From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: PREDICTMGT <predictmgt@usaid.gov> predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 3/31/2017 12:30:15 PM
Subject: Re: Please review mBio press release on your bats and MERS-CoV paper

Please send us links for the press release and study when they are issued next week so we can share with others. Thanks!

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Mar 31, 2017, at 11:47 AM, Andrew Clements <aclements@usaid.gov> wrote:

thanks. a few small suggestions (see attached).

On Thu, Mar 30, 2017 at 10:36 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Please find attached a draft press release for our paper being published on Tuesday on the MERS-like virus we identified in Uganda. Intention is for the release to go live simultaneously.
Hope it looks good to you,
Jonna

predictmgt+unsubscribe@usaid.gov
predictmgt@usaid.gov
https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/CAO5tDrGtsVWwpEZr0dCH%3D&B0k18mC02Eg9rD9%3DT6PHSq5%2BmEJw%40mail.gmail.com

--

Andrew Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
E-mail: aclements@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see http://www.usaid.gov/ept2

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Jonna Mazet (jkmazet@ucdavis.edu) <jkmazet@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>;Elizabeth S Chase (eschase@ucdavis.edu)" <eschase@ucdavis.edu>
CC: Alison Andre <andre@ecohealthalliance.org>;Brooke Watson <watson@ecohealthalliance.org>
Sent: 3/31/2017 8:21:42 PM
Subject: URGENT - need some edits to the Picture for the GVP paper

Hi Jonna, David, Liz,

Apologies for the urgency, but I just realized the figure for the GVP paper needs to be edited.

Can you re-do the text on the attached to say:

Top text bullet is good

Second bullet should say: "24 of these viral families likely contain species of pandemic potential"

Third bullet should say: "We can narrow our search by targeting surveillance to the most likely spillover hosts and their estimated 1.6 million unknown viral species"

Bottom text bullet should say: "The majority (85%) of the 650-840,000 viral species of zoonotic potential could be discovered for around $1.7 billion"

Cheers,

Peter

Peter Daszak
President

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www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Eri Togami <etogami@ucdavis.edu>
To: Jon Epstein <epstein@ecohealthalliance.org>
CC: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 9/24/2019 4:53:49 PM
Subject: RE: PREDICT EB scheduling

Thanks Jon!
-Eri

From: Jon Epstein [mailto:epstein@ecohealthalliance.org]
Sent: Tuesday, September 24, 2019 9:18 AM
To: Eri Togami
Cc: Jonna Mazet
Subject: Re: PREDICT EB scheduling

Hi Eri,
I think that would work for me.
Cheers,

Jon

On Fri, Sep 20, 2019 at 6:30 PM Eri Togami <etogami@ucdavis.edu> wrote:
Hi Jon,

I am reaching out with a scheduling question regarding future PREDICT EB calls. As you are aware, it is currently held biweekly on Wednesdays at 9am-11am PT/12-2pm ET, and I am scoping with all EB members to see if it could be moved to Tuesdays at 9:30am PT/12:30pm ET, and shortened to one hour. Will you be available at the proposed time?
I hope you had pleasant and safe travels from Bali.

Thank you,
Eri

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
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web: ecohealthalliance.org
Twitter: @epsteinjon
EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: Jon Epstein <epstein@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh, D.V.M <karesh@ecohealthalliance.org>
Sent: 1/29/2017 4:28:57 AM
Subject: Bangladesh report update

Jonna,
There are a few details from the report I wanted to discuss with you, when you've had a chance to review it. Send me a text anytime tomorrow or Monday when you have a moment to talk.

Thanks,
Jon

--

Jonathan H. Epstein DVM, MPH

Vice President for Science and Outreach

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Twitter:

-

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Jon Epstein <epstein@ecohealthalliance.org>
To: Brian Bird <bhbird@ucdavis.edu>
CC: David J Wolking <djwolking@ucdavis.edu>;Alison Andre <andre@ecohealthalliance.org>;Manjunatha N Belaganahalli <mbelaganahalli@ucdavis.edu>;William B. Karesh, D.V.M <karesh@ecohealthalliance.org>;Emily Hagan <hagan@ecohealthalliance.org>;Damien Joly <djoly@metabiota.com>;Katherine Leasure <kaleasure@ucdavis.edu>;Karen Saylors <ksaylors@metabiota.com>;Anthony, Simon J. <sja2127@cumc.columbia.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;Elizabeth S Chase <eschase@ucdavis.edu>;Eddy Rubin <erubin@metabiota.com>;Matthew LeBreton <mlebreton@metabiota.com>;Frantz Jean Louis <fjeanlouis@metabiota.com>;Emma Lane <lane@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;Amanda Fuchs <fuchs@ecohealthalliance.org>
Sent: 2/15/2017 2:28:25 PM
Subject: Re: Reminder: PREDICT Ebola Host Project Monthly Call - March 9th 9AM Pacific- 12pm Eastern

All,

A new paper in Nature's Scientific Reports on the correlation between Ebola outbreaks and forest fragmentation. Also discusses how putative bat reservoir species are impacted by forest fragmentation.

http://www.nature.com/articles/srep41613

Cheers,
Jon

On Feb 15, 2017 10:01 AM, "Brian Bird" <bhbird@ucdavis.edu> wrote:

Sorry folks for the discrepancy/typo on the day and the date.

Should be THURSDAY the 9th. Same times as listed.

Apparently the organizer needs some organizing!

-brian

From: Brian Bird <bhbird@ucdavis.edu>
Date: Tuesday, February 14, 2017 at 3:51 PM
To: David J Wolking <djwolking@ucdavis.edu>, Jonna Mazet <jkmazet@UCDAVIS.EDU>, Tracey Goldstein <tgoldstein@UCDAVIS.EDU>, "Anthony, Simon J." <sja2127@cumc.columbia.edu>, "William B. Karesh, D.V.M" <karesh@ecohealthalliance.org>, Jon Epstein <epstein@ecohealthalliance.org>, Matthew LeBreton <mlebreton@metabiota.com>, Damien Joly <djoly@metabiota.com>, Manjunatha N Belaganahalli <mbelaganahalli@ucdavis.edu>, Eddy Rubin <erubin@metabiota.com>, Karen Saylors <ksaylors@metabiota.com>, Frantz Jean Louis <fjeanlouis@metabiota.com>, Emma Lane <lane@ecohealthalliance.org>, Emily Hagan <hagan@ecohealthalliance.org>
Cc: Alison Andre <andre@ecohealthalliance.org>, Katherine Leasure <kaleasure@ucdavis.edu>, Elizabeth S Chase <eschase@ucdavis.edu>, Amanda Fuchs <fuchs@ecohealthalliance.org>

Subject: Reminder: PREDICT Ebola Host Project Monthly Call - March 9th 9AM Pacific- 12pm Eastern

Just a reminder for next month's call. Should have lots to share after the 3-country laboratory site assessment trip (Feb 20th-March 4th).

Agenda and other items to follow closer to the call date.

Thanks,

-Brian

PREDICT West Africa (3 Ebola Affected Countries)

COORDINATION CALL

Thursday: March 9th: 9-10AM Pacific, 12-1PM Eastern.

Toll-free number: 800-444-2801

Access Code: 1523158

International Dial-in number: 310-765-4820 (toll charges apply)

Brian H. Bird DVM, MSPH, PhD

One Health Institute

1089 Veterinary Medicine Dr.

School of Veterinary Medicine

University of California, Davis

bhbird@ucdavis.edu

From: William B. Karesh <karesh@ecohealthalliance.org>
To: Morzaria, Subhash (TCE) <Subhash.Morzaria@fao.org>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Hasibra, Mirela (TCE)" <Mirela.Hasibra@fao.org>
Sent: 2/23/2017 2:42:28 PM
Subject: Re: Sunchronized P-2-FAO surveillance and Ebola host country surveillance

Subhash, what is your Skype name ?

mine is: WilliamKaresh all one word

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

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President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

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On Feb 22, 2017, at 2:45 PM, Morzaria, Subhash (TCE) <Subhash.Morzaria@fao.org> wrote:

Dear Jonna,
Thanks, we will skype at 7.00 pm Addis time.
Best regards,
Subhash

Sent from my iPhone

On 22 Feb 2017, at 22:41, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Hi,
Thanks for making a time work. I'll join you. I'll only have 30 minutes. Will that be okay, as I pushed another meeting to accommodate.
Appreciate being kept in the loop and the anticipated discussion.
Jonna

On Wed, Feb 22, 2017 at 7:22 AM, Morzaria, Subhash (TCE) <Subhash.Morzaria@fao.org> wrote:
Dear Billy,

Thanks a lot. The latter option would also be better for me. Let us see what Jonna says.
Best,
Subhash

Sent from my iPhone

On 22 Feb 2017, at 17:56, William B. Karesh <karesh@ecohealthalliance.org> wrote:

Hi Subhash,

I'm in South Africa and can make the 5:00 your time work for me. That should be 4:00 for me, but I that's 6:00 AM for Jonna. Maybe two hours later would be better for Jonna (7:00 PM Addis, 6:00 PM Pretoria, 8:00 AM Davis). Let's wait and hear from her.

BK

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Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

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On Feb 22, 2017, at 9:04 AM, Mozzaria, Subhash (TCE) <Subhash.Mozzaria@fao.org> wrote:

Dear Billy/Jonna,
As you know we have been busy in the last few weeks revising our country work plans to be aligned with the GHSA Phase 1 country priorities as defined by the JEE process. In this regard a question has come up whether FAO would be able to conduct joint surveillance of the 'priority viral families' in GHSA Phase 1 countries as well as joint surveillance in "Ebola host" countries (Liberia, Guinea and SL).

I would like to discuss this with you various options before we can make a final decision. Please let me know when we can have a Skype call at your earliest. I am in now in Addis attending the ASL 2050 meeting. We finish this meeting tomorrow by 4.30 Addis time, so I can be available say from 5.00pm onwards local time.

Alternatively we can call early next week when I will be in Portugal.

Please let me know.

Thanks and with best regards,

Subhash

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Shana Gillette <sgillette@usaid.gov>
CC: Alisa Pereira <apereira@usaid.gov>;Leilani Francisco <francisco@ecohealthalliance.org>;PREDICTMGT <predictmgt@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 2/22/2017 6:30:14 PM
Subject: [predict] RE: Checking in on meeting with Leilani Francisco

Thanks Shana – makes sense, and we'll make sure we get an update to you rapidly.

Cheers,

Peter

Peter Daszak
President

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Shana Gillette [mailto:sgillette@usaid.gov]
Sent: Wednesday, February 22, 2017 2:10 PM
To: Peter Daszak
Cc: Alisa Pereira; Leilani Francisco; PREDICTMGT; predict@ucdavis.edu
Subject: Re: Checking in on meeting with Leilani Francisco

Ok, thank you Peter for the update. The table I sent was on new activities since last July...so there are likely gaps in activities that occurred before then...
Best,
Shana

On Wed, Feb 22, 2017 at 2:05 PM, Peter Daszak <daszak@ecohealthalliance.org> wrote:
Hi Shana (cc'ing Leilani also).

Many apologies for not responding sooner, and for missing the PREDICT Management Team call the other day when you discussed timing of a meeting with Leilani. This was due to travel for the GVP, then (with a one-day turnaround) to South Africa with EHA Board members – unavoidable and I've only just got back to the office.

Thanks for sending the attached table which Leilani will update and amend, so you get it back soon. I've already noticed that there are some gaps (e.g. Malaysia is missing) and we'll make sure they're filled in and up-to-date.

Second, apologies for any confusion or concerns about the timing of a meeting with you all in DC. Leilani is rapidly getting up to speed on all aspects of the project and meeting with the key people. Please bear with us, and we'll make sure that this happens as rapidly as possible. As a first step, Leilani has her first call with Karen Saylors today (Karen's

been in the field until now), and will be meeting in person with UCD and Metabiota around the 13th-15th March. She is really eager to meet with you and I'm sure we'll be able to schedule a trip rapidly after that.

Look forward to talking with you v. soon and, again, apologies for not responding more rapidly…

Cheers,

Peter

Peter Daszak
President

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www.ecohealthalliance.org

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From: Shana Gillette [mailto:sgillette@usaid.gov]
Sent: Wednesday, February 8, 2017 3:46 PM
To: Peter Daszak
Cc: Alisa Pereira
Subject: Checking in on meeting with Leilani Francisco

Hi Peter,

I have a few questions about the behavioral component now that Leilani is on board.

First, we would like to have an update of what is being done in terms of behavioral work in country. I am attaching the table that I made in terms of new activities since July--it is based off of the table that Chris sent us in October. If there are more activities to add now that it has been a few months, please let us know. If we could have this update fairly soon from Chris or Leilani, it would be helpful since we are getting questions from the Mission.

Second, could we set a date in the next few weeks to meet with Leilani in DC or New York about moving forward on the behavioral piece. We realize that she will need a few weeks to review the current activities and have internal discussions with everyone.

Let me know what may be possible. Thank you!

Best,
Shana
--
Shana Gillette, PhD
Senior Risk Mitigation Adviser
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (USAID)
Office Phone: 202-712-1456

Mobile: 970-581-4853
Email: sgillette@usaid.gov

--

Shana Gillette, PhD
Senior Risk Mitigation Adviser
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (USAID)
Office Phone: 202-712-1456
Mobile: 970-581-4853
Email: sgillette@usaid.gov

From:	Jon Epstein <epstein@ecohealthalliance.org>
To:	Jim Desmond <desmond@ecohealthalliance.org> Brian Bird <bhbird@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu> Anthony, Simon J. <sja2127@cumc.columbia.edu>
CC:	Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>
Sent:	3/7/2017 10:47:05 PM
Subject:	Shared Liberia trip report (via Google Docs) for comment

Dear Jim, Tracey, Brian, and Simon,

Welcome back! I've drafted a summary report of our meetings and key takeaways / action items from our week in Liberia and shared it via Google docs. Could you please have a look and add or correct anything you think important? It would be great if you could each review it by Friday. I'll then send it on to Jonna.

Cheers,
Jon

P.S let me know if you have trouble accessing the document.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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1.212.380.4467 (direct)
1.917.385.5315 (mobile)

web: ecohealthalliance.org

Twitter:

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From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Beth Edison <bedison@metabiota.com>;Ava Sullivan <sullivan@ecohealthalliance.org>;Molly Turner <turner@ecohealthalliance.org>;Diviband, Sherri <DivbandS@si.edu>;East, Larissa <EastL@si.edu>;Churchill, Carolina <cchurchill@wcs.org>
CC: Eddy Rubin <erubin@metabiota.com>;Karen Saylors <ksaylors@metabiota.com>;Evelyn Luciano <luciano@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;Zimmerman, Dawn <ZimmermanD@si.edu>;Murray, Suzan <MurrayS@si.edu>;Amanda Fine <afine@wcs.org>;Jonna Mazet <jkmazet@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Helen C Thompson <hcthompson@ucdavis.edu>
Sent: 3/6/2017 6:56:01 PM
Subject: Ordering information for PREDICT patches and vinyl stickers

Hi everyone. As noted on today's EB call, the information for ordering the PREDICT logo stitched patches (distributed at Dubai meeting) and vinyl stickers is included below for your reference. Let me know if you have any questions. Thanks!

For stitched patches, we used a company called Hero Patches – heropatches.com and had three separate designs made (horizontal and more square). You can ask the company to reference order #s HP22081A, HP22081B, and HP22081C and pick which style(s) you want to order. The woman who helped us with our original orders was Production Coordinator Amanda Russell - amanda.russell@heropatches.com

Vinyl stickers for equipment and other items can be purchased from the suppliers at the link below. We usually go with JM Wright and get a combination of square and long rectangular (horizontal) stickers.
https://www.usaid.gov/branding/suppliers

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: PREDICTMGT <predictmgt@usaid.gov> predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 3/21/2017 8:46:58 AM
Subject: Re: message of appreciation to the Center of Molecular Dynamics Nepal (CMDN)

Thanks! Good stuff.

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Mar 21, 2017, at 7:59 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Just an FYI
J

---------- Forwarded message ----------
From: **Claes, Filip (FAORAP)** <Filip.Claes@fao.org>
Date: Mon, Mar 20, 2017 at 11:43 PM
Subject: message of appreciation to the Center of Molecular Dynamics Nepal (CMDN)
To: Dibesh Karmacharya <dibesh@cmdn.org>
Cc: "Kalpravidh, Wantanee (FAORAP)" <Wantanee.Kalpravidh@fao.org>, "Black, Peter (FAORAP)" <Peter.Black@fao.org>, "Parajuli, Baikuntha (FAONP)" <Baikuntha.Parajuli@fao.org>, Jonna Mazet <jkmazet@ucdavis.edu>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Tracey Goldstein <tgoldstein@ucdavis.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>, Daniel Schar <dschar@usaid.gov>

Dear Dibesh,

I would like to thank you for the assistance that CMDN provided to the Central Veterinary Laboratory in Nepal.

Thanks to the kind provision of N8 primers and protocols, CVL was able to confirm the first outbreak of H5N8 within a week and report this to the OIE.

This shows how important the collaboration is within the EPT program and how PREDICT and FAO are working closer together.

Looking forward to work even closer together on the joint PREDICT-FAO/Government of Nepal surveillance at the wildlife-animal interface

Best wishes,

Filip

Filip Claes, PhD

Regional Laboratory Coordinator

Emergency Centre for Transboundary Animal Diseases (ECTAD)

Food and Agriculture Organization of the United Nations (FAO)

Regional Office for Asia and the Pacific

39 Phra Atit Road, Bangkok 10200

Thailand

Tel: (+662) 697-4104

Email: filip.claes@fao.org

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/CAO5tDrE39EqAnmEG0Y7B_A8JjzCp-biOxgQ4OEir2uqOxguwXQ%40mail.gmail.com.

From: William B. Karesh <karesh@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 3/29/2017 3:19:42 PM
Subject: Re: For SM call

Thanks, they filled me in, but also suggested that you were in support of dropping data meeting. What do you think about that? Good to discuss on SMT.

Well, I was a bit more general as in "I always think fewer meetings are better".

But, I do agree that a meeting with 40 people from around the world seems out of proportion for the value to be gained from small inputs from the other groups. We are already in discussions with P&R on sharing information to help each other and it's easy to meet up with two or three of them any time. Catherine is spending Monday with them for example, and we now have monthly calls with them and OHW. For WHO, it really comes down to Vietnam and LSN for the most part, or at country levels otherwise, so I'm not sure that is so important for a big meeting either. Same with CDC. For FAO, Jordan and Egypt teams work together and share data for all of the work they are doing, so that really leaves Asia as a big region and it seems silly to have them all come to New York to discuss collaborations in Asia.

The concern I have is that it is in the Yr3 work plan and its also Andrew's baby. So, I do think it would be good for the SMT call so he can weigh in.

I probably don't want to cancel the semi-annual because I think we need to pull together (those who will be left standing -- will explain soon), rather than fractionate more. Thoughts on that?

Yes!!, I agree. Also, I think for the Davis team, you probably feel like you have a fair sense of what everyone is doing and how it is coming together but everyone else is a bit more fragmented from each other. So, there is value there for others to see how things are coming together (or not). It also stimulates cross thinking and creativity when not only the different partners are in the room, but also when the different operational teams get to hang out with each other. The different team calls are really valuable for keeping things running smoothly and on target, but they don't provide a lot of cross pollination. And, in line with what you are saying, it will help with team building, which is always important, but even more so in times of stress.

Talk to you soon,

ps, this is Gwen's last week at FAO, Lidewij is taking her position temporarily.

B

Travel well,
J

On Tue, Mar 28, 2017 at 10:02 PM, William B. Karesh <karesh@ecohealthalliance.org> wrote:
Hi there,

On EB call last week Tracy suggested that we might not need the data meeting because FAO and others are not really generating enough data to have a worthwhile discussion. I suggested that we discuss with Andrew in next SM call, but feel free to drop that from the agenda if you would like to discuss in a different setting.

She also suggested that we drop the semi annual meeting because of the budget cuts. Not sure that needs to be a SM call discussion.

All food for thought, as well as paying for other meetings like WDA, etc this year, I say as I just landed in Rome 😱

BK

Sent from my iPhone

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Alisa Pereira <apereira@usaid.gov>;Anuthin Shek <ashek@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 4/5/2017 9:03:48 AM
Subject: Re: Ebola country caps

Thanks, Jonna. This looks great. Will discuss it with Dennis first and let you know if we need anything else.

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Apr 5, 2017, at 2:32 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Thanks for today.
Attached are our best estimates to which we can commit to making work for a one time reallocation.
Appreciate all of your efforts,
Jonna

On Thu, Mar 30, 2017 at 1:21 PM, Alisa Pereira <apereira@usaid.gov> wrote:
Yes, thank you. Would you also please send calendar invites to get it locked in.

Thanks
Alisa

Sent from my iPhone

On Mar 30, 2017, at 3:41 PM, Elizabeth S Chase <eschase@ucdavis.edu> wrote:

Greetings,

I am just confirming the SMT call is rescheduled for Tuesday, April 4 at 10-11 PDT / 1p-2m EDT.

Jonna suggested a discussion before the SMT and has 8:00am PDT/11:am EDT available. Shall I reserve that time for her to meet with you?

Thanks, Liz Chase

Liz Chase

Executive Assistant to Dr. Jonna Mazet

One Health Institute, University of California, Davis

530-752-3630

From: jonna.mazet@gmail.com [mailto:jonna.mazet@gmail.com] **On Behalf Of** Jonna Mazet
Sent: Thursday, March 30, 2017 12:32 PM
To: Elizabeth S Chase <eschase@ucdavis.edu>
Subject: Fwd: Ebola country caps

---------- Forwarded message ----------
From: **Andrew Clements** <aclements@usaid.gov>
Date: Thu, Mar 30, 2017 at 6:33 AM
Subject: Re: Ebola country caps
To: Alisa Pereira <apereira@usaid.gov>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>

fine for me as well

Andrew

On Thu, Mar 30, 2017 at 1:14 PM, Alisa Pereira <apereira@usaid.gov> wrote:

that works for me. Is this next Monday?

Alisa Pereira

Deputy Director

Emerging Threats Division

Global Health Bureau, USAID/Washington

Telephone: 202-712-5221

Cell: 202-997-9966

e-mail: apereira@usaid.gov

On Thu, Mar 30, 2017 at 12:26 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Hi Alisa & Andrew,

We have this as a discussion item for our next Management Team call. I anticipate this discussion to be potentially extremely sensitive and difficult. Would you like to do a pre-call on it with just me? I could do it at 8am Pacific on Tuesday.

Let me know what you think,

Jonna

[redacted]

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/pandemic

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Eddy Rubin <erubin@metabiota.com>
Sent: 4/18/2017 2:03:14 AM
Subject: Re: primer for Tuesday's call

Thanks for this good starting point.
Fine with me for Karen to join.
Have a good night,
Jonna

On Mon, Apr 17, 2017 at 4:31 PM, Eddy Rubin <erubin@metabiota.com> wrote:

Dear Jonna,

Look forward to chatting tomorrow. Just so you know how we are thinking and the directions we plan to go, I have included some material. Below is what we view would be the optimal Metabiota/ PREDICT Country by Country game plan going forward. This is similar to what I briefly mentioned to you when we were in DC for CUGH.

We are also working on a Sample and Data Quality Risk and Corrective Action plan which I will get to you before this Friday. I think with focus and putting in place the structures and QA and QC activities described in this document we can correct the sample/data quality/ safety… issues. We have also developed a Sierra Leone Data Report which will be completed in the next day or so. This report offers an overview of the SL data situation and includes: What happened with our data? How is our data being corrected? How will future data problems be avoided?

With regard to Tuesday's 9:00 AM call, I believe that it might be useful to have Karen participate on the call as she has a deep perspective on Metabiota's on the ground activities in all our countries though I defer to your decision on who should be on the call.

Best,

Eddy

Overview of Country-by-Country Game Plan

We are developing a **Sample and Data Quality Risks and Corrective Action** process, which includes new quality control checks and training plans in the following domains: 1) Animal field sampling (biosecurity, data capture, QC) refresher training; 2) Data Quality Control procedure of data from field to EIDITH; 3) lab sample quality, monitoring and analysis plan. This will be submitted to Davis upon completion (estimated timeline Wed, April 19th)

Metabiota is recommending focus on key country operations with unique field presence and discontinuation of management of China, Indonesia and ROC.

Metabiota proposes the following realignments:

Countries to be discontinued or for narrowed focus:

China : According to our analysis of the associated EIDITH data on those individuals enrolled from Dongguan and Shento hospitals, approximately 40% of the enrolled population has lifetime animal exposure, specifically: 20% handle live animals, 31% raise live animals 13% share a water source with animals, 21% have animals in the dwelling, 20% cook or handle live animals, 13% slaughter animals, and 23% hunter or trapped.

Based on this analysis, it does not seem that this level of exposure warrants continuing work in China. If Davis concurs, Metabiota will cease operations at our two hospitals in China.

Indonesia : Metabiota will cease operations and plans for hospital surveillance will be transferred to EHA.

Republic of Congo (RoC): MB will continue behavioral data collection in Brazzaville markets with the objective of collecting qualitative and questionnaire data in 5 bushmeat markets and restaurants. Karen has submitted an update on DRC/ROC Bushmeat market work and proposed work plan for ROC (April 14, 2017). We have ceased animal sampling and any syndromic surveillance in RoC. *Discussion points with Davis: 1) Davis to assume management of RoC*

Focus Countries:

Cameroon : We will keep leadership and maintain program in Cameroon, and conduct lab and data quality retraining within the next 3 months. After centralized training, we will deploy field specialists from Cameroon to other sites : Jean Michel (bat sampling specialist), Matthew LeBreton (wildlife ecologist) and Dr. Moctar Mouiche (wildlife vet) for field trainings in other countries.

Cote d'Ivoire: Continue operations working with Institute Pasteur de Cote d'Ivoire (IPCI) and LANADA partners but do not build out separate PREDICT lab space within IPCI.

Democratic Republic of Congo (DRC): We have ceased compensation to Prof Muyembe since December 2016 and are adjusting the subcontract with INRB accordingly. We will cut the second site of Buta after our April data collection trip and will provide retraining within the next quarter. (Re-training calendar to follow by Wed, April 19th)

Guinea : Per the retraining schedule, send Dr. Moctar and Jean Michel for intensive field sampling, data QC, and biosafety training refresher, with JM to stay for 2 weeks for intensive bat sampling. Put MOU in place with Ministry partners. Frantz will be fully retrained in all of SOPS training refreshers and will travel to Guinea every other month for field supervision.

Laos : We will continue operations and maintain program in Laos, and conduct lab and data quality retraining within the next 3 months. In late April, we will send the Laos team to Indonesia for lab training.

Sierra Leone : Team will immediately go through upgraded retraining, post quality control assessment and with a new supervision plan in place. We have assigned Jason (Data Quality and Implementation Manager) to assist Aish, James and Frantz in data cleanup. We have suspended field sampling work in SL until this training and recertification is complete. 1) Per the **Sample and Data Quality Risks and Corrective Action plan,** we will complete data cleanup. 2) Davis to approve new data QC plan and field/lab biosafety plans, and 3) staff biosafety training refresher will be completed before restarting field sampling. Frantz Jean Louis will be fully trained in all of these SOPS training

refreshers and to travel to SL every other month for field supervision.

Animal sample shipment: Metabiota will ship confirmatory samples to CDC in April and remaining wildlife samples to Davis once data verification is finalized.

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Alisa Pereira <apereira@usaid.gov>
Sent: 5/12/2017 6:17:27 PM
Subject: Re: Bullets on what assistance PREDICT can provide in DRC

Related to this, do you have DRC Ebola budget to cover any assistance requested or will you need to dip into the regular budget outbreak reserve?

And BTW, I may have suggested to others today that your ability to respond may be compromised by the existing country caps. Are the previously submitted country caps adjustments still valid or do you need to make some additional revisions. I've been asked to submit the revised cap numbers. Thanks!

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On May 12, 2017, at 6:53 PM, Angela Wang <awang@usaid.gov> wrote:

Hi Jonna,

I wasn't in the meeting before but Dennis came to my cube and said you would be sending me some bullets of what assistance PREDICT is able to provide in DRC. Alisa mentioned the messaging from Dennis may have been hazy so I just wanted to follow up..

Thanks!
Angela

--
Angela Wang, MSPH
Public Health Advisor
Emerging Threats Division, Office of Infectious Disease
USAID Washington, Bureau for Global Health
Phone: 202-712-1970 (O) | 571-213-3082 (C) | RRB-3.06.050
Email: awang@usaid.gov

From:	Alisa Pereira <apereira@usaid.gov>
To:	Jonna Mazet <jkmazet@ucdavis.edu>
CC:	Shana Gillette <sgillette@usaid.gov>;Dennis Carroll <dcarroll@usaid.gov>;AOTR/Grant Manager Andrew Clements <AClements@usaid.gov>;Peter Daszak <daszak@ecohealthalliance.org>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Cassandra Louis Duthil <clouisduthil@usaid.gov>;Leilani Francisco <francisco@ecohealthalliance.org>;Tracey Goldstein <tgoldstein@ucdavis.edu>;Billy Karesh <karesh@ecohealthalliance.org>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent:	5/20/2017 2:18:11 PM
Subject:	Re: PREDICT-2 Behavioral Risk Meeting First Follow-up First Piece

Thank you, Jonna. I will wait for others to chime in as well, but at first read, I think this submission is in line with what we discussed at our meeting, and appropriately positions PREDICT.

thanks

Alisa Pereira
Deputy Director
Emerging Threats Division
Global Health Bureau, USAID/Washington
Telephone: 202-712-5221
Cell: 202-997-9966
e-mail: apereira@usaid.gov

On Fri, May 19, 2017 at 8:03 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Dear Team,
In order to fulfill the request we discussed from the Mission in Sierra Leone/Guinea for a communications strategy timeline, as well as to follow-up on items we promised from the meeting last week, I have attached a confidential draft of the timeline.

We would greatly appreciate your feedback on this document before we provide it to the Mission or the GoSL MOH. It reads a bit strangely because almost all of it is dependent on interactions you are managing with partners to whom we have not yet been introduced. So sorry if it reads strangely. We could fix that in a version next week if those introductions are imminent.

We are also running this by our core team in Sierra Leone for their inputs.

Thanks in advance for your initial and confidential review & have a nice weekend,
Jonna

From: William B. Karesh <karesh@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Eddy Rubin <erubin@metabiota.com>;Peter Daszak <daszak@ecohealthalliance.org>;Alison Andre <andre@ecohealthalliance.org>;Taylor Elnicki <telnicki@metabiota.com>;Brooke Genovese <bgenovese@ucdavis.edu>
Sent: 5/23/2017 4:40:14 PM
Subject: Re: PBEJ calls

10-4

Sent from my iPhone

> On May 23, 2017, at 4:59 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
>
> Hi there,
> Since I'm meeting with all of you often to take care of issues, and I've been sitting alone on most of the pre-EB calls that we've set up for the four of us, I'd like to cancel them until further notice. We can continue with all of our purpose-based call scheduling and see how we do.
> So until we decide otherwise, please cancel all of the calls scheduled for 30 minutes prior to EB calls.
> Thanks and talk to all of you very soon ;)
> J

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>;Eddy Rubin <erubin@metabiota.com>;William B. Karesh <karesh@ecohealthalliance.org>
CC: Alison Andre <andre@ecohealthalliance.org>;Taylor Ehlicki <tehlicki@metabiota.com>;Brooke Genovese <bgenovese@ucdavis.edu>
Sent: 5/23/2017 8:00:25 PM
Subject: RE: PBEJ calls

No problem Jonna – good to get a half hour back….

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

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www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: jonna.mazet@gmail.com [mailto:jonna.mazet@gmail.com] **On Behalf Of** Jonna Mazet
Sent: Tuesday, May 23, 2017 10:59 AM
To: Eddy Rubin; William B. Karesh; Peter Daszak
Cc: Alison Andre; Taylor Ehlicki; Brooke Genovese
Subject: PBEJ calls

Hi there,
Since I'm meeting with all of you often to take care of issues, and I've been sitting alone on most of the pre-EB calls that we've set up for the four of us, I'd like to cancel them until further notice. We can continue with all of our purpose-based call scheduling and see how we do.
So until we decide otherwise, please cancel all of the calls scheduled for 30 minutes prior to EB calls.
Thanks and talk to all of you very soon ;)
J

From: Zandra Andre <zandre@usaid.gov>
To: Alison Andre <andre@ecohealthalliance.org>
CC: Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh <karesh@ecohealthalliance.org>;Alice Latinne <latinne@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>;Leticia Gutierrez-Jimenez <gutierrez@ecohealthalliance.org>;Karen Saylors <ksaylors@metabiota.com>;predict@ucdavis.edu <predict@ucdavis.edu>;Jonna Mazet (jkmazet@ucdavis.edu) <jkmazet@ucdavis.edu>;Marie Ahmed <mahmed@usaid.gov>;REGINA BLANDINE NGUESSAN KOKO <nkoko@usaid.gov>;Molly Turner <turner@ecohealthalliance.org>
Sent: 5/30/2017 10:08:34 AM
Subject: Re: setting up a phone call to discuss PREDICT work in Côte d'Ivoire

Great!
Until this afternoon,
Zandra

Zandra
Sent from my iPhone

On May 26, 2017, at 20:35, Alison Andre <andre@ecohealthalliance.org> wrote:

Dear All,

The meeting to discuss PREDICT work in Côte d'Ivoire has been scheduled for Wednesday, May 31st at 9:00am NY time, 1:00pm CI time. Call-in details below:

Dial in: +1-888-288-9321
Passcode: 5143987937#

If you would like to be called into the meeting, please send me the best number to reach you on.

Many thanks,
Alison

Alison Andre
Program Assistant

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

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www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Zandra Andre <zandre@usaid.gov>
Date: Wednesday, May 24, 2017 at 9:11 AM
To: Peter Daszak <daszak@ecohealthalliance.org>
Cc: "William B. Karesh" <karesh@ecohealthalliance.org>, Alice Latinne <latinne@ecohealthalliance.org>, Evelyn Luciano <luciano@ecohealthalliance.org>, Leticia Gutierrez-Jimenez <gutierrez@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>, Karen Saylors <ksaylors@metabiota.com>,

"predict@ucdavis.edu" <predict@ucdavis.edu>, "Jonna Mazet (jkmazet@ucdavis.edu)" <jkmazet@ucdavis.edu>, Marie Ahmed <mahmed@usaid.gov>, REGINA BLANDINE N'GUESSAN KOKO <nkoko@usaid.gov>
Subject: Re: setting up a phone call to discuss PREDICT work in Côte d'Ivoire

Hi Peter,

So good to hear from you! Indeed, it's great news that we'll be working together! And Billy too. I last saw him in Rome where I bid him adieu and enviously watched as he wheeled out of baggage claim, with all of his bags in tow while I was stuck dealing with lost luggage!

I'm available for a call next week. Tuesday or Wednesday look good in terms of availability. Tuesday any time from 8am until Noon, your time, will work. Wednesday, 9am to Noon, your time. Either of those windows work for you?

Thanks for the electronic introduction to your crew. Nice to meet everyone.

Best regards,
Zandra

Dr. Zandra Hollaway ANDRE
DVM, MPH, DACVPM
Senior One Health Team Lead
U.S. AGENCY FOR INTERNATIONAL DEVELOPMENT
US Embassy - Abidjan, Côte d'Ivoire
T: +225 27 49 43 35 M:+225 04 89 27 36
From the US: (301) 985 8627 x 4335
USAID.gov | ZAndre@usaid.gov | @USAIDWestAfrica

On Wed, May 24, 2017 at 1:29 AM, Peter Daszak <daszak@ecohealthalliance.org> wrote:

Hi Zandra,

I just wanted to reach out rapidly and say how pleased I am that we'll be working closely on the EPT/PREDICT program in Côte d'Ivoire! Jonna has already filled me in on her call yesterday with you, and I'm really looking forward to talking with you by phone to make sure we manage this transition efficiently and with minimal impact on the current momentum. That said, I didn't realize until today that you might not be in the office next week, so I don't want to miss the window. Please let me know when would be convenient and hopefully we can set up a time that works. To that end, I'm cc'ing Karen Saylors (who may be traveling over the next few days), Alice Latinne who'll be our 'country liaison' or point-person here at EHA for this work and Billy Karesh, who is in charge of partnerships for PREDICT. It would be ideal to have all of us on the call initially, but that might not be possible given travel.

I also want to introduce you to Evelyn Luciano, who manages admin for PREDICT here at EHA, Leticia Gutierrez-Jimenez who is helping manage wildlife surveillance in a number of countries, and Alison Andre who will help schedule the call.

Looking forward to hearing from you and to talking soon…

Cheers,

Peter

Peter Daszak

President

EcoHealth Alliance

460 West 34th Street – 17th Floor

New York, NY 10001

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From: Katherine Leasure <kaleasure@ucdavis.edu>
To: 'Cassandra Louis Duthil' <clouisduthil@usaid.gov>
CC: 'Predict inbox' <predict@ucdavis.edu>
Sent: 7/12/2017 5:02:51 PM
Subject: [predict] RE: PREDICT International Travel Requests

Hi Cassandra,

I just wanted to follow-up on my earlier email. Has a second request for concurrence been sent to the Cambodia mission? The trip is coming up on August 3, and flights are beginning to book up.

Thank you,
Katie

From: Katherine Leasure [mailto:kaleasure@ucdavis.edu]
Sent: Friday, July 07, 2017 9:03 AM
To: 'Cassandra Louis Duthil'
Subject: RE: PREDICT International Travel Requests

Hi Cassandra,

Could you send a second request to the Cambodia mission? They have not yet responded with concurrence.

Thanks!
Katie

From: Cassandra Louis Duthil [mailto:clouisduthil@usaid.gov]
Sent: Monday, July 03, 2017 11:40 AM
To: Sotheara Nop; Daniel Schar; Damrongwatanapokin, Sudarat (RDMA/OPH)
Cc: Andrew Clements; Alisa Pereira; Katie Leasure; Elizabeth Leasure; David John Wolking
Subject: Fwd: PREDICT International Travel Requests

Hi

ello team Cambodia,

the following travel approval requests have

come in from PREDICT. We appreciate your concurrence and welcome any questions you may have. *Please note: All travelers should be prepared to provide an in/out brief*

during the duration of their travel.

11. UC Davis would like to request travel approval for Dr. Tracey Goldstein to travel from Sacramento, California, USA to Phnom Penh, Cambodia from August 3-11, 2017 to attend

meetings with government and non-governmental partners, as well provide technical guidance to the field team during planned August sampling activities.

Trip purpose: Dr. Goldstein will meet with government and non-governmental partners regarding coordination of PREDICT-2 activities, and will join the field team to assist with technical guidance for the concurrence sampling of human, livestock and wildlife planned for August in a bat guano farming community in Kampong Cham.

Telephone: 202-712-5583 Cell: 407-731-3155 clouisduthil@usaid.gov

---------- Forwarded message ----------
From: **Katherine Leasure** <kaleasure@ucdavis.edu>
Date: Fri, Jun 30, 2017 at 2:23 PM
Subject: RE: PREDICT International Travel Requests
To: Andrew Clements <aclements@usaid.gov>
Cc: PREDICTMGT <predictmgt@usaid.gov>, Predict inbox <predict@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>

Thanks, Andrew. I have sent an email to EHA and will follow-up when I have received the requested information.

From: Andrew Clements [mailto:aclements@usaid.gov]
Sent: Thursday, June 29, 2017 3:22 AM
To: Katherine Leasure
Cc: PREDICTMGT; Predict inbox; Jonna Mazet
Subject: Re: PREDICT International Travel Requests

#3 approved.

I would like additional information on #8 as to how it relates to PREDICT.

All others approved subject to Mission concurrence.

On Thu, Jun 29, 2017 at 12:53 AM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:
Please find below international travel requests for your review and approval. Please let me know if you have any questions. Thanks!!

Travel Requests –

1. UC Davis would like to request travel approval for Dr. Corina Monagin to travel from Los Angeles, California, USA to Guinea, Conakry from July 22-29, 2017 for work plan and partner meetings related to the Ebola Host Project.

Trip purpose: Dr. Corina Monagin is traveling to Conakry as PREDICT Global Lead for the PREDICT program in Guinea. Dr. Monagin is planning to assist in transitioning the implementing partner from Metabiota to UC Davis. This will include meetings with Government Ministries (Health, Agriculture, Higher Education and Scientific Research), as well as in-country partners and stakeholders. She will be working with the PREDICT team on work plan, sampling strategy, as well as quality control of samples and data.

2. UC Davis would like to request travel approval for Dr. Terra Kelly to travel from Flagstaff, Arizona, USA to Accra, Ghana from August 5-12, 2017

Trip purpose: Dr. Terra Kelly will be traveling to Accra to meet with PREDICT implementing partners to discuss implementation of surveillance and diagnostic laboratory activities and scoping and planning for upcoming surveillance activities in Year 4. Dr. Kelly will also be conducting training for PREDICT human disease surveillance partners on questionnaire administration for the risk characterization and all laboratory partners on data entry and management in the EIDITH database for laboratory results reporting.

3. Metabiota would like to request travel approval for Tammie O'Rourke and Daniel O'Rourke to travel from Nanaimo, British Columbia, Canada to San Francisco, California, USA on August 23, 2017 to meet with PREDICT Senior Management. From San Francisco, California, USA, they will travel to Davis, California, USA from August 23 – 25, 2017 to meet with UCD global team and discuss USAID reporting and data extracts.

Trip purpose: In San Francisco, they will meet with PREDICT Senior Management to discuss PREDICT Information Management concerns, progress and issues. In Davis, they will meet with the UCD global team and discuss USAID reporting and data extracts and mapping to prepare for the PREDICT data meeting September 2017.

4. EcoHealth Alliance would like to request travel approval for Mr. Carlos Zambrana-Torrelio to travel from New York, New York, USA to Cartagena de Indias, Colombia from July 23-29, 2017, to attend and present at the International Congress for Conservation Biology.

Trip purpose: As part of continued work under the CBD-WHO Joint Work Programme, Mr. Zambrana-Torrelio will present on the indicators for health that links disease emergence and biodiversity loss and the One Health approaches operationalized by PREDICT-2. In addition, he will discuss on the methods and findings from the Deep Forest project to emphasize synergies in biodiversity and disease monitoring. Presentation title: "Integrating biodiversity in conservation planning for human health and well-being." Mr. Zambrana-Torrelio also was invited to participate in a workshop session on ecosystems and human health organized by the International Union for Conservation Nature.

5. EcoHealth Alliance would like to request travel approval for Simon Anthony to travel from New York, New York, USA to Kuala Lumpur, Malaysia from July 23-30, 2017 for in-country trainings with local partners and PREDICT staff.

Trip purpose: The purpose of this trip is to meet with local sequencing companies to discuss local implementation of new technologies developed at CII (VirCapSeq) (24th July). Dr. Anthony will also conduct a three-day training workshop with PREDICT staff at the National Public Health Lab (NPHL) on PCR, cloning and sequencing, as well as sequence analysis and assay design. Dr. Anthony will also conduct a one-on-one training with Mei Ho Lee in paper writing. Outcome: Enhanced local capacity for viral discovery, sequence analysis and assay design. Planning of PREDICT papers to be led by regional staff (Mei Ho Lee).

6. EcoHealth Alliance would like to request travel approval for Mr. Aleksei Chmura to travel from New York, New York, USA to Dali, Beijing, Guangzhou, and Shanghai China from July 31 to September 5, 2017 for meetings with in-country partners, field work, behavioral surveillance, and site selection work.

Trip purpose: Mr. Aleksei Chmura will meet with PREDICT-2 Field Coordinator Dr. Libiao Zhang at Guangxi Normal University in Guilin, and at our Partner Laboratory based at the Guangdong Entomological Institute in Guangzhou in Guangdong, as well as with Dr. Changwen Ke at the Guangdong CDC in Guangzhou. Dr. Zhu and Mr. Chmura will meet with Dr. Yunzhi Zhang of the Yunnan CDC. Together with Field Coordinator Dr. Guangjian Zhu, Mr. Chmura will coordinate and travel with full field team to sites in Yunnan Province to assist with human behavioral surveillance fieldwork, review field, lab, and data entry protocols, and prepare for 2017-18 PREDICT-2 field sampling. Field sites are prioritized along the wildlife trade pathways as per PREDICT-2 site selection criteria and protocols. Mr. Chmura will communicate with PREDICT-2 Metabiota partners in China as well as new Chinese Academy of Sciences Laboratory collaborators based in Beijing.

7. EcoHealth Alliance would like to request travel approval for Mr. Carlos Zambrana-Torrelio to travel from New York, New York, USA to Beijing, China from August 19-27, 2017, to attend and present at the International Association for Ecology (INTECOL).

Trip purpose: Mr. Zambrana-Torrelio will attend the International Association for Acology to present the results produced by Modeling and Analytics Working Group of the Global Virome Project. Presentation title: "The Global Virome Project: A network of viral-diversity monitoring."

8. EcoHealth Alliance would like to request travel approval for Dr. William Karesh to travel from New York, New York, USA to Paris, France from August 21-24, 2017 to participate in the World Organization for Animal Health's (OIE) ad hoc group on killing methods for farmed reptiles for their skins and meat.

Trip purpose: Dr. Karesh will participate in the World Organisation for Animal Health's (OIE) ad hoc group on killing methods for farmed reptiles for their skins and meat. Dr. Karesh will participate in setting health and IACUC related standards for wildlife farming for OIE code purposes.

9. UC Davis would like to request travel approval for Brett Smith to travel from Sacramento, California, USA to Freetown and Makeni, Sierra Leone from July 21 to August 10, 2017 to perform laboratory training.

Trip purpose: Mr. Smith will fly to Freetown, then travel on to Makeni to perform laboratory training. The training will include staff from UNIMAK and PREDICT with invitations to MAFFS and MOH to include staff from the TEKO veterinary lab and National Public Health lab to prepare, handle and test samples using Predict protocols.

10. UC Davis would like to request travel approval for Alexandre Tremeau-Bravard to travel from Sacramento, California, USA to Dakar, Senegal from August 12-25, 2017, then to Kigali, Rwanda from August 25-30, 2017 to perform laboratory trainings.

Trip purpose: Senegal – In Dakar, Mr. Tremeau-Bravard will train lab staff from ISRA and ICAD to prepare, handle and test samples using Predict protocols. Rwanda – In Kigali, he will do a refresher lab training for staff based at NRL and RAB.

11. UC Davis would like to request travel approval for Dr. Tracey Goldstein to travel from Sacramento, California, USA to Phnom Penh, Cambodia from August 3-11, 2017 to attend meetings with government and

non-governmental partners, as well provide technical guidance to the field team during planned August sampling activities.

Trip purpose: Dr. Goldstein will meet with government and non-governmental partners regarding coordination of PREDICT-2 activities, and will join the field team to assist with technical guidance for the concurrence sampling of human, livestock and wildlife planned for August in a bat guano farming community in Kampong Cham.

12. UC Davis would like to request travel approval for Diego Montecino to travel to Dar es Salaam and Morogoro, Tanzania from August 5-26, 2017 to support the PREDICT Tanzania team in the initiation of new in-depth methods for bat surveillance at high-risk urban interfaces.

Trip purpose: Mr. Montecino (UC Davis-based project scientist) will support the PREDICT Tanzania team to set up new methods for safely and effectively collecting non-invasive samples from a well-established urban straw-coloured fruit bat (*Eidolon helvum*) colony in Morogoro in order to test them for Coronaviruses and other priority viral threats. He will also introduce methods for counting bats present in a colony and assessing bat behavior and their interactions with people. Mr. Montecino will work hand-by-hand with the PREDICT Tanzania team to transfer the knowledge, skills, and capacity to conduct these activities following his return to the US.

Katherine Leasure

HR/Payroll/Financial Assistant
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https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/014901d2f061%246a1942a0%243e4bc7e0%24%40ucdavis.edu

--

Andrew Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4233
E-mail: aclements@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

--

You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
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To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/033801d2f1cd%24f99c1070%24ecd43150%24%40ucdavis.edu.

From: Jon Epstein <epstein@ecohealthalliance.org>
To: Sara Heydari <sheydari@usaid.gov>
CC: Manish Kakkar <manish.kakkar@phfi.org>;Bhatia, Rajesh (FAO/N) <Rajesh.Bhatia@fao.org>;Debapriyo Chakraborty <chakraborty@ecohealthalliance.org>;Angela Wang <awang@usaid.gov>;Schar, Daniel (RDMA/OPH) <dSchar@usaid.gov>;Reuben Swamickan <rswamickan@usaid.gov>;SHARMA, Anuj <sharmaan@who.int>;Black, Peter (FAO/RAP) <peter.black@fao.org>;Marietou Satin <masatin@usaid.gov>;Umesh Alavadi <ualavadi@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>;Alisa Pereira, (GH/HIDN) <apereira@usaid.gov>;Ava Sullivan <sullivan@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>
Sent: 7/17/2017 12:32:16 AM
Subject: [predict] Re: GHSA Work Planning Meeting in Delhi

Hi Sara,
I am planning to attend the workplanning meeting on the 23rd and 24th, pending ITA approval. I look forward to seeing you in Delhi.

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(e) epstein@ecohealthalliance.org
(o) 212.380.4467
(m) 917.385.5315
@epsteinjon

On Jul 5, 2017 9:13 PM, "Sara Heydari" <sheydari@usaid.gov> wrote:
Hi Anuj- Noted. Considering everyones travel and leave schedule, these were the only dates that worked for the team before September. Hopefully, you can spend a few hours with us on the 23rd. If the national consultation is held on the 24th and 25th, Peter and Dan can also attend part of the meeting on the 24th.

Thanks,
Sara

Sent from my iPhone

On 05-Jul-2017, at 5:16 PM, SHARMA, Anuj <sharmaan@who.int> wrote:

Dear Sara,

As mentioned, the national consultation to operationalise action against AMR is being planned for 24-25 Aug.

Regret my participation, unless the dates change again.

Thank you

Anuj

Dr Anuj Sharma | NPO – Antimicrobial Resistance, Laboratories | WHO Country Office for India, 332-A, Nirman Bhawan, New Delhi 110011

Phone: +91-11-66560800 ext/GPN: 23280 | Fax: +91-11-23062450 | Mobile: +91-8826247676 | Email: sharmaan@who.int | Website: www.searo.who.int/india

Fight antibiotic resistance … it's in your hands

http://www.fightantibiotic-resistance.net/ourhandsofthand.htm

From: Sara Heydari [mailto:sheydari@usaid.gov]
Sent: 05 July 2017 14:46
To: Bhatia, Rajesh (FAOIN); SHARMA, Anuj; Black, Peter (FAORAP); Schar, Daniel (RDMA/OPH); Angela Wang; Umesh Alavadi; Jon Epstein; Debapriyo Chakraborty; Manish Kakkar; Marietou Satin; Reuben Swarnickan
Subject: Re: GHSA Work Planning Meeting in Delhi

Hi all-

It looks like August 23rd and 24th works best for everyone. Please block your calendar for these dates. Please let us know if you have any questions.

Thanks,

Sara

On Thu, Jun 29, 2017 at 3:47 PM, Sara Heydari <sheydari@usaid.gov> wrote:

Hi all-

As discussed yesterday, We're proposing a work-planning meeting during the week of August of 21st. Please let us know what two days works best for you.

Thanks,

Sara Heydari

Program and Policy Advisor | USAID | India

email: sheydari@usaid.gov

Telephone: +91-11-2419-8021 | Mobile: +91-98111-68906

Website: http://www.usaid.gov/india

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Sara Heydari

Program and Policy Advisor | USAID | India

email: sheydari@usaid.gov

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Website: http://www.usaid.gov/india

UCDUSR00001117

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Peter Daszak <daszak@ecohealthalliance.org>
Sent: 7/27/2017 7:28:38 PM
Subject: Re: Quick question re. bats…

Thanks for checking-in. We already have their buy-in. In fact, Andrew is asking to see messaging and plan. So really no call needed, just move forward, so we can show them that we're making progress.
If you ask them any questions, we may get bogged down in revisiting something.
Move forward,
J

On Wednesday, July 26, 2017, Peter Daszak <daszak@ecohealthalliance.org> wrote:

Jonna – we had a good meeting yesterday – me, CKJ and Leilani - about bats and behavioral risk, as per the meeting in DC where we all told the USAID team that we would like to work on using behavioral risk approaches to propose intervention strategies around bats. We had some good ideas and I'm now going to push some of the modeling people to help out and work with Leilani to focus on some specific in-country examples.

Then I realized that we never really got a response from Shana or Dennis on that…. Is it ok with you if I call Shana/Dennis to just get their buy-in into the bat behavioral risk/intervention plan?

Cheers,

Peter

Peter Daszak

President

EcoHealth Alliance

460 West 34th Street – 17th Floor

New York, NY 10001

Tel. +1 212-380-4473

www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Leilani Francisco <francisco@ecohealthalliance.org>
CC: Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh <karesh@ecohealthalliance.org>
Sent: 8/2/2017 12:21:13 AM
Subject: Re: BR updates - consortium meeting

Hi Leilani,
Happy to work with you on a plan. Before you get too far, please wait for the tentative agenda for the meeting and reflect and make suggestions on that. It should be out for reaction this week. I think that agenda may be helpful in shaping your plans. My initial thoughts are that we would have a behavior/comms working session collaboratively across the partners, led by you, that would help provide the direction and firm up the content for what we present to the advisors and USAID. Of course, it is good to have the general pieces put together and prepared ahead of time, but we really want to work as a group to hone the messages for those stakeholder audiences.
As I think you know, behavior (pre-you) was the most criticized area at the last meeting with these groups, so we really want to make sure that we're careful and reflective from that meeting and shape our points sharply this time. They especially don't want to hear what they referred to as "shotgun" "anecdotes", so I'm concerned that we might be better off responding to the concerns outlined last time (Billy can share) and present more of a solid new plan, rather than past data that may reinforce their concerns. For example, drafts of the bat comms pieces might be the best things to present.
More soon & thanks for considering,
Jonna

On Tue, Aug 1, 2017 at 3:32 PM, Leilani Francisco <francisco@ecohealthalliance.org> wrote:

Hi Jonna,

I've been working with the Behavioral Risk team on analyzing data so we can present an update to USAID during the consortium meeting in September/before the end of the fiscal year.

It would be great to get your thoughts on the preliminary game plan.

Would you be interested in a quick run through?

Best,

Leilani

--

Leilani Francisco, PhD, MA, PMP
Senior Scientist | PREDICT-2 Senior Behavioral Risk Surveillance Coordinator

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From:	William B. Karesh <karesh@ecohealthalliance.org>
To:	David Wolking <djwolking@ucdavis.edu>;Alisa Pereira <apereira@usaid.gov>;Leilani Francisco <francisco@ecohealthalliance.org>;Cassandra Louis Duthil <clouisduthil@usaid.gov>;Chris Johnson <ckjohnson@ucdavis.edu>;PREDICTMGT <predictmgt@usaid.gov>;Andrew Clements <AClements@usaid.gov>;Eddy Rubin <erubin@metabiota.com>;Elizabeth Leasure <ealeasure@ucdavis.edu>;Lindsay Parish <lparish@usaid.gov>;Peter Daszak <daszak@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;Shana Gillette <sgillette@usaid.gov>
CC:	Catherine Machalaba <machalaba@ecohealthalliance.org>;Molly Turner <turner@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>;Brooke Genovese <bgenovese@ucdavis.edu>;Alison Andre <andre@ecohealthalliance.org>;Amanda Andre <amanda.andre@ecohealthalliance.org>
Sent:	8/7/2017 2:49:22 PM
Subject:	Re: Reminder: PREDICT Management Team Call - Monday August 7, 2017 (10AM PDT/1PM EDT)

Hi Everyone,

I have to be at a CFR meeting with CDC personnel today from 12:30 until 2:00. Peter and Leilani are both out of the office this week and if I can not slip out for the MT call today, please see the following notes (which given the shortened call today, we might not have discussed anyway):

Partners:

1. P&R is presenting a webinar on the P4P process on August 10th. If anyone wants to listen in, Rob Salerno at DAI can provide call in details.

2. We have been continuing monthly calls with P&R and OHW and recently reviewed draft One Health aspects of work plans with P&R to coordinate activities for year 4.

3. WBK worked on updating OIE standards for transport of biological materials to meet new UN and IATA recommendations. We will want to update the PREDICT protocols and training materials to reflect these changes for packaging, labeling and documentation.

Behavioral Risk Notes for MT meeting (Monday) and EB Meeting (Wednesday)

1. Leilani spoke with Amanda McClelland from the International Federation of Red Cross (IFRC)
    a. She was referred to PREDICT by Andrew to see if we could collaborate
    b. She sent an e-mail with her request:
        - They are looking to create a roster of consultants (individual or company) to support the roll out of a community and civil society focused epidemic preparedness program.
        - They are specifically looking for technical support to explore the idea of spatial anthropology and human geography, combined with risk mapping to inform community engagement and prevention interventions in an outbreak.
        - Link to the current advertisement for the roster: http://reliefweb.int/job/2135774/consultancy-epidemic-and-pandemic-preparedness-external-experts
        - They also plan to host a meeting to discuss the potential for this type of activity and how they would roll it out. She will send more details shortly on when this would

occur.

We are rolling out the Behavioral Risk In-depth Investigations as described in the 2-page BR Plan

We've developed a dashboard summarizing the BR topics and taxa being investigated in all 28 countries

We've finalized the interview guide which now includes intervention-focused probes; the focus group guide has been updated and is undergoing final review

We've finalized our working Universal Codebook for qualitative analysis

We've refined our analysis plan and developed a template to house our iterative analyses of qualitative and quantitative data to inform the holistic development of intervention recommendations

For the bat-human interaction intervention (for Sierra Leone and to be scaled up):

a. We have defined potential universal modes of communication, assessed viable modes in Sierra Leone, and refined the core messaging

b. The above has been compiled into a summary document

c. We discussed the viable modes as a group and selected story books and 2-page leave behinds as our primary modes

d. Illustration and storyboarding for the storybooks is in progress

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

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President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

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On Aug 4, 2017, at 12:24 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi again,

Below is the agenda for Monday's call. Please note that **this will be a shorter call (30 mins - 10:00-10:30AM/1:00-1:30PM EDT)** to accommodate a meeting in DC for our USAID partners.

Best,

David

PREDICT Management Team Agenda

Monday, August 7, 2017

10:00-10:30PM PDT/1:00-1:30pm EDT

#800-444-2801, Access code 5151894

International Dial-in number: 310-765-4820 (toll charges apply)

Standing items

USAID Updates

1. **Administrative items**
   a. Budget planning and next steps
   b. EPT-2 external evaluation updates
   c. August 2nd ETD M&E meeting update
   d. September 2017 semi-annual consortium meeting plans - see separate email with updated date and info on logistics and accommodation
   e. January 2018 Brussels All country meeting update
2. **Ebola Host Project updates**
   a. General updates
   b. SL communication partner and campaign strategy updates

On Thu, Aug 3, 2017 at 2:27 PM, David J Wolking <djwolking@ucdavis.edu> wrote:
Hi there,

Just a reminder about our PREDICT management team call this Monday (August 7, 2017 @10AM PDT/1PM EDT). I'll share the agenda and calendar invite soon.

Best,

David

From: Andrew Clements <aclements@usaid.gov>
To: Alisa Pereira <apereira@usaid.gov>;Angela Wang <awang@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;William Karesh <Karesh@ecohealthalliance.org>;Shana Gillette <sgillette@usaid.gov>;Cara Chrisman <cchrisman@usaid.gov>;Dennis Carroll <dcarroll@usaid.gov>;David J Wolking <djwolking@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Lisa Kramer (Nairobi/EA/R6H) <lkramer@usaid.gov>;Sarah Paige <spaige@usaid.gov>;Gregory Adams (GH/AA/GH) <gadams@usaid.gov>
Sent: 8/10/2017 1:26:49 AM
Subject: Fwd: PRO/EDR> Ebola-like illness - Uganda (02): (LW) EpiCore response [EXTERNAL]

FYI

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

Begin forwarded message:

From: promed-edr@promedmail.org
Date: August 9, 2017 at 9:14:20 PM EDT
To: promed-post@promedmail.org, promed-edr-post@promedmail.org
Subject: PRO/EDR> Ebola-like illness - Uganda (02): (LW) EpiCore response [EXTERNAL]
Reply-To: promedNOREPLY@promedmail.org

EBOLA-LIKE ILLNESS - UGANDA (02): (LUWERO) EPICORE RESPONSE
****
A ProMED-mail post
<http://www.promedmail.org>
ProMED-mail is a program of the
International Society for Infectious Diseases
<http://www.isid.org>

Date: 9 Aug 2017
Source: Dr. Henry Kyobe Bosa [edited]

Samples collected yesterday [8 Aug 2017] from the 3 surviving suspects in the Luwero VHF [viral hemorrhagic fever] alert have tested negative by PCR for all Ebola, Marburg, CCHF [Crimean-Congo Hemorrhagic Fever], RVF [Rift Valley Fever], and Sosuga viruses at UVRI [Uganda Virus Research Institute].

The district is already aware of these preliminary findings. Testing is underway for the one sample collected from the deceased case.

--
Communicated by:
ProMED-mail

<promed@promedmail.org>

[ProMED-mail greatly appreciates the additional information provided by Dr. Bosa on the 3 surviving contacts. Any further information on these cases or the primary case would be greatly appreciated. - Mod.JH

A HealthMap/ProMED-mail map can be accessed at: <http://healthmap.org/promed/p/97>.]

[See Also:
Ebola-like Illness - Uganda: (LW) RFI
http://promedmail.org/post/20170808.5237244]
.....jh/mod/jh
##
****
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<postmaster@promedmail.org>.
##
##

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From: Corwin, Andrew L <CorwinAL@state.gov>
To: David McIver <dmciver@metabiota.com>
CC: Clements, Andrew (GH/HIDN) <aclements@usaid.gov>;predict@ucdavis.edu" <predict@ucdavis.edu>;Huerta, Alexandria I <AHuerta@state.gov>;Karen Saylors <ksaylors@metabiota.com>;Bounheuang, Kounnavong" <BounheuangK@state.gov>;Schar, Daniel (RDMA/OPH) <dschar@usaid.gov>;Soubanh Silithammavong <sSilithammavong@metabiota.com>;Anchalee Jatapai <ajatapai@usaid.gov>;Kongchay, Vongsaiya (USAID) <KongchayV@state.gov>;Martz, Robin (USAID) <rmartz@usaid.gov>;Ricardo Echalar <rechalar@usaid.gov>;Damrongwatanapokin, Sudarat (RDMA/OPH)" <sdamrongwatanapokin@usaid.gov>
Sent: 9/7/2017 12:40:09 AM
Subject: [predict] RE: EPT-2 Meeting in Lao PDR

Thanks Dave,

We really would appreciate copies all such relevant documents. Excellent idea in establishing information sharing policy prior to Project start-up.

We would ask that as per Standard Practice, you complete the attached TDY Form in your request to Alex Huerta, USAID Country Representative for USAID Laos Mission Concurrence with regards to your visit. Please take note the Embassy approved hotels for USG sponsored travel at the bottom of the Form.

Looking forward to learning more.

Best regards,

Andy

Andrew L Corwin
Health Program Manager
USAID /Lao People's Democratic Republic (PDR)
Tel: 856.21.487305
Cell: 856.20.55521249
Email: corwinal@state.gov

From: David McIver [mailto:dmciver@metabiota.com]
Sent: Thursday, September 07, 2017 4:11 AM
To: Corwin, Andrew L
Cc: Clements, Andrew (GH/HIDN); predict@ucdavis.edu; Huerta, Alexandria I; Karen Saylors; Bounheuang, Kounnavong; Schar, Daniel (RDMA/OPH); Soubanh Silithammavong; Anchalee Jatapai; Kongchay, Vongsaiya (USAID); Martz, Robin (USAID); Ricardo Echalar; Damrongwatanapokin, Sudarat (RDMA/OPH)
Subject: Re: EPT-2 Meeting in Lao PDR

Hi Andy,

In terms of data sharing and virology surveillance, we have worked on a separate document that outlines rules and regulations surrounding sharing of data, samples, results, and the release of test results. In addition to the PREDICT-standardized data sharing agreements, our Lao PDR PREDICT team also went a step farther to create a document that specifically states when, and under which circumstances, data can be shared or viewed, and by whom. This document has been signed by representatives from PREDICT, DLF, DCDC, and FAO. I'll be happy to share copies of all these agreements with you when I'm in Laos, if you like.

While we have already collected some human samples already, testing has not yet began. Since we're still waiting for final USAID approval for contract agreements with NCLE, we've haven't been able to move forward with testing yet. Right now, we have about 180 human samples frozen in LN2 at NCLE. We're all very eager to get started on testing!

I'm looking forward to catching up with you in October, and I'll be happy to share our updates with you.

Thanks for your help.

Dave

—
David McIver, PhD
PREDICT Asia Regional Coordinator | Epidemiologist
Metabiota

e: dmciver@metabiota.com
c: +1 778-269-2965

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On Sep 5, 2017, 10:49 PM -0300, Corwin, Andrew L <CorwinAL@state.gov>, wrote:

Thanks David and Sudarat for the clarification. While there is an MoU arrangement between the MoH and MoAF, I thought the focus of the agreement was on information sharing and a one Health approach to outbreak investigations. I have not heard before of an arrangement in which MoAF provides permission on behalf of the MoH in terms of virological surveillance with associated laboratories diagnostics. But there may be indeed just such an agreement.

Have you already begun collecting human specimens and testing at NCLE? I would suggest scheduling a meeting with Dr Reiko who has replaced Dr Dapeng at WHO LAOS, if you have not already communicated with her. I would also be happy to brief her regarding this activity. It should be noted that all the virological work up at NCLE is supported by WHO Laos visa vi laboratory expertise and oversight.

With regards to your Lao travel, I will be available to meet with you the first week of October (except the 6th), and possibly the early afternoon of the 29th. We are all very excited to learn how this Activity is progressing.

Please address your request for Mission Concurrence to Alex Huerta, the Lao Country Representative.

Best regards,

Andy

From: David McIver <dmciver@metabiota.com
Date: September 5, 2017 at 8:37:59 PM GMT+7
To: Damrongwatanapokin, Sudarat (RDMA/OPH) >, Corwin, Andrew L <CorwinAL@state.gov
Cc: Anchalee Jatapai >, Schar, Daniel (RDMA/OPH) <dschar@usaid.gov>, Karen Saylors <ksaylors@metabiota.com>, Clements, Andrew (GH/HIDN) <aclements@usaid.gov>, Kongchay, Vongsaiya (USAID) <KongchayV@state.gov>, Ricardo Echalar <rechalar@usaid.gov>, Bounhouang, Koumsavong <BouahouangK@state.gov>, , <predict@ucdavis.edu>, predict@ucdavis.edu <predict@ucdavis.edu>, Martz, Robin (USAID) <rmartz@usaid.gov>, Soubanh Silthammavong <sSilthammavong@metabiota.com>, Huerta, Alexandria I Subject: Re: EPT-2 Meeting in Lao PDR

Hi Andy and Sudarat,

Sudarat is correct, in that the MOU was signed between Metabiota and the DLF/MoAF with the intention that they would subcontract to NCLE as the coordinator of the human surveillance portion of the program. To the best of my understanding, no further MOUs are required and human surveillance in the Khong District Hospital is ready to begin as soon as we have final approval from USAID Washington.

We do plan to make a visit to Champasack while I am in Laos, but we are not certain yet of the days - it will likely be the last week of September. I will work on processing a USAID Mission Concurrence Request and send that along to Alex. And of course, we'll be more than happy to be at an EPT meeting and give everyone an update on the PREDICT program.

Thanks very much,
Dave

—

David McIver, PhD
PREDICT Asia Regional Coordinator | Epidemiologist
Metabiota

e: dmciver@metabiota.com c: +1 778-269-2965

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On Sep 5, 2017, 7:15 AM -0300, wrote:

USAID Mission Concurrence Request

Lao PDR Temporary Duty Information Form (Last update: August 2017)
(send completed form to ahuerta@state.gov, manisonem@state.gov, and samaiphonet@state.gov)

Submitted by: Insert Name, Office

Dates of travel:	**From:** Click here to enter a date. **To:** Click here to enter a date.
TDY objective:	Click here to enter text.
USAID activity	Click here to enter text.
Individuals visiting Laos (from RDMA, Washington, Implementing Partner):	Click here to enter text.
Required meetings to be arranged:	
Site visits required:	
Data to be collected:	N/A
Is a DIP note or letter of introduction requested:	☐ Yes ☐ No *Note: DIP notes are required for site visits and meetings with high-level GOL officials. Names of GOL officials must also be provided.*
Is motor pool requested:	☐ Yes ☐ No
Is Embassy access requested:	☐ Yes ☐ No
Have the visitors met with the AMB/DCM before:	☐ Yes ☐ No
Is Laos staff recommended to accompany all meetings:	☐ Strongly recommended ☐ Optional, but at the Lace Office discretion
Additional Comments:	Embassy access is requested if a briefing for AMB is expected.

*Only a limited number of hotels meet Embassy Lao security and safety requirements for eCC travelers. As of August 2017 these are: (1) Lao Plaza Vientiane, (2) Landmark Mekong Riverside, (3) Settha Palace, (4) Dhavara Vientiane, and (5) Crowne Plaza.

From:	Andrew Clements <aclements@usaid.gov>
To:	Jonna Mazet <jkmazet@ucdavis.edu>;William Karesh <Karesh@ecohealthalliance.org>;Kevin Olival PhD <olival@ecohealthalliance.org>;Jon Epstein <epstein@ecohealthalliance.org>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;D. Phil Simon Anthony <anthony@ecohealthalliance.org>;Tracey Goldstein <tgoldstein@ucdavis.edu>
Sent:	9/7/2017 9:37:17 AM
Subject:	Fwd: Mongabay -- Bats and viruses: Beating back a bad reputation

FYI.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

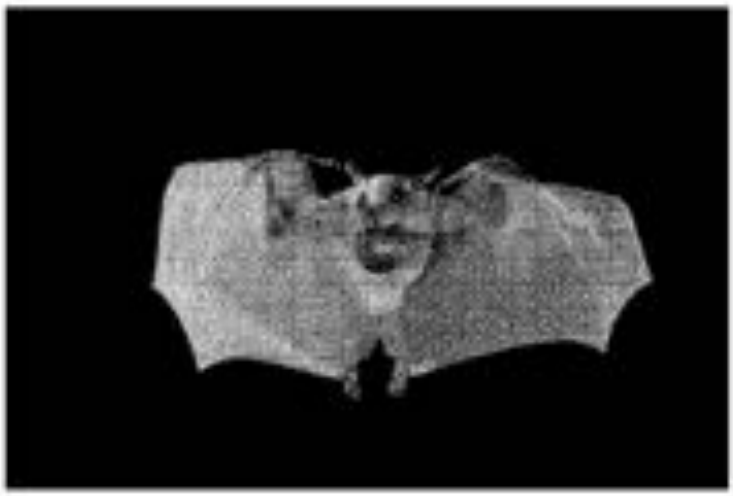
Begin forwarded message:

From: Kendra Chittenden <kchittenden@usaid.gov>
To: "GHSD Unit Mail List (USAID)" <ghsdunitmaillist@usaid.gov>
Subject: Fwd: FW: Mongabay -- Bats and viruses: Beating back a bad reputation

---------- Forwarded message ----------
From: **Monica Dea** <mdea@usaid.gov>
Date: Wed, Sep 6, 2017 at 12:45 PM
Subject: Fwd: FW: Mongabay -- Bats and viruses: Beating back a bad reputation
To: Kendra Chittenden <kchittenden@usaid.gov>

Very interesting reading....

From: Greg Folkers <gfolkers@niaid.nih.gov>
Date: Wednesday, September 6, 2017 at 7:21 AM
Subject: Mongabay -- Bats and viruses: Beating back a bad reputation



Bats and viruses: Beating back a bad reputation

Bat ecologists and conservationists worry that bats' exaggerated reputation for carrying disease-causing microbes leads to the baseless killing of millions of bats worldwide. by John C. Cannon on 29 August 2017

- *Ecologist Merlin Tuttle argues that too much research and media attention is focused on bats based on tenuous links to deadly disease-causing viruses such as Ebola.*
- *Live Ebola virus has never been found in bats, and virologists acknowledge that other animals may be involved.*
- *But scientists have plucked live strains of other dangerous viruses from bats, and researchers argue that continuing to study the association between viruses and bats (as well as other animals) will ultimately help us better prepare for future disease outbreaks.*

A burned-out stump was all that remained by the time a team of virologists arrived in Méliandou in 2014. They had been hunting for the source of the deadly outbreak of the disease caused by Ebola virus that had begun late the previous year. A patchwork of clues had led the researchers to the tree's charred remnants in this small Guinean village of not more than a few dozen families.

The tree had once been home to bats that locals would nab on occasion for a meal. It was also a spot where Emile Ouamouno might have been before he got sick. Emile, a toddler from Méliandou, is thought to be the first person to contract the illness in this outbreak. With little else to go on, scientists postulated that the origin of the virus that infected Emile might be the tree and its bats.

The virologists told a reporter for *Science* that they couldn't confirm if people from Méliandou had burned the tree to get rid of the bats that they feared might be carrying Ebola virus. But ecologist Merlin Tuttle has little doubt that was the case. To him, this type of persecution is part of the pattern set in motion when there's a whisper that bats might be involved in a disease outbreak.



A Wahlberg's epauletted fruit bat (*Epomophorus wahlbergi*), about to pollinate a baobab tree in Kenya. Countless thousands of epauletted bats live in African villages without record of harm to humans, Merlin Tuttle said. Photo and caption © Merlin Tuttle

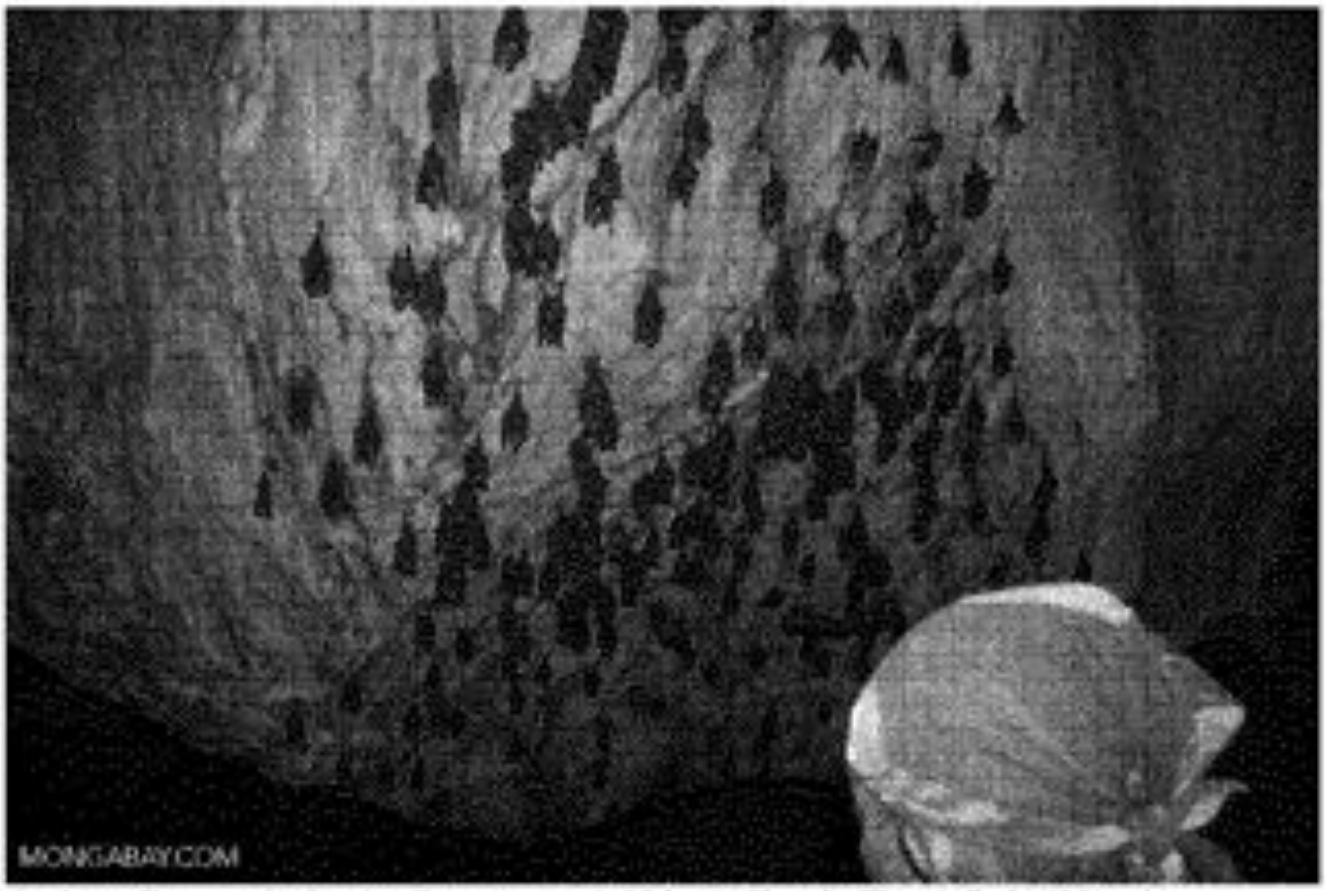
"I personally have documented cases where hundreds of thousands, sometimes millions of bats, were buried alive in their caves," he added, "just because somebody had one of these crazy ideas before it was even tested and found not to be true."

As recently as 2012, Tuttle and several colleagues traveled to a cave in Cuba's Alejandro de Humboldt National Park where they hoped to watch a bat colony emerge. But locals, fearful of the disease-causing microbes that they assumed the bats carried, had sealed it shut by the time they arrived, he said.

Tuttle, a research fellow at the University of Texas, contends that the accusations pegging bats as wellsprings of dangerous viruses to diseases including Ebola are often premature and grossly exaggerated He says that premature speculation can ignite the type of backlash that he witnessed in Cuba and that he suspects occurred in Guinea.

"When somebody comes out with a scary headline, the bats can all get eradicated before anyone even finds out that the bats weren't guilty," he told Mongabay.

The outbreak of Ebola in West Africa was scary indeed, killing more than 11,000 people in 10 countries before fizzling in 2016. Once bats are linked to such an event, "Who in his right mind is going to tolerate bats around under those circumstances?" Tuttle said.



A colony of insect-eating bats in a limestone cave in Malaysia. Photo by Rhett A. Butler / Mongabay

Bat fans

The septuagenarian has studied bats around the globe and continues his advocacy for bat conservation, not least for the benefits they provide us. The U.S. Forest Service reports that some 300 species of fruit trees need the pollination services of bats. And a study in Indonesia found that bats and birds boosted cacao yields by 31 percent, providing an annual bump in profits of $730 per hectare for farmers.

The biology and conservation of bats have been the focus of Tuttle's 55-year scientific career. Now, he's continuing his mission to vindicate them through his photographs, books, and popular articles, as well as a blog that rallies a vocal group of "bat fans."

An undue emphasis on bats as disease carriers has bled into scientific research, Tuttle says. In a consistent refrain, he argues that a frenzy of speculative scientific evidence, followed by even more speculative — and sometimes hyperbolic — storytelling on the part of journalists, leads to the unwarranted killing of bats.

In Tuttle's view, bats are about as suspect as other animals found in the forests of West and Central Africa, where all Ebola outbreaks have originated. Scientists have discovered that chimpanzees, gorillas, a skittish little antelope called a duiker and several rodents all tote Ebola virus RNA in their bloodstreams, although they've only found snippets, not entire genomes.

The isolation of a live strain of infectious Ebola virus from bats would indicate that bats are Ebola hosts, but so far that's been elusive. Researchers have turned up antibodies to Ebola in blood from bats, but from many other animals as well. The discovery of these remnants from a battle between a bat's immune system and a virus is often misinterpreted, said Jens Kuhn, a virologist at the National Institutes of Health in Bethesda, Maryland.

"That is very quickly taken as signs of [Ebola] infection by many people, but it doesn't mean that," Kuhn said. "Antibodies just means exposure to something that is Ebola-like."

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The upshot is that no one has found a definitive link between bats and any of 25 outbreaks since 1976. As a result, by the time the latest epidemic was winding down, studies began to emerge that expressed doubts about bats' role in the disease.



An Indian flying fox (*Pteropus giganteus*) in flight. Photo by Julie Larsen Maher © WCS

The hunt for origins

What scientists are looking for — and what some think that a bat species might be — is the organism that carries the Ebola virus continuously in its population, known as a reservoir. Whatever this reservoir is, it doesn't get sick or die itself, so it's an essential source of the virus to other organisms.

But not all scientists hunting for an Ebola reservoir are fixated on bats.

"There is something that doesn't quite fit in my head with this Ebola-bat story," said Siv Aina Leendertz, a virologist at the Robert Koch Institute in Berlin. "I don't think that it's enough evidence at the moment to say that Ebola continuously circulates in bats."

Leendertz published a review in 2016 where she posited that the chain of infection might include an aquatic insect like a mayfly. She said it was just an example to demonstrate how another animal could be involved that might be "completely wrong."

"If we are only focusing on the fruit bats," Leendertz added, "we might miss other things that could give us more information, more clues, more pieces to the puzzle."

Still, the antibodies that researchers have plucked out of bat blood demonstrate that bats "definitely have something to do with it," she said.



A common vampire bat (*Desmodus rotundus*) at the Bronx Zoo in New York City. Photo by Bill Meng © WCS

For most of us, pegging bats as dangerous harbors of disease-causing viruses isn't too much of a stretch, Kuhn said.

"It totally fits into our narrative about bats that they also carry very evil things."

Satan in Dante's *Inferno* takes a bat-like form. Their nocturnal nature touches on our most basic fear of the darkness and the unknown. And of course, the vampire Dracula can shapeshift into a bat in the famous Bram Stoker novel.

But like Leendertz, Kuhn advocates casting a broader net to track down the animals that connect us to viruses like Ebola. He has a hunch that an insect or another arthropod might be involved in the transmission of Ebola virus from animals to humans — perhaps a tick, delivering the infective agent into the blood of another host animal before it gets to us.

Our association with bats, both in lore and in real life, dates back millennia — think the cave dwellings of our early ancestors. And that's one reason Tuttle sees their reputation as flying disease distributors as so improbable.

"There are millions and millions of people every year that eat bats," he said. "I wish that there was a good reason that people shouldn't eat bats because it's caused the extinction of some, and it's certainly threatening many others.

"The truth is, there is no evidence that eating bats has caused any pandemics or major disease outbreaks," Tuttle added.

Kuhn agrees that this close relationship points to the involvement of some other organism. If bats are the sought-after reservoir of Ebola virus, Kuhn said, "Why don't we have one outbreak of Ebola after another?"

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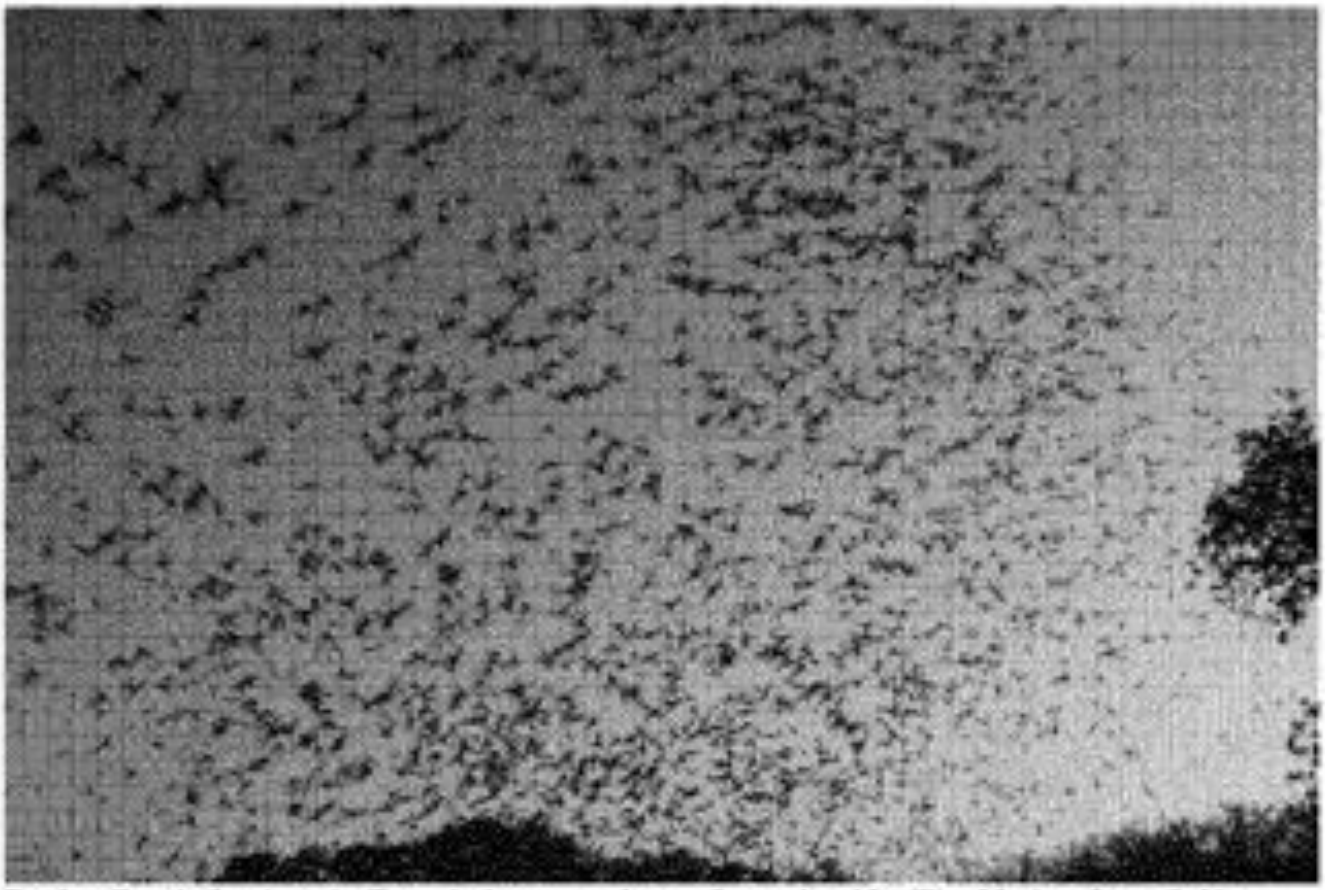
The answer? "There's more to [it] than just bats," he said.



Bracken Cave in San Antonio, Texas, is the summer home of more than 15 million Mexican free-tailed bats (*Tadarida brasiliensis*), making it the world's largest bat colony. Photo in the public domain by Ann Froschauer / U.S. Fish and Wildlife Service

An image problem

Until about 20 years ago, bats were known mostly for being carriers of the rabies virus — although then, as now, the chances of contracting rabies from a bat were astronomically small, with an average of fewer than three cases a year in the U.S.

Beginning in the late 1990s, however, scientific research to investigate bats' roles in the transmission of other diseases began in earnest. A bevy of viruses tied to bats stormed onto the epidemiological scene beginning in the late 1990s.

After that, "Bats became hip," Jens Kuhn said.

Nipah virus, which causes potentially fatal encephalitis, struck Malaysia in 1998. It made pigs sick, and it killed more than half of its victims, who were mostly pig farmers. In 2003, researchers isolated live Nipah virus from the urine and saliva of seemingly healthy bats, and studies now refer to the fruit bat genus *Pteropus* as the "wildlife reservoir" of the disease.

Severe acute respiratory syndrome (SARS) appeared in Asia in 2003, sickening 8,100 people. Scientists figured out that humans probably picked up the SARS-causing virus from civets for sale at local markets, and researchers have never pulled the live virus from a bat. However, in 2005 a paper, titled "Bats Are Natural Reservoirs of SARS-Like Coronaviruses," appeared in the prominent journal *Science*.

Once the science community had made the connection, however tenuous, between SARS and bats, that's what most people remembered, Tuttle said, not that they hadn't been able to find the live virus.

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"There's never been any proof that SARS came from bats," he added.

Indeed, many scientists who publish such research qualify their conclusions and explain that more work is needed. Yet such nuance is often lost on the media.

In a 2014 report on the inception of Ebola in Guinea published in the *New England Journal of Medicine*, for example, the authors refer to fruit bats as "potential reservoirs" of Ebola virus. But primed by what Tuttle sees as an overemphasis on bats in the realm of virology research, one news story on that paper stated unequivocally that fruit bats "are reservoirs of the virus."



A male straw-colored fruit bat (*Eidolon helvum*) from Kenya. Contrary to available evidence, this species was erroneously blamed for the index case, a child in Guinea, in the 2014 Ebola outbreak, Tuttle said. Photo and caption © Merlin Tuttle

Investigations probing the relationship between bats and viruses led to new hypotheses about the role of bats in the spread of disease, and they revealed new insights into how their immune systems handle viruses. Journalists and the public then latched onto aspects of bats' unique biology as the beginning and the end of the story of how viruses get from animals to humans.

Kuhn investigates many of the virus families associated with bats, and he said that the "weak" links that scientists have found, such as with Ebola, are easy to exaggerate.

For example, popular news outlets use the fact that bats fly to explain how these viruses get from one place to another. That's a "dangerous simplification," Kuhn said, that has been "completely overhyped in the media."

It also ignores other flying animals, Tuttle said.

"OK, they can travel long distances, but so do birds and insects," he said. "They're not the only thing that can travel long distances."

One news report, under the headline, "Why Killer Viruses Are On The Rise," called bats "arguably one of the

most dangerous animals in the world."

Part of the story had been reported from Gomantong Cave in Malaysian Borneo, home to the swiftlets that spin the nests used to make bird's nest soup, a favorite dish in parts of Asia. Workers climb to the cave's ceilings twice a year for the profitable harvest after the birds have vacated their homes. The boardwalk loop into the cavernous 90-meter-high (295-foot) gash in the forest is also popular with tourists, and they're not unlikely to pick up some sort of, ahem, souvenir dripping from the cave's ceiling and the millions of bats and birds that reside there.

The story warned, "There could be Ebola in the poop that lands on your shoulder."

Not only has Ebola virus never been found in Malaysia, but neither have any members of its family, the filoviruses. It's inaccurate to imply a risk of Ebola to cave visitors, but the sentence's broader, cheeky implication is that bats are constantly slinging around deadly viruses. If that's the case, Tuttle said, why haven't any of the nest harvesters or visitors gotten sick or touched off an outbreak after they left the cave, especially since humans have been doing pretty much the same thing there for hundreds of years?

"There is no evidence that any human in the whole world history has ever got any disease from poop landing on their shoulder from a flying bat," he said.

Tuttle uses his website to excoriate such media reports, which he argues put bats at risk of retaliation, including one on Mongabay in April 2016 that's since been corrected.



Gomantong Cave in Malaysian Borneo is home to millions of bats. Harvesters of swiftlet nests for soup and tourists are frequent visitors to the cave. Photo by John C. Cannon / Mongabay

The bat stops here

Just how big an effect does the intentional killing of bats have? In a 2016 study, a team of bat researchers tried to put some numbers to that question, as well as the other causes of bat decline worldwide, by reviewing cases of bat deaths going back to 1790.

Up until the beginning of the 21st century, they did find that "intentional killing" by humans was the most significant cause of deaths, often because people viewed them as pests. Then around 2000, as wind turbines began to pop up, they became a leading cause of death. So did white-nose syndrome, a potentially fatal disease in bats caused by a fungus. But the study didn't turn up evidence that people have ramped up efforts to destroy bats in the past 100 years, even when the bats-as-disease-carriers line of research began about two decades ago.

Paul Cryan, a bat biologist with the U.S. Geological Survey and an author of the research, recognizes that the perception of bats affects the way we treat these animals.

"It seems that people stigmatize and vilify things they don't understand, and bats are among the most misunderstood animals out there," Cryan wrote in an email. But, based on the team's research, "I would not expect extermination efforts to increase as new information on diseases and bats comes to light," he added.

Tuttle found the study's conclusions lacking. He said that Cryan and his coauthors' research did not account for the fact that journals stopped reporting "deliberate human killings" of bats in the 1980s, potentially ignoring more recent incidents.

Since that time, "Scientific journals have almost exclusively only published hypothesis-testing papers, meaning no further reporting of deliberate human killings that previously were at least sometimes reported," Tuttle said.

Even if they're not reported, he is adamant that bat killings continue. "In Mexico and the remainder of Latin America, it is sometimes difficult to find a hollow tree that hasn't been burned to kill bats (mistakenly feared as vampire bats)," Tuttle said. "And, with new speculation, bat killing there may get even worse.

"In my experience, wherever I go worldwide, people who fear bats attempt to kill them," he added.

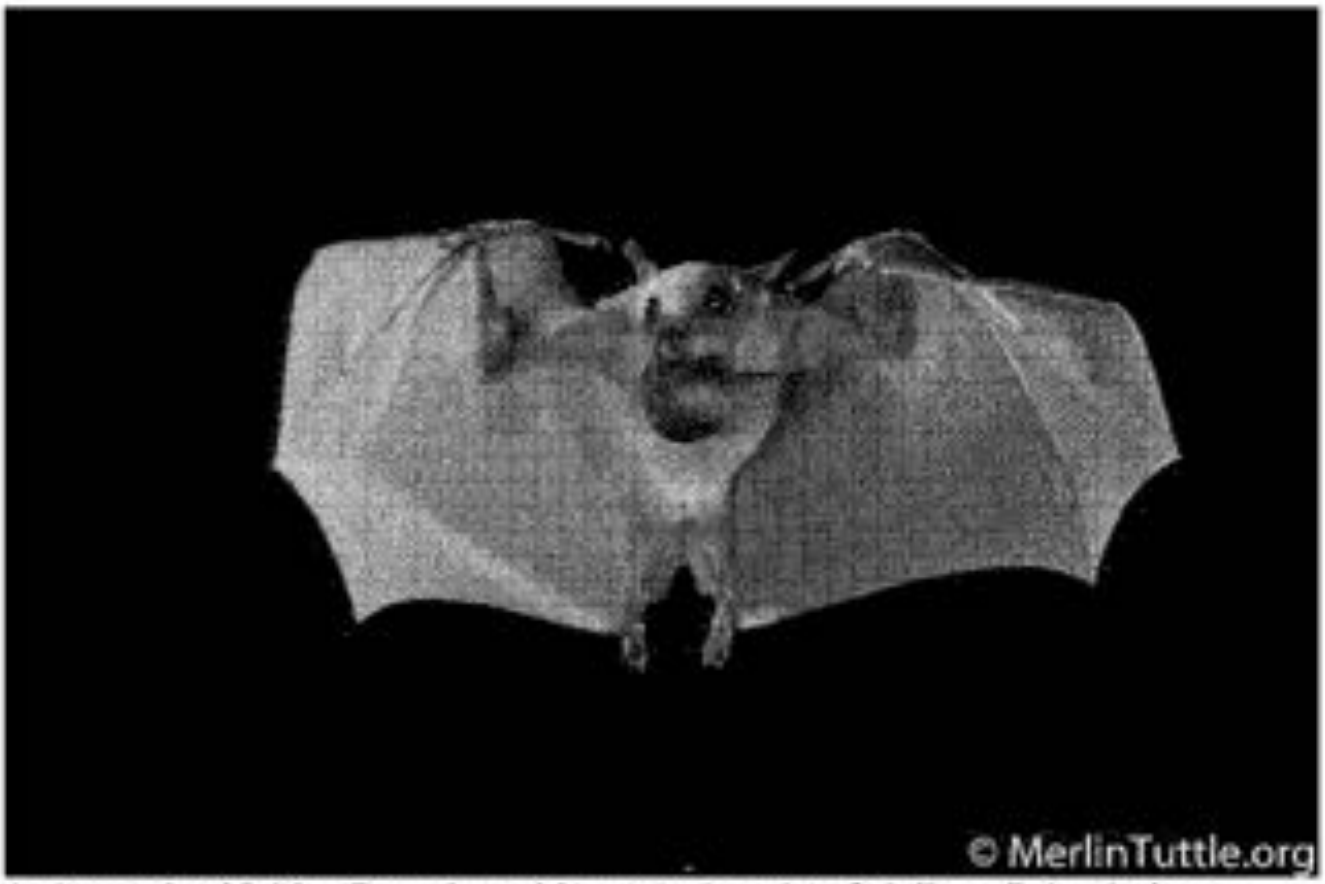
Tuttle is frustrated with his fellow scientists, many of whom have followed the fashionable line of bat-focused disease research to lucrative grants.

In late 2014, in the midst of the Ebola crisis, the U.S. House of Representatives approved $1.77 billion in funding for the Centers for Disease Control and Prevention (CDC) "for Ebola preparedness and response," which included money to support scientific research between 2015 and 2019.

That money hasn't all gone to bat research, but Tuttle says it's out of whack with the threat that Ebola poses to us. What's more, he suggests that the desire to keep that funding flowing is twisting the conclusions that researchers and journal publish, though he's hesitant to single out scientists by name.

These reports do often carry warnings about the value of bats to the ecosystem and that the evidence linking bats to viruses shouldn't be seen as a justification for killing them. Many news articles also highlight the importance of bats in controlling insects and pollinating crops as a way of discouraging retribution.

But, Tuttle said, such qualifying statements often appear late in the text, after the frightening, attention-grabbing, and potentially dangerous news appears.



A minor epauletted fruit bat (*Epomophorus labiatus minor*) carrying a fig in Kenya. Fruit-eating bats are seed dispersers vital to reforestation of tropical and subtropical areas worldwide. Photo and caption © Merlin Tuttle

One such study appeared in the journal *Virus Evolution* in early June 2017 and laid out a case for considering bats "the major evolutionary reservoirs" of coronaviruses, the group that includes the viruses that cause SARS and MERS.

The aim of this study was to find viruses that aren't yet known to science. It's part of an effort led by researchers with the PREDICT project, a $100-million effort funded by the U.S. Agency for International Development to cut the risk of global pandemics.

Tuttle upbraided the new study immediately, arguing in a written response he shared with Mongabay that bats are easy to catch in large numbers, making them good study subjects. As a result, finding a lot of viruses in them wasn't surprising. (Ironically, Tuttle said that many of the scientists looking for diseases in bats use a trap that he invented.)

"If I had many millions of dollars to look at you for viruses, I could find a lot of new viruses and I could make up a hell of a lot of scary tales about how they're related to things that were dangerous," he added.

Tuttle wrote in a June 14 post on his website that the research propagates "the needlessly sensational presentation of bats as exceptionally dangerous animals."

"Many viruses are innocuous or even beneficial, including some that are closely related to deadly ones," Tuttle wrote on July 2. "Also, the number of viruses found in bats is not necessarily indicative of risk."

He also said that the "exceptional diversity" of coronaviruses found in bats should be expected, given that bats themselves are "an exceptionally old, diverse, and widespread group." At around 1,300 species, one in every five known mammals is a bat.

The *Virus Evolution* study ran under the benign title, "Global patterns in coronavirus diversity." But it

spawned media coverage under headlines such as "Bats are global reservoir for deadly coronaviruses," which ran in the news section of the journal *Nature*.

The hunt for viruses that haven't yet caused an outbreak or been proven harmful to humans has drawn criticism from other scientists as well. Michael Osterholm questions the value of spending so much to find these previously unknown viruses. He is an epidemiologist at the University of Minnesota, and he also leads a team that's been working to rapidly develop a vaccine for Ebola virus since 2014.

Osterholm advocates putting more effort toward developing vaccines and getting them into the hands of healthcare workers, rather than building up our catalog of viruses with unknown consequences.

"I don't care if you have a fire truck that's big, red and shiny," he said. "If it doesn't have an engine in it, what good is it?"



Rodrigues fruit bats (*Pteropus rodricensis*) at the Bronx Zoo. Photo by Julie Larsen Maher © WCS

The bat we know

Still, Osterholm said bats are clearly linked to "very serious infectious diseases," and he voiced his concerns about disregarding all evidence that associates bats with disease.

"This concept that any description of bats carrying these viruses is somehow unwarranted or dangerous to bats — I think that's naive," he added.

Jens Kuhn agrees that given what we've learned about bats and viruses in the past two decades, especially with Ebola virus, further research is warranted.

"You have to go by the data that you have and not the data that you don't have," Kuhn said. "There is enough of this kind of anecdotal, weird evidence that would lead me to believe that bats are somehow involved in that [Ebola] puzzle."

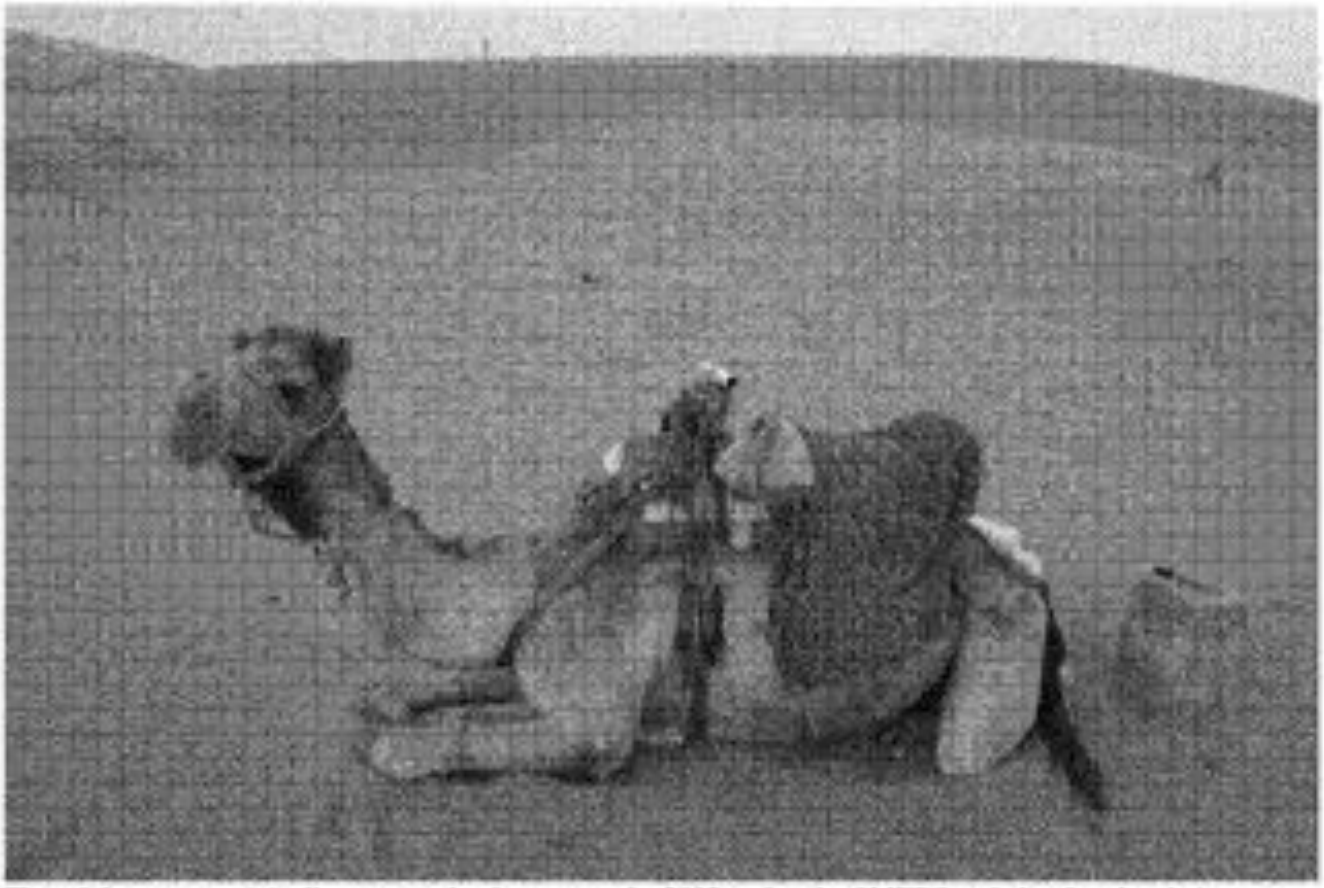
While Kuhn emphasizes how different these viruses are — "You can't throw them all together" — he offers an answer to Tuttle and Osterholm's challenge to the value of identifying viruses new to science. Understanding how these viruses evolve and are related to each other could ultimately help us be better prepared for outbreaks, he said.

Right now, it's a quest in which scientists sit at the very frontier of their knowledge. Never mind the tip, Kuhn said: "We haven't even seen the iceberg yet."

Middle East Respiratory Syndrome, or MERS, is one example of what researchers like Kuhn can glean from those relationships. The MERS coronavirus — in the same family as the SARS virus — can cause pneumonia and diarrhea. Of the roughly 2,000 people infected since 2012, 35 percent have died.

Tuttle pointed out that when MERS broke out in 2012, scientists and the media didn't look far for a culprit.

"Before they knew anything about it, they practically bet the bank — they predicted in writing — this is almost certainly coming from bats," he said.



Though bats were originally suspected to have caused a 2012 outbreak of MERS and closely related viruses have been found in bats, the virus that causes the disease most likely came from domesticated camels (*Camelus dromedarius*). Photo by Anne-Claire Benoit

In fact, epidemiologists eventually discovered that the virus had springboarded — or spilled over — into humans from a common animal in Saudi Arabia: camels (*Camelus dromedarius*). Epidemiologists use the term 'spillover' to refer to the juncture when a virus-carrying host slips the virus it is carrying to an organism of a different species.

But humans domesticated camels thousands of years ago. If our humped companions were the ultimate reservoirs of the MERS virus, meaning that they have been carrying the virus without showing signs of disease, it stands to reason that we would have noticed a spillover to humans before 2012.

Kuhn said that shared history left public health researchers with a big question: "How the heck did this virus

get into dromedaries?"

When virologists checked out the lineage of the MERS virus, they found that "Every single neighbor is a bat coronavirus," he said. "The most logical conclusion is that this is actually a bat virus that jumped into dromedaries," making bats a likely host and possibly a reservoir of MERS virus.

MERS isn't the only such disease. In 2009, a CDC-led team collected a live filovirus called Marburg from fruit bats known as Egyptian rousettes (*Rousettus aegyptiacus*) that roost in African caves by the tens of thousands.

Marburg virus infections have led to about a dozen outbreaks in humans since 1967, stemming mostly from contact with caves. Its deadliest recorded offensive in 2005 killed 90 percent of the 252 people who contracted the disease in Angola.

Researchers have since found that bats can carry an infectious form of Marburg virus for months in their colonies without visible symptoms. What's more — and this is a really important piece of the puzzle — they can eject bits of the virus in their saliva, feces and urine.

The fact that it can circulate in their systems for an extended period of time has led many scientists to deduce that bats are "at least a host" of Marburg in the environment, said Kuhn. That does not mean that Egyptian rousettes are the ultimate reservoirs. But such a strong connection to one filovirus does seem to hint that Ebola, another filovirus, might also reside in bats in a similar way.



Scientists have found that Egyptian rousettes (*Rousettus aegyptiacus*) can carry live Marburg virus, though no outbreak has ever been directly tied to contact between rousettes and humans. Photo by Zoharby (Own work), CC BY-SA 3.0 or GFDL, via Wikimedia Commons

The odds in our favor

The fact that bats can survive the effects of Marburg virus seems to lend support to the idea "that bats have unique physiological relationships with microbes," Paul Cryan said.

Part of that has to do with how bats live their lives. As flying mammals, bats expend a lot of energy, which raises their internal temperature. This constant feverish state can be particularly destructive to DNA unless an organism can evolve a solution. Cryan said he remembers "getting a chill" a few years ago as he read a study in *Science* postulating that bats' unique immune system, honed over millions of years of evolution to repair DNA damaged by flight, might help explain why they can handle such a close association with viruses.

Humans don't have such clever adaptations to handle microscopic invaders, so the thinking goes, and that leaves us more vulnerable than bats to the diseases that viruses and other organisms cause.

Even without such adaptations, the likelihood that humans will contract a virus from bats is infinitesimally small, Tuttle said. His hometown of Austin, Texas, has an enviable safety record with bats. Spectators from around the country gather on spring evenings to witness the exodus of perhaps 1.5 million bats from under a bridge on Texas' Colorado River. In the 1980s, public health officials worried that someone would contract rabies, but Tuttle campaigned for the bats to be left alone. Instead of getting rid of them, officials acted on his advice and posted signs asking visitors not to handle the bats.

"Thirty-five years later, we're still waiting for the first person to be harmed by a bat," he said.

Globally, people are much more likely to get rabies from dogs, as they're responsible for about 99 percent of cases.

Tuttle also points to his own extensive history with bats in dozens of countries with little more than a rabies shot as the only line of defense.

"I've done everything you can do to get exposed to some of these supposedly … deadly viruses," he said. "I'm still very healthy at 75."



Brazilian free-tailed bats (*Tadarida brasiliensis*) emerging from the Congress Avenue Bridge in Austin, Texas. Despite early health official warnings of danger, none of the millions of tourists has been attacked or harmed, Tuttle said. Photo and caption © Merlin Tuttle

The good health that most scientists enjoy from developed countries might be enough to keep a virus at bay, Kuhn said. Guinea and the other Ebola-endemic countries are among the world's poorest.

"It is very possible that you need to be immunosuppressed to get the first infection going," Kuhn said, "to make that species jump."

Tuttle draws on statistics to demonstrate the rarity of diseases associated with bats. He pointed out that in the past 40 years, Ebola, Marburg, MERS, Nipah, SARS, and a viral disease called Hendra have together caused just 15,000 human deaths. By comparison, he said, during that time frame some 2.2 million people are conservatively estimated to have died from rabies transmitted by dogs, which is itself considered to be rare.

"It just caught huge headlines because it was sensational and different," Tuttle said of Ebola. "This disease is trivial compared to a lot of other causes of human mortality."

But to Kuhn, that's a dangerous justification.

"This is, of course, true for any disease in history when it started," he said. "The moment you have an outbreak with 11,000 deaths, it's probably worthwhile trying to figure out where the virus is coming from."

Deforestation and roads continue to open up new areas of wilderness bringing us into closer contact with animals and any disease-causing viruses they carry. With that sort of novel exposure, along with humankind's increased mobility and rising population, the next Ebola outbreak could afflict a hundred thousand people, Kuhn said.

"Yes, it's a hypothetical scenario, but it's not necessarily an unlikely scenario," he added, "as this outbreak in western Africa has shown."

One thing is clear — that we will share our future with these zoonotic diseases, regardless of the reservoir and whether they spill over from bat, pig or camel.

"To be clear," Tuttle said in an email, "I recognize that bats can transmit some scary diseases, just like all other animals, especially humans."

As a population ecologist, he acknowledges our ever-shifting relationship with other species, and, bats aside, how difficult it is to predict just how bad the next spillover of disease from animals to humans will be.

"I don't know of anybody with my kind of training who doesn't think we're headed for some really serious bumps in the road," Tuttle added.

Shreya Dasgupta and Rebecca Kessler contributed reporting.

Banner image of a minor epauletted fruit bat in Kenya © Merlin Tuttle.

Follow John Cannon on Twitter: @johnccannon

Editor's note 8/31/17: At Merlin Tuttle's request three statements were amended to better reflect his views.

CITATIONS

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FEEDBACK: Use this form to send a message to the author of this post. If you want to post a public comment, you can do that at the bottom of the page.

Article published by John Cannon

Activism, Agriculture, Animal Behavior, Animals, Apes, Bat Crisis, Bats, Biodiversity, Birds, Charismatic Animals, Conservation, Deforestation, Ebola, Ecological Beauty, Ecology, Endangered Species, Environment, Featured, Forests, Hunting, Mammals, Research, Roads, Saving Species From Extinction, Wildlife, Wildlife Conservation, Wildlife consumption, Wind Power, Zoonotic Diseases

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+(211) 71 671 7226
+(211) 77 673 4677

--

Kendra Chittenden, Ph.D. | **Senior Infectious Disease Advisor, USAID** | mobile (703-209-5424) KChittenden@usaid.gov

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: David J Wolking <djwolking@ucdavis.edu>;Evelyn Luciano <luciano@ecohealthalliance.org>;Carlos Zambrana-Torrelio <zambrana@ecohealthalliance.org>
Sent: 9/13/2017 3:20:11 PM
Subject: RE: Feedback on Indonesia ideal work plan

Will do. I also spoke with Andrew yesterday and he's comfortable that this is probably a miscommunication. FYI I'll be meeting with Tim Meinke, Dan and Sudarat next week and will clear things up there.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4473
www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: jonna.mazet@gmail.com [mailto:jonna.mazet@gmail.com] **On Behalf Of** Jonna Mazet
Sent: Monday, September 11, 2017 11:29 AM
To: Peter Daszak
Cc: Kevin Olival, PhD; David J Wolking
Subject: Re: Feedback on Indonesia ideal work plan

I think what's happened is that whatever your planning hasn't made it into the workplan, so he's questioning the workplan, not the planned work. Please check the workplan and give us new text ASAP if appropriate, so we can finalize the process.
Thanks,
J

On Sun, Sep 10, 2017 at 10:18 AM, Peter Daszak <daszak@ecohealthalliance.org> wrote:
Thanks – it's a bit of a joke – we've been working closely with INDOHUN and Tim Meinke on this, and have had multiple meetings/phone calls with INDOHUN. Carlos and team were out there last week and I'm going out there next week. Tim's been aware of all of this at every step.

I explain that to Andrew et al. when they're in NYC next week.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4473
www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: joma.mazet@gmail.com [mailto:joma.mazet@gmail.com] **On Behalf Of** Joma Mazet
Sent: Friday, September 8, 2017 6:03 PM
To: Peter Daszak; Kevin Olival, PhD
Cc: David J Wolking
Subject: Fwd: Feedback on Indonesia ideal work plan

For your prep for discussions with Andrew next week.
Have a nice weekend.
J

---------- Forwarded message ----------
From: **Andrew Clements** <aclements@usaid.gov>
Date: Fri, Sep 8, 2017 at 3:58 AM
Subject: Feedback on Indonesia ideal work plan
To: Joma Mazet <jkmazet@ucdavis.edu>, David J Wolking <djwolking@ucdavis.edu>
Cc: Alisa Pereira <apereira@usaid.gov>, Shana Gillette <sgillette@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>, Amalhin Shek <ashek@usaid.gov>

Don't know how involved you've been with this…

Mission comment: "I'll follow up with more later but wanted to quickly share this SOW that PREDICT was using for their side of the DEAL work. This is based on conversation a year ago and very far off the mark of what we've been discussing in-country (and with the EHA tech team this week). I'll send comments next week but wanted to ask you if this was approved (I guess it was, as part of the global workplan?) but to the best of my knowledge we (Mission, UMN nor INDOHUN) hadn't seen it before."

Let's discuss with Peter next week before he goes to Indonesia. Something is not clicking on this project.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

From: Andrew Clements <aclements@usaid.gov>
To: Brian Bird <bhbird@ucdavis.edu>
CC: PREDICTMGT <predictmgt@usaid.gov>;PREDICT-outbreak <predict-outbreak@uccavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>
Sent: 9/18/2017 11:20:42 AM
Subject: Re: Cameroon gorilla die-off Official request for PREDICT assistance

Hi,

There is a mention of requesting approval from USAID/W in the report but I haven't seen an explicit request.

However, to save time I approve of Predict assisting with the diagnostic/response effort in Cameroon.

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Sep 16, 2017, at 1:16 AM, Brian Bird <bhbird@ucdavis.edu> wrote:

Hi everyone,

We've had a report of gorilla deaths in Cameroon and the government is requesting assistance with laboratory testing. Please see attached outbreak/health event rapid report and request letter.

We will update as more information becomes available.

-Brian

Brian H. Bird DVM, MSPH, PhD
Global Lead Sierra Leone and
Multi-Country Ebola operations
PREDICT-USAID

One Health Institute
1089 Veterinary Medicine Dr.
School of Veterinary Medicine
University of California, Davis
Email: bhbird@ucdavis.edu
Skype: brianhbird1
http://www.vetmed.ucdavis.edu/ohi/predict/index.cfm

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/312E978D-

3DC9-4515-8A47-E4C32A05CE12%40ucdavis.edu.

From:	Brian Bird <bhbird@ucdavis.edu>
To:	Andrew Clements <aclements@usaid.gov>
CC:	PREDICTMGT <predictmgt@usaid.gov>;PREDICT-outbreak <predict-outbreak@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>
Sent:	9/18/2017 3:40:44 PM
Subject:	Re: Cameroon gorilla die-off Official request for PREDICT assistance

HI Andrew,

My apologies if the PDF got lost amongst the interwebs. I've reattached the PDF of the request here.

-Brian

From: Andrew Clements
Date: Monday, September 18, 2017 at 4:21 AM
To: Brian Bird
Cc: PREDICTMGT , PREDICT-outbreak , Jonna Mazet , David J Wolking
Subject: Re: Cameroon gorilla die-off Official request for PREDICT assistance

Hi,

There is a mention of requesting approval from USAID/W in the report but I haven't seen an explicit request.

However, to save time I approve of Predict assisting with the diagnostic/response effort in Cameroon.

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
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We will update as more information becomes available.

-Brian

Brian H. Bird DVM, MSPH, PhD
Global Lead Sierra Leone and
Multi-Country Ebola operations
PREDICT-USAID

One Health Institute
1089 Veterinary Medicine Dr.
School of Veterinary Medicine

University of California, Davis
Email: bhbird@ucdavis.edu
Skype: brianhbird1
http://www.vetmed.ucdavis.edu/ohi/predict/index.cfm

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/312E978D-3DC9-4515-8A47-E4C32A05CE12%40ucdavis.edu.

Military Health Research Center (CRESAR),
P. O. Box 7039, Yaounde, Cameroon.
Tel : 00237-22229161
Email: nwobegahay@yahoo.com

September 15th, 2017

The Country Coordinator,
METABIOTA/USAID **PREDICT2** Project,
Yaounde, Cameroon.

Subject: **Request for USAID PREDICT2 technical assistance to CRESAR.**

Sir,

I wish to request for technical support from USAID PREDICT2 Project at Metabiota in Cameroon to investigate potential infections which could be associated, following the recent death of a gorilla in South East Cameroon.

CC:
- The Director General Metabiota Cameroon.

Sincerely,

Lt. Colonel Julius Nwobegahay, PhD
Head of the Military Health Research Center,
Yaounde, Cameroon.



From: Cara Chrisman <cchrisman@usaid.gov>
To: Eri Togami <etogami@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Dennis Carroll <dcarroll@usaid.gov>
Sent: 9/21/2017 10:00:24 PM
Subject: Re: PMAC 2018 GVP concept note

Hi Eri,

For when you're back - Dennis just updated that the deadline for these was extended to Oct. 15th. Additionally, since our understanding is that a sponsor is supposed to submit, he would be happy to send it in. We can also ask Sudarat to submit on our behalf.

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Developenent (AID)

Desk: (202) 712-1161
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

On Fri, Sep 1, 2017 at 5:31 PM, Eri Togami <etogami@ucdavis.edu> wrote:

Hi Eddy,

Thank you very much for your comments on the PMAC concept note.

Best,
Eri

Eri Togami DVM MPH

Fellow

One Health Institute

School of Veterinary Medicine

University of California, Davis

From: Eddy Rubin [mailto:erubin@metabiota.com]
Sent: Tuesday, August 29, 2017 12:00 PM
To: Eri Togami <etogami@ucdavis.edu>; Cara Chrisman <cchrisman@usaid.gov>; Dennis Carroll <dcarroll@usaid.gov>; Nathan Wolfe <nwolfe@metabiota.com>; Brooke Watson <watson@ecohealthalliance.org>; Peter Daszak <daszak@ecohealthalliance.org>; Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: PMAC 2018 GVP concept note

Good. A few small suggestions.

I do not think that GVP will better prepare us " to prevent accidental or intentional release of laboratory-enhanced virus variants."

From: Eri Togami <etogami@ucdavis.edu>
Sent: Monday, August 28, 2017 10:21 AM
To: Cara Chrisman; Dennis Carroll; Nathan Wolfe; Eddy Rubin; Brooke Watson; Peter Daszak; Jonna Mazet
Subject: PMAC 2018 GVP concept note

Hi everyone,

Please see a draft of our concept note for the PMAC launch. As per our previous discussions, we can propose one closed session and one open session. Jonna and I would appreciate your comments and suggestions by Wednesday 9/6.

Best wishes,
Eri

Eri Togami DVM MPH

Fellow

One Health Institute

School of Veterinary Medicine

University of California, Davis

From: Eri Togami <etogami@ucdavis.edu>
To: Cara Chrisman <cchrisman@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Dennis Carroll <dcarroll@usaid.gov>
Sent: 9/25/2017 6:03:32 PM
Subject: RE: PMAC 2018 GVP concept note

Hi Cara,

That sounds great, thank you. Would it be better to change the corresponding members to you and Dennis?

I hope you are well,
Eri

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Thursday, September 21, 2017 3:00 PM
To: Eri Togami ; Jonna Mazet ; Dennis Carroll
Subject: Re: PMAC 2018 GVP concept note

Hi Eri,

For when you're back - Dennis just updated that the deadline for these was extended to Oct. 15th.
Additionally, since our understanding is that a sponsor is supposed to submit, he would be happy to send it in.
We can also ask Sudarat to submit on our behalf.

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (AID)

Desk: (202) 712-1161
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

On Fri, Sep 1, 2017 at 5:31 PM, Eri Togami <etogami@ucdavis.edu> wrote:
Hi Eddy,

Thank you very much for your comments on the PMAC concept note.
Best,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Eddy Rubin [mailto:erubin@metabiota.com]
Sent: Tuesday, August 29, 2017 12:00 PM
To: Eri Togami <etogami@ucdavis.edu>; Cara Chrisman <cchrisman@usaid.gov>; Dennis Carroll <dcarroll@usaid.gov>; Nathan Wolfe <nwolfe@metabiota.com>; Brooke Watson <watson@ecohealthalliance.org>;

Peter Daszak <daszak@ecohealthalliance.org>; Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: PMAC 2018 GVP concept note

Good. A few small suggestions.

I do not think that GVP will better prepare us " to prevent accidental or intentional release of laboratory-enhanced virus variants."

From: Eri Togami <etogami@ucdavis.edu>
Sent: Monday, August 28, 2017 10:21 AM
To: Cara Cheisman; Dennis Carroll; Nathan Wolfe; Eddy Rubin; Brooke Watson; Peter Daszak; Jonna Mazet
Subject: PMAC 2018 GVP concept note

Hi everyone,

Please see a draft of our concept note for the PMAC launch. As per our previous discussions, we can propose one closed session and one open session. Jonna and I would appreciate your comments and suggestions by Wednesday 9/6.

Best wishes,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From:	Andrew Clements <aclements@usaid.gov>
To:	Jonna Mazet <jkmazet@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>;Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>
CC:	predictmgt@usaid.gov <predictmgt@usaid.gov>
Sent:	9/28/2017 5:35:12 PM
Subject:	Fwd: Important Information on Events Planned for Senegal

See below.

On Wed, Sep 27, 2017 at 7:56 AM, Cara Chrisman <cchrisman@usaid.gov> wrote:
Hi Team,

For those who didn't receive the message below directly, please see the information regarding meetings/events in Senegal.

Best,
Cara

Sent from my iPhone

Begin forwarded message:

From: Christopher Penders <cpenders@usaid.gov>
Date: September 27, 2017 at 7:12:10 AM EDT
To: Richard Greene <rgreene@usaid.gov>, Dennis Carroll <dcarroll@usaid.gov>, Christina Chappell <cchappell@usaid.gov>, Jeffrey Muschell <jmuschell@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>, Ashna Kibria <akibria@usaid.gov>, Cassandra Louis Duthil <clouisduthil@usaid.gov>, Monica Bautista <mbautista@usaid.gov>, Mackenzie Klein <mklein@usaid.gov>, Andrea Long-Wagar <alongwagar@usaid.gov>, Shana Gillette <sgillette@usaid.gov>, Amanda Paust <apaust@usaid.gov>, Latoya Armstrong <laarmstrong@usaid.gov>
Cc: Elizabeth Lugten <elugten@usaid.gov>, Carmen Tull <ctull@usaid.gov>
Subject: Important Information on Events Planned for Senegal

Dear Richard, Dennis, Jeffrey and Christina (and everyone else!)

Below is a message that we had drafted, initially for AORs and CORs, but really for anyone who might be planning a meeting or event in Senegal.

If you have an activity in Senegal or are considering planning a meeting or event in Senegal, we have some important news to share. There are three important takeaway messages:

1. The Ambassador has the right of first refusal to attend any event planned in Senegal. Therefore, sufficient advance notice must be given to the Mission and effort put in to preparing the required documents.

2. The Mission does not want trainings / workshops / meetings held in the resort cities (hotels) outside of Dakar; these meetings should be held in Dakar, and the Mission has suggestions for venues that are appropriate for use and approved by the RSO. (Please see the attached memo)

3. If you are planning, or even just at the stage of considering, to hold a meeting or event in Senegal, please reach out to the Country Team so that we can help you liaise with the Mission.

There is a substantial amount of additional information below; if it doesn't affect you now, please file this

email away for future reference and/or remember to contact the Country Team for detailed information and don't hesitate to let us know if you have any questions. Kindly share this info with colleagues as appropriate -- many thanks in advance!

Kind regards,
Carmen, Chris and Liz

Additional Information on Meetings, Workshops and Events in Senegal
[Edited from the original email communication]

The Ambassador has put forth the right of first refusal for events. Thus, we need to ensure there is sufficient time to produce and clear the required materials by the deadlines listed below. The information below has been shared with the IPs and Mission staff and this will be presented again to the IPs at an upcoming meeting

EVEN IF you do not have the date fixed or the invitees settled, the document drafting must begin. The information will be needed regardless, so there is no reason to wait until everything is known. Let the process start and drafting begin -- we can finalize specifics closer to the actual event. It is the responsibility of the AOR/COR or POC to hold your IP accountable for following the guidance.

GUIDANCE GIVEN TO THE MISSION AND IPs:

Communications
Good communications is essential for any Mission activity. This requires close coordination between IPs and their USAID counterparts – both AORs and CORs and the Development Outreach and Communications (DOC) Section.

The DOC Section is responsible for coordinating communications and engagement activities across the Mission portfolio. They are the point of contact for Front Office and the US Embassy. They are also responsible for quality control and ensuring branding and marking requirements are met.

Internal and External Communications
IP communications teams should work with the DOC Section to maintain close coordination throughout the life of projects and activities. This should include both ongoing internal communication – regular meetings from the start of the contract, shared planning, etc – and external communication activities, such as events, media work and engagement with key stakeholders, both in Senegal and the US.

Materials
The Mission typically produces several types of standard documents to capture the purpose and objectives of events and present key points. For most events involving the "Front Office" – the USAID Mission Director (MD) or Deputy Mission Director (DMD), or the Embassy Dakar Ambassador, Chargé d'Affaires, or Deputy Chief of Mission (DCM) – an Event Briefing Memo and either Talking Points, Remarks or a Speech will be required. There is sometimes confusion about the different documents and what they are used for. To clarify:

Event Briefing Memo – A brief overview of a proposed event (no more than three pages) providing enough information for the Front Office personnel to make a decision about whether to attend. Event Briefing Memos should always be prepared in English.

Talking Points – A clear, concise list (ca. 200-400 words) of statements or information a speaker should work to convey during her/his engagement, usually with someone outside the Mission. Talking points are not the same as remarks or speeches, which are meant to be read as a script at events. Talking Points can be prepared in either English or French.

Remarks – A short (ca. 200-250 words) prepared statement in script form, including acknowledgement of guests and touching on key points, but without the detail of a longer speech. Remarks can be prepared in either English or French.

Speeches – A longer (ca. 500 words) prepared statement in script form, including acknowledgement of guests, key points with supporting details, examples of actual people, groups, places or activities, and 'calls' for action in particular areas. Speeches can be prepared in either English or French.

Press release – A clear, concise summary (ca. 300-400 words) in standard format, with essential facts and statistics, quotes from USAID and other partners, and contact information. Press releases are usually prepared in French.

Events

Events involving the US Embassy and USAID Front Offices involve careful planning, preparation and execution. This takes time and an organized approach to ensure that the right people are involved at the right time. It also requires clear, consistent, and continuing communication and engagement between the various people and teams involved in the process.

The Mission coordinates many events each month, so it is important to let the DOC Section know as soon as possible to discuss what dates and representatives might be available.

Events involving the USAID/Senegal Front Office

In general, it takes at least two weeks to make the necessary arrangements for an event involving the USAID Front Office.
Below is an outline of the key steps that should be followed when organizing an event:

At least 2 weeks before the event.
AOR/COR or Team DOC approaches DOC Advisor to identify and agree a date for the event.
Technical Team and/or Team DOC and/or IP prepares an Event Briefing Memo in English.
The AOR/COR submits it to DOC Advisor.
DOC Advisor reviews and submits it to MD or DMD for approval.
Once approved, MD or DMD schedules a meeting with DOC Advisor and AOR/COR to identify and agree objectives, messaging and materials needed.
AOR/COR then manages the preparation of the necessary materials.

7 days before the event. All materials are sent to the Technical Team Director for sign-off.
6 days before the event. Technical Team Director passes all materials to the DOC Advisor for sign-off.
5 days before the event. DOC Advisor sign-off on materials and arranges for translation.
4 days before the event. Materials are translated and cleared by PRM.
3 days before the event. DOC Advisor passes speech to the Front Office for review. Comments sent back to the DOC Advisor who liaises with the Technical Team Director for final changes.
2 days before the event. Front Office receives final version of speech.
1 day before the event. Final check of all materials by the DOC Advisor and AOR/COR. Copies prepared for distribution, as needed.

Events involving the US Embassy Front Office

Events involving the US Embassy Front Office involve many of the same steps as events for the USAID/Senegal Front Office, but also require additional time to allow for review and planning by Embassy teams.

Below is an outline of the key steps that should be followed when organizing an event for the US Embassy Front Office:

At least 4 weeks before the event. AOR/COR or Team DOC approaches DOC Advisor to identify and agree a date for the event. Technical Team and/or Team DOC and/or IP prepares an Event Briefing Memo in English. The AOR/COR submits it to the DOC Advisor. DOC Advisor uses the Event Briefing Memo to prepare a Decision Memo and sends it to Embassy Front Office with the PAS Information Officer copied in. Once approved, DOC Advisor schedules a meeting with AOR/COR to identify and agree objectives, messaging and materials needed. AOR/COR then manages the preparation of the necessary materials.

At least 3 weeks before the event. The Speech/Remarks, drafted in English, are sent to the Technical Team Director for sign-off. Once cleared, the Technical Team Director passes them to the DOC Advisor for sign-off. The DOC Advisor then arranges for PRM and Front Office sign-off.

2 weeks before the event. The DOC Advisor sends the cleared Speech/Remarks to the PAS Information Officer who reviews and clears the document and arranges Embassy Front Office sign-off.

1 week before the event. The DCM and the Ambassador sign-off. The Speech/Remarks are then translated into French.

3 days before the event. PAS Information Officer and DOC Advisor confirm preparation of Speech/Remarks.

1 day before the event. Final check of all materials by DOC Advisor and AOR/COR; copies prepared for distribution, as needed.

Event checklist
We've prepared a checklist to help ensure the various components of event preparation are addressed.

--
Christopher Penders, MS, MPH
Africa Regional Team Lead
Global Health Bureau | *Office of Country Support*
USAID|Washington
Phone: +1.571.551.7271
Mobile: +1.571.242.9550
Email: cpenders@usaid.gov

Leading Public Health Development



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From: William B. Karesh <karesh@ecohealthalliance.org>
To: Andrew Clements <aclements@usaid.gov>;David J Wolking <djwolk@gmail.com>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 10/3/2017 3:28:11 PM
Subject: Re: Invitation: SMT call @ Tue Oct 3, 2017 10am - 11am (PDT) (PREDICTMGT)

I'm jumping on the 1:00 train to DC so will be able to connect after we get through the tunnel and pop up in MJ. Probably by 1:10.

BK

From: Andrew Clements <aclements@usaid.gov>
To: David J Wolking <djwolking@ucdavis.edu>
CC: Alisa Pereira Emerging Threats Division <apereira@usaid.gov>;PREDICTMGT <predictmgt@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>;Prof. Jonna Mazet <jkmazet@ucdavis.edu>;klwood@ucdavis.edu <klwood@ucdavis.edu>
Sent: 10/19/2017 8:41:42 AM
Subject: Re: PREDICT FY18 GHSA workplan

Update:

Ghana and Kenya Missions have reported that they do not have any comments on the proposed work plans.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Oct 17, 2017, at 6:09 PM, Andrew Clements <aclements@usaid.gov> wrote:

Hi David,

See attached for feedback from Missions and our ETD team on the Year 4 GHSA work plans submitted by Predict. There is a summary Word document that contains information for all countries; other comments are included in the specific country work plans that are also attached to this email.

Since most/all of the comments are related to small corrections or seeking additional clarification/information, I propose the following course of action:

1. For administrative purposes, I am providing approval for these work plans (in their current form) as part of your overall annual work plan; (I will review the regular budget country work plans in the near future).

2. I am also requesting that you have your in-country or country backstops provide the specific edits and requested detail directly to the Missions so that the staff have a final updated work plan.

Please let me know if you have any questions.

Andrew

On Thu, Sep 14, 2017 at 2:47 PM, David J Wolking <djwolking@ucdavis.edu> wrote:
Hi Andrew and Alisa,

Attached are PREDICT's FY18 GHSA workplan and accompanying narrative. Thanks again for working with us on the continuing budget challenges and for your flexibility with this submission timeline.

Please let us know if you have any questions.

Best,

David

--

Andrew Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
E-mail: aclements@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/epidemic

<2. PREDICT Ethiopia_FY18 GHSA Workplan Gantt chart(9.13.17) YB comments.xlsx>
<2. PREDICT_FY18 GHSA Workplan (9.13.17)_Tanzania EM comment_October 8_2017.xlsx>

From: aclements@usaid.gov
To: jkmazet@ucdavis.edu <jkmazet@ucdavis.edu>;tgoldstein@ucdavis.edu <tgoldstein@ucdavis.edu>;subhash.morzaria@fao.org <subhash.morzaria@fao.org>;vankerkhovem@who.int <vankerkhovem@who.int>;karesh@ecohealthalliance.org <karesh@ecohealthalliance.org>;lparish@usaid.gov <lparish@usaid.gov>;ckjohnson@ucdavis.edu <ckjohnson@ucdavis.edu>;sophie.vondobschuetz@fao.org <sophie.vondobschuetz@fao.org>;ahmed.elidrissi@fao.org <ahmed.elidrissi@fao.org>;lidewij.wiersma@fao.org <lidewij.wiersma@fao.org>;djwolking@ucdavis.edu <djwolking@ucdavis.edu>;apereira@usaid.gov <apereira@usaid.gov>;dcarroll@usaid.gov <dcarroll@usaid.gov>;mirela.hasibra@fao.org <mirela.hasibra@fao.org>;cchrisman@usaid.gov <cchrisman@usaid.gov>;lkramer@usaid.gov <lkramer@usaid.gov>
Sent: 10/19/2017 3:17:13 PM
Subject: Invitation: RE: USAID MERS investments @ Thu Oct 19, 2017 10am - 11am (jkmazet@ucdavis.edu)

RE: USAID MERS investments

more details »

teleconference line: +41 22 79 18643

Thu Oct 19, 2017 10am – 11am

jkmazet@ucdavis.edu

- aclements@usaid.gov
- tgoldstein@ucdavis.edu
- jkmazet@ucdavis.edu
- subhash.morzaria@fao.org
- vankerkhovem@who.int
- karesh@ecohealthalliance.org
- lparish@usaid.gov
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- lidewij.wiersma@fao.org
- djwolking@ucdavis.edu
- apereira@usaid.gov
- dcarroll@usaid.gov
- mirela.Hasibra@fao.org
- cchrisman@usaid.gov
- lkramer@usaid.gov

Yes · **Maybe** · **No** more options »

Google Calendar

Learn More

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Dennis Carroll <DCarroll@usaid.gov>;PREDICTMGT <predictmgt@usaid.gov>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>;Peter Daszak <daszak@ecohealthalliance.org>;Cara Chrisman <cchrisman@usaid.gov>;Eri Togami <etogami@ucdavis.edu>
CC: Brooke Genovese <bgenovese@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>;Kevin J. Olival <olival@ecohealthalliance.org>
Sent: 10/25/2017 7:06:17 PM
Subject: Great Predict & GVP coverage in the Atlantic!

Could have gone horribly wrong, as they were calling for a response to a paper that said don't bother trying to collect data & predict epidemics & pandemics, but it didn't:

https://www.theatlantic.com/science/archive/2017/10/pandemic-prediction-challenge/543954/

Phew & congrats team,
Jonna

From: Brooke Watson <watson@ecohealthalliance.org>
To: Dennis Carroll <dcarroll@usaid.gov>
CC: Eri Togami <etogami@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>
Sent: 11/15/2017 7:13:03 PM
Subject: Re: Request for GVP materials for BCG team before Nov.21 meeting

Hi Dennis,

Thanks for sending this list. I've attached a spreadsheet with 3 tabs for bullet points 1-3: Outreach-to-date, Upcoming Funding Conversations, and Interested Countries. (also available in our shared Google Drive.) I've updated Cara's old tracking document with the information I have, but there are many missing fields, and likely some additional outreach we've done that wasn't in any of my notes. **Eri, if you notice any outreach that I've missed, could you please update the spreadsheet?**

I was traveling during last week's call, so i imagine you discussed bullets 4-6 (and that Jonna and Eri have access to at least #4 and #6.)

We can discuss tomorrow on the weekly call.

Thanks!

Best,

Brooke

On Mon, Nov 13, 2017 at 3:04 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:
Eri and Brooke, as a follow up to the discussion I had with BCG - they have asked for the materials below. Can you pull these together? Some of these can be topics in our next phone call. Let me know if there are ones you dont have

thanks

d

Hello Dennis,

I hope your week has started off well.

I wanted to follow up here to confirm that you will be able to share the below materials, ideally by week's end, so that BCG and our team can get up to speed on everything before next week's meeting.

Please let us know if there's anyway that we can help you here.

Thanks,
Jen

Materials Needed before Nov.21 from GVP technical team of Dennis, EcoHealth Alliance, UC-Davis and/or Metabiota

- Table of investors/funders approached with feedback and current status of these discussions (Arie to provide?)
- Calendar of upcoming meetings with potential GVP investors
- List of countries interested in GVP and how they are interested in engaging
- Draft paper on the PREDICT project

- Published paper on MERS virus and its many variants
- Draft MOU in discussion with the Chan-Zuckerberg BioHub

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Brooke Watson, MSc
Research Scientist

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www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

	A	B	C	D
1	**Institution/Individual**	**Region**	**Contact**	**Type of Org**
2	Beijing Genomics Institute	Beijing	Henry Yang	industry (pharma/tech)
3	Bill & Melinda Gates Foundation	Seattle	Chris Elias	foundation
4	BioHub	SF/Bay Area	Cristina Tato	industry (pharma/tech)
5	Bloomberg Philanthropies	NYC area	missing info	foundation
6	Boston University	Boston/NE	Jerry Keusch	academia
7	Bush/Scowcroft	Dallas	Andrew Natsios	NGO
8	Canada - IDRC	Canada	Dominique Charron	government
9	CDC-Atlanta	Washington DC	Stuart Nichol, John Towner	government
10	CEPI	London	Richard Hatchett	NGO
11	Chan-Zuckerberg	SF/Bay Area	Cori Bargmann	foundation
12	Chatham House	London	David Heymann/David Harper	NGO
13	China Academy of Science/C-CDC*	Beijing	George Gao	government
14	China CAS	Beijing	George Gao	government
15	Columbia University	NYC area	Ian Lipkin, Simon Anthony	academia
16	Costa Rica/Academy of Science	Costa Rica	Roman Macaya Hayes, Pedro Leon	government
17	CSIS	Washington DC	Steve Morris	NGO
18	Dan Janzen UPenn	Costa Rica	NA	academia
19	DARPA	Washington DC	Matt Hepburn	government
20	David Nabarro	NYC area	David Nabarro	influencer
21	Dean Jamison	SF/Bay Area	Dean Jamieson	influencer
22	DFID	London	missing info	government
23	Donald McNeil Jr. (NY Times)	NYC area	Don McNeil	media
24	DTRA	Washington DC	Lance Brooks	government
25	England CMO	London	Sally Davies	government
26	GAVI	Geneva	Seth Berkeley	NGO
27	Georgetown	Washington DC	Sam Habibi	academia

	A	B	C	D
28	Global Virus Network	Washington DC	Bob Gallo	NGO
29	Gordon and Betty Moore Foundation	SF/Bay Area	Harvey Feinberg	foundation
30	Graduate Institute of Geneva	Geneva	Gian Luca Burca	academia
31	Harvard University	Boston/NE		academia
32	Hemsley Charitable Trust	NYC area	Stephanie Cluskey (CEO), Bob Cook	foundation
33	HHS/ASPR	Washington DC	Maria-Julia Marinissen	government
34	Hong Kong University	Hong Kong	Keiji Fukuda	academia
35	ICONIQ	SF/Bay Area	NA	VC
36	Illumina	SF/Bay Area	Christiane Honisch	industry (pharma/tech)
37	Institute Pasteur	Paris	Christine Gilliet	NGO
38	Japan - JICA/MOFA	Japan	missing info	government
39	Johnson & Johnson	NYC area	Alan Tennenberg	industry (pharma/tech)
40	Korea - KDCA	Korea	missing info	government
41	Lancet	London	Richard Horton	media
42	Laurie Garrett	NYC area	Laurie Garrett	influencer
43	London School	London		academia
44	Merck	NYC area	Amy Espeseth	industry (pharma/tech)
45	Merieux Foundation	Paris	Guy	industry (pharma/tech)
46	Michael McCullough (entrepreneur, investor)	SF/Bay Area	Michael McCullough	influencer
47	Microsoft Research	Seattle	Lucas Joppa, Ethan Jackson, Jonathan Carlson	industry (pharma/tech)
48	NAMRU	Washington DC	Fanca Jones	government
49	NIH/NIAID/Fogerty	Washington DC	Tony Fauci, Roger Glass, Mike Kurilla	government
50	No More Epidemics	Boston/NE	Jonathan Quick	NGO
51	Noweigian MOH	Oslo	NA	government

	A	B	C	D
52	NSC	Washington DC	Tim Ziemer	government
53	OIE	Paris	Monique Eloit(CEO)/Billy Karesh	multilateral
54	OSTP	Washington DC	Jean-Paul Chretien	government
55	Paul Allen/Vulcan	Seattle	Richard Reagan	foundation
56	Peggy Hamburg	Washington DC	Kate Bond	government
57	Rockefeller	NYC area	Michael Meyers	foundation
58	Science Philanthropy Alliance	SF/Bay Area	Marc Kastner, Valerie Kohn	foundation
59	Skoll Global Threats	SF/Bay Area	Larry Brilliant/Mark Smolinski	foundation
60	UCSF	SF/Bay Area	Richard Feachem	academia
61	UNESCO	Paris	Dr Casimiro Vizzini	multilateral
62	University of Washington	Seattle	Marguerite Pappaioanou	academia
63	US Embassy in China	Beijing	Miles Toder	government
64	Wellcome Trust	London	Jeremmy Farrar + Mike Turner and Philip Price	NGO
65	Wellcome Sanger	London	Mike Stratton	NGO + industry (pharma/tech)
66	WHO	Geneva	Maria van Kerkhove, Steve Solomon	multilateral
67	Thailand / Mahidol University	Thailand	Prasert Auewarakul	academia
68	GfSAID	SF/Bay Area	Peter Bogner	NGO
69	Yale University	Boston/NE	David Stanton	academia

	E	F	G
1	**Funder Type (if applicable)**	**Date of last contact**	**Core Team Member**
2	in-kind	Oct-17	Eddy, Peter
3	direct	Mar-17	Jonna
4	direct and in-kind	Sep-17	Jonna
5	direct	missing info	Dennis
6	NA	NA	Dennis
7	direct	Oct-17	Dennis
8	direct	Oct-17	Dennis, Eddy, Billy Karesh
9	in-kind	Jan-17	Jonna
10	NA	Oct-17	Dennis/Peter
11	direct and in-kind	NA	Nathan/Dennis
12	NA	Jul-17	Dennis
13	direct and in-kind	Oct-17	Peter
14	in-kind	Oct-17	Peter
15	in-kind	Oct-17	Peter
16	in-kind	Oct-18	Dennis/Cara
17	NA	missing info	missing info
18	in-kind	Nov-17	Nathan, Jonna
19	direct	Nov-17	Dennis
20	NA	NA	Dennis
21	NA	Mar-17	Dennis
22	direct	missing info	missing info
23	NA	NA	Peter
24	direct	missing info	Peter/Dennis
25	direct	Jun-17	Dennis/Peter
26	in-kind	NA	none yet
27	NA	Oct-17	Dennis, Cara

	E	F	G
28	NA	missing info	missing info
29	direct	Aug-17	Dennis
30	NA	Oct-17	Dennis, Cara
31	NA	NA	missing info
32	direct	NA	Dennis
33	direct	Oct-17	Cara/Dennis
34	NA	Sep-17	Peter
35	direct	NA	none yet
36	direct and in-kind	Mar-17	Nathan/Eddy
37			
38	direct	missing info	missing info
39	direct and in-kind	Jul-17	Peter
40	direct	Jul-17	Peter
41	NA	Jul-17	Ron/Dennis
42	NA	NA	Dennis
43	NA	Jul-17	Dennis
44	direct and in-kind	Aug-16	Cara/Dennis
45	direct and in-kind	Aug-17	Jonna
46	NA	Sep-16	Nathan
47	direct and in-kind	Jun-17	Peter
48	direct	missing info	Dennis
49	direct	Oct-17	Peter/Dennis
50	NA	NA	missing info
51	direct	NA	Peter, Dennis

	E	F	G
52	direct	Jul-17	Dennis/Cara
53	direct and in-kind	Oct-17	Peter/Dennis
54	NA	Dec-17	Dennis/Cara
55	direct	Sep-17	Dennis/Cara
56	NA	missing info	
57	direct	Apr-17	Dennis/Peter
58	direct	Jan-17	Jonna/Nathan
59	direct	Sep-17	Jonna
60	NA	Sep-17	Dennis
61	NA	missing info	missing info
62	direct	NA	missing info
63	direct and in-kind	Oct-17	Dennis, Peter, Eddy
64	direct	Jul-17	Dennis/Cara
65	in-kind	Jul-17	Eddy
66	NA	Aug-17	Dennis
67	in-kind	Jun-17	Jonna
68	in-kind	Aug-17	Dennis
69	NA	NA	Cara/Dennis

	H
1	**Comments**
2	Verbally and via email have committed to sequencing 30% of the discovered virome at own cost.
3	Dennis previously meet with Chris Karp and Scott Dowell - seemingly not folks with funding decision-making power. Jonna leading a workshop/panel with Bill Gates in April at NEJM in Boston
4	Very interested, moving forward with MOUs
5	missing info
6	missing info
7	Dennis spoke at an event recently. Interested, but have not had in-depth funding conversations
8	Good interactions at Ontario meeting, want to continue to be involved
9	offered free help around negotiating in country
10	Supportive partner but non-funder. Necessary voice to get buy-in from Gates etc.
11	Either connection through Nathan or Cristina at BioHub
12	Dennis gave talk in July - likely not funders but David Heymann is influential and good to have on our side.
13	Most recent engagement via Eddy at Beijing Genome Conference. Eager, interested, need firm financial commitment.
14	Most recent engagement via Eddy at Beijing Genome Conference. Eager, interested, need firm financial commitment.
15	Ian Lipkin is chair of the Lab Platform working group. Have discussed costs of sequencing, but has not offered to provide any discounted or in-kind sequencing
16	In frequent conversation, likely not bringing any funds.
17	Center for Strategic and International Studies.
18	frequent email interactions, most recent in-person meeting on 10/04/17.
19	Dennis in conversation with Matt Hepburn and setting up additional meetings
20	Gian Luca Burzi (ELSI WG lead) is(was?) David's legal aid.
21	Briefed (along with Larry Summers) on GVP, interested.
22	missing info
23	EHA's contact at the Times. May be useful for press
24	EHA interfaces with DTRA often through other grants. Dennis knows well. Great candidate for GVP funding
25	Dennis and Peter met in July and seemed eager to learn more, recommended several contacts in London. Potential advocate
26	Also have a DC office
27	engaged with the ELSI group via Sam Habibi

	H
28	missing info
29	Have had conversations with Harvey and GVP does not fall within their mandate. However he seems interested and supportive and is a valuable influencer in the field - good to keep on as advisor if possible. Perhaps a potential board member? Also, speaking at PMAC on Plenary 0.
30	engaged with the ELSI group via Gian Luca Burca
31	missing info
32	missing info
33	In contact with MJM
34	Keiji on steering committee. Need to involve the bird flu group on the waterbird work. Not a funder.
35	venture funding arm of Mark Zuckerberg and others. Not yet contacted, but discussed in relation to the Chan-Zuckerberg Initiative
36	Very keen to get involved. Not clear that they've committed to funding (even in-kind support), but very interested in our data.
37	
38	Eri can facilitate communication in Japanese
39	Dennis, Peter and Brooke have call scheduled for 12/06. Interested but uncommitted. Alan is the GHSA rep for J&J
40	Peter gave a talk in July, no direct funding conversations.
41	Non-funder. Offered to publish editorial in time with PMAC launch, but need at least ~6 months for review process.
42	science writer, has written extensively on pandemics / pandemic preparedness.
43	Dennis gave talk in July - likely not funders but David Heymann is influential and good to have on our side.
44	Was not able to attend Beijing. Involved at Bellagio. Little recent followup, no financial commitments.
45	Interested, but don't seem ready to become a funding partner.
46	Was or is on the board of Metabiota. No apparent recent contact
47	Peter and Brooke met over the phone in June. Interesting group but focused in the US and on vector technology not useful to us. Potentially should continue conversations around data platform / data hosting.
48	Naval Medical Research Unit. Dennis gave talk?
49	Mike Kurilla an advocate and on the steering committee.
50	missing info
51	Contacts via Richard Hatchett/CEPI, which is housed in/adjacent to the Norwegian Department of Public Health.

	H
52	Tim Ziemer very interested.
53	Billy on an advisory board. Keen to take on much of the waterbird work. Dennis and Eddy met with a group in Ottowa recently.
54	Spoke to a large mixed group - seemed supportive but pre-Trump administration.
55	Org going through a lot of turmoil. Have been pitched twice, possibly to wrong people (i.e. not Paul). Tabled until there is some consistency.
56	Former FDA administrator, perhaps less relevant now.
57	Peter involved with Rockefeller via the Planetary Health Alliance. Knows of GVP. Alternate contact: Cori Bargmann, suggested by Christine Tato at BioHub.
58	Met in Jan 2017. Pitch was still too broad (asking for ~$ bil, when the SPA is made up of smaller donors. Need a revamped pitch with $300,000-$500,000 sized asks.
59	Jonna working on convincing him to commit to funding GVP in one country, likely Thailand. Interested but has not yet committed.
60	Richard is very supportive but not a funder. Potentially could play a board role.
61	missing info
62	Strongly linked to Gates. No recent outreach that I know of.
63	Most recent engagement via Eddy at Beijing Genome Conference. Eager, interested, working to get GVP on the Trump-Xi meeting agenda.
64	Not the right contact at Wellcome. Need to get to Jeremy. Likely needs a British lead for this to work - Wellcome rarely donates to American NGOs. Much of the funding is controlled in-country.
65	Interested but focused as an organization more on human + bacterial sequencing. Mike a good friend of Eddy's. Trying to figure out how they could get involved - Eddy suggested in-kind sequencing.
66	Maria & Steve on steering committee. Need buy-in, but agree that this shouldn't be housed in the WHO.
67	Prasert has obtained a government grant and is seeking to use it toward GVP-style activities. MOUs in draft process, may be shared with Thailand team
68	head of the GISAID platform for sharing bird flu samples. Provided guidance on the data platform for GVP. Not a funder, but could potentially provide expertise/hosting for data.
69	Eri also has connection

	A	B	C
1	**Institution/Individual**	**Region**	**Contact**
2	Beijing Genomics Institute	Beijing	Henry Yang
3	BioHub	SF/Bay Area	Cristina Tato
4	Canada - IDRC	Canada	Dominique Charron
5	China Academy of Science/C-CDC*	Beijing	George Gao
6	DARPA	Washington DC	Matt Hepburn
7	DFID	London	?
8	DTRA	Washington DC	Lance Brooks
9	Illumina	SF/Bay Area	Christiane Honisch
10	Johnson & Johnson	NYC area	Alan Tennenberg
11	Rockefeller	NYC area	Michael Meyers
12	Science Philanthropy Alliance	SF/Bay Area	Marc Kastner, Valerie Kohn
13	Skoll Global Threats	SF/Bay Area	Larry Brilliant/Mark Smolinski
14	Wellcome Trust	London	Jeremy Farrar + Mike Turner and Philip Price

	D	E
1	**Funder Type (if applicable)**	**Funding ask**
2	in-kind	30-50% of China virome sequenced pro-bono
3	direct and in-kind	?
4	direct	300-500K
5	direct and in-kind	300-500K
6	direct	
7	direct	
8	direct	
9	direct and in-kind	
10	direct and in-kind	$1M?
11	direct	none yet
12	direct	none yet
13	direct	"commit to GVP in one country" - no specific monetary value discussed yet
14	direct	none yet

	F	G
1	**Contact planned**	**Core Team Member**
2	Eddy / Dennis / Peter seeking formal commitment from Henry (date?)	Peter, Eddy, Dennis
3	MOU currently being drafted	Jonna
4	Dennis arranging meetings (date?)	Dennis, Eddy, Billy Karesh
5	Peter seeking formal commitment from George	Peter
6	Dennis in conversation with Matt Hepburn and has set up additional meetings.	Dennis
7	none yet	?
8	none yet	Peter/Dennis
9	none yet	Nathan/Eddy
10	Peter and Dennis have a call with Alan Tennenberg on 12/06/18	Peter
11	none yet	Dennis/Peter
12	none yet	Jonna/Nathan
13	?	Jonna
14	none yet	Dennis/Cara

	H
1	**Comments**
2	Verbally and via email have committed to sequencing 30% of the discovered virome at own cost. No formal commitments or monetary value yet assigned to this.
3	Very interested, moving forward with MOUs regarding the data platform. Unsure if they have funding resources.
4	Very interested in funding the hub. Mentioned that a 300-500K donation would be palatable without all the regulatory hurdles that come with larger sums.
5	Most recent engagement via Eddy at Beijing Genome Conference. Eager, interested, need firm financial commitment.
6	Dennis in conversation with Matt Hepburn and has set up additional meetings.
7	?
8	EHA interfaces with DTRA often through other grants. Dennis knows well. Great candidate for GVP funding
9	Very keen to get involved. Not clear that they're committed to funding (even in-kind support), but very interested in our data.
10	Dennis, Peter and Brooke have call scheduled for 12/06. Interested but uncommitted. Alan is the GHSA rep for J&J
11	Peter involved with Rockefeller via the Planetary Health Alliance. Knows of GVP. Alternate contact: Cori Bargmann, suggested by Christine Tato at BioHub.
12	Met in Jan 2017. Pitch was still too broad (asking for ~3 bil, when the SPA is made up of smaller donors. Need a revamped pitch with $300,000-$500,000 sized asks.
13	Jonna working on convincing him to commit to funding GVP in one country, likely Thailand. Interested but has not yet committed.
14	Not the right contact at Wellcome. Need to get to Jeremy. Likely needs a British lead for this to work - Wellcome rarely donates to American NGOs. Much of the funding is controlled in-country.

	A	B	C	D
1	**Country**	**Contact**	**Level of engagement**	**Type of interest**
2	Australia	DFAT health lead (name?)	Medium	Primarily funder
3	China	George Gao, Henry Yang, Miles Toder @ US Embassy	High	Funder and project site
4	Costa Rica	Roman Macaya Hayes, Pedro Leon	High	Primarily project site
5	UK	Sally Davies, Chief Medical Officer	Medium	Primarily funder
6	Korea	?	Low	Primarily project site
7	Thailand	Prasert Auewarakul, Supaporn Wacharapluesadee	High	Primarily project site
8	Norway	dept. of public health via Richard Hatchett	Medium	Funder and project site

	E	F
1	**Date of last contact**	**Core Team Member**
2	Oct-17	Dennis/Peter
3	Oct-17	Peter
4	Oct-17	Dennis/Cara
5	Jun-17	Dennis/Peter
6	Jul-17	Peter
7	Jun-17	Jonna
8	Jul-17	Peter/Dennis

	G
1	**Comments**
2	Dennis met DFAT health lead recently, who was very enthusiastic and set up additional meetings with DC-based counterparts. Peter has contacts at CSIRO.
3	Lots of enthusiam from US Embassy in China to push this forward. Encouragement also from BGI (Henry Yang) and China CDC/CAS (George Gao). Stated hesitance around a US-based NGO organizational structure.
4	In frequent conversation, likely not bringing any funds.
5	Dennis and Peter CMO in July, who seemed eager to learn more. Jonna has met with the British tech consulate in SF who are also interested.
6	Peter gave an invited talk in July, no funding conversations yet.
7	Prasert has obtained a government grant and is seeking to use it toward GVP-style activities. MOUs in draft process, may be shared with Thailand team
8	Contacts via Richard Hatchett/CEPI, which is housed in/adjacent to the Norwegian Department of Public Health.

From: David J Wolking <djwolking@ucdavis.edu>
To: Andrew Clements <aclements@usaid.gov>;Alisa Pereira Emerging Threats Division <apereira@usaid.gov>;Amalhin Shek <ashek@usaid.gov>;Shana Gillette <sgillette@usaid.gov>
CC: Prof. Jonna Mazet <jkmazet@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>;David M Zachgo <dzachgo@ucdavis.edu>;Matt Blake <mblake@ucdavis.edu>
Sent: 11/21/2017 11:05:29 PM
Subject: Re: PREDICT-2 Q4Y3 Quarterly Financial Report

Andrew,

Please find attached our Q4Y3 country by category financial report. Apologies for the delay.

Please let us know if you have any questions.

David

On Mon, Nov 13, 2017 at 11:54 PM, Andrew Clements <aclements@usaid.gov> wrote:
Thanks, David.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Nov 13, 2017, at 10:27 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Andrew,

Just an update that we are working hard on this country by category financial report. This report will include the Ebola funding report, the CORE funding report, and the combined report that includes both CORE and Ebola funds.

This is my first attempt pulling these figures together and we want to provide accurate information, so I'll do my best to deliver the report as soon as possible.

Best,

David

PREDICT-2 Expenses Quarter 3 Year 3 (04/01/17-06/30/17) - Combined (Core + Ebola)

Cost Category	US Central	Bangladesh	Cambodia	Cameroon	China	Cote d'Ivoire	DRC	Egypt	Ethiopia
Salaries	125,800	41,942	64,778	70,678	42,942	30,554	130,092	20,971	32,294
Fringe	62,469	14,553	17,066	27,307	14,553	24,978	66,686	7,277	25,139
Equipment	0	475	475	475	475	475	475	238	238
Domestic Travel	38,639	2	36,082	5,022	932	3	9,693	1	6,430
Foreign Travel	16,766	16,669	12,067	7,859	7,944	18,231	36,476	2,046	1,936
Services	0	337,757	3,757	25,461	202,948	54,560	21,992	117,862	2,340
Supplies	30,894	320	2,401	0	0	3,955	1,590	0	0
Other	15,595	2,318	109,845	78,866	2,418	12,664	34,092	1,159	4,708
Indirects	132,976	53,444	43,267	92,369	74,465	53,367	128,125	13,042	31,437
Total Costs	**$430,549**	**$267,675**	**$268,748**	**$307,336**	**$345,677**	**$199,790**	**$429,019**	**$162,756**	**$107,518**

Cost Category	Gabon	Ghana	Guinea	India	Indonesia	Jordan	Kenya	Lao PDR	Liberia
Salaries	0	46,167	138,679	41,942	71,544	20,971	47,457	59,243	37,455
Fringe	0	30,826	77,137	14,553	23,819	7,277	21,403	21,004	43,097
Equipment	0	475	31,305	475	475	238	238	475	475
Domestic Travel	0	4,534	80,488	2	2	1	3	4,709	516
Foreign Travel	0	10,982	9,546	11,300	8,286	2,046	6,202	12,488	4,347
Services	0	2,373	12,847	62,834	97,925	118,836	42,219	3,757	179,441
Supplies	0	22,102	82,516	0	168	0	536	10,085	36,433
Other	0	22,102	-536	2,318	2,318	1,159	1,286	5,907	17,679
Indirects	0	64,380	182,003	50,697	47,968	16,224	25,512	49,852	89,629
Total Costs	**$0**	**$224,032**	**$613,984**	**$183,923**	**$253,526**	**$166,781**	**$143,657**	**$167,561**	**$409,543**

Cost Category	Malaysia	Mongolia	Myanmar	Nepal	RoC	Rwanda	Senegal	Sierra Leone	South Sudan
Salaries	42,942	39,570	84,125	68,860	42,572	68,824	64,768	124,055	0
Fringe	14,553	15,146	36,238	20,221	14,899	31,669	38,254	74,358	0
Equipment	475	238	15,475	475	475	475	39,079	475	0
Domestic Travel	2	4,974	2	5,138	2	5,082	2,394	13,824	0
Foreign Travel	4,092	2,674	24,361	23,678	23,798	6,550	10,716	16,451	0
Services	157,217	1,878	28,702	16,606	7,204	9,406	2,907	40,251	0
Supplies	1,258	49,701	7,586	3,400	0	992	43,957	31,055	0
Other	2,318	16,331	2,417	103,268	24,534	22,469	9,681	245,124	0
Indirects	26,519	35,127	42,925	86,400	45,958	35,671	65,643	253,334	0
Total Costs	**$248,347**	**$165,643**	**$230,830**	**$328,025**	**$159,763**	**$181,119**	**$275,568**	**$796,694**	**$0**

Cost Category	Sudan	Tanzania	Thailand	Uganda	Vietnam
Salaries	0	77,732	42,942	54,268	67,879
Fringe	0	49,823	14,553	63,568	27,002
Equipment	0	475	475	475	475
Domestic Travel	0	3,992	2	6,111	1,777
Foreign Travel	0	11,928	8,203	624	8,353
Services	0	2,858	3,757	8,426	3,757
Supplies	0	6,009	0	3,225	1,980
Other	0	30,225	2,318	94,142	6,077
Indirects	0	64,747	27,693	47,921	36,133
Total Costs	**$0**	**$267,639**	**$99,137**	**$280,660**	**$153,524**

$7,874,107 Q3Y3 PREDICT-2 Costs (Combined)

$39,649,692 Balance Remaining

$97,000,000 Obligated to Date

($43.7M Core for YR 1-3 + $53.3M Ebola for YR 2-5)

PREDICT-2 Expenses Quarter 3 Year 3 (04/01/17-06/30/17) - CORE

Cost Category	US Central	Bangladesh	Cambodia	Cameroon	China	Cote d'Ivoire	DRC	Egypt	Ethiopia
Salaries	100,213	41,942	64,778	0	41,942	0	0	20,971	0
Fringe	36,247	14,553	17,066	0	14,553	0	0	7,277	0
Equipment	0	475	475	475	475	475	475	238	238
Domestic Travel	27,765	2	16,082	0	932	0	0	1	0
Foreign Travel	36,166	16,860	32,067	0	7,984	0	0	2,066	0
Services	0	187,757	3,757	0	202,948	0	0	117,982	0
Supplies	27,160	520	2,403	0	0	0	0	0	0
Other	14,629	2,318	109,845	0	2,418	0	0	1,159	0
Indirects	92,994	53,444	43,267	0	74,463	0	0	13,042	0
Total Costs	**$334,970**	**$267,673**	**$289,740**	**$475**	**$345,677**	**$475**	**$475**	**$162,736**	**$238**

Cost Category	Gabon	Ghana	Guinea	India	Indonesia	Jordan	Kenya	Lao PDR	Liberia
Salaries	0	0	0	41,942	72,544	20,971	0	59,263	0
Fringe	0	0	0	14,553	23,819	7,277	0	21,004	0
Equipment	0	475	475	475	475	238	238	475	475
Domestic Travel	0	0	0	2	2	1	0	4,709	0
Foreign Travel	0	0	0	11,300	9,286	2,066	0	12,488	0
Services	0	0	0	62,894	97,925	108,836	0	3,757	0
Supplies	0	0	0	0	168	0	0	10,085	0
Other	0	0	0	2,318	2,318	1,159	0	5,907	0
Indirects	0	0	0	57,697	47,968	16,234	0	49,832	0
Total Costs	**$0**	**$475**	**$475**	**$313,923**	**$253,526**	**$166,781**	**$238**	**$167,561**	**$475**

Cost Category	Malaysia	Mongolia	Myanmar	Nepal	RoC	Rwanda	Senegal	Sierra Leone	South Sudan
Salaries	41,942	59,579	84,125	69,960	42,672	68,824	0	0	0
Fringe	14,553	15,146	36,238	20,221	14,899	31,649	0	0	0
Equipment	475	238	15,675	475	475	475	475	475	0
Domestic Travel	2	4,976	2	5,158	2	5,082	0	0	0
Foreign Travel	4,090	2,674	24,361	23,678	23,798	6,550	0	0	0
Services	157,217	1,878	38,702	16,606	7,204	9,406	0	0	0
Supplies	1,228	49,701	7,586	3,400	0	992	0	0	0
Other	2,318	16,331	2,417	105,748	24,334	22,469	0	0	0
Indirects	26,518	31,327	42,925	86,400	45,958	35,671	0	0	0
Total Costs	**$248,347**	**$165,641**	**$230,830**	**$328,625**	**$159,763**	**$181,119**	**$475**	**$475**	**$0**

Cost Category	Sudan	Tanzania	Thailand	Uganda	Vietnam
Salaries	0	0	41,942	0	67,879
Fringe	0	0	14,553	0	27,002
Equipment	0	475	475	475	475
Domestic Travel	0	0	2	0	1,777
Foreign Travel	0	0	8,201	0	8,353
Services	0	0	3,757	0	3,757
Supplies	0	0	0	0	1,980
Other	0	0	2,318	0	6,077
Indirects	0	0	27,801	0	36,123
Total Costs	**$0**	**$475**	**$99,137**	**$475**	**$153,524**

$3,703,140 Q3Y3 PREDICT-2 Costs (CORE)

$10,079,519 Balance Remaining

$43,700,000 Obligated to Date

($13.6M/YR for YR 1-2 + $16.3M for Y3 + $200K for Jordan)

PREDICT-2 Expenses Quarter 3 Year 3 (04/01/17-06/30/17) - Ebola

Cost Category	US Central	Cameroon	Cote d'Ivoire	DRC	Ethiopia	Ghana	Guinea	Kenya	Liberia
Salaries	23,587	70,678	30,554	130,091	31,284	66,617	138,679	47,457	57,925
Fringe	25,212	27,107	24,978	66,656	29,139	30,826	77,137	21,403	43,097
Equipment	0	0	0	0	0	0	30,830	0	0
Domestic Travel	10,894	5,022	5	9,693	6,430	4,534	80,488	3	516
Foreign Travel	0	7,639	18,231	36,476	1,936	10,982	9,546	6,202	4,347
Services	0	25,461	54,560	21,992	2,340	2,373	11,847	41,219	179,445
Supplies	23,734	0	3,955	1,390	0	22,012	81,516	538	36,431
Other	1,170	78,856	12,664	54,091	4,706	22,022	-536	1,286	17,679
Indirects	39,982	92,269	53,367	128,123	31,437	64,190	181,603	25,312	89,629
Total Costs	**$124,579**	**$307,063**	**$198,315**	**$428,343**	**$107,273**	**$223,556**	**$610,509**	**$143,439**	**$429,068**

Cost Category	Senegal	Sierra Leone	Tanzania	Uganda
Salaries	64,166	124,053	77,732	54,248
Fringe	38,254	74,158	49,823	63,588
Equipment	38,603	0	0	0
Domestic Travel	1,394	11,824	3,892	8,111
Foreign Travel	10,716	16,451	11,928	624
Services	2,907	40,251	2,808	8,426
Supplies	41,927	11,025	6,009	3,225
Other	9,481	245,124	30,225	94,142
Indirects	65,643	253,334	64,747	47,821
Total Costs	**$275,093**	**$796,219**	**$287,164**	**$290,165**

$4,170,967 Q3Y3 PREDICT-2 Costs (Ebola) **$53,300,000 Obligated to Date**

$29,570,174 Balance Remaining

From: David J Wolking <djwolking@ucdavis.edu>
To: Andrew Clements <aclements@usaid.gov>
CC: Amalhin Shek <ashek@usaid.gov>;Shana Gillette <sgillette@usaid.gov>;Prof. Jonna Mazet <jkmazet@ucdavis.edu>;Alisa Pereira <apereira@usaid.gov>
Sent: 11/22/2017 3:09:36 PM
Subject: Re: PREDICT-2 Q4Y3 Quarterly Financial Report

Hi Andrew,

It appears I attached the Y3Q3 report (4/1/2017 to 6/30/17) by mistake, they have almost identical file names. I really am not very good at this job am I?

Attached is the Y3Q4 report, apologies for the confusion.

Best,

David

On Wed, Nov 22, 2017 at 1:54 AM, Andrew Clements <aclements@usaid.gov> wrote:
Hi David,

A follow up on this based on a separate email from Jonna saying that core funds will run out late December/early January.

In the attached table, it shows about 10 million of core remaining at the end of FY17 quarter 3. Using the projected monthly burnrate (1.5 million) from Jonna's email or the quarterly burnrate from your table (3.7 million), the pipeline would appear to be sufficient to go well past the beginning of January. Or am I reading the information incorrectly?

Thanks!

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Nov 22, 2017, at 1:05 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

Andrew,

Please find attached our Q4Y3 country by category financial report. Apologies for the delay.

Please let us know if you have any questions.

David

On Mon, Nov 13, 2017 at 11:54 PM, Andrew Clements <aclements@usaid.gov> wrote:

Thanks, David.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

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This is my first attempt pulling those figures together and we want to provide accurate information, so I'll do my best to deliver the report as soon as possible.

Best,

David

pdf>

PREDICT-2 Expenses Quarter 4 Year 3 (07/01/17-09/30/17) - Combined (Core + Ebola)

Cost Category	DS Central	Bangladesh	Cambodia	Cameroon	China	Cote d'Ivoire	DRC	Egypt	Ethiopia
Salaries	96,960	45,525	69,776	69,227	45,524	58,974	116,377	22,762	79,639
Fringe	42,896	22,081	24,579	33,756	22,081	22,340	42,098	11,040	28,044
Equipment	0	0	0	0	0	0	0	0	21,000
Domestic Travel	55,087	0	29,092	6,569	0	0	8,640	0	36,830
Foreign Travel	5,188	9,348	6,837	36,782	18,658	13,576	7,447	1,490	3,931
Services	0	198,559	2,294	34,450	132,941	30,900	50,059	71,250	5,852
Supplies	55,435	4,013	6,342	9,694	9	0	6,358	0	1,053
Other	14,508	5,996	121,466	44,951	1,996	1,771	26,242	749	30,726
Indirects	224,599	41,743	40,337	87,249	35,668	45,411	91,699	23,926	64,264
Total Costs	**$504,400**	**$327,226**	**$360,921**	**$334,288**	**$256,899**	**$170,672**	**$353,311**	**$131,197**	**$241,344**

Cost Category	Gabon	Ghana	Guinea	India	Indonesia	Jordan	Kenya	Lao PDR	Liberia
Salaries	0	43,446	75,760	45,524	77,002	22,762	62,200	37,004	6,642
Fringe	0	11,695	27,856	22,081	39,055	13,040	20,332	26,381	2,634
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	0	14,722	2,344	0	0	0	1,217	20,399	331
Foreign Travel	0	9,631	10,225	5,447	6,600	14,313	5,315	7,997	47
Services	0	2,145	336	45,757	103,649	232,491	29,670	6,088	299,326
Supplies	0	1,556	623	16,439	0	0	5,160	263	3,961
Other	0	21,372	72,469	1,496	1,542	749	1,271	21,330	47
Indirects	0	42,304	100,819	48,467	32,668	18,030	36,047	49,020	34,472
Total Costs	**$0**	**$146,990**	**$299,132**	**$187,211**	**$270,597**	**$299,384**	**$161,153**	**$168,382**	**$327,220**

Cost Category	Malaysia	Mongolia	Myanmar	Nepal	RoC	Rwanda	Senegal	Sierra Leone	South Sudan
Salaries	45,524	25,639	84,225	71,443	45,524	69,366	100,749	100,253	0
Fringe	22,081	16,803	32,810	29,648	22,081	35,625	54,337	37,352	0
Equipment	0	0	0	17,820	0	0	41,679	0	0
Domestic Travel	0	2,658	658	15,592	2,403	10,233	16,666	30,296	0
Foreign Travel	5,961	1,490	29,493	9,842	12,240	7,466	17,835	25,958	0
Services	212,456	1,117	31,335	9,773	5,460	5,967	5,832	20,678	0
Supplies	332	6,313	20,774	36,541	229	22,805	21,703	1,857	0
Other	1,496	11,348	1,497	242,030	8,196	4,658	59,845	52,356	0
Indirects	28,807	24,279	46,748	71,904	36,763	36,934	79,039	124,326	0
Total Costs	**$316,657**	**$111,683**	**$247,581**	**$477,591**	**$132,095**	**$193,217**	**$397,765**	**$391,856**	**$0**

Cost Category	Sudan	Tanzania	Thailand	Uganda	Vietnam
Salaries	0	139,691	45,524	105,536	79,457
Fringe	0	32,788	22,081	42,554	26,512
Equipment	0	2,743	0	0	0
Domestic Travel	0	32,664	0	3,100	8,146
Foreign Travel	0	8,832	4,964	4,747	3,137
Services	0	68,473	423,345	12,999	88,095
Supplies	0	18,292	20	30,271	7,078
Other	0	39,523	1,496	17,400	42,679
Indirects	0	107,209	27,960	67,603	57,798
Total Costs	**$0**	**$456,415**	**$515,390**	**$284,239**	**$362,902**

$8,169,470 **Q4Y3 PREDICT-2 Costs (Combined)**

$31,480,222 **Balance Remaining**

$97,000,000 Obligated to Date

($43.7M Core for YR 1-3 + $53.3M Ebola for YR 2-5)

PREDICT-2 Expenses Quarter 4 Year 3 (07/01/17-09/30/17) - CORE

Cost Category	US Central	Bangladesh	Cambodia	Cameroon	China	Cote d'Ivoire	DRC	Egypt	Ethiopia
Salaries	68,773	45,525	69,776	0	45,524	0	0	22,762	0
Fringe	29,347	22,081	24,378	0	22,081	0	0	11,060	0
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	37,145	0	19,092	0	0	0	0	0	0
Foreign Travel	5,186	9,348	6,857	0	18,658	0	0	1,490	0
Services	0	198,320	2,244	0	132,941	0	0	71,230	0
Supplies	10,371	4,013	6,342	0	3	0	0	0	0
Other	10,130	5,996	125,946	0	1,996	0	0	749	0
Indirects	73,923	41,743	40,337	0	35,688	0	0	13,926	0
Total Costs	**$235,075**	**$327,226**	**$284,921**	**$0**	**$256,893**	**$0**	**$0**	**$121,197**	**$0**

Cost Category	Gabon	Ghana	Guinea	India	Indonesia	Jordan	Kenya	Lao PDR	Liberia
Salaries	0	0	0	45,524	77,002	22,762	0	37,084	0
Fringe	0	0	0	22,081	39,055	11,040	0	26,383	0
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	0	0	0	0	0	0	0	10,399	0
Foreign Travel	0	0	0	5,447	6,690	14,313	0	7,997	0
Services	0	0	0	45,757	103,640	232,491	0	6,088	0
Supplies	0	0	0	38,439	0	0	0	263	0
Other	0	0	0	1,496	1,542	748	0	11,230	0
Indirects	0	0	0	48,467	52,668	18,030	0	49,020	0
Total Costs	**$0**	**$0**	**$0**	**$187,211**	**$279,597**	**$299,384**	**$0**	**$168,382**	**$0**

Cost Category	Malaysia	Mongolia	Myanmar	Nepal	RoC	Rwanda	Senegal	Sierra Leone	South Sudan
Salaries	45,524	25,659	84,255	73,441	45,524	69,366	0	0	0
Fringe	22,081	36,803	32,810	29,448	22,081	35,823	0	0	0
Equipment	0	0	0	32,870	0	0	0	0	0
Domestic Travel	0	2,658	688	13,382	1,403	18,233	0	0	0
Foreign Travel	5,961	1,490	29,495	9,842	12,240	7,466	0	0	0
Services	212,426	3,222	31,333	9,773	3,660	5,967	0	0	0
Supplies	332	6,313	10,724	36,541	226	22,805	0	0	0
Other	1,496	11,348	1,497	242,030	8,196	4,628	0	0	0
Indirects	28,807	24,270	46,748	71,904	36,765	36,934	0	0	0
Total Costs	**$316,627**	**$111,643**	**$237,351**	**$477,381**	**$132,095**	**$193,217**	**$0**	**$0**	**$0**

Cost Category	Sudan	Tanzania	Thailand	Uganda	Vietnam
Salaries	0	0	45,524	0	79,457
Fringe	0	0	22,081	0	76,512
Equipment	0	0	0	0	0
Domestic Travel	0	0	0	0	9,166
Foreign Travel	0	0	4,968	0	3,337
Services	0	0	413,345	0	68,095
Supplies	0	0	20	0	7,078
Other	0	0	1,496	0	41,679
Indirects	0	0	27,960	0	57,708
Total Costs	**$0**	**$0**	**$515,394**	**$0**	**$362,812**

$4,506,604 **Q4Y3 PREDICT-2 Costs (CORE)**

$5,572,915 **Balance Remaining**

$43,700,000 Obligated to Date

($13.6M/YR for YR 1-2 + $16.3M for Y3 + $200K for Jordan)

PREDICT-2 Expenses Quarter 4 Year 3 (07/01/17-09/30/17) - Ebola

Cost Category	US Central	Cameroon	Cote d'Ivoire	DRC	Ethiopia	Ghana	Guinea	Kenya	Liberia
Salaries	28,195	89,127	58,974	118,377	79,639	43,446	75,760	62,200	6,642
Fringe	13,348	33,756	22,540	42,194	28,044	11,695	27,936	20,331	2,614
Equipment	0	0	0	0	21,000	0	0	0	0
Domestic Travel	17,942	8,309	0	8,840	16,830	14,722	2,144	1,117	111
Foreign Travel	0	16,782	11,576	7,447	3,933	9,651	19,225	5,315	47
Services	0	34,450	30,900	50,059	5,852	2,145	136	28,670	299,326
Supplies	45,084	9,664	0	6,354	1,055	1,554	623	5,181	3,961
Other	4,178	44,951	1,271	26,142	20,726	21,372	72,489	1,271	47
Indirects	50,676	97,249	45,411	93,899	64,264	42,304	100,518	36,047	14,472
Total Costs	**159,423**	**334,288**	**170,672**	**353,311**	**$241,344**	**146,890**	**299,132**	**161,133**	**327,220**

Cost Category	Senegal	Sierra Leone	Tanzania	Uganda
Salaries	100,740	100,233	129,891	105,534
Fringe	34,337	37,152	32,788	42,554
Equipment	41,679	0	2,743	0
Domestic Travel	16,666	30,296	32,664	3,100
Foreign Travel	17,835	23,938	8,832	4,747
Services	5,852	20,678	68,473	12,999
Supplies	21,703	1,857	19,292	30,221
Other	39,845	52,356	39,523	17,400
Indirects	79,109	124,526	102,209	67,685
Total Costs	**357,765**	**391,036**	**436,415**	**284,239**

$3,662,867 Q3Y3 PREDICT-2 Costs (Ebola)

$25,907,307 Balance Remaining

$53,300,000 Obligated to Date

From: Andrew Clements <aclements@usaid.gov>
To: William Karesh <Karesh@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>
Sent: 12/4/2017 10:17:18 AM
Subject: Fwd: International Conference on Emerging Infectious Diseases (ICEID) and IMED

FYI

CDC will host the next International Conference on Emerging Infectious Diseases (ICEID) on **August 26–29, 2018** in Atlanta at the Omni Atlanta Hotel at CNN Center.

Abstracts open **Jan 15 and close March 2, 2018**. Attached is a list of the abstract categories (not posted yet). The website is - https://www.cdc.gov/iceid/index.html

The **International Meeting on Emerging Diseases and Surveillance (IMED) 2018** will take place in **Vienna, Austria on November 9-12, 2018.**

--

Andrew Clements, Ph.D.
Senior Scientific Advisor
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For more information on USAID's Emerging Pandemic Threats program, see http://www.usaid.gov/ept2

1. **Laboratory Diagnostics and Systems**
   - _ Laboratory Capacity for Infectious Disease Surveillance and Outbreak Response
   - _ New Diagnostics, including Culture-independent Diagnostic Tests
   - _ Characterizing Novel and Emerging Pathogens
   - _ Bioinformatics

2. **Improving Infectious Disease Surveillance and Outbreak Response**
   - _ Genomic and Molecular Epidemiology
   - _ New Data Systems/Platforms for Surveillance
   - _ Novel Surveillance Strategies
   - _ Response Systems and Networks
   - _ Global Health Security and the IHR
   - _ Infectious Disease Modeling

3. **Human/Animal/Environmental Factors Affecting Disease Emergence and Control**
   - _ Foodborne Infections
   - _ Waterborne Infections
   - _ Vector-Borne Diseases
   - _ Zoonotic and Animal Diseases—One Health
   - _ Ebola and other Viral Hemorrhagic Fevers
   - _ Tropical Infections and Parasitic Diseases

4. **Healthcare-Associated Infections**
   - _ Tracking and Preventing Healthcare-associated Infections
   - _ Detecting Emerging Threats in Healthcare
   - _ Antimicrobial Use and Resistance
   - _ Blood, Organ, and Other Tissue Safety

5. **Global Health Threats**
   - _ Viral Hepatitis
   - _ Emerging Aspects of HIV
   - _ Sexually Transmitted Diseases
   - _ Tuberculosis
   - _ Malaria

6. **Influenza and Other Respiratory Diseases**
   - _ Novel Influenza Viruses
   - _ Seasonal Influenza
   - _ MERS, RSV, and other Respiratory Infections
   - _ Challenges in Respiratory Disease Control

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7. **Vaccines and Beyond**
   - Challenges for Vaccine-Preventable Diseases
   - New Vaccines
   - New Therapeutics
   - Disease Elimination and Eradication

8. **Policy, Preparedness, and Emergency Response**
   - Policy-level Interventions for Infectious Disease Control
   - Improving Infectious Disease Emergency Preparedness and Response
   - Research and Ethics during Infectious Disease Epidemics
   - Health Communications for Infectious Diseases

9. **Special Populations and Settings**
   - Travelers' Health
   - Immigrant and Refugee Health
   - Perinatally transmitted Infections
   - Health Equity and Infectious Diseases
   - Infectious Diseases in Disaster Settings

10. **Host Factors**
   - Host Genetics
   - The Microbiome
   - Infectious Causes of Chronic Diseases

UCDUSR0001198

From:	Andrew Clements <aclements@usaid.gov>
To:	Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
CC:	predictmgt@usaid.gov <predictmgt@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Lelani Francisco <francisco@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;Tracey Goldstein <tgoldstein@ucdavis.edu>;William B. Karesh <karesh@ecohealthalliance.org>;Megan M Doyle <mmdoyle@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent:	12/23/2017 11:53:28 AM
Subject:	Re: Quarterly surveillance activities summary Dec 2017

(Continued) ...all those who contributed to the assembling of the report.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Dec 23, 2017, at 1:51 PM, Andrew Clements <aclements@usaid.gov> wrote:

Thanks, Chris and all those

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
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On Dec 22, 2017, at 11:15 PM, Christine Kreuder Johnson <ckjohnson@ucdavis.edu> wrote:

Greetings.
Sharing our summary of PREDICT surveillance activities by country. As usual, all counts are based on data in EIDITH to date.
Be sure to let us know if you have any questions.
Looking forward to seeing many of you soon.
Happy Holidays and all the best in 2018!
Chris

Christine Kreuder Johnson, VMD, PhD
Professor of Epidemiology and Ecosystem Health
Senior Biological and Ecological Surveillance Coordinator, Emerging Pandemic Threats PREDICT Project
One Health Institute
VM3B 1089 Veterinary Medicine Drive
One Health Institute
School of Veterinary Medicine
University of California
Davis, California 95618
+1.530.752.1238

From: Sacchetti, Ben <Sacchetti.Ben@bcg.com>
To: Dennis Carroll <dcarroll@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>;Brooke Watson <watson@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>;Jennifer Fluder <jfluder@usaid.gov>;Stroman, Trish <Stroman.Trish@bcg.com>
Sent: 1/18/2018 3:56:00 PM
Subject: RE: Slides for "Open Session"

Thanks, Dennis. Can we discuss this in today's Core Team meeting? We were anticipating that the revised set of pitch materials (which I will send out in about 15 minutes) could be used for the open session, in place of the CUGH slide deck. If that sounds ok, we will of course make sure to incorporate any of the updates you refer to below.

Ben Sacchetti
Principal
THE BOSTON CONSULTING GROUP
Mobile +1 3125763836

From: Dennis Carroll [mailto:dcarroll@usaid.gov]
Sent: Thursday, January 18, 2018 11:51 AM
To: Jonna Mazet ; Peter Daszak ; Eddy Rubin ; Brooke Watson ; Eri Togami ; Sacchetti, Ben ; Jennifer Fluder
Subject: Slides for "Open Session"

All, I have gone back to the CUGH slide deck - made some updates and broke it out with an eye to my giving the opening background; Jonna doing the "Proof of Concept"; Peter doing the "Strategic Underpinnings"; and Eddy doing the Impact - which was pretty much the way we did it before

Any way, first cut - look at it - make any modifications, changes you want.

We'll also need to work with BCG to see if they have inputs..

Note: the file is saved in the Power Point 1997-2003 format. Later versons of PP reject the file as corrupted. Go figure

d

--
Dr. Dennis Carroll
Director, Emerging Threats Program
Bureau for Global Health
U.S. Agency for International Development

Office: 202-712-5009
Mobile: 301-646-6235

From: Andrew Clements <aclements@usaid.gov>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Amalhin Shek <ashek@usaid.gov>;Alisa Pereira <apereira@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 2/1/2018 6:02:07 PM
Subject: Re: PREDICT-2 December 2017 Ebola Financial Report

Thanks

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Feb 1, 2018, at 6:53 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Hi Andrew. Please find attached the December 2017 Ebola Financial Report for PREDICT. Let me know if you have any questions.

Thanks,
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Andrew Clements <aclements@usaid.gov>
To: Katherine Leasure <kaleasure@ucdavis.edu>
CC: PREDICTMGT <predictmgt@usaid.gov>;David J Wolking <djwolking@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Brian Bird <bhbird@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>
Sent: 3/14/2018 4:26:29 PM
Subject: Any upcoming travel planned for Guinea?

If so, let's discuss. Sounds a little dicey in Conakry at the moment.

--

Andrew Clements, Ph.D.
Senior Scientific Advisor
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For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/eid2

From: Andrew Clements <aclements@usaid.gov>
To: Jim Desmond <desmond@ecohealthalliance.org>;Jonathan Epstein <epstein@ecohealthalliance.org>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;William Karesh <Karesh@ecohealthalliance.org> Peter Daszak <daszak@ecohealthalliance.org>
Sent: 4/12/2018 3:13:10 PM
Subject: Fwd: PRO/AH/EDR> Monkeypox - Africa (07): Liberia

FYI

---------- Forwarded message ----------
From: <promed-edr@promedmail.org>
Date: Thu, Apr 12, 2018 at 12:04 AM
Subject: PRO/AH/EDR> Monkeypox - Africa (07): Liberia
To: promed-post@promedmail.org, promed-edr-post@promedmail.org, promed-ahead-post@promedmail.org

MONKEYPOX - AFRICA (07): LIBERIA
****
A ProMED-mail post
<http://www.promedmail.org>
ProMED-mail is a program of the
International Society for Infectious Diseases
<http://www.isid.org>

Date: Wed 11 Apr 2018
Source: Xinhua Net [edited]
<http://www.xinhuanet.com/english/2018-04/11/c_137101492.htm>

Liberian health authorities on Tuesday [10 Apr 2018] issued an alert on the possible outbreak of monkeypox, an infectious disease found mostly in central and western Africa.

Liberia's chief medical officer Francis Kateh said the disease, caused by the monkeypox virus, has already been discovered in the southern county of River Cess.

Kateh said there are currently 4 confirmed cases of the disease. A couple of suspected cases have also been sent for testing.

According to the health official, the time from exposure to the onset of symptoms of monkeypox is around 10 days, while the duration of symptoms is typically from 2-5 weeks.

He said the virus may be spread from handling bushmeat, an animal bite or scratch, body fluids, contaminated objects, or close contact with an infected person.

Monkeypox was 1st identified in 1958 amongst laboratory monkeys. The 1st human cases were discovered in 1970 in the Democratic Republic of Congo.

Fever, itchy toes, headache, muscle pain, and swollen lymph nodes, among others, have been identified as the symptoms of the disease.

The disease is not deadly [West Africa virus clade] and can be cured [partially prevented] through the smallpox vaccine.

Last year [2017], the west African country Nigeria recorded 172 suspected and 61 confirmed cases of monkeypox disease between September and December 2017.

--
Communicated by:
ProMED-mail from HealthMap Alerts
<promed@promedmail.org>

[The above report provides no information about the situation in which these 4 cases became infected, nor any information about the clade the responsible monkeypox virus belongs to.

Monkeypox (MPX) virus infections are not as benign as the above report suggests. As noted in an earlier post (Monkeypox - Africa (04) http://promedmail.org/post/20180327.5712702), monkeypox is a zoonotic orthopoxvirus with a similar disease presentation to smallpox in humans, with the additional distinguishing symptom of lymphadenopathy. After an initial febrile prodrome, a centrifugally distributed maculopapular rash develops, with lesions often present on the palms of the hands and soles of the feet. The infection can last up to 4 weeks, until crusts separate, and a fresh layer of skin is formed. Sequelae include secondary bacterial infections, respiratory distress, bronchopneumonia, gastrointestinal involvement, dehydration, encephalitis, and ocular infections, which can result in permanent corneal scarring. The virus occurs in 2 clades: The West Africa clade, with low to nil mortality, and the Central Africa clade that has a 10-17 percent fatality rate.

The main reservoirs of monkeypox virus are suspected to be rodents, including rope squirrels (_Funisciurus_ spp; an arboreal rodent) and terrestrial rodents in the genera _Cricetomys_ and _Graphiurus_). Halting the bushmeat trade and consumption of wild animals in order to halt MPX virus exposure will be culturally and economically difficult, so continued occurrence of cases can be expected.

Although ProMED-mail has not posted cases of MPX in Liberia before, a recent publication indicates that there have been 4 cases in that country in Grand Gettah in 1970 and 2 cases in Rivercess and Maryland counties in 2017. There have been MPX cases this year (2018) in Nigeria and the Central African Republic.

Reference
Durski KN, McCollum AM, Nakazawa Y, et al. Emergence of Monkeypox -- West and Central Africa, 1970-2017. MMWR Morb Mortal Wkly Rep 2018;67:306-310. DOI: <http://dx.doi.org/10.15585/mmwr.mm6710a5>.

A map showing the location of Liberia in West Africa can be accessed at: <http://healthmap.org/promed/p/54>. - Mod.TY]

[See Also:
Monkeypox - Africa (06): Nigeria
http://promedmail.org/post/20180405.5728330
Monkeypox - Africa (05):Central African Republic (HK)
http://promedmail.org/post/20180403.5726159
Monkeypox - Africa (04) http://promedmail.org/post/20180327.5712702
Monkeypox - Africa (03): Central African Republic (HK) comment
http://promedmail.org/post/20180322.5703720
Monkeypox - Africa (02): Central African Republic (HK)
http://promedmail.org/post/20180321.5700108
Monkeypox - Africa: Nigeria
http://promedmail.org/post/20180120.5572204]
.....sb/mpp/ty/msp/mpp
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For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 5/21/2018 1:11:11 PM
Subject: Re: UPDATE PREDICT DRC EVD outbreak 19 May 2018

Thanks

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On May 20, 2018, at 11:20 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Brief Sunday update in today's form -- more tomorrow.
Best,
Jonna

Jonna AK Mazet, DVM, MPVM, PhD
Professor of Epidemiology & Disease Ecology
Executive Director, One Health Institute
Global Director, PREDICT Project of USAID Emerging Pandemic Threats Program

School of Veterinary Medicine
University of California
1089 Veterinary Medicine Drive
Davis, CA 95616, USA
+1-530-752-3630
onehealthinstitute.net

For scheduling and logistical issues, please contact:
Ms. Brooke Goncveaa
bgoncveaa@ucdavis.edu
+1-530-752-3630

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/CAO5tDrGi3gCW8jm%3D8f9D%3DC9DQ3vesfPARuZ89O5LKXgQ5950g%40mail.gmail.com.

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 6/4/2018 8:50:42 AM
Subject: Re: UPDATE PREDICT DRC EVD outbreak 2 June 2018

Thanks

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jun 3, 2018, at 6:43 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Brief update,
Jonna

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/CAO5tDrFUQ4QKbUZEoG%2BsyHVmU5kuUO45S86m10_T3RbLBkuPhQ%40mail.gmail.com.

From: Jon Epstein <epstein@ecohealthalliance.org>
To: aneeshareacode@gmail.com <aneeshareacode@gmail.com>
CC: Rajesh Bhatia <rajeshbhatia@ecohealthalliance.org>;Predict inbox <predict@ucdavis.edu>;William B. Karesh, D.V.M <karesh@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>
Sent: 6/11/2018 7:31:34 PM
Subject: [predict] Nipah virus inquiry

Dear Aneesh,
I am replying to your inquiry sent to PREDICT regarding the Nipah virus outbreak. I am part of the PREDICT global coordination team, and the technical lead for our work in India. We are, indeed aware of the situation and have been paying attention to the investigation. Federal and local government authorities have been managing the outbreak response and I would encourage you communicate with your local health officers directly with technical questions or concerns. PREDICT India is working in the northern part of the country, but we are happy to provide technical information about Nipah virus as resources allow.

Here is a link to the PREDICT website where you will find more information about the project globally, including in Bangladesh where we have worked with government during Nipah virus outbreaks.

www.vetmed.ucdavis.edu/ohi/predict/index.cfm

WHO and CDC websites also have publicly available information about Nipah virus ecology and epidemiology.

www.who.int/csr/disease/nipah/en/

www.cdc.gov/vhf/nipah/index.html

Lastly, I've attached some papers related to Nipah virus ecology in bats in Malaysia, Bangladesh, and India, which I hope will provide useful information.

We are hopeful that the outbreak is nearly over in Kerala.

Sincerely,

Dr. Jonathan Epstein

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

1.212.380.4467 (direct)
1.917.385.5315 (mobile)

web: ecohealthalliance.org

Twitter:

-

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: predict-request@ucdavis.edu <predict-request@ucdavis.edu> on behalf of aneesh kumar <aneesharesearch@gmail.com>
Sent: Saturday, June 9, 2018 12:10:42 AM
To: predict@ucdavis.edu
Subject: [predict] Nipah Outbreak at Kerala, India

Dear Sir,
I am Assistant Professor at Medical College,Calicut, Kerala, India. I would like to invite your kind attention to the Nipah Disease, out break in our district, which caused 16 deaths out of 18 diagnosed through RT PCR. The source of out break is not yet clear. 12 fruit bats were being examined for Nipah virus in the sorrounding regions and was found negative. In this circumstances, I request your expertise to investigate in to this Nipah outbreak..
Thanking you in anticipation
Aneesh

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

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web: ecohealthalliance.org

Twitter:

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

Convergence of Humans, Bats, Trees, and Culture in Nipah Virus Transmission, Bangladesh

Emily S. Gurley,[1] Sonia T. Hegde,[2] Kamal Hossain, Hossain M.S. Sazzad, M. Jahangir Hossain,[3] Mahmudur Rahman, M.A. Yushuf Sharker,[4] Henrik Salje, M. Saiful Islam, Jonathan H. Epstein, Salah U. Khan, A. Marm Kilpatrick, Peter Daszak, Stephen P. Luby

Preventing emergence of new zoonotic viruses depends on understanding determinants for human risk. Nipah virus (NiV) is a lethal zoonotic pathogen that has spilled over from bats into human populations, with limited person-to-person transmission. We examined ecologic and human behavioral drivers of geographic variation for risk of NiV infection in Bangladesh. We visited 60 villages during 2011–2013 where cases of infection with NiV were identified and 147 control villages. We compared case villages with control villages for most likely drivers for risk of infection, including number of bats, persons, and date palm sap trees, and human date palm sap consumption behavior. Case villages were similar to control villages in many ways, including number of bats, persons, and date palm sap trees, but had a higher proportion of households in which someone drank sap. Reducing human consumption of sap could reduce virus transmission and risk for emergence of a more highly transmissible NiV strain.

Emerging zoonoses pose a substantial threat to human health and well-being (*1*). Some of the most devastating human disease pandemics have been caused by diseases originating in livestock or wildlife, including HIV infection, influenza, bubonic plague, and a large Ebola outbreak in West Africa (*1*,*2*). For this reason, there is considerable scientific and public health interest in predicting which emerging pathogens have the potential to cause pandemics so that these pandemics can be prevented. Emerging lethal zoonotic pathogens that have crossed the species barrier and can be transmitted from 1 person to another, albeit without sustained person-to-person transmission, are particularly concerning because they could evolve to become more highly transmissible and cause large outbreaks or pandemics (*3*). It is therefore critical to focus resources on limiting the opportunity of these pathogens to spillover from wildlife and livestock to infect persons and to better adapt to human hosts.

Effectively preventing cross-species transmission of zoonotic pathogens depends on our ability to determine how transmission occurs, including transmission pathways and determinants of human risk. Efforts to identify and predict risky geographic areas for emerging zoonoses have focused primarily on publicly available data, remote sensing of species habitat, and other large-scale population measures (*4*,*5*). A major limitation of these risk mapping approaches is that they typically rely on crude measures of spatial risk, including presence or absence of species or population densities. Human behavior patterns are rarely taken into account, although the risk for transmission probably involves complex, time-varying interactions between humans and their environment that are often driven by culture, climate, and economic development (*1*,*6*,*7*).

Infection with Nipah virus (NiV), an emerging zoonotic pathogen, can cause encephalitis in humans; the virus can also be transmitted between humans, although somewhat inefficiently (*8*). NiV was first identified as the etiologic agent causing outbreaks in pigs and encephalitis in humans in Malaysia and Singapore during 1998–1999 (*9*). Shortly thereafter, this virus was identified as the cause of outbreaks of human encephalitis in Bangladesh and India

Author affiliations: icddr,b, Dhaka, Bangladesh (E.S. Gurley, S.T. Hegde, K. Hossain, H.M.S. Sazzad, M.J. Hossain, M.A. Yushuf Sharker, M.S. Islam, S.U. Khan, S.P. Luby); Centers for Disease Control and Prevention, Atlanta, Georgia, USA (S.T. Hegde, S.P. Luby); Ministry of Health and Family Welfare, Bangladesh, Dhaka (M. Rahman); Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA (H. Salje); Institut Pasteur, Paris, France (H. Salje); EcoHealth Alliance, New York, New York, USA (J.H. Epstein, P. Daszak); University of Florida, Gainesville, Florida, USA (S.U. Khan); University of California, Santa Cruz, California, USA (A.M. Kilpatrick); Stanford University, Stanford, California, USA (S.P. Luby)

DOI: https://doi.org/10.3201/eid2309.161922

[1]Current affiliation: Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA.

[3]Current affiliation: University of Michigan School of Public Health, Ann Arbor, Michigan, USA.

[4]Current affiliation: Medical Research Council, Banjul, The Gambia.

UCDUSR0001210

during 2001 (*10*,*11*). Nearly every year since 2001, NiV has caused outbreaks among humans in Bangladesh; cases are also reported in bordering areas of India (*12*). Initial spillovers during these outbreaks have been amplified by person-to-person transmission; the largest of these outbreaks involved 66 persons, primarily patients and healthcare workers, in Siliguri, India, in 2001 (*10*). In addition, an outbreak in Faridpur, Bangladesh, in 2004 involved 5 generations of transmission (*13*). Although the case-fatality rate for patients in Malaysia and Singapore was ≈40%, it exceeds 70% in Bangladesh and India (*12*).

The natural reservoir for NiV is Old World fruit bats of the genus *Pteropus*, which are found in eastern Africa and throughout Asia, Australia, and the Pacific islands (*14*,*15*). Antibodies against NiV or NiV-like viruses have been found in pteropid bats throughout Asia, including Malaysia, Thailand, Cambodia, India, and Bangladesh (*16*–*20*). *Pteropus medius* (formerly *P. giganteus*) is the only pteropid bat species present in India and Bangladesh and is the putative reservoir for NiV in this region (*21*). The widespread evidence of henipavirus infection in *Pteropus* bats suggests that this virus may have co-evolved with bats and has probably been present in these areas for as long as the bats have been there. Infected bats shed NiV in their saliva and urine (*22*,*23*), and spillover might occur between humans and bats throughout this region. Types of contact that could result in NiV transmission include hunting bats for human consumption; living nearby and under bat roosts; and sharing food resources, including bats drinking date palm sap and humans consuming fruit partially eaten by bats (*8*,*16*,*24*). Despite this information, the geographic scope and scale of reported cases of infection with NiV remains limited: only Bangladesh regularly reports cases (*25*). Furthermore, even within Bangladesh, there is unexplained substantial spatial heterogeneity in case occurrence; virtually all cases are detected in the central and northwestern parts of the country (Figure 1) (*25*).

The purpose of our study was to identify differences in endogenous risk and risky human behavior across these areas that drive these human disease patterns. Outbreak investigations in Bangladesh showed that a major risk factor for NiV infection was consumption of raw date palm sap, a national delicacy (*12*). Date palm trees (*Phoenix sylvestris*) are tapped overnight to collect the sap in clay pots, and the sweet sap is retrieved from the tree first thing in the morning and drunk raw (*26*). Wildlife studies have shown that date palm sap is commonly consumed by *Pteropus* bats, particularly during winter months when other fruits are not available (*27*). We sought to understand causes of geographic variation in NiV transmission from bats to humans across Bangladesh. We performed a large-scale, case–control study that used villages as study units and quantified the distribution of bats, humans, date palm sap trees, and human behavior that might influence interactions with bats, such as date palm sap harvesting and consumption.

Methods

Data Collection

We conducted a village-level case–control study to identify characteristics associated with NiV transmission from bats to humans in Bangladesh. Case villages were those in which human infections were identified during 2001–2012 with no evidence that the source of infection was another

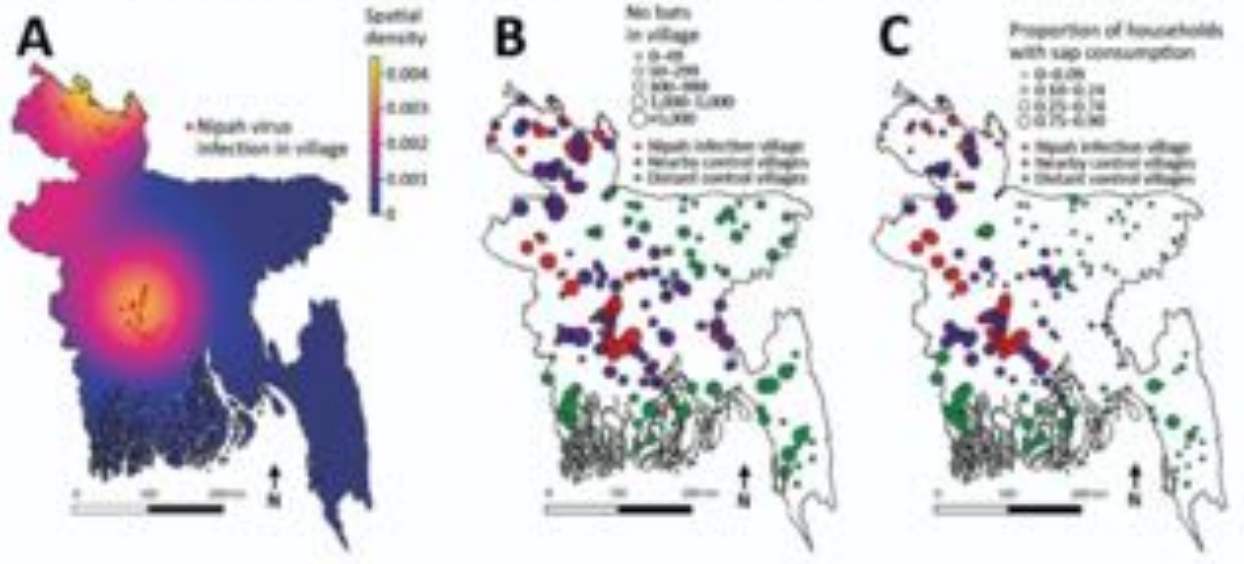

Figure 1. A) Locations of identified bat-to-human transmission of Nipah virus and spatial intensity of transmission events, Bangladesh, 2001–2012. B) Relative sizes of the *Pteropus medius* bat populations in case and control villages (including within 5 km of each village). C) Proportion of households in case and control villages with persons who regularly consume fresh date palm sap.

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human case of infection with NiV and thus was probably caused by spillover from bats. We mapped these case villages and drew 50-km buffers around them to define the area of Bangladesh to which NiV was endemic (Figure 1, panel B). This distance chosen was arbitrary but reasonably represents the distance that a person could travel within a day, even without access to good roads, and is within the typical nightly foraging radius of *Pteropus* bats, which has been observed as 20–50 km (*28*–*30*). We then selected control villages by randomly generating 2 sets of geographic points on a map. The first set was chosen from within the area to which NiV was endemic (nearby controls) but >5 km from a case village. The second set was chosen from points >50 km from case villages (distant controls). We chose control villages near and distant from villages with cases of infection with NiV to determine if characteristics driving transmission were different at varying spatial scales. We sought to enroll 75 controls from nearby villages and 75 controls from distant villages.

Our approach for identifying control villages could have misclassified some villages where cases of infection with NiV have occurred but gone undetected. However, all outbreaks due to NiV have been observed exclusively in the part of the country that includes our case and nearby control villages, despite the fact that surveillance for outbreaks frequently identifies outbreaks of other diseases throughout the country (*31*).

We collected data for study villages at 2 time points: during December 2011–February 2012 and during December 2012–February 2013. These times were chosen to align our surveys with the season that has a high incidence NiV infection in Bangladesh (*12*). Trained data collection teams used hand-held devices to identify the latitude and longitude of the randomly selected points and enrolled the village with that coordinate or the village located closest to that point as a control village. Teams visited case and control villages and identified a group of key village informants who assisted with mapping the village boundary and estimating the number of households located in each village. The teams then asked local residents to identify all of the bat roosts they knew of in their village and within 5 km of the village boundary. Trained data collectors located all of the roosts and counted the number of *Pteropus* bats roosting. In addition, they counted all date palm sap trees in the village and within 500 m of the village boundary.

We then requested that 25 randomly selected households from each village participate in a structured survey. After identifying the village boundary, the field team used a random number table to choose a cardinal direction: north, east, south, or west. The household on the edge of the village in that direction was approached for participation. The team then divided the estimated number of households in the village by the desired sample size (25) and skipped that number of households to choose the next for participation. This process continued until 25 households were enrolled. For villages with <25 households, all households were enrolled. Data collectors administered the structured survey to an adult household member to obtain data for household demographics, date palm sap consumption practices, experience with observing and hunting bats, number of fruiting trees on their household premises, and behavior regarding eating fruit with animal bite marks off the ground.

Data Analysis

To estimate the number of persons in each village, we multiplied the number of estimated households in each village by the mean number of household residents in households sampled for the study from that particular village. We measured data for each village by direct observation, such as the number of bats roosting, or through the surveys at sampled households. We compared case villages to both sets of controls in terms of human and bat population size, as well as human behavior patterns regarding date palm sap and fruit consumption.

We estimated means and proportions with 95% CIs and compared case and control villages by using generalized linear models with binomial distributions and a logit link, which used robust variance estimates to account for model misspecification. For exposures measured at the household level, we accounted for clustering within the village in the model. Analyses were conducted by using the generalized linear model package in Stata version 13.0 (StataCorp LLC, College Station, TX, USA). Variables that were highly skewed were log-transformed to equalize leverage.

We used multivariable logistic regression models to estimate independent associations (odds ratios with 95% CIs) between village characteristics and being a village with a case of NiV infection. For multivariable regression, each village had 1 value for each exposure, and household-level data from each village was aggregated to estimate the proportion of all village households reporting each exposure or behavior. Therefore, we did not need to account for clustering of observations, but we did calculate the 95% CIs for the odds ratios by using robust variance to account for imprecision in exposures estimated from a sample of households. We first built an inclusive model comparing each set of controls to the case villages on the basis of our a priori hypothesis that NiV spillover risk is determined by human population, number of bats present, number of date palm trees, and proportion of persons in the village who commonly consumed raw date palm sap. In addition, any other behavior patterns that were associated with an increased risk for NiV spillover by univariable analysis were also included in the model. Associations were considered statistically significant if p values were <0.05.

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Ethical Considerations

All study participants provided informed consent before participation. The study protocol was reviewed and approved by the institutional review board of the icddr,b.

Results

Data collection teams visited all 60 case villages and 73 nearby control villages and 74 distant control villages where they surveyed 5,024 persons (Figure 1, panel B). Three selected control villages could not be visited because of local security concerns or logistical constraints.

Villages that had cases of infection with NiV were similar to nearby and distant control villages for most characteristics, including human population, bat population, and number of date palm sap trees (Table 1; Figure 2). However, both groups of control villages had a lower proportion of households who reported that ≥1 person commonly drank fresh date palm sap than households in case villages (61% in case villages vs. 49% in nearby control villages and 31% in distant control villages) (Table 1; Figure 1, panel C; Figure 2).

In addition, the average number of household residents who drank ≥1 glass of raw sap when it was in season

Table 1. Characteristics of villages with cases of Nipah virus infection and control villages, Bangladesh 2011–2013*

Characteristic	Villages with cases, n = 60	Nearby control villages, n = 73	p value†	Distant control villages, n = 74	p value‡
Human population					
No. persons in village	1,476 (1,202–1,749)	1,389 (1,102–1,676)	0.20	1,392 (1,010–1,774)	0.10
No. persons/km²	1,168 (1,167–2,169)	1,173 (582–1,754)	0.78	1,335 (456–2,213)	0.95
Pteropus bat population					
Proportion of villages where *P. medius* bats were observed roosting in village or within 5 km of village boundary	0.85 (0.76–0.94)	0.86 (0.78–0.94)	0.86	0.76 (0.66–0.86)	0.19
No. bats roosting in village or within 5 km of village boundary	554 (319–789)	620 (364–875)	0.60	407 (226–587)	0.37
Proportion of respondents reporting large fruit bats					
Roosted nearby during the day in past month	0.25 (0.17–0.34)	0.37 (0.29–0.45)	0.060	0.40 (0.31–0.49)	0.024
Fly overhead at dusk	0.51 (0.43–059)	0.64 (0.56–0.70)	0.019	0.77 (0.71–0.83)	<0.001
Visit fruit trees at night	0.43 (0.35–0.51)	0.52 (0.45–0.60)	0.10	0.53 (0.45–0.61)	0.090
Date palm sap and fruiting trees					
No. trees in village or within 500-m radius of village boundary	120 (88–152)	95 (78–111)	0.91	101 (65–138)	0.14
Proportion of households with fruiting trees on premises	0.97 (0.94–0.99)	0.97 (0.94–0.98)	0.61	0.94 (0.92–0.96)	0.14
No. fruiting trees on each household premise	56 (46–68)	52 (43–61)	0.61	108 (45–170)	0.47
Human behavior					
Proportion of villages with ≥1 date palm sap collector	0.60 (0.47–0.63)	0.40 (0.29–0.52)	0.026	0.51 (0.40–0.63)	0.32
No. sap collectors in villages	4.5 (1.8–7.3)	2.3 (1.0–3.6)	0.41	3.7 (1.9–5.6)	0.54
Proportion of villages with ≥1 fresh date palm sap seller	0.38 (0.28–0.51)	0.32 (0.21–0.43)	0.45	0.39 (0.26–0.51)	0.92
No. (%) fresh sap sellers in villages	1.9 (0.6)	0.9 (0.2)	0.16	2.4 (0.6)	0.47
Proportion of households where ≥1 person drank raw sap	0.61 (0.54–0.68)	0.49 (0.42–0.56)	0.014	0.31 (0.24–0.39)	<0.001
Proportion of households where someone drank raw sap >1×/wk during the past harvest season	0.35 (0.27–0.43)	0.29 (0.23–0.35)	0.26	0.21 (0.16–0.27)	0.005
No. household residents who drank ≥1 glass of raw date palm sap when in season	3.3 (2.7–3.9)	2.1 (1.8–2.5)	0.001	1.5 (1.1–1.9)	<0.001
Proportion of villages where >1 household fed raw date palm sap to livestock	0.16 (0.10–0.21)	0.12 (0.06–0.18)	0.66	0.14 (0.08–0.21)	0.78
Proportion of villages where ≥1 person hunted bats	0.53 (0.40–0.66)	0.64 (0.53–0.75)	0.22	0.27 (0.17–0.38)	0.002
Proportion of households that reported residents ate bitten fruits dropped on the ground	0.42 (0.37–0.48)	0.58 (0.53–0.62)	<0.001	0.66 (0.61–0.71)	<0.001

*Values are mean (95% CI) except as indicated.
†Comparison of villages with cases of Nipah virus infections with nearby control villages by using generalized linear models that account for correlations within villages for characteristics measured in household surveys.
‡Comparison of villages with cases of Nipah virus infections with distant control villages by using generalized linear models that account for correlations within villages for characteristics measured in household surveys.

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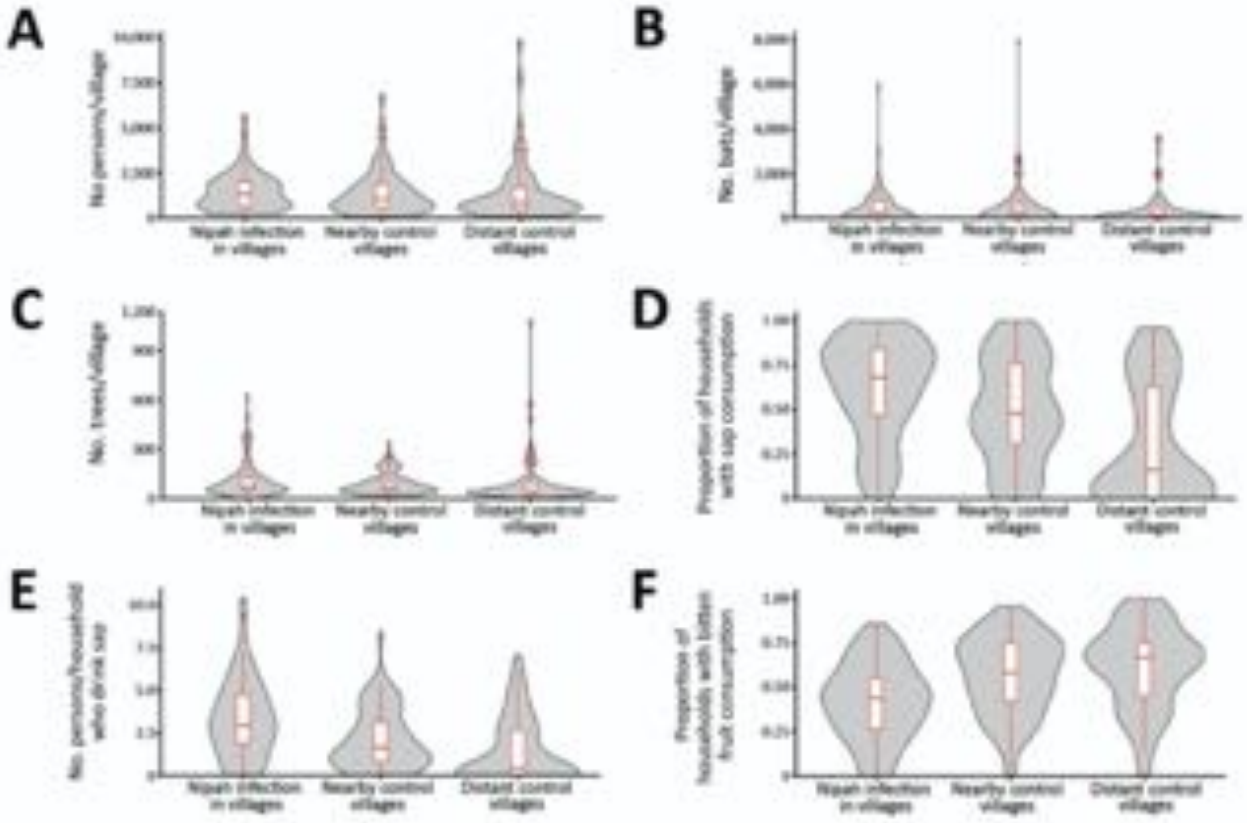

Figure 2. Comparisons of villages with Nipah virus infections with nearby and distant control villages, Bangladesh, 2011–2013. A) Human population size, B) *Pteropus medius* bat population size, C) no. date palm trees, D) proportion of households with members who consume fresh date palm sap, E) average no. of persons per household who consume fresh date palm sap, and F) proportion of households that reported their residents eat bitten fruits dropped on the ground. Gray shading in violin plots indicates distribution of values for each variable. Box plots indicate 25th and 75th percentiles (bottom and top lines), medians (horizontal lines within boxes), and 95 CIs (whiskers). Red dots indicate maximum (outlier) values.

was higher in case villages (3.3 glasses) than in nearby control villages (2.1 glasses) and distant control villages (1.5 glasses) (Table 1; Figure 2, panel E). A larger proportion of villages that had cases of infection with NiV had ≥1 bat hunter than distant control villages (53% vs. 27%; p = 0.002) (Table 1). Households in nearby and distant control villages were more likely to report that someone in the house ate fruits bitten by animals off the ground and saw bats roosting nearby during the day and flying overhead at dusk than were households in villages with cases of infection with NiV (Table 1).

Multivariable analyses showed that, compared with nearby control villages, each additional 10% increase in the proportion of households reporting that someone regularly consumed raw sap was associated with a 6.39 (95% CI 1.61–25.40) increase in odds of being a village with cases of NiV infection (Table 2). Compared with distant control villages, the odds of being a village with cases of NiV infection were 1.18 (95% CI 1.02–1.37) times higher for each order of magnitude increase in bat populations and 26.97 (95% CI 5.98–121.67) times higher for each 10% increase in households that reported someone who regularly consumed sap.

Discussion

NiV is a highly fatal pathogen and poses a risk for pandemic spread because it can be transmitted from person-to-person. To reduce opportunities for a more transmissible strain to emerge, which could lead to regional outbreaks or a pandemic, we must prevent spillover from bats to humans. Bangladesh is the only place where spillover events are predictably identified each year. Therefore, preventing bat-to-human transmission of NiV in rural Bangladesh should be a global public health priority.

Our study reported 2 key findings to achieve this priority. First, our data suggest that human infection, and as a result, selective pressure to adapt to humans (*3*), is determined by the joint probability of a human consuming raw sap in rural Bangladesh and of sap being contaminated by the urine or saliva of a bat that is shedding the virus

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Table 2. Odds ratios from logistic regression models estimating associations between village characteristics and Nipah virus spillovers, Bangladesh, 2011–2013*

Characteristic	OR (95% CI) for villages with NiV infections vs. nearby control villages	p value	OR (95% CI) for villages with NiV infections vs. distant control villages	p value
Per each order of magnitude increase in no. persons in village	1.36 (0.90–2.07)	0.14	1.57 (0.90–2.8)	0.12
Per each order of magnitude increase in no. bats ≤5 km from village	1.00 (0.86–1.16)	0.97	1.18 (1.02–1.37)	0.029
Per each order of magnitude increase in no. date palm sap trees ≤5 km from village	0.75 (0.49–1.12)	0.16	.69 (0.45–1.04)	0.078
Per each 10% increase in households reporting that someone consumed raw date palm sap during the harvest season	6.39 (1.61–25.40)	0.008	26.97 (5.98–121.67)	<0.001
Per each 1% increase in villages reporting that someone hunts bats	NA	NA	1.80 (0.80–4.06)	0.16

*ORs were calculated by using robust variance. NA, not applicable; NiV, Nipah virus; OR, odds ratio.

(*22*,*32*). Bangladesh has a population of 160 million persons, and according to a United Nations report (http://esa.un.org/unpd/wup/Country-Profiles/), 70% of Bangladeshi residents in 2015 lived in rural areas where date palm sap is collected. We found that ≥30% of rural households have ≥1 regular date palm sap drinker, which implies that there are millions of persons drinking fresh sap each year. The reservoir for NiV (the *P. medius* bats) is nearly ubiquitous across the landscape (Figure 1, panel B), and previous studies show that bat visits to date palm sap trees are common (*27*), which suggests that much of the fresh date palm sap consumed is probably contaminated with bat saliva or excreta. Despite this finding, human infections with NiV are rare, which suggests that shedding of transmissible virus by bats is also rare during the date palm sap harvesting season or occurs too infrequently to cause human infection.

Date palm sap consumption was common in control villages, although less common than in case villages. These findings suggest that we need not eliminate date palm sap consumption to reduce NiV spillovers. Date palm sap is deeply rooted in Bengali culture (*32*), and because the risk associated with consumption at the individual level is low, eliminating this practice could be difficult. However, even if we are unable to eliminate sap consumption, modest reductions in consumption of contaminated date palm sap could meaningfully reduce incidence rates for infection with NiV. Case villages were also more likely to have more bats roosting nearby than distant control villages but not nearby control villages. This finding suggests that although large increases in bat population sizes could increase risk for spillover, odds ratios indicate that human behavior patterns are a greater risk for driving NiV transmission than bat population size. Extermination of bats would not be an appropriate approach to mitigating the risk for NiV infection because of the major ecologic role of *P. medius* bats in tree pollination and seed dispersal. Public health messages during outbreaks stress the need for bats in the local ecology, but greater efforts to preserve bat habitat during outbreaks should be considered.

Second, our data suggest that we should target interventions to communities that consume large amounts of raw sap. We identified that consumption of date palm sap was common in many areas across Bangladesh, even in areas where no cases of infection with NiV have been detected. The ability to target resources is key when funding for public health prevention is limited. Our data suggest that areas with high consumption of raw sap should be targeted for enhanced surveillance to track changes in NiV epidemiology and quickly respond to outbreaks and for interventions to interrupt transmission through consumption of contaminated sap. Interventions to reduce human consumption of contaminated sap have been developed and include efforts to reduce fresh sap consumption in general and using physical barriers to keep bats from accessing and contaminating sap (*32*–*36*). However, sustained changes in behavior patterns regarding consumption of date palm sap will probably require long-term efforts to promote these interventions because this consumption is ingrained in local culture, and there is evidence that knowledge per se about risk for infection with NiV is not associated with behavior patterns regarding date palm sap consumption in areas to which NiV is endemic (*32*,*36*).

Residents of nearby and distant control villages were more likely to report seeing bats roosting nearby during the day. One possible explanation for this finding could be an association between experiencing an outbreak of infection with NiV and destruction of bat habitat. Local investigation teams have observed that residents in villages in which outbreaks have occurred often cut down trees in which bats roost within the village after the outbreak. Residents of nearby and distant control villages were also more likely than residents of case villages to report eating animal-bitten fruits off the ground. Investigations of the first outbreak of infections with NiV in Malaysia suggested that the most probable pathway of transmission from bats to pigs was through consumption of bat-bitten fruits (*37*). However, there is no evidence that this transmission route plays a major role in human infections in Bangladesh, despite more than a decade of investigation

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(*38*), and this study provides further evidence that this factor is not a major contributor to human infection in this setting, given the strong association between human date palm sap consumption and being a village with cases of NiV infection. No outbreaks of infection with NiV have been linked with bat hunting, but Old World fruit bats are hypothesized to be reservoir hosts for several major zoonotic pathogens, including Marburg virus and Ebola virus (*39*,*40*). In addition to NiV, our group reported evidence of 55 novel viruses in *P. medius* bats (*41*), and evidence for human exposure to these or other bathorne pathogens through this type of bat contact should be explored. Efforts to reduce bat hunting would be beneficial for conservation of these species and reduction of disease risk.

Our study objective was to identify the major drivers of spatial patterns of NiV spillovers across Bangladesh by drawing upon evidence we have about individual risk factors for NiV infection. There might be other rare drivers of risk that were not detected because of limited statistical power. However, these drivers would have a smaller role in explaining disease risk than those identified in this study. *P. medius* bats are found throughout Bangladesh (*42*) but spillover of NiV to humans could be driven by spatial or temporal variation in NiV incidence in bats. More evidence about this possible contributor to spatial heterogeneity would improve our understanding of risk.

Our study provides an example of how epidemiologic studies can be used to describe the ecologic drivers of zoonotic disease emergence. The risk for cross-species transmission is complex and depends on the presence of reservoir hosts and permissive contact patterns with humans, as well as the frequency of these interactions. Future studies to explain spatial risk for similar emerging zoonotic infections should incorporate data on all aspects of the transmission, including human behavior patterns.

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At the time of this study, Dr. Gurley was an epidemiologist at the icddr,b, Dhaka, Bangladesh. She is currently an associate scientist in the Department of Epidemiology, John Hopkins University School of Public Health, Baltimore, MD. Her primary research interests are Nipah virus, infectious diseases, and disease transmission.

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Pteropid Bats are Confirmed as the Reservoir Hosts of Henipaviruses: A Comprehensive Experimental Study of Virus Transmission

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Abstract. Bats of the genus *Pteropus* have been identified as the reservoir hosts for the henipaviruses Hendra virus (HeV) and Nipah virus (NiV). The aim of these studies was to assess likely mechanisms for henipaviruses transmission from bats. In a series of experiments, *Pteropus* bats from Malaysia and Australia were inoculated with NiV and HeV, respectively, by natural routes of infection. Despite an intensive sampling strategy, no NiV was recovered from the Malaysian bats and HeV was reisolated from only one Australian bat; no disease was seen. These experiments suggest that opportunities for henipavirus transmission may be limited; therefore, the probability of a spillover event is low. For spillover to occur, a range of conditions and events must coincide. An alternate assessment framework is required if we are to fully understand how this reservoir host maintains and transmits not only these but all viruses with which it has been associated.

INTRODUCTION

Hendra virus (HeV) and Nipah virus (NiV) are zoonotic viruses responsible for outbreaks of respiratory and neurological disease in livestock and humans. Both belong to the genus *Henipavirus*, subfamily *Paramyxovirinae* family *Paramyxoviridae*, and order *Mononegavirales*.

Originally isolated from humans and domestic animals, pteropid bats have been identified as the reservoir for both viruses. HeV antibody was first identified in the serum of *Pteropus* sp. bats in 1996 followed by the isolation from a grey-headed flying fox, *Pteropus poliocephalus* and a black flying-fox, Pteropus alecto.[1,2] Subsequently, both *Pteropus* spp. occurring in Malaysia were found seropositive for NiV neutralizing antibodies, and the virus has been isolated from *Pteropus hypomelanus* and *Pteropus vampyrus*.[3–5]

HeV was initially isolated from the uterine fluid of a *P. poliocephalus* female that had miscarried and from fatal tissues.[2] NiV has been isolated from pools of voided urine of *P. hypomelanus* collected by Chua and others[4] from under roosting bat colonies, from urine *of Pteropus lylei* in Cambodia, using similar techniques, and from the urine of a wild-caught *P. vampyrus* in peninsular Malaysia.[3,6]

In this study, we attempted to identify the routes of transmission between bats and their spillover hosts by using geographically appropriate henipaviruses and hosts. Specifically, we aim to determine routes of virus excretion in bats and whether their gender or pregnancy status influenced the amount and route of excreted virus. This work outlines the experimental studies and the detailed findings.

MATERIALS AND METHODS

Animals. Twenty wild-caught adult *Pteropus alecto* bats from Queensland, Australia (12 pregnant females [Bats 1–12], five non-pregnant females [Bats 13–17], and three males [Bats 18–20]) and eight wild-caught adult *P. vampyrus* bats from Malaysia (four non-pregnant females [Bats 21–24] and four males [Bats 25–28]) were used in these experiments. *Pteropus alecto* was chosen because its distribution overlaps the locations where HeV outbreaks have occurred and it is the most abundant species of flying fox in *Australia*. *Pteropus vampyrus* was chosen because its distribution overlaps the putative location of the NiV spillover in Malaysia, which led to the 1998–9 outbreak.

Australian bats were kept in captivity in Queensland (3 weeks) before shipment to the Commonwealth Scientific and Industrial Research Organization (CSIRO) Australian Animal Health Laboratory (AAHL). The Malaysian bats were kept at Taiping Zoo (3 months) before export to *Australia*. All animals were seronegative to henipavirus infection on the basis of virus neutralization tests (VNTs) at the time of capture and for the period before the experiment. Animal husbandry methods and experimental design were endorsed by the CSIRO AAHL's Animal Ethics Committee (protocol no. 1023). For the duration of the study, bats were housed in a single room at Biosafety level 4 (BSL-4). Room temperature was maintained at 22°C with 15 air changes/hour. Humidity varied between 40% and 60%. Bats were housed individually in *squeeze* bottom cages (750 mm wide by 570 mm *deep* and 600 mm high). They were fed a variety of fresh fruit and provided with water ad lib. Bat weights were recorded before the start and periodically throughout the study.

Before experimentation, animals were immobilized with a mixture of ketamine HCl (5 mg/kg) (Ketamil; Ilium, Glendenning, Australia) and medetomidine (50 μg/kg) (Domitor; Novartis, Pendle Hill, Australia) by intramuscular injection. For reversal, *atipamezole* (Antisedan; Novartis) was given intramuscularly at 50% of the dose used for medetomidine. At termination of the study, bats were immobilized as above, with euthanasia by cardiac exsanguination. Serology, virus isolation, and the initial stages of RNA extraction were also carried out at BSL-4; staff wore fully encapsulated suits with breathing apparatus.

Viral inoculum. HeV used to infect Australian bats was originally isolated from *P. poliocephalus*.[2] *P. alecto* bats were infected with Vero cells (passage #6) cell culture supernatant (1.5×10^7 $TCID_{50}$/mL). Because of the unavailability of a bat

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nolate for NiV, the virus used to infect the Malaysian bats was originally isolated from the central nervous system of persons with fatal NiV encephalitis during the 1999 outbreak in Malaysia. A stock of low passage virus was grown in Vero cells and used to infect *P. vampyrus* individuals. The cell culture supernatant had a titer of 5×10^7 $TCID_{50}$/mL.

Experimental infections. The study was conducted in three parts: Part 1, 12 pregnant *P. alecto*; Part 2, 8 *P. alecto*; and Part 3, 8 *P. vampyrus*. The *P. alecto* were exposed oronasally as described previously with 50×10^7 $TCID_{50}$ HeV. The *P. vampyrus* were exposed by dripping 1 mL of inoculum (50×10^7 $TCID_{50}$ NiV) into the nostrils and throat and then rechallenged on Day 28 with the same virus inoculum by the same route. Clinical signs were assessed daily. In Part 1 and 2, animals were sampled, and rectal temperatures recorded every second day for 19 days. In Part 3, animals were sampled every second day for 21 days, and every second day from Days 30 to 42. Blood, urine, throat, and rectal swabs were collected at each sampling. Urine was collected by gentle manual compression of the bladder. Blood was collected from either the marginal wing vein or the uropatagial vein using a 25 gauge needle and 3 ml syringe. Swabs were placed immediately into 1 mL of viral transport medium (phosphate buffered saline [PBS] containing 100 U Penicillin, 100 μg/mL Streptomycin, and 500 μg/mL Fungizone). All specimens were stored at −80°C. Blood for serology was collected from Australian bats on either Day 10 or 11 and at postmortem, and from Malaysian bats on Days 14, 21, 28, 35, 42, and at postmortem.

The Australian bats were euthanized on Day 20, 21, or 22 and a wide range of tissues were collected for analysis. The Malaysian bats were rechallenged on Day 28, and the experiment terminated on Day 49, 50, or 51 when a wide range of tissues were collected at postmortem.

Samples were analyzed for the presence of henipavirus genome by TaqMan analysis. Virus isolation was only attempted on samples that were positive by TaqMan analysis. Seroconversion was assessed by virus neutralization. Tissues were also preserved in formalin and prepared for immunohistochemical staining and histopathological analysis.

Serology. A VNT was used, with either 100 $TCID_{50}$ NiV or 100 $TCID_{50}$ HeV and Vero cells as previously described.[7] Serum neutralizing titers were recorded as the reciprocal of the serum dilution. Positive and negative controls and a back-titration of the virus were included in each test. Serum samples with a titer of 1/10 and above were assessed to be positive. Serology was carried out at BSL-4. At the time of these experiments other assays including Bioplex assays were not available.

HeV and NiV genome Taqman polymerase chain reaction assays. Samples collected during the study and tissues collected aseptically at postmortem were assayed for the detection of henipavirus genome by TaqMan assay as previously described.[7,9]

Primers and TaqMan probe to detect HeV genome and NiV genome were designed from the N gene sequence of HeV (Genbank accession no. AF017149) and NiV (Genbank accession no. AF212302), respectively, using specified criteria in the Primer Express Software version 1.5 (Applied Biosystems, Foster City, CA). The specific HeV oligonucleotide primers were: Hendra-N1433F 5′-atc tca gat cca gat tag ctg caa-3′ and Hendra-N1572R 5′-atc att tig ggc agg ttt gg-3′. The fluorogenic 5′ nuclease (TaqMan) probe was Hendra 1642comp 5′-[6-carboxy-fluorescein (FAM)]-cct ggt cat ctt tcc ttc ct-3′-[MGBNFQ]. The specific NiV oligonucleotide primers were: Nipah-N1198F 5′-tcagcaggaaggcaagagtgtaa-3′ and Nipah-N1297R 5′-ccccttcatgatatcttgatcc-3′. The fluorogenic 5′ nuclease (TaqMan) probe was Nipah1247comp5′-[6-carboxy-fluorescein (FAM)]-tgctggtaccagacttgcctc-3′-[6-carboxy-tetramethyl rhodamine (TAMRA)].

Assays were performed using a two-step protocol consisting of an initial reverse transcription (RT) reaction followed by complementary DNA (cDNA) amplification. The appropriate virus inoculum was used as the positive control in the TaqMan assays. All TaqMan reagents were purchased from Applied Biosystems except primers, which were manufactured by Geneworks (Hindmarsh, Australia). RNA was reverse transcribed using the TaqMan Gold RT-polymerase chain reaction (PCR) kit (Applied Biosystems). RNA (3.5 μL) diluted to 500 μg/3.5 μL (tissue samples) or undiluted (swabs, urine, and blood) was added to 6.5 μL of a reaction mix containing 1× TaqMan RT buffer, 5.5 mM magnesium chloride, 2 mM deoxyNTP mixture, 2.5 μM random hexamers, 0.4 U/μL RNase inhibitor, and 1.25 U/μL MultiScribe reverse transcriptase. The samples were reversed transcribed in a Px2 thermal cycler (Hybaid; Thermo Scientific, Wilmington, MA) at 22°C for 15 min, 48°C for 30 min, and 95°C for 5 min. The cDNA (5 μL) was added to 20 μL of PCR reaction mix in each well of a MicroAmp (Applied Biosystems) optical reaction plate containing 12.5 μL of Taqman Universal PCR mastermix, 3.35 μL distilled water, 1.25 μL each of 18 μM forward and reverse primers, and 1.25 μL of 5 μM labeled probe.

The samples were tested in duplicate and amplified in a GeneAmp 7700 Sequence Detection System (Applied Biosystems) using the following program: 50°C for 2 min, 1 cycle; 95°C for 10 min, 1 cycle; 50 cycles at 95°C for 15 s, 60°C for 60 s. Primer and probe optimization experiments were done as recommended in the AB7700 Sequence Detection System protocol. A dilution series was made of each primer and probe set to determine the optimum concentrations (data not shown). Samples were positive if the cycle threshold (C_T) value was < 45 cycles. If a sample tested positive it was then retested in triplicate along with a random selection of negative samples that were also tested in triplicate. The average retested C_T value was recorded. Where only one or two wells in the triplicate testing registered a C_T value < 45, an indeterminate result was recorded.

Virus isolation. Samples that tested positive or indeterminate for henipavirus genome by TaqMan assay were then processed for virus isolation in Vero cells. A 10% w/v homogenate of tissue samples was prepared. Blood was diluted 1 in 10 with PBS, and the fluids from swabs and urine were tested neat, as previously described.[9]

Histopathologic and immunohistochemical methods. Submandibular lymph node, submandibular salivary gland, adrenal gland, tonsil, lung, kidney, bladder, spleen, heart, forebrain, hindbrain, liver, pancreas, mesenteric lymph node, ileum, genital and gonadal tissues (placenta, ovary, uterus, vagina, testis, penis), and bone marrow (hyoid and laryngeal bones) were collected. From Part 1, fetal tissues were collected from the pregnant bats, and these typically included intestine, kidney, lung, liver, brain, pancreas, adrenal, heart, and spleen. Tissues were fixed in 10% neutral-buffered formalin, processed through to paraffin. A rabbit polyclonal anti-Nipah virus antibody was used as the primary antibody for tissues collected from the Malaysian bats and a rabbit polyclonal anti-Hendra

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virus antibody was used as the primary antibody for tissues collected from the Australian bats. Immunohistochemistry protocols were as described previously.[9]

RESULTS

Animals. The 12 pregnant *P. alecto* bats were captured in south-east Queensland in July 2003. The remaining *P. alecto* bats were captured from the same site in January 2004, with this timing overlapping the end of the birthing season for this species. The *P. vampyrus* bats were captured in Peninsular Malaysia in late 2005. The weights for all bats (*P. alecto* and *P. vampyrus*), ranged from 540 g to 1,000 g.

Clinical observations. All bats remained clinically well throughout the study period. No febrile responses were recorded in either Part 1 or 2 of the experiment after virus inoculation. Because of the absence of a febrile response, rectal temperatures were not recorded in Part 3. All animals maintained their initial bodyweight or exhibited a slight gain in weight and ate copious amounts of fruit.

Detection of henipavirus genome. All samples collected were screened by TaqMan RT-PCR for either HeV or NiV genome, depending on the inoculum. Positive HeV TaqMan results for urine, blood, throat, and rectal swab samples are shown in Table 1. The table indicates the average cycle number (C_t value) at which the sample was positive for the detection of HeV genome when tested in triplicate. Indeterminate samples, where only one or two wells registered a C_t value of < 45 were also recorded. There were 46 samples that were positive for the detection of HeV genome, and an additional 18 indeterminate results.

At postmortem, a limited range of tissues were positive for the detection of HeV genome and these all came from bats that had samples test positive for HeV genome during the clinical sampling period (Table 2). The data does not indicate an association between virus replication and virus shedding with pregnancy. It should be noted that as animal numbers were unavoidably limited (because of the restrictions working within a BSL-4 environment) no statistical analyses could be undertaken.

Only two samples tested positive for NiV genome, both from Bat 22; one from a throat swab on Day 4, and one from a rectal swab on Day 8 (data not shown). No postmortem tissues tested positive for NiV genome (data not shown).

Virus isolation. Samples positive or indeterminate for henipavirus genome were inoculated onto cells for virus isolation. For Parts 1 and 2, this amounted to 64 premortem samples and 10 postmortem samples (Table 2), and in Part 3, only two samples (throat swab and rectal swab from Bat 22). Virus was isolated from one non-pregnant female bat (Bat 16), on three occasions, twice from urine on consecutive sampling days (Days 6 and 8) and once from a rectal swab on Day 6. The amount of virus recovered was at the limit of detection (virus titer < 1/8).

Postmortem. No gross abnormalities were identified on gross postmortem examination of the bats. At postmortem Bat 15 was noted to be in the early stages of pregnancy.

Histopathology and immunohistochemistry. Histopathological abnormalities were few. In the adrenal gland of Bat 8 there was severe, diffuse, subacute necrosis and hemorrhage of the zona fasciculata and zona reticularis extending into the adrenal medulla consistent with the exhaustive phase of a stress response. The fetal liver from Bat 6 had mild periportal mononuclear cell infiltration suggesting antigenic exposure. The endometrial glands of Bats 13 and 16 were distended, indicating possible oestrus or periestral activity, and Bat 15 was in the early stages of pregnancy. The testicular tissue was in active spermatogenesis in Bat 18 only. All tissues examined were negative on immunohistochemical staining for HeV or NiV antigen including the kidney and bladder of Bat 16.

Serology. Table 3 shows a summary of the serology results from Parts 1 and 2 indicating the virus neutralizing titer and

TABLE 1

C_t values for the HeV TaqMan positive samples from *Pteropus alecto*.

Bat number and sample type	days post inoculation									
	0/1	2/3	4/5	6/7	8/9	10/11	12/13	14/15	16/17	18/19
1 throat swab				35						
5 throat swab			31	35						
7 throat swab		33								
9 throat swab		29		34						
10 throat swab		28								
6 rectal swab		33	30		36					
10 rectal swab		30	31	30						
13 rectal swab			31		*					
16 rectal swab			*	31	*	*				
17 rectal swab				35				37		
19 rectal swab				35						
10 urine		33								
13 urine						38	35	*		
16 urine			*	35	32	33	32	32	30	30
17 urine			*		*	36	37	33		
8 blood							*			
13 blood				*	*	34	36		*	
16 blood			*	35	*	34	33	38		*
17 blood			31	36	33	37	36	36		
20 blood						*	*		37	39

*C_t values represent the cycle number at which a sample became positive for the detection of HeV genome. (*) represents an indeterminate result (i.e., only one or two wells in a triplicate were positive). The pattern of genome detection is shown with the circles. The black circle highlights the detection of genome on mucosal surfaces. The broken circle highlights the detection of genome in blood and urine, representing a systemic infection. Virus was isolated in cell culture from urine collected from Bat 16 on Days 6 and 8.

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TABLE 2

Bats that tested positive for the detection of HeV genome during the sampling period and at postmortem, together with their antibody status at postmortem

Sex (M/F), pregnant (P)	Bat number	TaqMan + ve samples	Sampling day number (postinoculation) of the positive sample	TaqMan + ve PM tissues	Antibody status at post mortem
F (P)	3	Throat swab	6	Lung	−ve
F (P)	5	Throat swab	4, 6	None	−ve
F (P)	7	Throat swab	2	None	−ve
F (P)	9	Throat swab	3, 7	Spleen	1/10
		Rectal swab	3, 5, 9		
		Blood	13		
F (P)	10	Throat swab	3	None	−ve
		Rectal swab	3, 5, 7		
		Urine	3		
F	13	Rectal swab	4	Spleen	1/20
		Urine	10, 12		
		Blood	10, 12		
F	16	Rectal swab	7, 15	Spleen	−ve
		Urine	7, 9, 11, 13, 15, 17, 19	Liver	
		Blood	7, 9, 11, 13, 15	Kidney	
F	17	Rectal swab	7	Spleen	1/40
		Urine	11, 13, 15	Lung	
		Blood	5, 7, 9, 11, 13, 15	Liver	
M	19	Rectal swab	7	None	−ve
M	20	Blood	16, 18	Spleen	−ve

day of collection. In Part 1, by postmortem, 50% (6/12) bats had virus neutralizing titers ranging from 1/10 to 1/40. There was an additional bat that showed fleeting virus neutralization in serum at Day 10 with a titer of 1/10. In Part 2, three bats showed virus neutralization by the time of postmortem, with the maximum titer being 1/40. Table 4 shows a summary of the serology from Part 3, where for the first 3 weeks of the experiment, virus neutralization patterns mirrored those seen in the Australian bats and by Day 21 two bats had titers of 1/10. However, 7 days later, this had risen to 5/10 animals. It was at this point that bats in Part 3 were rechallenged. Seven days after this rechallenge another bat showed virus neutralization by serum, and by the conclusion of the experiment (Day 49+), the serum of 7/8 bats neutralized NiV.

DISCUSSION

This study confirms that while healthy *Pteropus* bats can be experimentally infected with henipaviruses productive infections (generation of high titer progeny viruses) were not established. One non-pregnant female *P. alecto* shed HeV in urine on Day 6 and Day 8 postexposure and had HeV genome in kidney at postmortem examination. Isolation of henipavirus from bat urine is consistent both with previously published laboratory data and field surveillance. In one study using a native Australian bat (*P. poliocephalus*), NiV was isolated on three occasions from the urine of a single bat.[10] Similarly, Chua and others[4] recovered the first pteropid NiV isolate from urine collected beneath the roost of *P. hypomelanus* and, subsequently, NiV was similarly isolated from the urine of *P. lylei* and from a wild-caught *P. vampyrus*.[34] The presence of live virus in a rectal swab of the same bat on Day 6 is quite likely to be a contaminant from urine as the sampling procedure started with urine collection. Urine expression by manual bladder palpation in females did result in some contamination of fur in the urogenital region. Additionally, there was no other rectal swab isolate of HeV from this or any other bat.

In this study NiV was not recovered from exposed Malaysian bats. Nipah virus genome detection in samples was also very low (2/512). Both positive samples were from the same female bat; one being a throat swab on Day 4 and the other a rectal swab on Day 8. Although it is possible these results reflected primary inoculum on mucosal surfaces, it is our experience (in other species) that clearance of henipavirus inoculum occurs within 48 hours of its administration (unpublished data). Detection of genome without the subsequent detection

TABLE 3

The HeV serum neutralizing titers of the *Pteropus alecto* bats at 10 days postinoculation and at postmortem; all other bats (3, 5, 6, 7, 10, 14, 15, 16, 19, 20) remained seronegative (≤ 1/5) throughout the experiment

Bat no.	Hendra virus serum neutralizing titer	
	Day 10 pi[a]	Postmortem[a]
1	1/20	1/10
2	1/20	1/10
4	1/40	1/20
8	1/20	1/40
9	1/20	1/10
11	1/80	1/40
12	1/10	≤ 1/5
13	≤ 1/5	1/20
17	≤ 1/5	1/40
18	1/20	1/20

[a] Postmortems were conducted on either Day 26, 27, or 32 postinoculation.

TABLE 4

NiV serum neutralizing titers of the *Pteropus vampyrus* bats[a]

Bat no.	Nipah virus serum neutralizing titer					
	Day 14	Day 21	Day 28	Day 35	Day 42	Postmortem[b]
21	≤ 1/5	≤ 1/5	1/10	1/10	1/80	1/80
22	≤ 1/5	1/10	1/10	1/20	1/40	1/20
24	≤ 1/5	≤ 1/5	≤ 1/5	≤ 1/5	1/40	1/20
25	≤ 1/5	≤ 1/5	1/10	1/20	1/20	1/40
26	≤ 1/5	≤ 1/5	≤ 1/5	1/20	≤ 1/5	1/10
27	1/80	1/10	1/40	1/40	1/20	1/40
28	≤ 1/5	≤ 1/5	≤ 1/5	≤ 1/5	≤ 1/5	1/10

[a] Bats were rechallenged with NiV after serum sampling on Day 28. Bat 22 remained seronegative (≤ 1/5) throughout the experiment.

[b] Postmortems were conducted on either Day 49, 50, or 51 days postinoculation.

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of live virus has been seen in other studies. In a recent study involving *P. alecto* Japanese encephalitis virus was transmitted from experimentally infected bats to mosquitoes despite the absence of a detectable viraemia.[31] In only one experimentally infected bat was Japanese encephalitis virus genome detected by TaqMan RT-PCR and this was at a very high cycle number, indicating very low levels of genome. The sample did not yield viable virus when inoculated onto cells, confirming the very low levels of virus.

The greatest incidence of HeV genome detection in rectal and throat swabs was in the first 7 days post challenge, whereas the majority of urine and blood samples with detectable HeV genome were collected after Day 7 (Table 1). This is consistent with intranasal exposure of HeV being followed by replication in mucosal surfaces with subsequent systemic infection. In this and other experiments virus isolation from exposed *Pteropus* bats coincided with the timing of the proposed systemic infection, at least 6 days after exposure to the virus.[30,32]

Only 1 in 20 bats shed infectious HeV. The virus was at low titers and was detected over a narrow time frame. Previous studies have not reported the titer of henipavirus recovered from bats; however, the low frequency of virus isolation is consistent with field data. We conclude that the opportunity for spillover of HeV from healthy bats is limited both by the amount of excreted virus and the time over which it is excreted. It follows that for an outbreak of Hendra virus to occur, a susceptible spillover species would need to be exposed, most likely to urine from an infected bat, within a very narrow window of opportunity. It is possible that this window is enlarged by certain physiological or immunological factors in some individual bats. Our data do not support either pregnancy or stress in the conventional sense being such a factor, however it should be noted that because of low experimental numbers the finding may not reflect the situation in nature. Similarly, when naive colonies are exposed to HeV and many individuals become simultaneously infected, there may be an increased likelihood of a susceptible host receiving an infectious dose. The latter mechanism has been proposed as an explanation for the sporadic nature of HeV outbreaks in horses.[11]

Inoculated bats survived Nipah virus challenge without developing clinical disease consistent with previous studies.[30] We conclude that the opportunity for spillover of NiV from healthy bats is also rare, and similarly constrained by the short infectious period and the low intensity of infection.

Regarding the finding from VNTs on post-challenge serum samples, all positive samples had relatively low titers consistent with previous studies.[32] One animal in a previous study did mount a significant antibody response with a titer > 1:640.[30] However in this study, an Australian bat species (*P. poliocephalus*) was infected with heterologous virus (i.e., virus that naturally infects a closely related species of bat; NiV) and this may explain the increased titer seen.

The consistently low virus neutralizing titers in experimental and natural henipavirus infections in bats is in contrast to the high titers often observed during infection of other species.[30] In this study, the VNT profile of the NiV-infected bats was similar to that of the HeV-infected bats up to Day 21 pi, with low titers and only a small proportion of bats (2/8) testing positive in the serum neutralizing test. However, by Day 28, 50% of the *P. vampyrus* had virus neutralization at low serum dilutions. After rechallenge on Day 28, three more bats showed virus neutralization by the termination of the experiment but in neither time frame were the patterns particularly suggestive of either a primary or anamnestic antibody response.

Leonard, Allen, and Sulkin[33] suggested that the immune response of bats to (arbovirus) infection enhanced their effectiveness as reservoir hosts. Chakravarty and Sarkar[34,35] found a high percentage (~82%) of peripheral circulating B cells in *P. giganteus* and suggested that this was evidence, which corroborated earlier suggestions that the immune status of bats could be described as relatively immunodeficient. From our observations we do not believe that the immune status of bats is necessarily compromised, but rather the key immune responses to co-evolved pathogens may require alternate methods of evaluation to those described above.

Plowright and others[19] showed that seroprevalence rates in *Pteropus scapulatus* suggested that pregnancy and lactation are risk factors for viral infection. In our study pregnancy did not influence recovery of live virus from infected bats. Plowright and others[19] also reported elevated seroprevalence in a nutritionally stressed population, and suggested that there may be an increased susceptibility to viral infection caused by substantial energetic costs of immune responses. Although the bats used in this study were in good health, and did not lose bodyweight over the course of the experiment, it would be difficult to ascertain whether they were stressed in a physiological sense.

Absence of disease in infected animals is consistent with previous studies. Long-term coexistence of viruses and their hosts has given co-evolution a good chance to reach a relative equilibrium, and consequently many viruses do not cause disease in their reservoir host.[36] The theory of viral co-evolution with chiropteran hosts has been previously suggested, and the findings of this study support this.[37]

Our studies provide valuable insight into aspects of the dynamics of henipavirus infection in the natural flying fox reservoir, but many questions remain unanswered. Current assumptions about ecology and conventional host/pathogen relationships, and how such data is fed into models, must be challenged. The most significant finding of this work is that infected animals exhibited little clinical or serological evidence of henipavirus infection or associated disease. The data from this study and others[30] show that pteropid bats are susceptible to henipavirus infection but, in general, the infections (experimental and field) are non-pathogenic. Collectively, these characteristics indicate that pteropid bats are true reservoir host species[31–37] for henipaviruses. The data may be indicative that for an effective spillover event to occur, ecologically, physiologically or immunologically 'primed' bats may be necessary. To test this hypothesis further experimental trials are required to assess the impact of henipavirus infection on such animals. Finally, it must be noted that the inferences gained from the data described in this study are drawn from low numbers of experimental animals.

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Short Report: Detection of Nipah Virus RNA in Fruit Bat (*Pteropus giganteus*) from India

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Abstract. The study deals with the survey of different bat populations (*Pteropus giganteus*, *Cynopterus sphinx*, and *Megaderma lyra*) in India for highly pathogenic Nipah virus (NiV), Reston Ebola virus, and Marburg virus. Bats ($n = 140$) from two states in India (Maharashtra and West Bengal) were tested for IgG (serum samples) against these viruses and for virus RNAs. Only NiV RNA was detected in a liver homogenate of *P. giganteus* captured in Myanaguri, West Bengal. Partial sequence analysis of nucleocapsid, glycoprotein, fusion, and phosphoprotein genes showed similarity with the NiV sequences from earlier outbreaks in India. A serum sample of this bat was also positive by enzyme-linked immunosorbent assay for NiV-specific IgG. This is the first report on confirmation of Nipah viral RNA in *Pteropus* bat from India and suggests the possible role of this species in transmission of NiV in India.

Bats are known reservoirs for many highly infectious viruses such as Ebola virus (EBOV), Marburg virus (MARV), severe acute respiratory syndrome corona virus, and Nipah virus (NiV).[1] Nipah virus was first recognized in India during an encephalitis outbreak in Siliguri, West Bengal, 2001[2] and in Nadia District, West Bengal, in 2007.[3] The adjacent country, Bangladesh has had multiple outbreaks of NiV during 2001–2011.[4–7]

Nipah virus is a member of the family *Paramyxoviridae* and the genus *Henipavirus*. The henipaviruses are naturally harbored by *Pteropid* fruit bats (flying foxes) and are characterized by a large genome, a wide host range, and their recent emergence as zoonotic pathogens capable of causing illness and death in domestic animals and humans.[8] *Pteropus* bats are the known vectors of this disease, and their involvement has been reported in many countries (Malaysia, Bangladesh, Australia, Thailand, Cambodia, Indonesia, and Madagascar).[9–11]

The route of infection of NiV from bats to humans is by ingestion of NiV-contaminated fresh date palm sap, consumption of partially eaten fruits, or contact with infected domestic animals (cattle, pigs, and goats). Large numbers of persons in Bangladesh and India showed development of disease after person-to-person transmission of the virus.[12] *Pteropus giganteus* bats are widely distributed across Bangladesh and India.[13] A recent study reported the seropositivity for NiV in *P. giganteus* bats in northern India.[14] Similar finding have been reported from Bangladesh.[4] We have surveyed two states (Maharashtra and West Bengal) in India for viral RNA and IgG against NiV, MARV, and REBOV viruses in different bat populations.

With the permission of Chief Conservator of Forests, West Bengal and Maharashtra State, India, bats were caught at roosts either by using mist nets or harp traps. Bats were anesthetized and bled from either the brachial or cephalic arteries; in some cases, blood samples were collected by cardiac puncture. One hundred forty bats of three species, *P. giganteus* (31), *Cynopterus sphinx* (30), and *Megaderma lyra* (79), were captured in Maharashtra and West Bengal States during May 2009–October 2010.

Some bats were euthanized with isoflurane, dissected, and organs were collected. Organs were stored in liquid nitrogen and blood was stored at 4°C during transport. Sex, age, body condition score, pregnancy status, lactation status, weight, and morphologic details were recorded in field laboratory. During capturing the bats and postmortem surgery, proper protecting equipments were used to avoid any infection to the workers. Bat specimens were transported to Biosafety Level 3 Laboratory of National Institute of Virology, Pune, India for further testing.

Liver and spleen were homogenized in phosphate-buffered saline by using a homogenizer (GenoGrinder 2000; BT&C Inc., Lehavon, NJ). Tissue homogenates were used to extract RNAs by using an RNA extraction machine (ABI 6100; Applied Biosystems, Foster City, CA). Quantitative reverse transcription–polymerase chain reactions (RT-PCRs) specific for REBOV, MARV, and NiV were performed.[15,16] A diagnostic nested RT-PCR for the NiV nucleocapsid gene was performed as described.[2] Partial glycoprotein, phosphoprotein, and fusion gene sequences were amplified. Mitochondrial DNA of bat was amplified by using PCR and sequenced for further species confirmation.[17]

Serum was separated from blood and tested by indirect enzyme-linked immunosorbent assay for IgG against MARV, NiV, and REBOV by using kits provided by the Centers for Disease Control and Prevention, Atlanta, GA and described protocols.[18] Each serum sample was tested at 4 dilutions (1:100, 1:400, 1:1,600, and 1:6,400). Isolation of virus was attempted from liver and kidney tissue suspensions in *Vero E6* cells that were blindly passaged three times.

Of 140 bat specimens, only one liver homogenate was positive for NiV viral RNA in a *P. giganteus* bat from Myanaguri, West Bengal, India. The NiV-positive bat was a healthy male adult (weight = 650 grams). The quantitative RT-PCR result for the liver homogenate was positive for NiV (cycle threshold value = 31.6), and the kidney homogenate was negative. However, results of a diagnostic NiV-specific RT-PCR were positive for liver and kidney homogenates. This bat serum sample was also found positive for NiV-specific IgG at dilutions of 1:100 and 1:400. Serum and tissues from this *Pteropus* bat were negative for REBOV and MARV by ELISA and quantitative RT-PCR. The remaining 139 bat specimens were negative for IgG against all three viruses and for viral RNA.

During virus isolation attempts in *Vero E6* cells, NiV-positive liver and kidney homogenates from *P. giganteus* did not show

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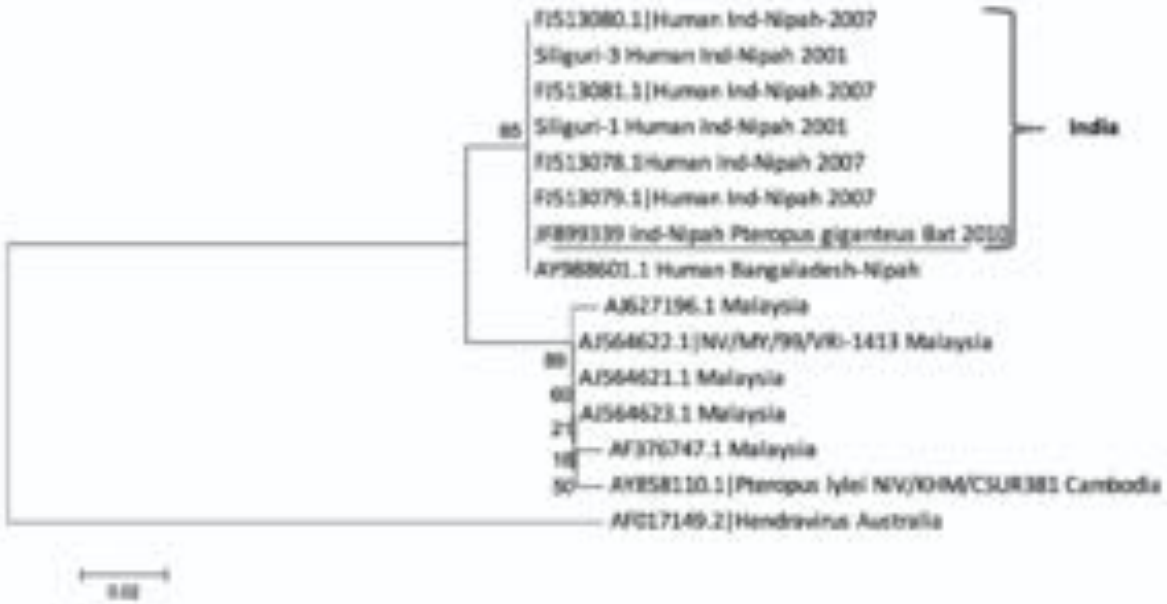

FIGURE 1. Phylogenetic tree of partial nucleocapsid gene (339 basepairs) sequence of Nipah virus from *Pteropus giganteus* from India and other reported Nipah viruses from GenBank constructed by using the neighbor-joining method with 1,000 bootstrap replicates. Scale bar indicates nucleotide substitutions per site.

a cytopathic effect. The sample was blind passaged in *Vero E6* cells for three passages without evidence of a cytopathic effect.

A 2,021-basepair fragment of the viral genome was sequenced for NiV, which includes partial gene fragments for the nucleocapsid gene (205 basepairs), the glycoprotein gene (954 basepairs), the phosphoprotein gene (338 basepairs,), and the fusion protein gene (524 basepairs) (Genbank accession nos. JF899339-JF899420). Partial mitochondrial gene of a *Pteropus* bat was sequenced, and the identity of the bat was confirmed as *P. giganteus*.

The nucleotide and amino acid sequences of partial nucleocapsid gene of *Pteropus*-derived NiV showed 100.0% homology with NiV sequences reported during 2001 (Siliguri) and 2007 (Nadia) outbreaks in India and with Bangladesh sequences. Partial nucleocapsid gene sequences of NiV showed 96.0% identity with Cambodia and Malaysia strains and 81.0% with Hendra virus from Australia at the nucleotide level. *Pteropus* NiV amino acid sequences from India showed 100.0% identity with all NiV sequences except with AF017149 (Australia) and NiV from *Pteropus* bats from Malaysia (AY858110) (98.0% identity).

Bat NiV glycoprotein gene sequence showed 99.0% and 100.0% identity with virus sequences from Nadia outbreak (AF513078), and with Bangladesh sequence (Ay988601) and 100% identity at the amino acid level. Bat NiV sequence

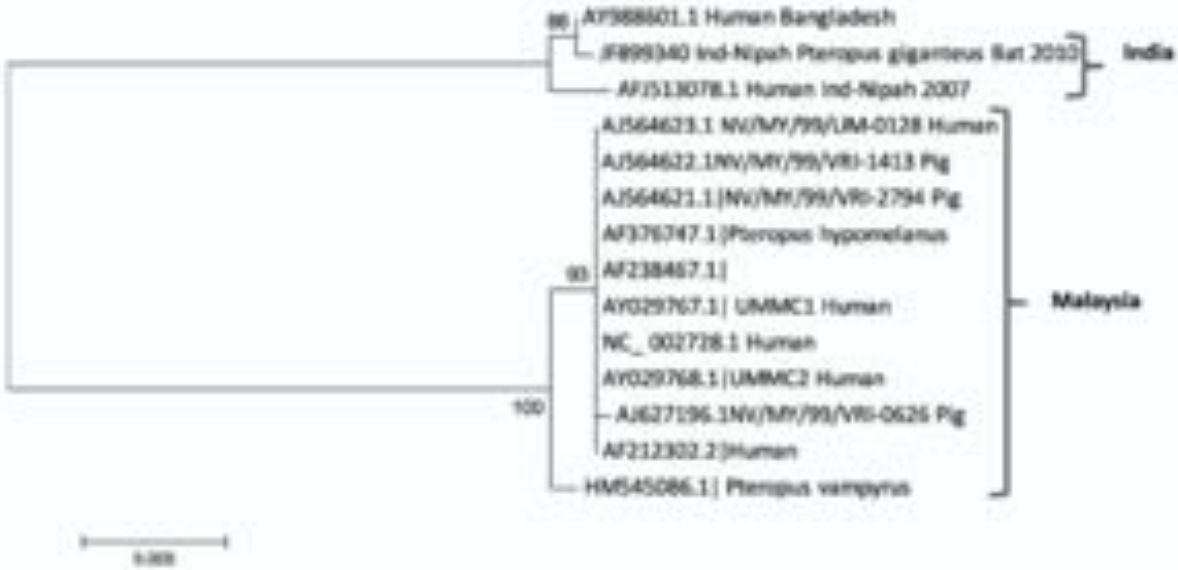

FIGURE 2. Phylogenetic tree of partial glycoprotein gene (954 basepairs) sequence of Nipah virus from *Pteropus giganteus* from India and other reported Nipah viruses from GenBank constructed by using the neighbor-joining method with 1,000 bootstrap replicates. Scale bar indicates nucleotide substitutions per site.

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had identities of 92.0% and 96.0% with Malaysia strains at the nucleotide and amino acids levels, respectively, except for HM585086.1 sequence (derived from *P. vampyrus*), which showed 97.0% identity at the amino acid level. Two phylogenetic lineages were formed for NiV nucleocapsid and glycoprotein gene sequences: Bangladesh and India sequences and Malaysia and Cambodia sequences (Figures 1 and 2).

Partial sequences of glycoprotein and nucleocapsid genes of NiV from India detected in *Pteropus* bats showed that NiV was present in the captured bat. Viral sequences from India were similar to those from Bangladesh in the same phylogenetic lineage. The same NiV strain might circulate in India and Bangladesh. Thus, we believe that when the bat was captured, the viremia phase had ended but there was still some virus in the liver. The healthy body condition of the bat, the positive quantitative RT-PCR result for liver, and the presence of IgG suggest that the virus infection likely had no adverse effect on the bat, which overcome the infection. Our results suggest that *Pteropus* bats may be a reservoir for NiV in India. A systematic survey is required in different states of India to understand the distribution of this virus.

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Original Contribution

Use of Infrared Camera to Understand Bats' Access to Date Palm Sap: Implications for Preventing Nipah Virus Transmission

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Abstract: *Pteropus* bats are commonly infected with Nipah virus, but show no signs of illness. Human Nipah outbreaks in Bangladesh coincide with the date palm sap harvesting season. In epidemiologic studies, drinking raw date palm sap is a risk factor for human Nipah infection. We conducted a study to evaluate bats' access to date palm sap. We mounted infrared cameras that silently captured images upon detection of motion on date palm trees from 5:00 pm to 6:00 am. Additionally, we placed two locally used preventative techniques, bamboo skirts and lime ($CaCO_3$) smeared on date palm trees to assess their effectiveness in preventing bats access to sap. Out of 20 camera-nights of observations, 14 identified 132 visits of bats around the tree; 91 to the shaved surface of the tree where the sap flow originates, 4 at the stream of sap moving toward the collection pot, and no bats at the tap or on the collection pots; the remaining 6 camera-nights recorded no visits. Of the preventative techniques, the bamboo skirt placed for four camera-nights prevented bats access to sap. This study confirmed that bats commonly visited date palm trees and physically contacted the sap collected for human consumption. This is further evidence that date palm sap is an important link between Nipah virus in bats and Nipah virus in humans. Efforts that prevent bat access to the shaved surface and the sap stream of the tree could reduce Nipah spillovers to the human population.

Keywords: bats, date palm sap, food contamination, infrared camera, nipah virus, transmission

Introduction

Nipah virus is an emerging zoonotic paramixovirus causing encephalitis with 40–70% case fatality in humans (Goh et al., 2000; Luby et al., 2009). Fruit bats of the genus *Pteropus*, are the apparent natural reservoir for the virus, and occasionally secrete Nipah virus in their saliva and excrete it in their urine (Young et al., 1996; Yob et al., 2001; Olson et al., 2002; Wacharapluesadee et al., 2005). Studies in Bangladesh, India, and Malaysia also identified neutralizing antibodies against Nipah virus in *Pteropus* bats (*P. vampyrus* and *P. hypomelanus*) (Yob et al., 2001; Epstein et al., 2008; Homaira et al., 2010). *P. giganteus*, one of the most common fruit bats in Bangladesh, have been found to carry antibodies against Nipah virus (Bates and Harrison, 1997; Hsu et al., 2004; Epstein et al., 2006).

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Eight Nipah virus outbreaks have been recognized in Bangladesh between 2001 and 2008 (ICDDR,B, 2008; Luby et al., 2009). All of these outbreaks in Bangladesh coincided with the date palm sap harvesting season that occurs from mid-October to early April (Nahar et al., 2010; Luby et al., 2009). In the January 2005 human Nipah outbreak in Tangail District, Nipah cases were eight times more likely than controls to report drinking raw date palm sap ($P < 0.001$). Date palm sap collectors in the area reported that the large *Pteropus* fruit bats frequently visited the date palm sap collection pots (Luby et al., 2006).

Drinking raw date palm sap is a seasonal delicacy in Bangladesh. Local sap collectors (*gachhis*) harvest the sap by shaving approximately 1 inch depth of the bark approximately 8 × 12 inches on one side of the top of the date palm tree (*Phoenix sylvestris*) just below the base of the branches. The sap collectors shave the bark in a V-shape so that the sap flows into the tap and then into a clay pot that is hung below (Fig. 1.1.a). In Bangladesh, people used date palm sap for two primary purposes: most is made into molasses and a small amount is consumed raw. During winter, the *gachhis* collect sap from date palm trees early in the morning; they sell it within a few hours to consumers who drink it almost immediately, because it ferments within a few hours and loses its sweet taste (Luby et al., 2006; Nahar et al., 2010).

Date palm sap collectors identified bats as one of the nuisances that decrease the quality of raw sap. They report that bats drink the sap and, occasionally, spoil the contents of the sap collection pot with urine or feces (Nahar et al., 2010). Traditionally, a few of them use techniques that they thought could prevent bats' access to date palm sap. A review of these techniques concluded that smearing lime ($CaCO_3$) on the sap stream and covering the sap-producing surfaces with a bamboo skirt, comprised of several bamboo sticks woven together, were the two techniques most likely to prevent bats access to date palm sap (Nahar et al., 2010).

This pilot study aimed to understand the frequency and ways that bats contacted date palm sap, and to gain a preliminary understanding of the effectiveness of these locally used preventive techniques.

Materials and Methods

Site Selection

We conducted the study from February 26 to March 21, 2008 in Faridpur District, Bangladesh, at a location (N23° 33′ 55.0″ E89° 42′ 26.0″) which had about 1000 date palm sap-producing trees and a bat roost (N23° 34′ 19.0″ E89° 42′ 18.0″)

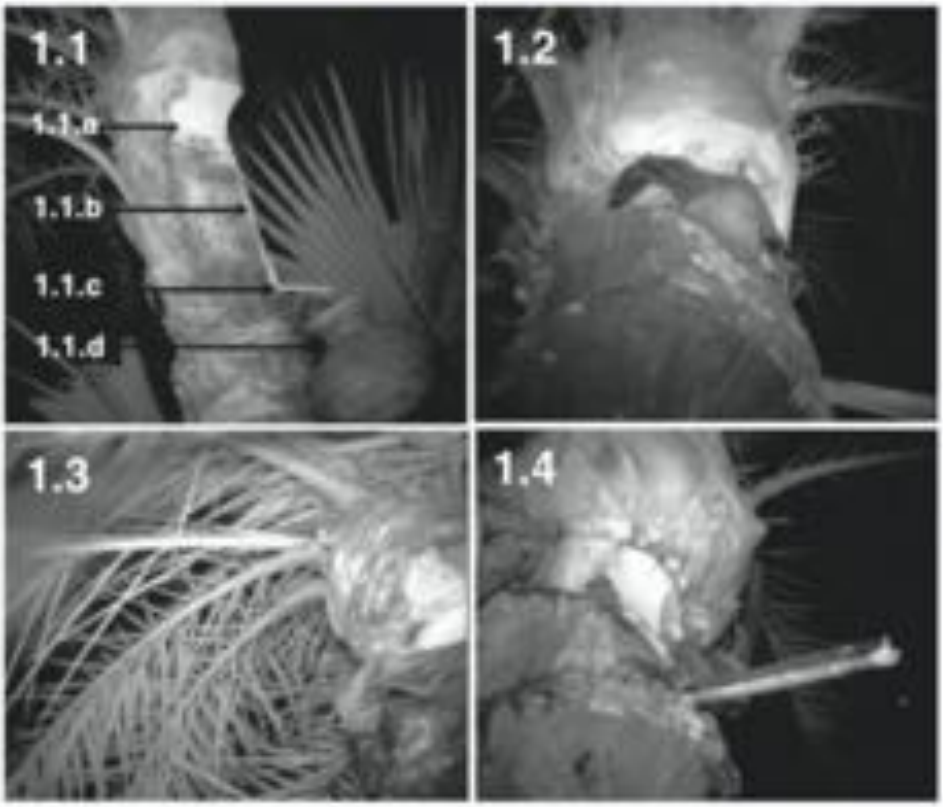

Figure 1. Date palm sap-producing tree, and ways of bats contaminating the shaved surface of the tree.

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containing approximately 200 *Pteropus* bats, located 1 km away.

Date Palm Tree Selection

Among the date palm sap-producing trees, we selected 14 tall, newly shaved trees that the local sap harvesters' and residents reported were often visited by bats.

Observation

Direct Human Observation

A trained data collector observed a tree each night from dusk (5:00 pm) to dawn (6:00 am). In total, they observed 14 trees over 14 nights, 1 night per tree. The data collector observed the selected date palm trees, maintaining a distance of approximately 30 m from the tree, so as not to alter the bats' natural feeding behavior. The observer noted the number of bat visits on and around the date palm tree, the number of bats feeding on and around the date palm tree, and the frequency of bats visiting the tree while recording the time of each observation.

Camera Observation

We used two motion sensor-tripped infrared cameras (Silent Image™ Model RM30 digital cameras, RECONYX, Inc., Holmen, WI)[3] that included an infrared illuminator and a passive infrared motion detector. We observed 10 date palm sap-producing trees for 20 camera-nights without any local protective technique. We defined a camera-night of observation as an infrared camera focused on the shaved surface, sap stream, tap, and the collection jar hung on the date palm tree from 5:00 pm in the evening to 6:00 am in the morning. We used two cameras per night, both of which were mounted on a single tree, set to the left and right angle to the shaved surface, and focused on the sap flowing from the shaved part into the collection pot (Fig. 2). If there was any movement in the sap collection area, each camera took one picture per second for the next 5 seconds. The cameras were placed in the same tree that the people were observing, but because there were two cameras, they recorded two camera-nights of observation for each night of human observation.



Figure 2. Two infrared cameras mounted in a date palm tree from the left and right angle to the shaved surface, focused on the sap flowing from the shaved surface into the collection pot.

In the morning, these cameras were recovered and the pictures were transferred to a computer and reviewed.

Applied Local Protective Techniques

In addition to the previously described camera observations, we also observed two local techniques, lime paste and bamboo skirts for eight camera-nights. These methods were used to explore if they could prevent bats access to sap. We applied a thin layer of lime paste ($CaCO_3$) over the cut surface on two trees (four camera-nights of observation). We also applied bamboo skirts covering the shaved surface, sap stream, tap, and the opening of the pot on another two trees (four camera-nights of observation) (Fig. 3).

Data Extraction

We defined bat visits by both human and camera observation. For human observation, this was any sighting of a bat flying in or around the date palm tree. For camera observation, this was when a bat was seen in the focus area of the

[3]Inclusion of trade names is for identification only and does not imply endorsement by ICDDR,B, by CDC or the Department of Health and Human Services.

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Figure 3. Bamboo skirt, covering a date palm sap-producing tree's shaved surface, sap stream, tap, and the mouth of the pot.

camera. The visit continued until the bat was no longer seen. We recorded the camera data in a structured field data sheet, which included the frequency of bat visits and any contact with date palm sap. We defined bat–sap contact as an instance of a bat landing, licking (i.e., the bat's tongue contacted the date palm sap), or urinating either on the date palm's shaved surface, sap stream, or the parts of the tap or collection pot that came in contact with the sap. The focus of each of the two cameras placed on the same tree did not always fully overlap, so the total bat visits identified by each camera were counted individually. Because each bat could not be individually identified, it was not possible to assess if the same bat made multiple visits at different times of the night. We analyzed the results as the frequency of "bat visits" per "camera-nights" of observation.

We classified the bats into *Pteropus* and non-*Pteropus* groups. We distinguished the *Pteropus* bats by their larger body mass, dog or fox-like face, long and pointed ears, and fur characteristics (Kunz and Jones, 2000a, b), and the non-*Pteropus* bats based on their relatively smaller body mass and fur characteristics (Nowak et al., 1994). The infrared camera we used only produced low resolution black and white photos, so we were not able to clearly distinguish the species of non-*Pteropus* fruit bats.

Statistical Methods

We calculated the total, mean, and median bat visits per tree per camera-night of observation. Distribution of the duration of bat–sap contact was skewed, so we presented the medians of the duration of contact with 95% CI (Bonett and Price, 2002). We also performed Wilcoxon rank sum test among *Pteropus* and non-*Pteropus* bats' durations of bat–sap contacts to assess equality of medians (Siegel and Castellan, 1988).

Results

Frequency of Bat Visits to Date Palm Tree

Out of 20 camera-nights of observation of the date palm trees without any intervention, 14 identified 185 bat visits on and around the tree: 151 (82%) at the shaved surface, 4 (2%) at the sap stream, no bats at the tap or the collection pot hung on the tree, and the rest ($n = 30$) did not land on the tree; the remaining 6 nights of observation did not identify any bat visiting the trees. Out of 20 camera-nights of observations on date palm trees without any intervention, the cameras identified 132 visits of bats at and around the tree (mean: 7.7 visits per night; standard deviation [SD] 15 visits), 91 bat visits at the shaved surface (mean: 7.6 visits per night; SD 8 visits), and 4 bat visits at the sap stream (mean: 0.7 visits per night; SD 1.6 visits).

Human observers during 10 nights without any intervention reported 72 visits of bats (mean: 7.2 visits per night; SD 5.5 visits) in and around the tree. Their observation was unable to identify whether bats landed on the shaved surface, sap stream, tap, or the collection pot and contaminated the sap.

Characteristics of Bats Contacting Date Palm Sap

Pteropus and non-*Pteropus* bats accessed date palm sap differently. The non-*Pteropus* bats, primarily landed directly on the shaved surface ($n = 82$, 54%) (Fig. 1.2). The second most frequent mode of accessing the sap was to land directly to the left or right of the shaved surface ($n = 63$, 42%) of the tree and climb to it (Fig. 1.3). The *Pteropus* bats accessed the shaved surface by landing on higher branches and climbing down to the shaved surface ($n = 8$, 100%) (Fig. 1.4).

Both *Pteropus* and non-*Pteropus* bats contacted sap at the date palm trees shaved surface and the sap stream 157

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Table 1. Visits, Ways, and Duration of *Pteropus* and Non-*Pteropus* Bats Contacting Date Palm Sap

28 Camera-nights of observations	Pteropus	Non-Pteropus	Total
Bats on and round the date palm tree			
Times landed on the tree	8 (4%)	149 (81%)	157 (85%)
Times did not land on the tree	4 (2%)	24 (13%)	28 (15%)
Total	12 (6%)	173 (94%)	185 (100%)
Frequency of bats contacting date palm sap			
Shaved surface (bat visit-times)	8 (5%)	145 (92%)	153 (97%)
Sap stream (bat visit-times)	0 (0%)	4 (3%)	4 (3%)
Total	8 (5%)	149 (95%)	157 (100%)
Ways of bat–sap contact			
By landing and licking (bat visit-times)	8 (5%)	130 (83%)	138 (88%)
By landing only (bat visit-times)	0 (0%)	19 (12%)	19 (12%)
Total	8 (5%)	149 (95%)	157 (100%)
Duration of bat–sap contact			
No. of observations	8	149	157
Total duration of contamination (seconds)	4826	12,252	17,078
Median duration in seconds (range)	483 (124–1094)	20 (1–711)	29 (1–1094)
95% CI for median	216–1085	11–41	15–50

times during a total of 28 camera-nights of observations (mean 5.8 bat–sap contacts per night; SD 11.7). All ($n = 8$) of the *Pteropus* bats contacted sap at the shaved surface of the date palm tree by licking (Table 1).

During one camera observation, a *Pteropus* bat urinated while hanging on the branches of the tree. The urine did not directly contact the shaved surface or the pot, because the bat was hanging on a branch on the right side about 2 feet away (Fig. 4).

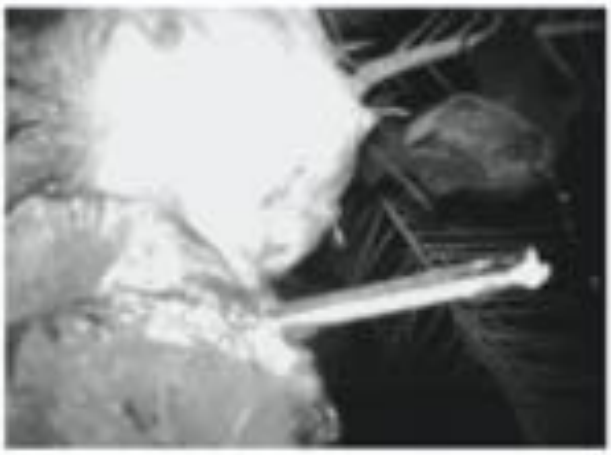

Figure 4. A bat urinating while hanging on the date palm tree branch.

Duration of Visits on the Tree and Bats' Contact with Sap

Bats visited the trees from 1 second to 93 minutes (median: 33.5 seconds). The median duration for the *Pteropus* bats contacting date palm sap (483 seconds, 95% CI 216–1085) was 23 times higher than the non-*Pteropus* bats (21 seconds (95% CI: 11–41) ($P = 0.01$) (Table 1).

Bats Visit at Different Times of Night

Bats visited date palm trees from 6:00 pm to 5:00 am. Camera observation identified that the bats visited the trees most commonly from 9 pm to midnight (37%) and from 2:00 am to 5:00 am (45%) (Fig. 5). The number of *Pteropus* fruit bat visits ($n = 12$) were very few compared to the non-*Pteropus* fruit bat visits ($n = 173$) (Table 1), and all of the *Pteropus* fruit bats visited between 8:00 pm and 12:00 am. The cameras consistently identified more bat visits (mean: 5 visits per camera night) than the human observers (mean: 0.4 visits) per night especially between 2:00 am and 5:00 am (95% CI for mean difference: −8.8 to −0.8).

Local Protective Techniques and Bat Visits

Out of four camera-nights of observations of date palm trees treated with lime paste, the cameras identified 49 bat

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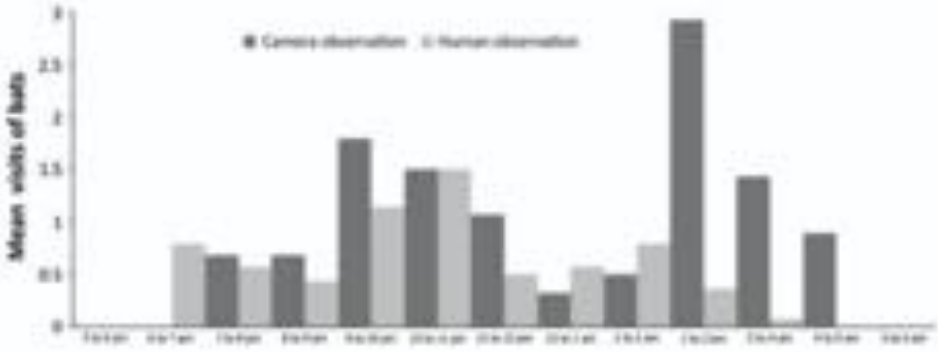

Figure 5. Bats seen by 28 infrared camera and 14 human observations at different hours of the night around the tree.

visits on and around the tree where no sap contact was noted (mean: 13 visits per night; SD 24 visits) and 56 visits at the shaved surface where bats contacted the sap by landing and/or licking (mean: 15 visits per night; SD 27 visits). On several occasions, bats contaminated sap multiple times on a single visit to the tree. During the four camera-nights of observation on trees protected with the bamboo skirt, one bat visited on and around the tree, and no bats contacted the shaved surface, sap stream, tap, or the collection pot.

The human observer collected data on two date palm trees treated with lime smear and two covered with a bamboo skirt. The observer identified 10 bat visits on and around the tree (mean: 5 visits per night; SD 1.4 visits) when lime smear was applied on two trees for two nights. The observer also identified 12 visits of bats on and around the tree (mean: 6 visits per night; SD 5.6 visits) when the trees were protected with bamboo skirt intervention and observed for two nights.

Discussion

As one step to understanding the transmission of Nipah virus from bats to humans, this study used infrared cameras to observe and explore the frequency and process of bats making physical contact with date palm sap. The infrared photos, taken in areas of previous Nipah outbreaks in Bangladesh, identified that multiple species of bats frequently visited date palm trees and contacted sap by landing on the shaved surface and licking the sap stream.

The majority of the bats physically contacted date palm sap by landing and licking (88%) and, in most cases, it was the shaved surface of the tree. This provided the bats with more surface area to hold on to and gave them easier access to lick the date palm sap (Fig. 1). Physical contact of bats with date palm sap allows microbiological flora from bats to enter sap. Bats that licked the shaved surface potentially contaminated the sap through the transfer of their saliva, though in the vast majority of these instances, we would not expect this flora to include Nipah virus; in capture studies of wild *Pteropus* bats, fewer than 1% of throat swab specimens had Nipah virus RNA detected (Chua et al., 2002, Wacharapluesadee et al., 2005).

These camera observations also suggest that urine is a potential vehicle of transmission for Nipah virus. Nipah virus RNA and whole virus has been recovered from *Pteropus* bat urine (Yob et al., 2001; Wacharapluesadee et al., 2005, 2010; Wacharaplusesadee and Hemachudha, 2007). Our study results differ from a previous study, which reported that fruit bats do not urinate at their feeding ground (Chua et al., 2002). Our observation of fruit bats, particularly the flying foxes urinating at their feeding ground (Fig. 4), may be due to their rapid gastrointestinal transit time, highly liquefied diet, the long duration of stay, their large consumption of date palm sap (Hall and Richards, 2000), or they could have fed elsewhere prior to their date palm tree visits. The urine might come into contact with the bats' body fur and feet, and be transferred to sap when the bats land directly on the shaved surface and/or the sap stream of a date palm tree. Another possibility is that bats could urinate on the shaved surface, sap stream, tap of the tree, and/or the collection pot hung on the tree, though we did not directly observe this in 28 camera-nights of observations.

Our camera observations made detailed records of the frequency and timing of bat visits to the date palm tree at night. Previous studies report that *P. giganteus* bats begin to leave their roost 15 to 20 minutes after sunset and may fly up to 50 km searching for feeding grounds (Lawrence, 1939; Davis, 1966; Marshall, 1985; Kunz and Jones, 2000b). Our findings indicate similar patterns of

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feeding behavior; the bats started to visit the date palm tree about 1 hour after sunset. This study also identified a distinct feeding pattern, where frequency of bats' visits peaked twice during the night (Fig. 5), leading to the possibility that they leave the roost several times for foraging, or different bats visited the tree from different distances (Singaravelan and Marimuthu, 2004). This also suggests that interventions for sap protection from bats should be in place for the entire night. The mean number (7.7 visits; SD 13) of bats that visited the date palm sap varied from what was observed in another study of nectar-feeding behavior of several species of fruit bats which found that *Cynopterus sphinx* mean visits varied from 6.6 (SD 2.6) to 39.3 (SD 14.2) visits every night, and for *P. giganteus*, it was 2.9 (SD 2.1) to 17.3 (SD 3.1) visits in three locations under natural conditions (Singaravelan and Marimuthu, 2004). Bats forage on date palm sap as they do on nectar and fruit juices (Banack, 1998; Singaravelan and Marimuthu, 2004). Date palm sap is an agricultural product that would not be available for bats in natural settings. This indicates that these bats have become opportunistic feeders during winter in Bangladesh; they might drink date palm sap for food, as well as for rehydration (Walton and Trowbridge, 1983). Continuous deforestation and integrated farming have reduced the availability of naturally occurring food sources including flowers, nectars, pollens, and fruits (Kunz and Jones, 2000a,b; Khan, 2001). Although both nectar and date palm sap are liquid plant- produced sources of food, and easy to access, the high sugar content and the availability of the date palm sap might promote higher frequency of bat visits (Aidoo et al., 2006). The date palm trees usually produce more than a liter of sap/tree/day that consist of about 10% sucrose (FAO, 1993). Whereas, the volume of nectar production is generally much lower (ranging from 0.3 to 103 μL in a day) depending on the species of tree with a sucrose content ranging from 10% to 100% (Wolff, 2006). The date palm sap production starts to decline in mid-February, during the beginning of Spring in the Indian subcontinent, and it is about the same time when nectar becomes available (Mitra et al., 2010).

This study identified that multiple species of fruit bats physically contacted date palm sap, including *Pteropus* spp. The only *Pteropus* species present in Bangladesh is *P. giganteus* (IUCN, 2000). Researchers found that both *Pteropus* and non-*Pteropus* bats were serologically positive in several studies in Asia (Yob et al., 2001; Hsu et al., 2004; Li et al., 2008) and Africa (Hayman et al., 2008); in Thailand, Nipah virus RNA was identified in the saliva of *Pteropus* and non-*Pteropus* fruit bats (Wacharapluesadee et al., 2005). This indicates that the non-*Pteropus* fruit bats could also be involved in the transmission of Nipah virus or other zoonoses in Bangladesh. Although the frequencies of non-*Pteropus* bat visits were higher than the *Pteropus* fruit bats, the *Pteropus* bats contacted the sap for a longer time. Further research might clarify the potential role of non-*Pteropus* bats in zoonotic virus transmission.

To prevent bats from feeding on the date palm sap, the date palm tree harvesters in the western part of Bangladesh apply lime to the shaved surface. The sap collectors who practiced this method believed that the bitter acrid taste of lime would keep bats away (Nahar et al., 2010). In the limited data we collected, the application of lime did not appear to prevent bats from feeding and making contact with date palm sap. The lime might have been washed away by either the sap flow or by rain that occurred during one of the nights of observation. Another preventative technique we observed being used by sap collectors was the bamboo skirts. In the two trees this was tried, the bamboo skirt apparently did protect the sap from bats. The physical barrier formed by the bamboo skirts covering the shaved surface, sap stream, tap, and mouth of the sap collection pot at the tree kept bats from physically contacting the sap.

Bat observation through infrared camera was a useful method to study bat feeding behavior of date palm sap. These cameras provided more accurate detail of bats' visits than did the human observation. Our human observers did not have optimum night-viewing capabilities to detect bats contacting date palm sap. They may have lost concentration, or fallen asleep in the early hours of the morning, but had a wider field of view. We could only compare bats' visits on and around the tree between human and camera observations. The human observer noted that the frequency of bats' visits started to decline after 2 am, and failed to detect any bats after 4:00 am, whereas the camera observation had opposite results. The cameras identified limited numbers of *Pteropus* bat visits, which may not reflect the actual nature of date palm tree visits at different times of the night. Despite the benefits of the cameras' exclusive focus on the shaved surface, sap stream, tap, and collection pot, it could have been possible that the cameras took pictures of the same non-*Pteropus* fruit bat flying around the tree several times due to this narrow view. The non-*Pteropus* fruit bats have a tendency to forage around fruit

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trees multiple times (Singaravelan and Marimuthu, 2004), and we identified that most (94%, $n = 175$) of the bat visits on and around the trees were by non-*Pteropus* bats. Similarly, the camera might have missed other bats picked up by human observation that were flying around the tree and were out of camera focus. In 4 out of 28 observations, heavy fog reduced visibility for a couple of hours; this could also have reduced our bat count. Our method identifies the frequency of bat visits; this probably underestimates the number of bats visiting each night. *Pteropus* bats have their preferred feeding grounds where they forage for several hours at night (Walton and Townbridge, 1983); non-*Pteropus* fruit bats, such as *Cynopterus* spp, often make their roost very close to their feeding ground and shuttle back and forth (Storz and Kunz, 1999). This particular feeding behavior of the fruit bats could have led us to count the same bat visiting multiple times.

Conclusion

Bats commonly visited date palm trees and physically contacted sap collected for human consumption. This study provides further evidence that date palm sap is an important link between Nipah in bats and Nipah in humans. Efforts that prevent bat access to the shaved surface and the sap stream of the tree from dusk to dawn could reduce Nipah spillovers to the human population. Further study is needed to identify the efficacy of bamboo skirt to prevent date palm sap contamination by bats.

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Recurrent Zoonotic Transmission of Nipah Virus into Humans, Bangladesh, 2001–2007

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Human Nipah outbreaks recur in a specific region and time of year in Bangladesh. Fruit bats are the reservoir host for Nipah virus. We identified 23 introductions of Nipah virus into human populations in central and northwestern Bangladesh from 2001 through 2007. Ten introductions affected multiple persons (median 10). Illness onset occurred from December through May but not every year. We identified 122 cases of human Nipah infection. The mean age of case-patients was 27 years; 87 (71%) died. In 62 (51%) Nipah virus–infected patients, illness developed 5–15 days after close contact with another Nipah case-patient. Nine (7%) Nipah case-patients transmitted virus to others. Nipah case-patients who had difficulty breathing were more likely than those without respiratory difficulty to transmit Nipah (12% vs. 0%, p = 0.03). Although a small minority of infected patients transmit Nipah virus, more than half of identified cases result from person-to-person transmission. Interventions to prevent virus transmission from bats to humans and from person to person are needed.

Human Nipah virus infection, characterized primarily by fever and encephalitis, was first recognized in a large outbreak of 276 reported cases in peninsular Malaysia and Singapore that occurred from September 1998 through June 1999 (*1*,*2*). Contact with sick pigs was the primary risk factor for infection (*3*). A newly identified porcine respiratory and neurologic syndrome developed in some pigs infected with the Nipah virus; this syndrome was characterized by fever, barking cough, behavioral changes, uncoordinated gait, spasms, and myoclonus (*4*). The outbreak of Nipah virus infection in humans ceased when the infected herds of pigs in the region were culled (*5*).

Substantial data implicate fruit bats (*Pteropus* spp.) as the natural reservoir host of Nipah virus. In initial studies after the Malaysia outbreak, 16/64 (25%) *P. vampyrus* and *P. hypomelanus* fruit bats had neutralizing antibodies to Nipah virus (*6*). Nipah virus was subsequently isolated from urine specimens collected under a *P. hypomelanus* roost from partially eaten fruit dropped during feeding activity in Malaysia (*7*) and from urine collected under a *P. lylei* roost in Cambodia (*8*). Nipah virus–specific RNA was identified in saliva and urine samples from *P. lylei* fruit bats in Thailand (*9*).

The nucleotide sequences of Nipah virus strains isolated from pigs and persons in Malaysia were remarkably similar (*3*,*10*,*11*) and suggest that the entire outbreak was caused by 1 or 2 closely related strains. Indeed, all human cases of Nipah infection in Malaysia and Singapore could have originated from a single or perhaps 2 introductions of Nipah virus from its bat reservoir into pigs (*10*,*12*).

In Bangladesh, by contrast, recurrent Nipah outbreaks have been recognized since 2001 (*13*–*17*), and the strains of Nipah isolates show substantial heterogeneity in their nucleotide sequences (*11*). This heterogeneity suggests repeated introductions of Nipah virus from its host reservoir into the human population in Bangladesh.

A single species of fruit bats of the genus *Pteropus*, *P. giganteus*, lives in Bangladesh and is widely distributed throughout the country (*18*). Blood samples from *P. giganteus* bats in Bangladesh and neighboring India commonly have antibodies to Nipah virus (*13*,*19*). The conditions that

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permit recurrent introduction of Nipah virus from fruit bats to persons in Bangladesh are unknown. Besides the tendency for Nipah virus outbreaks to reoccur in Bangladesh, a second notable difference in Nipah virus epidemiology in Bangladesh is that, in contrast to Malaysia, where person-to-person transmission of Nipah virus was not confirmed (*20*), person-to-person transmission has been repeatedly observed in Bangladesh (*15*,*16*).

The high prevalence of antibodies to Nipah virus among *Pteropus* spp. bats suggests that Nipah virus is well adapted to transmission between individual bats of this genus. We hypothesize that when a *Pteropus* spp. bat sheds Nipah virus in Bangladesh, this virus occasionally infects 1 or more persons. Once people are infected, the epidemic chain of transmission can be perpetuated by person-to-person transmission (*16*).

A more complete understanding of the character of Nipah virus infection in Bangladesh has been limited by the analysis of relatively small individual outbreaks. We combined data from the 7 recognized human outbreaks and the identified sporadic cases of Nipah virus in Bangladesh from 2001 through 2007. The objective was to describe the introduction of Nipah virus into the human population and the epidemiology of person-to-person transmission.

Methods

We reviewed available data from investigations of all of the human Nipah infections recognized in Bangladesh from 2001 through 2007. Information from the separate investigations was combined into a single database. Not all variables of interest were collected from the earliest outbreaks, but because many of the same investigators were involved across the outbreaks, data were collected in similar formats.

Persons were classified as being infected with Nipah virus if they had fever with new onset of altered mental status, seizures, or severe shortness of breath and either had specific antibodies against Nipah virus or were part of a cluster of similar case-patients in the same region, with at least 1 of the case-patients being Nipah-antibody positive. In addition, if a person had fever and immunoglobulin (Ig) M antibody to Nipah, that person was classified as being infected with Nipah virus.

We classified Nipah cases as part of a cluster if at least 1 other Nipah case was identified in the same community within 3 weeks of onset of illness. If no other cases appeared in the same community within 3 weeks, the Nipah case was classified as an isolated case.

We counted distinct introductions of Nipah virus into the human population. Each cluster of Nipah case-patients and each sporadic case was counted as a separate Nipah introduction.

We classified persons as primary case-patients if illness developed without known contact with any other Nipah case-patients, as secondary case-patients if Nipah disease developed 5–15 days after close contact with other Nipah case-patients, and as Nipah spreaders if at least 1 person with whom that person had close contact had Nipah illness develop 5–15 days after that contact. We collected geographic coordinates by using global positioning systems from the home of each case-patient.

Laboratory Methods

The field team, which involved a large number of different people over the course of the many outbreak investigations, centrifuged whole blood specimens and brought the separated serum on wet ice to the laboratory at the International Center for Diarrheal Diseases Research, Bangladesh (ICDDR,B), where it was stored at –70°C. Before 2007, serum samples were shipped on dry ice to the US Centers for Disease Control and Prevention (CDC) and tested with an IgM capture enzyme immunoassay (EIA), which detects Nipah IgM, and with an indirect EIA for Nipah IgG (*21*). Nipah (Malaysia prototype) virus antigen was used in both assays. In 2007, the Nipah antibody testing was conducted at the government of Bangladesh's Institute of Epidemiology Disease Control and Research using reagents provided by the Special Pathogens Branch of CDC in Atlanta. All positive samples were confirmed at CDC.

Statistics

We assessed whether differences in proportions were more extreme than would be expected by chance by using the χ^2 test or the Fisher exact test when the expected cell size was <5. The basic reproductive number (R_0) is the average number of persons infected by an infectious person during his or her entire infectious period when he/she enters a totally susceptible population (*22*). We estimated R_0 by dividing the number of persons infected by a primary case-patient by the total number of primary case-patients.

Ethics

Many of these data were collected as part of routine surveillance or emergency outbreak investigations, so study protocols did not undergo human subjects review. In 2005, a protocol for establishing a formal Nipah surveillance system and the strategy for outbreak investigations were reviewed and approved by the Ethical Review Committee of the ICDDR,B.

Results

A total of 122 Nipah case-patients were identified; 74 (61%) were male, and the mean of all case-patients age was 27 years (range 2–75). Eighty-seven (71%) of 122 died. Fifty-nine (48%) infections were serologically confirmed. Of the 63 case-patients that were not laboratory confirmed, 59 (94%) died before any blood was collected; 4 (6%) had

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an initial serum specimen without detectable antibodies but died before a follow-up specimen could be collected.

We identified 23 introductions of Nipah virus into human populations in central and northwestern Bangladesh from 2001 through 2007 (Figure 1). Ten introductions involved clusters with a median of 10 affected persons (range 2–35). Thirteen Nipah introductions resulted in isolated human infections.

The onset of illness for the index cases for the 23 human Nipah introductions occurred from December 31 through April 20 (Figure 2). The probability that all 23 index cases would randomly occur in 5 contiguous months is $(5 / 12)^{23} \times 12 = 0.00000002$. The number of Nipah case-patients varied by year; most cases were recognized in 2004, and no cases were recognized in 2002 and 2006 (Figure 3).

In 62 (51%) Nipah case-patients, illness developed from apparent person-to-person transmission. None of these cases were professional healthcare workers exposed to Nipah case-patients on the job. The case-fatality ratio was similar for primary and secondary cases (75% vs. 66%, respectively; $p = 0.28$).

Nine case-patients (7%) were Nipah spreaders who transmitted Nipah infection to other persons. All Nipah spreaders died. 4 of these were classified as secondary cases. Nipah case-patients who had difficulty breathing during their illness were more likely to be Nipah spreaders (12% vs. 0%, $p = 0.03$). Similarly, Nipah case-patients who had cough were more likely to be Nipah spreaders (12% vs. 2%, $p = 0.080$). Patients classified as secondary cases were just as likely to have difficulty breathing as those classified as primary cases (65% vs. 66%, $p = 0.94$).

Nipah case-patients who died were more likely to be Nipah spreaders than were Nipah case-patients who survived (10% vs. 0%; Fisher exact test, $p = 0.057$). Persons who spread Nipah were no more likely to be primary Nipah case-patients than were Nipah patients who did not spread Nipah (56% vs. 49%, odds ratio 1.3, 95% confidence interval 0.34–5.1, $p = 0.74$). Nipah spreaders transmitted Nipah to a mean of 7 persons (range 1–22).

Among the 10 clusters, 5 involved person-to-person transmission ranging from 2 to 5 generations of transmission. The 60 primary Nipah case-patients infected 29 subsequent persons. The estimated basic reproductive number was 0.48.

Fourteen secondary Nipah case-patients had contact with a primary Nipah case-patient for ≤2 days. The median incubation period of these secondary cases was 9 days (range 6–11 days).



Figure 1. Locations of human Nipah virus introductions (red dots), Bangladesh, 2001–2007.

Discussion

These introductions of Nipah virus from its presumed reservoir in *Pteropus* bats to humans in Bangladesh were clustered, both in time of year as well as in specific years. Occurring during winter and spring in certain years, this clustering in Bangladesh suggests that the specific conditions necessary for Nipah virus transmission from bats to humans occurs only periodically. Perhaps shedding of Nipah virus by *Pteropus* bats is seasonal, and because of population dynamics and the accumulation of susceptible juvenile bats over time, transmission is quite low in some years compared with other years when widespread shedding and transmission occur.

The presumed wildlife reservoir of Nipah virus, bats of the genus *Pteropus*, is widely distributed across Bangladesh, the rest of the Indian subcontinent, and Southeast Asia (*18*). Wherever *Pteropus* bats have been collected and tested, they commonly have had antibodies against Nipah or a related virus (*8,9,13,23,24*). Human Nipah infections in Bangladesh, however, have been recognized in a confined geographic area. The Institute of Epidemiology Disease Control and Research in Bangladesh has national surveillance for disease outbreaks. Outbreaks involving the deaths of several previously healthy persons, which is characteristic of Nipah outbreaks, typically generate substantial local concern, media attention, and notification of local and

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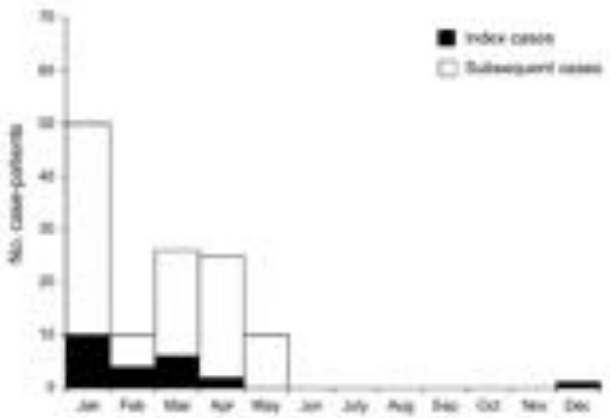

Figure 2. Human Nipah virus infections in Bangladesh, by month of illness onset, 2001–2007.

central health authorities. Despite investigations of outbreaks in all regions of the country, all confirmed Nipah outbreaks have occurred in the same central and northwestern regions (Figure 1). Notably, the only 2 outbreaks that have been reported from India have been in regions within 50 kilometers of the border with Bangladesh and immediately contiguous with the affected areas in Bangladesh (*25*,*26*). One hypothesis that would explain this geographic concentration of human cases is that the bats are attracted to specific foods available in these areas during the winter and spring; people living in these communities are occasionally exposed to foods contaminated with bat urine or saliva that contains Nipah virus. One outbreak of Nipah virus was associated with consumption of raw date palm sap, which is harvested from December through March in this region (*14*). In 21 of the 23 recognized index case-patients, Nipah virus illness developed during this harvest season.

Person-to-person transmission is a major pathway for human Nipah virus infection in Bangladesh, accounting for 51% of recognized cases in this review. By contrast, in Malaysia and Singapore, person-to-person transmission was not confirmed, although 1 nurse who cared for Nipah patients in an intensive care unit in Malaysia and reported no clinical illness had serologic evidence of Nipah virus infection and brain magnetic resonance imaging consistent with Nipah virus infection (*27*). Even if occasional unrecognized person-to-person transmission of Nipah virus occurred in the outbreak in Malaysia, person-to-person transmission is much more apparent and common in Bangladesh. Moreover, the outbreak in Siliguri, India, in 2001 was also characterized by widespread person-to-person transmission (*25*).

Three factors likely contributed to the higher frequency of person-to-person transmission of Nipah virus in Bangladesh than was observed in Malaysia. First, respiratory disease associated with Nipah infection was more common and more severe in Bangladesh compared with that in Malaysia and Singapore (*28*–*30*). Earlier studies demonstrated that Nipah virus was present in respiratory secretions of some Nipah virus–infected patients (*11*,*31*). We found that Nipah case-patients who had difficulty breathing were much more likely to be Nipah spreaders. Together, these findings suggest that when a Nipah virus–infected patient has a symptomatic respiratory tract infection associated with Nipah virus, the patient can shed an infectious inoculum of Nipah virus in his respiratory secretions. In the largest recognized Nipah outbreak in Bangladesh, touching a patient who had respiratory difficulties was a risk factor for developing Nipah infection (*16*). The personal care typically provided to ill and dying relatives in Bangladesh is likely a second important contributor to person-to-person transmission. This care is characterized by close physical interaction, frequent contact with a patient's saliva, and a lack of basic infection control practices because the paradigm of communicable disease is inconsistent with the prevailing cultural interpretation of illness (*32*). Third, all Nipah virus strains from human cases in Malaysia were genetically similar, in contrast to the marked diversity of the strains in Bangladesh (*11*). Some strains possibly possess genetic characteristics that facilitate person-to-person transmission.

Our 0.48 estimate of the basic reproductive number of Nipah virus in rural Bangladesh, a resource-poor setting with extremely limited infection control practices, suggests that Nipah virus is unlikely to cause a sustained human pandemic from person-to-person transmission. This conclusion is further supported by our observation of 23 separate introductions of the virus into the human population; none of these introductions resulted in sustained person-to-person transmission. Indeed, only 1 of the introductions exceeded 2 generations of transmission (*16*). However, we could study only 9 patients who transmitted the Nipah virus. Thus, our understanding of the variability in transmission of different strains of the virus in different contexts is limited.

This analysis has limitations. First, we almost certainly did not identify all human Nipah virus infections that occurred in Bangladesh from 2001 through 2007. Many persons in Bangladesh, especially the impoverished, do not access the formal healthcare system, even when seriously ill (*33*,*34*). The available data on human Nipah virus infection in Bangladesh are biased toward infections acquired in outbreaks recognized by public health authorities. Because meningoencephalitis is a common cause of hospitalization in Bangladesh, sporadic cases that are unrecognized as Nipah virus infection may be the more common presentation of Nipah virus infection in the country. Indeed, during 2004 and 2007, years when multiple outbreaks were iden-

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tified, many patients who sought treatment for symptoms of encephalitis in hospitals located near identified outbreak areas were tested for Nipah virus. This testing identified several additional patients infected with the virus who lived quite a distance from the outbreak villages and who had no apparent connection to other cases. Thus, surveillance almost certainly underestimates the public health impact of Nipah virus infection in Bangladesh and may underestimate its geographic and seasonal range. Because outbreaks are more likely to lead to recognition of Nipah virus infection than sporadic cases and person-to-person transmission can occur only in clusters, the overall proportion of Nipah virus infections in Bangladesh that are transmitted person to person is probably <50%.

A second limitation is that the calculation of the basic reproductive rate assumed that all persons infected by a primary case-patient were identified. The investigation team could have failed to recognize all cases, especially in persons with milder or asymptomatic infection. In Malaysia, among 178 persons without symptoms who lived on farms where at least 1 person with confirmed Nipah encephalitis was identified, 20 (11%) had antibodies against Nipah virus (*3*). This possibility of asymptomatic infection suggests that our estimate of the basic reproductive rate is a minimal estimate. However, in outbreaks, when mild or asymptomatic persons were screened in Bangladesh, few additional Nipah cases were identified (J. Hossain, pers. comm.). Moreover, only patients who died transmitted the infection, so the possible infection of persons in whom mild illness developed is unlikely to contribute to the risk for pandemic transmission.

A third limitation is that we identified only 9 persons who transmitted Nipah virus and so have limited statistical power to assess their characteristics. Indeed, the association of cough with Nipah virus transmission and death with Nipah transmission are above the traditional guideline for statistical significance. However, the weight of the evidence, including an association with respiratory illness that meets the traditional criterion for statistical significance and the isolation of Nipah virus in respiratory secretions, suggests that person-to-person transmission occurs occasionally from virus-infected patients who are efficient respiratory transmitters of the virus.

A fourth limitation is that this analysis assumes that persons in whom Nipah illness developed 5–15 days after contact with a Nipah patient were considered infected by the contact. If the subsequent case-patient had a similar environmental exposure to Nipah virus as the initial case-patient, this approach may overestimate the proportion of cases that result from person-to-person transmission. However, Nipah virus is readily recovered from the saliva of infected persons (*11*,*31*), and epidemiologic studies of individual outbreaks implicate contact with Nipah-infected patients as a risk factor for transmission (*16*). Moreover, the observed 6–11-day window between exposure and disease is consistent with incubation periods for other human viral infections. Thus, person-to-person transmission is the most likely route of transmission in these scenarios.

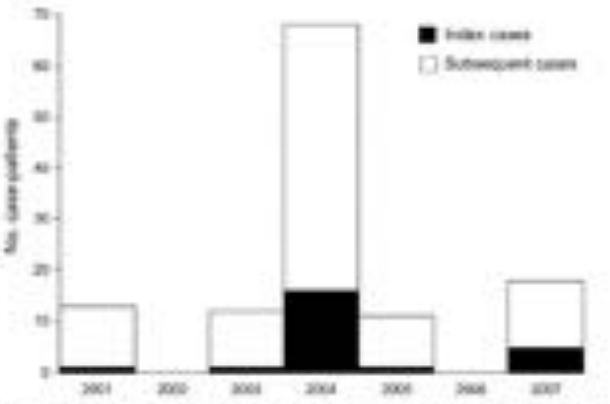

Figure 3. Human Nipah virus infections in Bangladesh, by year of illness onset, 2001–2007.

The recurrent introduction of Nipah virus from its fruit bat reservoir to humans in Bangladesh causes outbreaks with high fatality rates and substantial neurologic sequelae among survivors (*35*). Fruit bats have a critical niche in the ecosystem, contributing to both plant pollination and distribution of seeds (*36*,*37*). Preventing human Nipah virus infections in Bangladesh is difficult because these infections are relatively rare compared with many other serious and more common health threats faced by the large population of this low-income country. Improved understanding of the mechanism of zoonotic transmission from bats to humans may help identify feasible approaches to prevent future introductions of the virus into the human population. Interventions to reduce the risk for pathogen exposure by minimizing saliva contact or improving hand hygiene among persons who care for seriously ill patients in severely resource-constrained settings could reduce person-to-person transmission of Nipah as well as transmission of other dangerous pathogens. In confirmed or highly suspected cases of Nipah virus infection, respiratory droplet precautions may also be warranted.

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Original article

Isolation of Nipah virus from Malaysian Island flying-foxes

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Abstract

In late 1998, Nipah virus emerged in peninsular Malaysia and caused fatal disease in domestic pigs and humans and substantial economic loss to the local pig industry. Surveillance of wildlife species during the outbreak showed neutralizing antibodies to Nipah virus mainly in Island flying-foxes (*Pteropus hypomelanus*) and Malayan flying-foxes (*Pteropus vampyrus*) but no virus reactive with anti-Nipah virus antibodies was isolated. We adopted a novel approach of collecting urine from these Island flying-foxes and swabs of their partially eaten fruits. Three viral isolates (two from urine and one from a partially eaten fruit swab) that caused Nipah virus-like syncytial cytopathic effect in Vero cells and stained strongly with Nipah- and Hendra-specific antibodies were isolated. Molecular sequencing and analysis of the 11,200-nucleotide fragment representing the beginning of the nucleocapsid gene to the end of the glycoprotein gene of one isolate confirmed the isolate to be Nipah virus with a sequence deviation of five to six nucleotides from Nipah virus isolated from humans. The isolation of Nipah virus from the Island flying-fox corroborates the serological evidence that it is one of the natural hosts of the virus. © 2002 Éditions scientifiques et médicales Elsevier SAS. All rights reserved.

Keywords: Nipah virus; Fruitbat; Isolation; Characterization

1. Introduction

A novel paramyxovirus, named Nipah virus (NiV), was first isolated from the cerebrospinal fluid (CSF) of a patient from Sungai Nipah village in March 1999 [1,2] and subsequently identified as the aetiological agent responsible for the outbreak of fatal encephalitis in Malaysia [3,4]. This virus is antigenically related to, but distinct from, Hendra virus first isolated in September 1994 during an outbreak of a severe respiratory illness in horses and resulted in the deaths of 14 horses and two humans in Queensland, Australia [5–7]. The outbreak of NiV encephalitis in Malaysia started in September 1998 and reached its peak in March 1999 with 265 human cases reported and 105 fatalities [3,8]. The virus also caused a respiratory and central nervous system illness in pigs, and the majority of the human cases occurred in individuals who had occupational exposure to the infected pigs [9–11]. The spread of the outbreak was due to the movement of infected pigs from farm to farm. The outbreak was only controlled after successful isolation and identification of the aetiological agent followed by the culling of more than a million pigs in the infected and immediate surrounding areas [3,8].

With the outbreak under control, there is an urgent need to identify the natural reservoir of the virus to obtain a better understanding of the mode of introduction of the virus into livestock and prevention of future reintroduction. Surveillance of wildlife species for evidence of the origin of the virus was an integral part of the outbreak investigation. A survey of bat populations in peninsular Malaysia was undertaken, with emphasis on fruit bat species based on the

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experience of the isolation of Hendra virus from large fruit bats [12] and the presence of neutralizing antibodies to Hendra virus in these bats [13,14]. During the initial phase of surveillance, blood and tissue samples were collected from 324 bats, comprising 14 species, caught by mist-netting and shooting. Neutralizing antibodies to NiV were found mainly in Island flying-foxes (*Pteropus hypomelanus*) and Malayan flying foxes (*Pteropus vampyrus*) [15] but no virus reactive with anti-Nipah virus antibodies was isolated.

Based on the above serological results, we undertook a novel approach by collecting urine samples from the Island flying-foxes, *P. hypomelanus*. We report here the isolation and identification of NiV from two pooled urine samples of Island flying-foxes and a swab sample of partially eaten fruit.

2. Methods

2.1. Bat urine sample collection

Collection sites were chosen based on information obtained from the Malaysian Wild Life Protection Department and village headmen of islands along the coastal region of the country. A survey of the roosting places of the fruit bats was made and the exact spots where the urine and faeces of fruit bats expected to be deposited (indicated by the presence of previous dropping on the ground) were carefully delineated during the day. Half-an-hour before the Island flying foxes returned to roost the following morning (usually about 5.00 a.m.), clean translucent plastic sheets measuring 1.6 × 2.7 metres were placed at the marked spots directly under the roosting fruit bats. Sterile cotton swabs were used to soak up the urine as soon as it landed on the plastic sheet, 4–5 drops per swab, and kept at 4 °C in viral transport medium [1X Hank's balanced salt solution (ICN Biomedicals, Inc., USA), 1% bovine albumin, pH 7.4] containing amphotericin B (15 μg/ml), penicillin G (100 units/ml) and streptomycin (50 μg/ml). During the night, trips were made to the feeding ground of the fruit bats consisting of fruiting 'Mango' (*Mangifera indica*) and 'Jambu Air' (*Eugenia aquea*) trees, which was located 1–2 km from the roosting place. Careful observation was made on the feeding pattern of these fruit bats and swab samples were taken from partially eaten fruits as soon as they landed on the ground.

2.2. Virus isolation and identification

In the laboratory, each swab in viral transport medium was lightly vortexed and 200 μl of the medium containing the swab from each pooled urine specimen or each partially eaten fruit were carefully transferred into each well of a 24-well tissue culture plate pre-seeded with 1×10^5 Vero cells (ATCC, CCL-81) in 1 ml of Eagle's minimal essential growth medium. Single inoculation was performed for each sample. The plates were carefully sealed and incubated at 37 °C. Daily examination was made and any sample showing cytopathic effect (CPE) was inoculated into a flask of confluent Vero cells. Once the cell monolayer showed 75% CPE, the cells were washed with sterile phosphate buffered saline and collected by centrifugation at 600 *g* for 10 min. Multiple cell smears were prepared on Teflon-coated slides and air-dried in a class II type A/B3 biosafety cabinet under UV irradiation. After fixing in cold acetone for 10 min, the slides were stained by indirect immunofluorescence using convalescent serum sample from a patient who had recovered from Nipah encephalitis as well as with Hendra-specific hyperimmune mouse ascitic fluid. Non-infected Vero cells were similarly stained with the convalescent Nipah serum and Hendra-specific antibodies to serve as the negative control. In addition, the slides were also stained with mono-specific antibodies (Chemicon Co., USA) against mumps virus, measles virus, respiratory syncytial virus, and parainfluenza virus 1, 2, 3.

Virus re-isolation was attempted from the original positive specimens as well as from 20 original negative specimens stored at −70 °C for 2 months as control.

2.3. Molecular characterization

A 75-cm^2 flask of Vero cells was inoculated with 0.5 ml of the bat virus isolated from one of the urine samples. When the CPE was almost complete, the cells were pelleted and total RNA was extracted by using the RNeasy Mini Kit (Qiagen, Germany). Synthesis of single-strand viral cDNA was performed by using the Thermoscript RT™ Kit (GIBCO BRL, USA) in a 20-μl reaction mix. Ten pairs of NiV-specific primers were synthesized based on the published nucleotide (nt) sequence information of the NiV nucleocapsid (N), phosphoprotein (P) and matrix (M) genes (GenBank accession number AF212302) [16], and selective amplifications of the virus cDNA with these primers were performed separately in ten tubes, each with 50 μl of PCR mix. Thirty cycles of 30 s at 94 °C, 30 s at 55 °C, and 1 min at 72 °C were performed. The amplified products were analysed by electrophoresis in 1% (w/v) agarose gel and subsequently compared with those of NiV isolated from humans.

The PCR products of the bats' isolate were gel-purified and extracted with the QIAquick PCR Purification Kit (Qiagen, Germany). Nucleotide sequences of both strands of each purified PCR product were determined by first performing the sequencing reactions with appropriate viral-specific forward and reverse primers using the ABI Big Dye Terminator Cycle Sequencing Kit (Applied Biosystems, USA). Detection of the sequencing products were performed on an ABI 377 automated DNA sequencer (Applied Biosystems, USA). The segments of sequence data were aligned using Clone Manager 5/Align Plus 4 programme (S&E Software, USA) and further overlapping viral-specific forward and reverse primers were then synthesized using

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the sequence information obtained, to sequence through the previous primers sites that were based on the NiV sequence information deposited in the GenBank. Following the availability of sequence information of the NiV fusion protein (F) and glycoprotein (G) genes in the GenBank (accession numbers AF238466 and AF238467) [16], a similar process was carried out to sequence the F, G and respective intergenic regions of the virus isolated from fruit bat. Thus, each nucleotide was sequenced at least four times.

2.4. Management and genetic analysis of nucleotide and deduced amino acid sequences

The sequence data derived from PCR products were routinely managed using the Clone Manager 5 and Align Plus 4 programme package. Multiple sequence alignments were performed using standard linear scoring matrix with the following parameter settings: mismatch penalty of 1, open gap penalty of 4, extended gap penalty of 1 and similarity significance value cut-off of 60%.

Multiple sequence alignments and neighbour-joining phylogram were generated using the Clustal X programme [17]. Phylogenetic analysis was conducted using the PROTDIST and KITSCH programmes in the PHYLIP software package Version 3.5c [18]. Most likely evolutionary relationships were determined by evaluation of trees from 100 randomized resampling cycles. Bootstrap verification of the resulting phylogenetic tree was performed by analysis of 100 bootstrapped replicates using the SEQBOOT, NEIGHBOURING-JOINING and CONSENSE programmes of the same package. Final tree files were visualized using the Treeview programme [19].

3. Results

3.1. Sample collection

Between August 1999 and June 2000, three field trips were made to collect samples for virus isolation from the same colony of Island flying-foxes (Fig. 1) roosting in trees along the beach in Tioman island, located about 25 km off the eastern coast of peninsular Malaysia. On the first trip (17th August 1999), 50 pooled urine samples were collected and each pool consisted of 4–5 drops of bat urine. A second trip (23rd August 1999) was made 6 d later resulting in the collection of 275 similarly pooled urine samples. On the third field trip (11th June 2000), the collection of bat urine samples was carried out over three consecutive mornings. A total of 263 pooled urine samples and 27 swabs of partially eaten fruits were collected.

3.2. Virus isolation

Four virus isolates that caused CPE in Vero cells with the formation of multinucleated giant cells were isolated from four pooled urine samples collected during the first field trip. All the isolates were identified as a novel paramyxovirus, named Tioman virus [20], belonging to the genus *Rubulavirus*. No NiV was isolated during that trip. During the second field trip, no infectious agent was isolated from the pooled urine samples despite performance of a blind passage. Twenty virus isolates causing three different patterns of syncytial CPE with formation of giant cells in Vero cells were obtained from 19 pooled urine samples as well as from a swab of a partially eaten Jambu Air (*E. aqueu*) fruit



Fig. 1. A colony of Island flying-foxes (*P. hypomelanus*), roosting in a 'Ketapang' tree on Tioman island situated about 25 km off the eastern coast of peninsular Malaysia.

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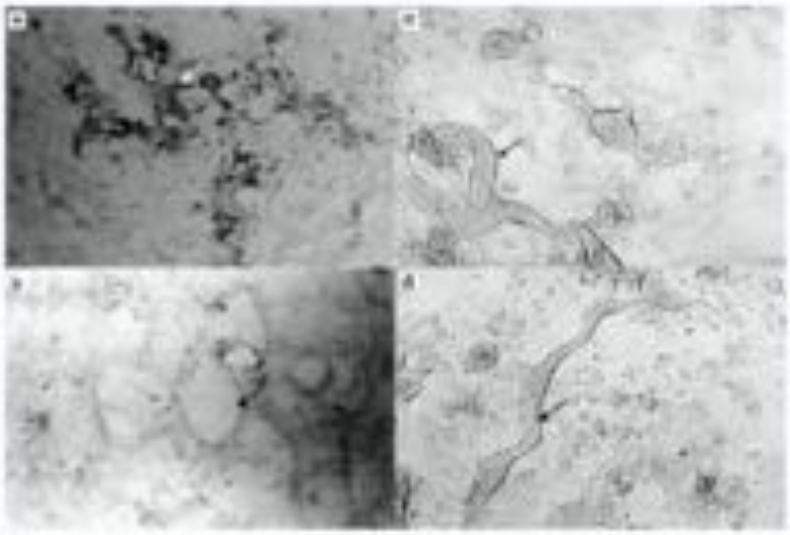

Fig. 2. Composite photograph of Vero cells (ATCC, CCL-81) showing syncytial CPE due to infection by various type of viruses. The photograph was taken 24 h after inoculation, except for (A) which was taken 48 h post-inoculation. Original magnification: 100× for all components. Arrows indicate multi-nucleated syncytial giant cells. A) Vero cells infected with Tioman virus. B) Vero cells infected with another yet to be characterized virus isolated from the urine of *P. hypomelanus*. C) Vero cells infected with Nipah virus isolated from the urine of *P. hypomelanus*. D) Vero cells infected with Nipah virus isolated from human CSF.

collected on the third field trip. Five of the isolates caused CPE in Vero cells similar to that of Tioman virus (Fig. 2a), 12 isolates produced syncytial CPE yet to be characterized (Fig. 2b) and three isolates [two from urine (sample nos B13/6-18 and B13/6-43) and one from the swab of a partially eaten fruit (sample no. 3A13/6-4)] caused CPE (Fig. 2c) similar to that of NiV isolated from humans (Fig. 2d). Of the three isolates that caused Nipah-like CPE, CPE was noted on the 6th and 8th day post-inoculation for the urine samples and the 9th day post-inoculation for the swab of the partially eaten fruit. The wells with positive Nipah-like CPE were located in three different 24-well culture plates.

3.3. Immunofluorescent antibody staining

The infected Vero cells from all 20 isolates did not react with a range of commercial monoclonal antibodies against known human paramyxoviruses. The Vero cells infected with Tioman virus did not stain with a Nipah convalescent human serum as well as with Hendra-specific hyperimmune mouse ascitic fluid. Similarly, the Vero cells infected with the yet to be characterized virus did not react with the Hendra-specific hyperimmune mouse ascitic fluid but gave a weak positive speckled pattern of staining with Nipah convalescent human serum. However, the infected Vero cells from the three virus isolates that caused Nipah-like CPE stained strongly with Nipah convalescent human serum as well as with Hendra-specific hyperimmune mouse ascitic fluid (Fig. 3a, b). The non-infected Vero cells did not give positive staining with either Nipah convalescent serum or Hendra-specific hyperimmune mouse ascitic fluid (figure not shown).

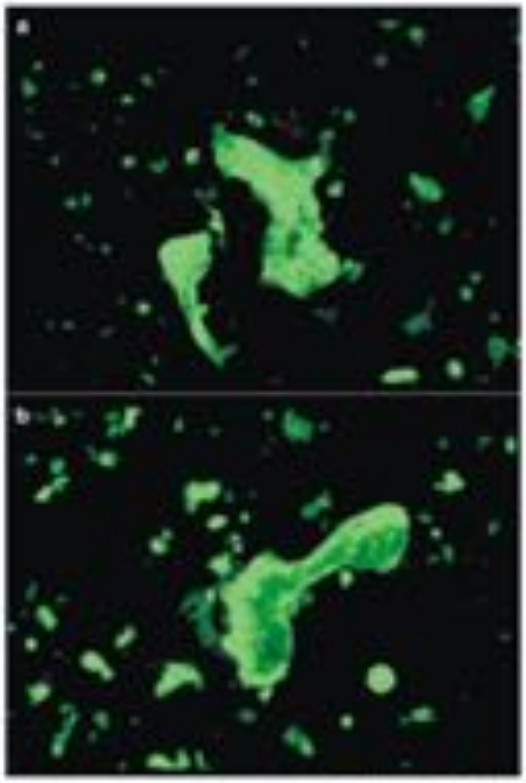

Fig. 3. Positive immunofluorescent staining of Vero cells infected with Nipah virus isolated from the urine of *P. hypomelanus*. A) Stained with a convalescent human serum infected with Nipah virus. B) Stained with Hendra-specific hyperimmune mouse ascitic fluid. Original magnification: 400×.

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3.4. Virus re-isolation

All three viruses that stained positively with Nipah and Hendra-specific antibodies were successfully re-isolated from the original specimens 2 months after storage. No virus was re-isolated from the original negative control specimens. All three re-isolated viruses gave similar CPE in Vero cells and staining reaction by indirect immunofluorescent antibody staining.

3.5. Molecular characterization

Selective amplifications of one of the Nipah-like isolates by PCR using the initial ten pairs of Nipah-specific primers yielded PCR products of the expected size from each of the ten separate reaction tubes. The results were comparable to those obtained previously using cDNA of NiV isolated from humans (Fig. 4). A continuous 11,200-nt fragment was generated by sequencing all the PCR amplicons including the F and G genes, followed by alignment of the derived nucleotide sequences using the Clone Manager 5/Align Plus 4 program. This fragment represents the partial nucleotide genome of NiV isolated from the urine of Island flying-fox and it comprises the N, P, M, F and G genes with the trinucleotide CTT as the intergenic sequence. The sequence data have been deposited in the GenBank under the accession number AF376747.

Alignment and analysis using the same computer programme showed that the bat NiV shared 99% sequence homology with the NiV isolated from human (Nipah-H) over the nucleotide region extending from the beginning of the N-gene (nt 56) to the end of the G-gene (nt 11,255) (GenBank accession number AF212302). Detailed analysis over the same nucleotide region shows that bat NiV differed from the Nipah-H by six nucleotides at nucleotide positions 201 (T to C), 2381 (T to C), 3022 (T to C), 7696 (C to T), 9248 (T to C) and 9392 (A to G). We also compared this bat NiV sequence with the complete nucleotide sequences of two Nipah viruses isolated from the only surviving encephalitic patient with positive virus isolation from his CSF (unpublished data). These two human isolates were designated UMMC1 (isolated from CSF) and UMMC2 (isolated from throat secretion). Bat NiV differed from UMMC1 by five nucleotides; nucleotide positions 201 (T to C), 3022 (T to C), 7696 (C to T), 9248 (T to C) and 9392 (A to G). It differed from UMMC2 by six nucleotides occurring at the same position with similar nucleotides changed as the Nipah-H. That means UMMC2 has an identical nucleotide sequence to Nipah-H and both differed from UMMC1 by only one nucleotide at position 2381. Nt 2381 is located at the 3′ non-coding region of the P gene. The change of nucleotide at position 201 results in an amino acid (aa) change (isoleucine to threonine) at position 30 of the N protein. The change in nucleotide at position 3022 results in an aa change (leucine to proline) at position 206 of the P protein. Similarly, the change in nucleotide at position 7696 results in an aa change (threonine to methionine) at position 348 of the F protein. Nt 9248 and nt 9392 are both located at the coding region of the G gene and both nucleotide changes do not result in any aa change. There is no base deletion or insertion detected over the 11,200-nt region.

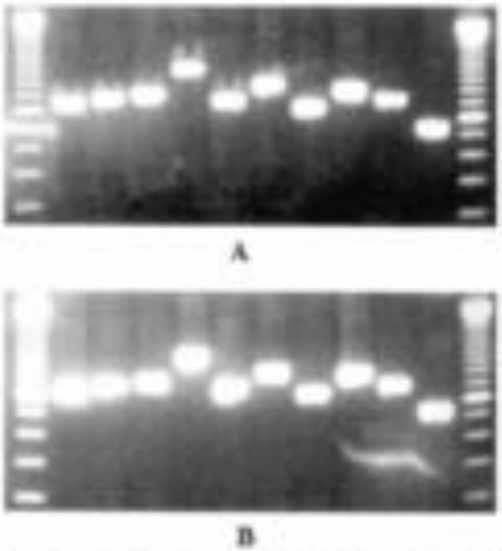

Fig. 4. Ethidium bromide-stained agarose gel of ten PCR products derived from (A) Nipah virus isolated from humans and (B) the virus isolated from the urine of *P. hypomelanus*. The two outer lanes contained the 100-bp DNA ladder (GIBCO BRL, USA), starting with the 200-bp marker.

4. Discussion

A novel paramyxovirus named Nipah virus emerged in Malaysia in late 1998, and caused fatal disease in domestic pigs and humans as well as substantial economic loss to the local pig industry. Epidemiological features of the outbreak indicate that infection in humans is due to close contact with live infected pigs and the spread of the outbreak was due to the movement of infected pigs [10–11]. A wildlife reservoir was suspected to be the source of the virus. Though neutralizing antibodies to NiV were detected in Malayan flying foxes (*P. vampyrus*) and Island flying foxes (*P. hypomelanus*) [15], no virus reactive with anti-Nipah virus antibodies was isolated. The finding that anti-NiV antibodies cross-neutralized Hendra virus, though at a lower titre and vice versa [4], led to the need to isolate NiV from its natural host to confirm the suspicion that fruit bats of the *Pteropus* species are the natural reservoir.

The conventional approach of collecting specimens for virus isolation from these fruit bats involves mist-netting or shooting [15]. These methods of collection are labour-intensive and the shooting of these protected animals requires a special license. The number of animals collected by these methods is therefore limited. The approach we used in this study is based on the fact that fruit bats will urinate followed by defecation soon after they return from their foray for food, and their excreta are discharged almost

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vertically downwards (due to their adopted position during urination and defecation) onto the ground. To preclude rapid evaporation, the urine samples have to be collected from the plastic sheet almost immediately. Moreover, care must be taken to collect the urine samples quickly before contamination by faecal materials. To the best of our knowledge, the urine samples were of bat origin as no other animals were noted to share the same roosting place, and urine and faecal samples were deposited on the plastic sheets only upon the return of the fruit bats. The method adopted here is novel, simple and easy to perform, allowing for many specimens to be collected in a single morning. The collection process can be repeated, as none of the flying-foxes is killed. This is particularly important if virus infection and excretion from the host is intermittent and periodic in nature. The isolation of virus from the urine sample also shed some understanding on the mode of virus transmission. From our experience, fruit bats did not urinate or defecate while feeding at the feeding ground and only appeared to urinate and defecate at the roosting place. The likelihood of the partially eaten fruit being contaminated by urine was low. There is a possibility of transmission of NiV via contaminated fruit that could be readily devoured by pigs.

The results of this study show that the isolation rate of NiV from the urine of Island flying-foxes was low, suggesting that only a few bats in the colony were excreting the virus. This finding is not in concordance with the earlier serological finding that 25% (11/44) of fruit bats from this colony had neutralizing antibodies to NiV [15]. The discrepancy may be due to the low virus excretion rate in the urine of these infected bats or the small sampling size of the serological study. The other possibility for the discrepancy may be due to the fact that urine or saliva may not be the only (or major) routes of excretion of virus. Epidemiological and experimental data from Field et al. [21] suggested infected foetal tissues or fluids as a possible mode of transmission of Hendra virus. Our study also shows that the excretion of NiV from these fruit bats is probably periodical in nature as no NiV was isolated on the first two attempts.

There is always the possibility of laboratory contamination, although highly unlikely in this study because 1) no human Nipah virus isolation work was performed for at least 2 months prior to the work on the isolation of virus from bats, 2) three isolates of bat Nipah virus were isolated from three different 24-well culture plates, and 3) the virus was re-isolated from the original positive samples and not from the original 20 negative samples.

The identification of the isolates as NiV was based on characteristic cytopathic effect in Vero cells and the staining reaction with specific Nipah and Hendra antibodies. The identification of one of the isolates was further confirmed by sequencing of its structural genes (N, P/C/V, M, F and G) and comparison of the nucleotide sequences of these genes with the published sequences of the NiV strain isolated from humans.

The near identical sequence similarity among the three Nipah viruses isolated from human patients during the outbreak of febrile encephalitis and their minor sequence variation from the bat isolate suggest that the spill-over of NiV from its natural reservoir, Pteropid bats, is most probably a recent event. The hypothesis is compatible with the epidemiological features of the outbreak due to the virus [8,12,22].

The finding of NiV in the Malaysian Island flying-foxes does not exclude the possibility of other bat or animal species as a reservoir for this virus. However, this finding may demonstrate one way in which the virus can be introduced into the pig farm through fruit bat secretions. In the re-structuring of pig farms in Malaysia, this may have to be taken into account and certain fruit trees likely to attract flying-foxes should be excluded from such farms. Since flying-foxes, especially *P. vampyrus*, are migratory in nature, this information should be of interest to neighbouring countries where pig farming is an important industry.

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Henipavirus Infection in Fruit Bats (*Pteropus giganteus*), India

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We tested 41 bats for antibodies against Nipah and Hendra viruses to determine whether henipaviruses circulate in pteropid fruit bats (*Pteropus giganteus*) in northern India. Twenty bats were seropositive for Nipah virus, which suggests circulation in this species, thereby extending the known distribution of henipaviruses in Asia westward by >1,000 km.

Nipah virus (NiV) and Hendra virus (HeV) are zoonotic paramyxoviruses (genus *Henipavirus*) that have caused human deaths in Australia, Malaysia, Singapore, India, and Bangladesh (*1*–*4*). Known reservoirs for henipaviruses are *Pteropus* spp. fruit bats, which are distributed across the Indo-Pacific region from Madagascar eastward to the South Pacific islands (*5*). Evidence of henipavirus infection has been reported in *Pteropus* bats from Malaysia, Bangladesh, Australia, Thailand, Cambodia, Indonesia, and Madagascar, which supports the theory that these bats have co-evolved with henipaviruses (*6*–*8*).

The first known outbreak of NiV encephalitis in India occurred in 2001 in Siliguri, West Bengal (*1*). The fruit bat (*P. giganteus*) is present across the Indian subcontinent and, although it is suspected as the reservoir host for NiV in Bangladesh, its status as a reservoir for henipaviruses in India is unknown. Seven outbreaks of NiV encephalitis were recognized in Bangladesh from 2000 through 2008, and antibodies to NiV have been found in *P. giganteus* in several colonies there, including colonies adjacent to human case-patients (*3*,*5*,*9*). In the current study, we examined a population of *P. giganteus* bats in India, >1,000 km west of Siliguri, for antibodies to henipaviruses.

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The Study

We captured 41 *P. giganteus* bats from a colony in Haryana State in northern India from June 24 through June 30, 2003, by using mist nets. Blood was collected from the brachial or cephalic artery or from the vein by using a heparinized 3.0-mL syringe and a 22-gauge or 27-gauge needle and stored for 24 hours at 4°C to allow for plasma separation; the separated plasma was then stored at −20°C until use. Sex, age, body condition score, pregnancy status, lactation status, weight, and forearm length were recorded. Age was estimated by the presence of secondary sexual characteristics and dental wear. Body condition was assessed by digital palpation of the pectoral muscles and individuals were assigned a body condition score (BCS) of "poor," "fair," or "good." Unweaned juveniles were not assigned a BCS because of their physical immaturity. Pregnancy was determined by digital palpation, and a bat was considered "lactating" if milk could be expressed from either teat. All bats were released after sampling.

All 41 plasma samples were screened for antibodies to NiV and HeV by using virus-specific indirect ELISAs. Thirty-nine samples (2 samples had insufficient amounts of plasma remaining) were analyzed by using NiV and HeV serum neutralization tests (SNTs) under Biosafety Level 4 conditions (*10*). For the ELISA, coating antigen was derived from purified HeV- and NiV-infected Vero cells, and positive control serum specimens were obtained from experimentally infected horses (HeV) and pigs (NiV). Protein A/G conjugate was used to detect bound bat serum. A final serum dilution of 1:50 was used for the bat samples. A sample was considered reactive if the ratio of its average optical density at 450 nm (OD_{450}) of infected Vero cell antigen-coated wells (each sample was tested in duplicate) to uninfected Vero cell antigen-coated wells was >2.0 and the average OD_{450} value for the sample in the infected Vero cell antigen-coated wells was >0.2. Positive control serum samples were confirmed by both ELISA and SNT. SNT results were considered positive if virus neutralization occurred at ≥1:5 dilution (*11*). If neutralizing antibodies were present for both HeV and NiV, the higher titer was considered the positive test only if the difference between them was >4-fold (*11*). Samples that had positive titers to both viruses that differed by <4-fold were considered positive for an unspecified henipavirus.

The results of the serologic tests are presented in the Table, including comparisons of the results by gender, lactation status (females), and BCS. Twenty-six (63%) of 41 samples (95% confidence interval [CI] 47%–78%) were reactive in the NiV ELISA, 5 of which were also reactive in the HeV ELISA. No plasma samples reacted only in the HeV ELISA. Twenty (51%) of 39 samples (95% CI 35%–68%) had neutralizing antibodies to NiV, and 10 (26%) of 39 (95% CI 13%–42%) had neutralizing antibodies to

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HeV. One (3%) of 39 samples (95% CI 0%–13%) had a neutralizing titer of 5 to NiV and HeV. This sample reacted in the NiV ELISA, but not in the HeV ELISA, although because it had equivalent neutralizing titers to both viruses, it was considered positive for an unspecified henipavirus. The ELISA showed 95% sensitivity and 75% specificity compared with the SNT.

Each of 2 unweaned pups matched their mother's serostatus, with 1 pup positive by SNT (pup 80, mother >640). Samples of the other mother–pup pair were seronegative. There were no significant differences in the NiV seroprevalence in male bats on SNT (8/12) compared to female bats (12/27) by using a Fisher exact test (FET; p = 0.300) or in lactating female bats (8/19) compared to nonlactating (5/8) female bats (FET; p = 0.420). We found significant differences in seroprevalence between bats with a poor and fair BCS (FET; p = 0.005), with bats in poor condition having a lower antibody prevalence than those with fair BCS. No difference in seroprevalence was found between the poor and good BCS groups or the fair and good groups.

Conclusions

Our study provides evidence that NiV, or a closely related henipavirus, circulates in Indian fruit bats (*P. giganteus*), thereby extending the range of the genus *Henipavirus* in Asia westward by >1,000 km. Our results are consistent with reports of NiV in *P. giganteus* bats in Bangladesh (*3*) and with *Pteropus* spp. being the primary reservoir of henipaviruses (*5*). Logistical limitations prevented us from attempting virus isolation and testing for viral RNA.

Previous studies have demonstrated that ELISAs, although less specific than SNTs, are useful screening tests for henipaviruses (*11*). Our results support this assertion, with the ELISA showing a high sensitivity. In our study, neutralizing antibodies to HeV and NiV were detected in 11 bats, 10 of which exhibited a >4-fold titer to NiV antibodies. Concurrent HeV and NiV titers are considered due to cross-neutralization rather than exposure to both viruses (*8*,*11*,*12*). Serologic studies provide information about the proportion of a population exposed to NiV, but not about the prevalence of bats that may be shedding virus or the virus itself. Further work in this area is required to fully characterize the henipavirus(es) involved and to confirm the status of *P. giganteus* as a reservoir.

Researchers have suggested that pregnancy plays a key role in henipavirus transmission among Australian *Pteropus* spp. and from bats to other species (*13*,*14*). In our study, we found no significant difference in seroprevalence between sexes, or between lactating and nonlactating females. Of the 2 lactating females carrying pups, 1 had a high titer of >640 and its pup had a titer of 80 against NiV, which suggests the passive transfer of antibodies; the other dam–pup pair was seronegative. Seroprevalence appeared to be significantly greater in bats with fair BCS when compared with those with poor BCS; however, no significant differences were found between good and poor or good and fair BCS groups. The findings that bats with fair BCS had a higher seroprevalence than poor BCS bats, but that there was no difference between good BCS bats and the other 2 groups, may be explained by the subjective classification of a bat's body condition. Those bats deemed to have fair body condition may have been more similar to those with robust bodies (good BCS) than those with thin, emaciated bodies (poor BCS). In fact, if one combines the good and fair categories, and compares the seroprevalence (18/28) with that of the poor group, the difference is still significant ($p = 0.007$); by contrast, combining the fair and poor categories (17/32) and comparing that seroprevalence to the good category results in no significant difference ($p = 0.660$). Having a lower seroprevalence in bats with the

Table. ELISA and SNT results and univariate associations between serostatus and other variables for wild-caught *Pteropus giganteus* bats in India*

Characteristic	ELISA		SNT	NiV SNT comparisons, p value†
	No. NiV reactive/ no. tested	No. HeV reactive/ no. tested	No. NiV positive/total (%) [median titer; range]	
Total	26/41	5/41	20/39‡ (51) [80; 5–640]	
Male	10/12	3/12	8/12 (67) [80; 20–640]	0.300
Female	16/29	2/29	12/27‡ (44) [80; 5–640]	
Lactating	12/20	2/20	8/19‡ (42) [80;20–640]	1.00
Nonlactating	4/9	0/9	4/8‡ (50) [80;5–80]	
Body condition score§				
Poor	5/9	0/9	1/9 (11) [640; NA]	P v F: 0.005; F v G: 0.315; P v G: 0.506
Fair	16/24	5/24	16/23 (70) [80; 5–640]	
Good	3/6	0/6	2/5 (40) [80; 40–80]	

*SNT, serum-neutralization test; NiV, Nipah virus; HeV, Hendra virus; NA, not applicable; P, poor; F, fair; G, good.
†Fisher exact test p value significant at <0.05.
‡Two samples had insufficient plasma for SNT (both were ELISA negative); sample 1 was from a nonlactating adult female with a good body condition score (BCS) and the other was from a lactating adult with a fair BCS. A third sample, a nonlactating adult female with a good BCS had equivocal NiV/HeV SNT titers (5), which was attributed to an unspecified henipavirus and considered negative for NiV and HeV.
§Two pre-weaned pups (1 male, NiV SNT negative; 1 female, NiV SNT positive titer 80) were excluded from the BCS dataset because of their physical immaturity.

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poorest BCS may be explained as an artifact of the nonrandom sampling (we sampled those bats that were first to be captured), by the limited sample, or it could suggest that NiV infection causes death in *P. giganteus* bats that are in poor physical condition. The latter explanation is less plausible because experimental infections of *Pteropus* spp. with henipaviruses produce only subclinical infection with no illness or death (*15*).

In northern India, as in Bangladesh, *P. giganteus* bats live in close association with the human population. Indeed, the colony examined in this study lives in a busy town above a major tourist attraction. Previous studies of NiV encephalitis outbreaks in Bangladesh have identified fresh date palm juice or fruit as plausible foodborne routes of transmission between bats and humans (*3*,*16*). The multiple outbreaks of NiV in Bangladesh, and the 2001 outbreak in West Bengal, show a continued risk for spillover infection between bats and humans in this region. Our findings suggest that the risk for NiV spillover to humans should be considered over a much wider area than previously regarded.

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Risk Factors for Nipah Virus Infection among Pteropid Bats, Peninsular Malaysia

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We conducted cross-sectional and longitudinal studies to determine the distribution of and risk factors for seropositivity to Nipah virus (NiV) among *Pteropus vampyrus* and *P. hypomelanus* bats in Peninsular Malaysia. Neutralizing antibodies against NiV were detected at most locations surveyed. We observed a consistently higher NiV risk (odds ratio 3.9) and seroprevalence (32.8%) for *P. vampyrus* than *P. hypomelanus* (11.1%) bats. A 3-year longitudinal study of *P. hypomelanus* bats indicated nonseasonal temporal variation in seroprevalence, evidence for viral circulation within the study period, and an overall NiV seroprevalence of 9.8%. The seroprevalence fluctuated over the study duration between 1% and 20% and generally decreased during 2004–2006. Adult bats, particularly pregnant, with dependent pup and lactating bats, had a higher prevalence of NiV antibodies than juveniles. Antibodies in juveniles 6 months–2 years of age suggested viral circulation within the study period.

Nipah virus (NiV) disease emerged in Peninsular Malaysia during September 1998–April 1999 and resulted in 105 human deaths (>40%) and compulsory culling of 1.1 million pigs (*1*). NiV disease has been successfully controlled in Malaysia. However, elsewhere in Bangladesh and India, 12 NiV outbreaks have since occurred (*2*). Pteropid bats (family Pteropodidae, genus *Pteropus*) were the most likely reservoir host of the virus, and evidence of NiV in these bats had been consistently found in populations across southern Asia (*3–6*) and Africa (*7*) despite an absence of outbreaks in some areas.

Characteristics of bats that promote their competency as a natural host and reservoir for many emerging pathogens from evolutionary, ecologic, sociobehavioral, and immunologic perspectives are progressively being reported (*8–11*). In Malaysia, previous surveillance work suggest 2 pteropid species, *Pteropus hypomelanus* (variable flying fox) and *P. vampyrus* (large flying fox) bats, as reservoir hosts for NiV (*12*). *P. hypomelanus* bats reside on offshore islands along the eastern (n = 14) and western (n = 4) coasts of the peninsula (*13*). NiV was first isolated from pooled urine samples from these bats on the island of Pulau Tioman off the eastern coast of the state of Pahang (*14*). *P. vampyrus* bats, the pteropid species identified during the first NiV disease outbreak location in 1998 (*3*), are anthropogenic-susceptible bats residing in remote and inaccessible areas such as mangroves and dense forests (*13*). *P. vampyrus* bats roost mainly on the mainland but may have focal transitory points on surrounding islands as they travel (*16,17*).

Our recent follow-up work on a cohort of *P. vampyrus* bats (*18,19*) showed a possible NiV recrudescent event leading to horizontal viral transmission to other bats in the colony. The findings further elucidated maintenance and transmission dynamics of the virus within and among roosts, colonies, and the bat metapopulation. In this report, we present results of 2 studies conducted concurrently to determine the geographic extent and prevalence of

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[1]Members of the Henipavirus Ecology Research Group are listed on the group's website (www.ecohealthalliance.org/herg).

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NiV-neutralizing antibody for *P. vampyrus* and *P. hypomelanus* bats, and to identify the sexual and reproductive maturity determinants for NiV seropositivity in the wild.

Materials and Methods

Study Design and Study Populations

Cross-sectional Study of NiV (Distribution Study)

During March 2004–May 2007, we sampled *P. hypomelanus* bat colonies from several roost sites in Pulau Kapas and Pulau Perhentian on the northeast coast of Terengganu, Pulau Tioman on the southeast coast of Pahang, and Pulau Pangkor on the northwest coast of Perak. We also sampled *P. vampyrus* bats in the states of Perlis; Perak (Teluk, Mcrisah, and Lenggong); Terengganu (Kampung Alor Lek, Setiu, and Kuala Berang); Pahang (Tanjung Agas, Pasir Panjang, and Gunchong); and Johor (Bentat and Kesang) (Figure 1). We determined these sites using published information on pteropid roost locations (*15*), reports from the Malaysia Department of Parks and Natural Resources authority (PERHILITAN), information from local hunters and residents, and field observations. A complete list of observed roost sites was published by Epstein et. al. (*16*). Colonies were selected for this study on the basis of observed presence of bats, accessibility for bat capture, and roost size (e.g., number of bats). A sample size of 35 bats was targeted at each location or for each sampling effort to be able to detect a NiV-seropositive bat given a minimum prevalence of 10% with 10% precision at a confidence level of 95% (*20*).

Permission for the study was granted by PERHILITAN, and Institutional Animal Care and Use Committee approval was obtained from the Wildlife Trust Institutional Animal Care and Use Committee (New York, NY, USA). A special permit to trap and humanely kill the bats was obtained from PERHILITAN. Bats were captured nonrandomly by using 2 methods: opportunistic sampling of hunted bats (hunters were not solicited or incentivized to hunt bats for this study) and mist nets.

Hunted bats were sampled at the site of hunting, and bats were attributed to the location of the nearest known roost. Blood samples were collected by cardiac puncture, and the kidneys were harvested. The blood, urine, and kidney samples were processed as described (*18*). Bats captured in mist nets were extracted from the nets immediately after capture and anesthetized before sampling by using medetomidine, a combination of medetomidine/ketamine (*21*), or isoflurane gas. Blood (3 mL) was collected from the cephalic vein or brachial vein and placed into serum-separator tubes (Vacutainer, Becton Dickinson, Franklin Lakes, NJ, USA). Sterile cotton swabs were used to collect oropharyngeal and urogenital samples. All samples were

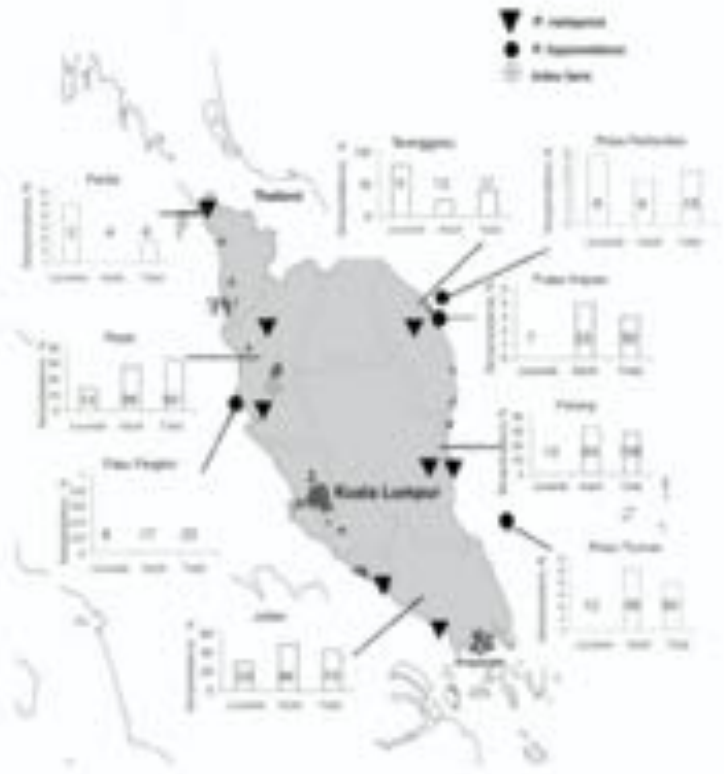

Figure 1. Trapping sites for *Pteropus hypomelanus* and *P. vampyrus* bats and seroprevalence of Nipah virus in 6 sites, Peninsular Malaysia, January 2004–September 2006. Values in the small graphs indicate number of positive samples.

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stored in liquid nitrogen at −190°C) and transported to the Veterinary Research Institute in Ipoh, Perak, Malaysia.

For each bat hunted or captured, information on the date of sampling, species, location, sex, reproductive status, and estimated age was recorded. We assigned each bat an age category of adult (secondary sexual characteristics visible/reproductive), juvenile (no observable secondary sexual characteristics, not pregnant, dental wear characteristics), or pup (dependent and attached to its dam) (*3*). We categorized the reproductive status as pregnant, carrying a pup (adult females with attached pup), nursing (adult females without attached pup but with evidence of lactation), or dry (not in any of the previous categories) using published criteria (*15*). The total number of bats sampled for each pteropid species is shown in Tables 1 and 2. Bats captured in mist nets were released at the site of capture after recovery from anesthesia.

We performed descriptive analysis to describe the seroprevalence on the basis of species of bats and locations. Differences among positive antibody titers (range <8–1,025) between species were tested by using the Mann-Whitney *U* test. Comparison of the seroprevalence rates between the 2 pteropid species was performed by using the χ^2 test. When there were sufficient data to perform the analysis, several factors were examined for its association to NiV seropositivity by using the χ^2 test.

Longitudinal Study on Risk Factors for *NiV* (Risk Factor Study)

We performed a longitudinal study on a population of *P. hypomelanus* bats in Pulau Tioman in which 50 bats from the same colony were captured by using mist nets and sampled approximately every 6–8 weeks during January 2004–October 2006. Monsoonal rains prevented access to the island of Pulau Tioman during December–February, which extended the interval between some sampling points. Captured bats were tagged by using a thumb band or implantable microchip (Avid Identification Systems, Inc., Norco, CA, USA) and unique identification numbers to ensure that sampling was not repeated on the same bat. The bats were anesthetized by using ketamine and xylazine (*22*). Data, blood, and swab samples were collected as described in the previous section.

We investigated associations between serostatus (positive or negative) and each of the hypothesized risk factors (sex, age, reproductive categories, time) using the χ^2 test or Fisher exact test when the χ^2 test was not appropriate. Our previous study (*15*) suggested a correlation between the serologic status of pups and their dams. Therefore, serologic data for *P. hypomelanus* pups were excluded from further analysis. Logistic regression with generalized estimating equations was used to analyze longitudinal data to control for the effect of clustering, assuming that bats sampled between various times were from the same population. To compare the categories across sexual and reproductive maturity, we reclassified the data on the basis of sex (male and female) and reproductive maturity (juvenile, adult, dry, pregnant, carrying a pup, and nursing) and renamed the variable the sexual and reproductive maturity factor. The logistic regression analysis includes the sexual and reproductive maturity categories and sampling time for the bats. All hypothesis testing was 2-sided, with $\alpha = 0.05$, and was performed by using SPSS version 19 (SPSS Inc., Chicago, IL, USA).

Laboratory Analysis

Plasma-neutralizing antibodies against NiV were measured by using the serum neutralization test (SNT) (*23*) with plasma diluted 1:2–1:1,024. A titer ≥8 was considered a positive titer for specific antibody against NiV because serum samples were usually toxic to Vero cells at higher concentrations (i.e., 1:2 or 1:4). Virus isolation was attempted by using rabbit kidney and Vero cells in a biosafety level 3 facility until the third passage before a sample was considered negative (*23*). According to the Malaysian Government Act on Control and Prevention of Infectious Diseases 1988 (revised May 25, 2006), NiV is categorized in risk group 3, which enables the virus to be handled in a biosafety level 3 facility. Any tissue culture with an NiV-like cytopathic effect was confirmed by using a PCR as described (*24*). All laboratory diagnostics (SNT, virus isolation, and PCR) were conducted at the Veterinary Research Institute in Ipoh.

Results

Distribution of *NiV*

P. vampyrus Bats

NiV-neutralizing antibodies were detected in bats at all locations (Table 1). Overall, 82 (32.8%) of 253 bats were seropositive. We found no significant difference in seroprevalence rates in bats from the 5 states ($p = 0.213$, by Fisher exact test). NiV-neutralizing antibody titers ranged from <8 to 1,024 (median <8), and among seropositive bats, the median titer was 64. All culture and PCR results were negative. Among pups, juvenile, and adult bats, 0% (0/1), 25% (14/56), and 35.2% (68/193), respectively, were seropositive (Table 1). Age, sex, and female reproductive status were examined for their effects on serostatus of *P. vampyrus* bats. Univariate analysis showed that age and sex were not associated with seroprevalence of NiV. However, among nursing bats, a higher risk for NiV seropositivity was observed than in other adult females (Table 3).

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Table 1. *Pteropus vampyrus* bats with Nipah virus–neutralizing antibody titers, Peninsular Malaysia, January 2004–October 2006[a]

Location	Sex	Age	No.	SNT titer	No. positive	% Seroprevalence (95% CI)
Perlis, n = 6	M	Adult	4	≤8	0	16.7 (1.1–58.2)
		Juvenile	0	NA	NA	
		Pup	0	NA	NA	
	F	Adult	0	NA	NA	
		Juvenile	2	≤8	1	
		Pup	0	NA	NA	
Perak, n = 50	M	Adult	18	≤8–32	3	24 (14.1–37.5)
		Juvenile	11	≤8–64	2	
		Pup	0	NA	NA	
	F	Adult	18	≤8–512	7	
		Juvenile	3	≤8	0	
		Pup	0	NA	NA	
Terengganu, n = 18	M	Adult	6	≤8–128	1	38.9 (20.2–61.5)
		Juvenile	5	≤8–64	4	
		Pup	0	NA	NA	
	F	Adult	6	≤8–16	2	
		Juvenile	0	NA	NA	
		Pup	1	≤8	0	
Johor, n = 73	M	Adult	23	≤8–128	12	42.4 (31.7–53.9)
		Juvenile	16	≤8–128	6	
		Pup	0	NA	NA	
	F	Adult	26	≤8–128	12	
		Juvenile	8	≤8–16	1	
		Pup	0	NA	NA	
Pahang, n = 106	M	Adult	44	≤8–1,024	10	29.2 (21.4–38.5)
		Juvenile	9	≤8	0	
		Pup	0	NA	NA	
	F	Adult	50	≤8–1,024	21	
		Juvenile	3	≤8	0	
		Pup	0	NA	NA	
Overall, N = 253		Adult	193	≤8–1,024	0	32.8 (27.3–38.8)
		Juvenile	68	NA	14	
		Pup	1	NA	68	

[a]SNT, serum neutralization test; NA, not applicable (no samples).

P. hypomelanus Bats

Of 119 plasma samples collected from island sites, 2 were not used because of inadequate amounts of plasma. Of the remaining 117, 13 (11.1%) were seropositive. NiV antibodies were detected in 13 (13.8%) of 94 bats from islands off the east coast (Pulau Perhentian, Pulau Kapas, Pulau Tioman) of Peninsular Malaysia. Titers ranged from <8 to 256 (median <8); among seropositive bats, the median titer was 32. Samples from Pulau Pangkor (n = 24) were negative for NiV-neutralizing antibodies. All culture and PCR results were negative. Pups were not captured, but among juvenile and adult bats, 0% (0/31) and 11.1% (13/73), respectively, were seropositive (Table 2). Univariate analysis showed that sex was not associated with NiV seropositivity. Stratified data for various reproductive categories were sparse and lacked power for meaningful analysis (Table 3).

Comparison of *P. vampyrus* and *P. hypomelanus* Bats

The antibody titer difference between *P. vampyrus* and *P. hypomelanus* bats was significant ($p<0.001$, by Mann-Whitney U test. The difference in seroprevalence for NiV between *P. hypomelanus* (13/117, 11.1%) and *P. vampyrus* (82/253, 32.8%) bats was significant (χ^2 19.54, $p<0.001$), and risk for a seropositive reaction to NiV was 3.9× higher for *P. vampyrus* bats than for *P. hypomelanus* bats.

Longitudinal Study of NiV *P. hypomelanus* Bats

Characteristics of bats sampled are shown in Table 4. All *P. hypomelanus* bat samples had negative culture and PCR results. The overall NiV seroprevalence for *P. hypomelanus* bats from Pulau Tioman was 9.8%. Differences in seroprevalence between sampling times were significant ($p<0.001$). The highest seroprevalence rate was in 2004, which then waned in 2005 and 2006 (Figure 2).

The seroprevalence of NiV in adult bats (12.8%) was significantly higher than in juveniles (3.7%; $p<0.001$), and adults were ≈4× more likely to be seropositive (odds ratio 3.9). Seroprevalence was not significantly different between male (11.1%) and female bats (8%; $p = 0.258$). However, when data for female bats were examined by their reproductive categories, a significant difference ($p<0.001$) was observed. Bats that were pregnant, carrying a pup, and lactating were 3.9×, 4.8×, and 3.0× more likely

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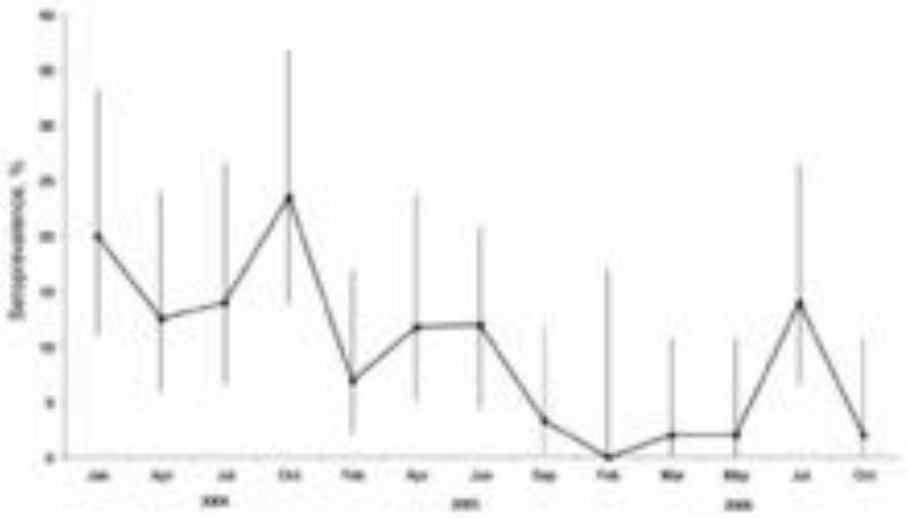

Figure 2. Seroprevalence of Nipah virus among *Pteropus hypomelanus* bats in Pulau Tioman, Peninsular Malaysia, January 2004–September 2006. Error bars indicate 95% CIs.

to be seropositive than adult female bats that did not show these features (Table 5).

Although our data were not sufficiently powered to detect significant differences among various sex and reproductive maturity categories (sample size was not large enough within each category level), when we controlled for the effect of time, the likelihood of seropositivity to NiV among pregnant, carrying, and nursing females remained higher than other female bats, and the highest risk was observed among those females carrying pups. Juvenile female bats were the least likely to have detectable NiV antibodies compared with other bats. Most seropositive cases appeared to cluster in 2004 and decreased toward the end of the study (Table 6).

Anthropic disturbance to roosting sites during our study resulted in dispersal of *P. hypomelanus* bats to smaller (<20), more disparate cohorts that roosted higher in the trees and finally relocation to another site on Pulau

Table 2. *Pteropus hypomelanus* bats with Nipah virus–neutralizing antibody titers, Peninsular Malaysia, January 2004–October 2006*

Location	Sex	Age	No.	SNT titer	No. positive	% Seroprevalence (95% CI)
Pulau Pangkor, n = 23	M	Adult	13	≤8	0	0 (0–16)
		Juvenile	4	≤8	0	
		Pup	0	NA	NA	
	F	Adult	4	≤8	0	
		Juvenile	2	≤8	0	
		Pup	0	NA	NA	
Pulau Perhentian, n = 15	M	Adult	2	≤8–128	0	13.3 (2.5–39.1)
		Juvenile	1	≤8	1	
		Pup	0	NA	NA	
	F	Adult	7	≤8–64	1	
		Juvenile	5	≤8	0	
		Pup	0	NA	NA	
Pulau Kapas, n = 29	M	Adult	7	≤8	0	3.3 (0.01–18.1)
		Juvenile	0	NA	NA	
		Pup	0	NA	NA	
	F	Adult	15	≤8	1	
		Juvenile	7	≤8–32	0	
		Pup	0	NA	NA	
Pulau Tioman, n = 50	M	Adult	27	≤8–128	6	20 (11.1–33.2)
		Juvenile	4	≤8	0	
		Pup	0	NA	NA	
	F	Adult	11	≤8–256	4	
		Juvenile	8	≤8	0	
		Pup	0	NA	NA	
Overall, N = 117		Adult	73	≤8–256	13	11.1 (6.5–18.2)
		Juvenile	31	NA	0	
		Pup	0	NA	0	

*SNT, serum neutralization test; NA, not applicable (no sample)

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Table 3. Univariate analysis of independent variables and Nipah virus serostatus of 2 *Pteropus* bat species surveyed in a cross-sectional survey (without pup data), Peninsular Malaysia, January 2004–October 2008*

Species and risk factor	No. positive/no. tested (%)	p value†	OR (95% CI)
P. vampyrus			
Age			
Juvenile	14/56 (25)	Referent	1.00
Adult	68/193 (35.2)	0.151	1.63 (0.83–3.19)
Sex			
M	38/135 (28.1)	Referent	1.00
F	44/114 (38.6)	0.081	1.6 (0.94–2.73)
Female reproductive status			
Dry	21/58 (36.2)	Referent	1.00
Pregnant	6/14 (42.9)	0.645	1.32 (0.40–4.33)
Carrying a pup	3/7 (42.9)	0.731	1.32 (0.27–6.48)
Nursing	11/17 (64.7)	0.042	3.23 (1.04–9.99)
Juvenile	3/18 (16.7)	0.130	0.35 (0.09–1.36)
P. hypomelanus			
Age			
Juvenile	0/31 (0)	NA	NA
Adult	13/86 (15.1)	NA	NA
Sex			
M	7/58(12.1)	Referent	1.00
F	6/59 (10.2)	0.744	0.85 (0.26–2.62)
Female reproductive status			
Dry	2/23 (8.7)	Referent	1.00
Pregnant	4/14 (28.6)	0.112	4.20 (0.65–26.89)
Carrying a pup	NA	NA	NA
Nursing	NA	NA	NA
Juvenile	0/22 (0)	NA	NA

*OR, odds ratio; NA, not applicable.
†By χ^2 test, Fisher exact test, or simple logistic regression.

Tioman, ≈6 km from the previous site. We believe roost size affected seroprevalence rates and thus reduced risks for seropositivity, as observed toward the end of the study.

Discussion

All bats captured during the study, including NiV-seropositive bats, appeared healthy, which was consistent with observations from experimental infections of pteropid bats with NiV (*25*,*26*). Our cross-sectional survey found that seroprevalences of NiV in *P. vampyrus* and *P. hypomelanus* bats were 32.8% and 11.1%, respectively, which differed from results of a study Yob et al. (*12*) after the first NiV outbreak (17% vs. 31%, respectively). Although both studies support the hypothesis that *Pteropus* spp. are the natural reservoir for NiV in Malaysia, we believe that this difference may be attributed to our study having a larger sample size for each species and a wider geographic sampling scale, as well as potential differences among the diagnostic assays used.

The presence of NiV-seropositive *P. vampyrus* bats across Peninsular Malaysia was expected because satellite telemetry studies by Epstein et al. (*16*) and Breed et al. (*17*) showed that *P. vampyrus* bats are highly mobile, moving beyond state and national borders and making contact with other conspecifics across the region probable. These findings are consistent with the findings of studies of Hendra virus in Australia and NiV in Bangladesh, in which evidence for circulation has been observed across a broad expanse of the home range of each pteropid species (*27*–*29*). The higher seroprevalence of NiV among *P. vampyrus* bats than among

Table 4. Characteristics of *Pteropus hypomelanus* bats tested for Nipah virus, Pulau Tioman, Peninsular Malaysia, January 2004–October 2008*

Sex	Age group	No.	Reproductive status	No.	SNT titer range	No. (%) seropositive	% Seroprevalence (95% CI)
Male, n = 407	Adult	314	NA	NA	≤8–512	39 (12.4)	10.80 (8.16–14.27)
	Juvenile	81	NA	NA	≤8–32	5 (6.1)	
	Pup	12	NA	NA	≤8	0	
Female, n = 243	Adult	124	Dry	62	≤8–256	4 (6.5)	8.20 (5.30–12.4)
			Pregnant	19	≤8–256	4 (21.1)	
			Attached	20	≤8–256	5 (25)	
			Nursing	23	≤8–128	4 (17.4)	
	Juvenile	113	NA	NA	≤8–64	2 (1.8)	
	Pup	6	NA	NA	≤8–64	1 (16.6)	
Overall, N = 650	NA	650	NA	NA	≤8–512	64	9.80 (7.77–12.39)

*SNT, serum neutralization test; NA, not applicable.

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Table 5. Univariate analysis of independent variables and Nipah virus seropositivity (without pup data) in 632 samples from *Pteropus hypomelanus* bats surveyed in Pulau Tioman, Peninsular Malaysia, January 2004–October 2006

Risk factor	No. positive/no. tested (%)	p value*	Odds ratio (95% CI)
Sampling time			
Jan 2004	10/50 (20)	Referent	1.00
Apr 2004	7/50 (14)	0.297	0.57 (0.20–1.64)
Jul 2004	7/50 (14)	0.427	0.65 (0.23–1.88)
Sep 2004	12/51 (6.3)	0.668	1.23 (0.48–3.18)
Feb 2005	4/54 (6.9)	0.052	0.29 (0.08–1.01)
Apr 2005	5/41 (6.9)	0.262	0.53 (0.18–1.59)
Jun 2005	6/50 (12)	0.280	0.54 (0.18–1.63)
Sep 2005	2/61 (3.3)	0.013	0.13 (0.03–0.65)
Feb and Mar 2006†	1/71 (1.4)	0.007	0.05 (0.01–0.45)
May 2006	1/50 (2)	0.019	0.08 (0.01–0.66)
Jul 2006	7/50 (14)	0.427	0.65 (0.23–1.88)
Oct 2006	1/50 (2)	0.019	0.08 (0.10–0.66)
Age			
Juvenile	7/194 (3.7)	<0.001	1.00
Adult	56/438 (12.8)		3.91 (1.75–8.75)
Sex			
M	44/395 (11.1)	0.213	1.00
F	19/237 (8.1)		0.69 (0.39–1.22)
Female reproductive status			
Dry	4/66 (6.5)	Referent	1.00
Pregnant	4/19 (21)	0.077	3.87 (0.86–17.29)
Carrying a pup	5/20 (25)	0.031	4.83 (1.15–20.24)
Nursing	4/23 (17.4)	0.139	3.05 (0.69–13.40)
Juvenile	2/113 (1.8)	0.128	0.26 (0.05–1.47)

*By χ^2 test, Fisher exact, or simple logistic regression.
†Data were combined to enable analysis.

P. hypomelanus bats suggests that exposure to NiV is more common among the *P. vampyrus* bats, which is consistent with higher rates of NiV seroprevalence among juvenile *P. vampyrus* bats than among juvenile *P. hypomelanus* bats. These findings suggest that viral circulation and exposure are probably more common among *P. vampyrus* bats.

We believe that the greater connectivity of *P. vampyrus* bats among colonies in the region create a metapopulation structure in which there is more opportunity for virus to circulate by migration, resulting in a higher rate of exposure. Island bats have limited connectivity (*30*). Thus, herd immunity tends to wane over time, creating a relatively lower seroprevalence (*11*). This phenomenon may be illustrated by our survey of *P. hypomelanus* bats on Pulau Pangkor, in which we did not detect any seropositive bats. We sampled 24 bats, which would have enabled us to detect a seropositive bat, given a prevalence >10% with 95% confidence. The fact that we did not detect any seropositive bats suggests a lower seroprevalence, which could also be attributed to the relatively high degree of urbanization on Pulau Pangkor and consequently smaller colonies and a decreased seroprevalence.

The longitudinal study of *P. hypomelanus* bats showed that prevalence of neutralizing antibodies to NiV fluctuated during the study (range 1%–20%) and, although unpredictable, seroprevalence generally waned in the final 2 years (Figure 2). We did not observe any consistent and discernible seasonal seroprevalence pattern. However, other studies have suggested periodic patterns of antibody prevalence that are connected to the reproductive cycle of bats for other viruses such as Hendra virus (*31*), filovirus, and lyssavirus (*8*,*9*). With the exception of the first NiV outbreak in Malaysia, other studies have linked NiV outbreaks to bat reproductive seasons (*32*–*34*). We believe that the waning seroprevalence during our study is partly explained by anthropic disturbances that occurred at the original study site in Pulau Tioman, which resulted in relocation and dispersal of the original colony into smaller roost sizes. In addition to waning immunity in bats, smaller roost size decreases viral transmission to other susceptible bats, resulting in decreasing seroprevalence over time. The lack of viral isolation from any sample collected during our studies may have been caused by a low incidence of viral shedding or low viral excretion doses within the colony, which is supported by studies of henipavirinses (*1*,*4*,*5*,*18*,*35*).

Sex was not a risk factor for NiV exposure, which is consistent with results of other studies (*28*,*31*,*36*). However, when we stratified the analysis on the basis of sexual and reproductive maturity of the bats, we found that female bats that were pregnant, had an attached pup, and were lactating had a consistently higher likelihood of exposure to NiV than adult males or dry adult females. Analysis of data from a cross-sectional survey of bats of both species suggests an increasing risk for exposure to NiV when female bats were pregnant or lactating. This finding was strengthened in the longitudinal study because female bats that were pregnant, had an attached pup, or were nursing had a higher risk for

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Table 6. Risk factors for Nipah virus seropositivity (without pup data) in *Pteropus hypomelanus* bats sampled in Pulau Tioman, Peninsular Malaysia, January 2004–October 2006*

Variable	β	SE	p value	OR (95% CI)
Time				
Jan 2004	Referent	Referent	Referent	1.00
Apr 2004	−0.58	0.57	0.310	0.55 (0.17–1.72)
Jul 2004	0.52	0.59	0.373	1.69 (0.53–5.43)
Sep 2004	0.38	0.51	0.457	1.46 (0.53–3.97)
Feb 2005	−1.31	0.62	0.034	0.26 (0.07–0.90)
Apr 2005	−1.17	0.78	0.135	0.30 (0.06–1.44)
Jun 2005	−0.44	0.59	0.459	0.64 (0.19–2.07)
Sep 2005	−1.54	0.76	0.045	0.21 (0.04–0.96)
Feb and Mar 2006†	−2.59	1.09	0.018	0.07 (0.00–0.63)
May 2006	−2.13	1.09	0.051	0.11 (0.01–1.00)
Jul 2006	−0.32	0.56	0.564	0.72 (0.24–2.17)
Oct 2006	−2.47	1.08	0.022	0.08 (0.01–0.70)
Sexual and reproductive maturity				
Adult males	Referent	Referent	Referent	1.00
Juvenile males	−0.78	0.52	0.132	0.45 (0.16–1.27)
Dry females	−0.84	0.53	0.114	0.42 (0.14–1.22)
Pregnant females	0.50	0.62	0.421	1.65 (0.48–5.61)
Carrying a female pup	1.24	0.69	0.074	3.48 (0.88–13.6)
Nursing females	0.50	0.63	0.427	1.65 (0.47–5.74)
Juvenile females	−2.34	0.70	0.001	0.09 (0.02–0.38)

*β, estimated coefficient; OR, odds ratio.
†Data were combined to enable analysis.

NiV when we controlled for the potential confounding effect of sampling time (or seasonality).

Among mammals, *Pteropus* spp. bats are known to carry their pups for ≤3 months (*30*) after birth and continue to nurse for ≤4 months after the pup is independent. Pregnancy and lactation are the most metabolically demanding periods of mammalian life (*37*). Therefore, the cumulative stress from reproductive activities, followed by physical exertion from carrying an attached pup to lactation, may have led to the increased risk for NiV infection among this group of bats, consistent with the findings of Plowright et al. (*31*). We speculate that NiV spillover events are most likely to occur during these periods.

Our study has several limitations, including sampling bias, which results from the nonrandom sampling technique used. Sample numbers were often suboptimal because of extreme difficulty in catching pteropid bats. In addition, there are major challenges associated with interpretation of serologic data in wildlife populations. Although we detected differences in the prevalence of neutralizing antibodies between species and increased risk among bats in different reproductive categories, there is still little known about the timing of actual infection or the duration of NiV antibodies in bats. One technique used to overcome this difficulty was to examine age-stratified serologic data, which has been used in similar epidemiologic studies (*31*). *P. hypomelanus* bats reach sexual maturity at ≈12 months of age (*30*) and *P. vampyrus* at 24 months of age (*38*), which enabled us to infer that NiV antibodies in weaned juveniles (≈6–24 months of age) may indicate recent viral circulation. Our previous study among captured *P. vampyrus* bats demonstrated horizontal transmission of NiV from an adult to juvenile bats within the same colony after a brief shedding episode (*18*). Our finding of juvenile *P. hypomelanus* bats with antibodies to NiV during the longitudinal study support the possibility that virus had been circulating in this population within the lifetime of the juvenile, assuming that the juvenile bats were old enough to have lost maternal antibodies.

Our finding of neutralizing antibodies to NiV in both species of *Pteropus* bats at almost all locations we studied in Malaysia, coupled with isolation of NiV from these bats by our group and another group, strengthened the theory that NiV is enzootic in both *Pteropus* bat species, and that these species serve as the natural reservoir for NiV in Malaysia. Longitudinal surveys of *P. hypomelanus* bats suggest size and colony density may cause lower seroprevalence, and female bats that were pregnant, carrying a pup, and lactating generally had higher rates of NiV exposure than males or nonpregnant adult females, which lend further support to the hypothesis that infection rates may be higher during periods of pregnancy and lactation. Further study of NiV infection and shedding rates in pteropid bats will help elucidate seasonal and intracolonial viral dynamics.

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Address for correspondence: Latiffah Hassan, Department of Pathology and Microbiology, Faculty of Veterinary Medicine, Universiti Putra Malaysia, Serdang, Selangor, Malaysia; email: latiffah@vet.upm.edu.my

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UCDUSR0001262

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 6/12/2018 8:10:22 AM
Subject: Re: UPDATE PREDICT DRC EVD outbreak 11 June 2018

Thanks

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jun 12, 2018, at 2:14 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Today's report,
Jonna

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/CAO5tDrG45gjKpz8jMpmP-Fxrua1dTgC-Um8GmPgoUvprkKC5Q%40mail.gmail.com.

From:	William B. Karesh <karesh@ecohealthalliance.org>
To:	Andrew Clements <aclements@usaid.gov>
CC:	Jonna Mazet <jkmazet@ucdavis.edu>;djwolking@ucdavis.edu" <djwolking@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;MurrayS@si.edu <MurrayS@si.edu>;cchrisman@usaid.gov" <cchrisman@usaid.gov>;Alisa Pereira <apereira@usaid.gov>
Sent:	8/10/2018 3:05:40 PM
Subject:	Re: Smithsonian presentation

It was a confluence of a few concepts that came up at the Midyear meeting in Napa, including : people's availability, early enough to stimulate enthusiasm about an EPT-3, and not too late to be heavy into the Mid-term election cycle if we want to get Hill staffers and some attention there.

Sent from my iPhone

BK

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
460 West 34th Street - 17th Floor
New York, NY 10001 USA

+1.212.380.4463 (direct)
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www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On Aug 10, 2018, at 10:29 AM, Andrew Clements <aclements@usaid.gov> wrote:

Hi all,

Turns out Dennis, Alisa, and I will not be available for this presentation on the current date.

Can you remind me if there was a specific reason you/we selected this date? Would a future date be possible (assuming there is availability at the castle)?

Thanks!

Andrew

Andrew P. Clements, Ph.D.

Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclement@usaid.gov

From:	David J Wolking <djwolking@ucdavis.edu>
To:	Amalhin Shek <ashek@usaid.gov>
CC:	Clements, Andrew (GH/HIDN) <aclements@usaid.gov>;Vallutto, Marc <ValluttoM@si.edu>;Wolking David <djwolking@ucdavis.edu>;Alisa Pereira Emerging Threats Division <apereira@usaid.gov>;Cara J. Chrisman <cchrisman@usaid.gov>;Cassandra Louis Duthil <clouisduthil@usaid.gov>;Elizabeth Leasure <eleasure@ucdavis.edu>;Prof. Jonna Mazet <jkmazet@ucdavis.edu>;Eunah Regina Cho <eecho@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent:	8/28/2018 3:47:30 PM
Subject:	Re: Save the Date: USAID PREDICT Briefing- Findings & Implications, September 12 in Washington, D.C.

Hi Amalhin,

Attached is the list of RSVPs received to date maintained by Marc and the Smithsonian team. We'll follow-up with our list of invitees soon.

David

On Tue, Aug 28, 2018 at 7:37 AM Amalhin Shek <ashek@usaid.gov> wrote:
Hi David,

While a call is scheduled, could you share a list of pending invitations and those who have RSVP'd so far?

Thanks in advance,

Amalhin Shek | Budget & Communications Analyst
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
Phone: 571-551-7102(o) 571-236-0989(c) |CP3 8092
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USAID-HECFAA, VP of Community Engagement

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On Tue, Aug 28, 2018 at 2:56 AM Andrew Clements <aclements@usaid.gov> wrote:
No problem. I'm available Wednesday through Friday of this week.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Aug 27, 2018, at 10:59 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Andrew,

Jonna is on vacation today and admittedly I don't have a great handle on where we stand with our own internal organization and plans for this briefing. I'll consult with her tomorrow and we'll be in touch with either another day/time to connect or thoughts for next steps and plans.

Best,

David

On Sat, Aug 25, 2018 at 12:01 AM Andrew Clements <aclements@usaid.gov> wrote:
Sounds good David. Does Tuesday around 1:00 EDT work?

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Aug 25, 2018, at 12:50 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Amalhin, Andrew, and Alisa,

Just wanted to connect again on invites for this Castle briefing, coming up quick (2.5 weeks)!

We had a good discussion last week on our management team call but I think we should touch base briefly on the overall plan for ensuring the attendees are strategically aligned with the goals for the meeting and so we make the best use of the available space. As Jonna mentioned on the call we have a list of folks we can share invites with (and we plan to create an official invitation with an abstract and speaker bios that can be shared) so maybe we can connect early next week on next steps so we're well coordinated and all on the same page?

Enjoy the weekend,

David

On Tue, Aug 21, 2018 at 8:58 AM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

From: predict-request@ucdavis.edu <predict-request@ucdavis.edu> **On Behalf Of** Amalhin Shek
Sent: Tuesday, August 21, 2018 6:53 AM
To: GHSD Unit Mail List (USAID) <ghsdunitmaillist@usaid.gov>; Predict inbox <predict@ucdavis.edu>; E3 FAB Mail List (USAID) <e3.fab@usaid.gov>; Korde, Sonali <skorde@usaid.gov>; Damien Joly <djoly@metabiota.com>; Jonna Mazet <jkmazet@ucdavis.edu>; Andrew Tobiason <atobiason@usaid.gov>; GH List <phscontactsotherbureaus@usaid.gov>; Rodriguez, Michelle A. <rodriguezmi@si.edu>; rosenth@fiosd.fic.nih.gov; Woods, Debra <woodsd@si.edu>; Ronald Waldman <ronwaldman@email.gwu.edu>; murrays@si.edu; ASHLEYEL <ashleyel@ucia.gov>; Billy Karesh <karesh@ecohealthalliance.org>; ian.watson@ultra.mil; Palmer, Bill <palmerb@si.edu>; stm2@cdc.gov; Tracey Goldstein <tgoldstein@ucdavis.edu>; lisa.hensley@nih.gov; david.spiro@nih.gov; dcharng@umn.edu; fahrlingp@niaid.nih.gov; Peter Daszak <daszak@ecohealthalliance.org>; jose.fernandez@hhs.gov; Ramella, Mark <ramellam@si.edu>; Norton, Benjamin <nortonben@si.edu>; chiggs@niaid.nih.gov; pbright@usgs.gov; Paul Mahanna <pmahanna@usaid.gov>; Megan Fotheringham <mfotheringham@usaid.gov>; wsteiger@usaid.gov; Irene Koek <ikoek@usaid.gov>; David Stanton <dstanton@usaid.gov>; Alma Golden <agolden@usaid.gov>; catchison@usaid.gov; Carter, Hillary H. EOP/NSC <Hillary_H_Carter@nsc.eop.gov>; Luciana L. Borio@nsc.eop.gov; jean.m.richards5.civ@mail.mil; Barton Behravesh, Casey (CDC/OID/NCEZID) <dlx9@cdc.gov>; Health and Climate Change <healthandclimatechange@usaid.gov>
Cc: ValituttoM@si.edu
Subject: [predict] Save the Date: USAID PREDICT Briefing- Findings & Implications, September 12 in Washington, D.C.

Dear Colleagues,

This year marks the 100th anniversary of the 1918 influenza pandemic that killed more than 50 million people worldwide in just one year. Since then, there have been numerous other emerging infectious diseases from animals (particularly wildlife) that have spilled over to humans and caused regional epidemics and global pandemics. Diseases such as Ebola, 2009 H1N1 influenza, HIV/AIDS, MERS-CoV, Nipah, SARS, and Zika have demonstrated ability to cause serious health, economic, and social impacts at the country, regional, or global levels. At present, there is a lack of available medicines and vaccines to address many of these diseases which puts a premium on understanding the dynamics of how and where spillover occurs so that risk mitigation measures can be developed and applied.

Since 2005, USAID has been a global leader in addressing emerging infectious diseases spilling over from animals to humans. The USAID/PREDICT project was started in 2009 to begin filling gaps in the understanding of spillover risk of known threats as well as identifying possible future threats. At the same time, PREDICT has strengthened in-country surveillance and laboratory capacity and assisted in outbreak response in Africa, Asia, and the Middle East. PREDICT's work is closely coordinated the other U.S. Government agencies, donors, and international organizations and supports the Global Health Security Agenda which helps protect countries worldwide, including the U.S., from the impacts of disease epidemics and pandemics.

The PREDICT briefing at the Smithsonian Institute on September 12, 2018 will provide an update on key results to date from this unique project as well as expected results over the last year of PREDICT.

See you there!

Amalkin Mack
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
Phone: 571-551-7102(o) 571-236-0989(c) 1 CP3 8092
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USAID-HECFAA, VP of Community Engagement

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	A	B	C	D	E	F
1	USAID PREDICT PROGRESS MEETING					
2						
3	1	Baldwin	Lisa	USAID	lbaldwin@usaid.gov	
4	2	Bright	Patricia	USGS	pbright@usgs.gov	
5	3	Carlin	Ellen	EHA/ SI	CarlinE@si.edu	
6	4	Carter	Hillary	NSC	Hillary_H_Carter@nsc.eop.gov	
7	5	Chrisman	Cara	USAID	cchrisman@usaid.gov	
8	6	Costello	Robert	SI - NMNH	COSTELLR@si.edu	
9	7	Higgs	Elizabeth	NIH/NIAID	ehiggs@niaid.nih.gov	
10	8	Karesh	William	EHA	karesh@ecohealthalliance.org	
11	9	Maset	Jonna	UCD	jkmaset@ucdavis.edu	
12	10	Meyer	Annalisa	SI - SCBI	MeyerAn@si.edu	
13	11	Monfort	Steve	SI - SCBI	monforts@si.edu	unconfirmed
14	12	Pereira	Alisa	USAID	apereira@usaid.gov	
15	13	Rhodes	Rachel	USAID	rarhodes@usaid.gov	
16	14	Shek	Amalhin	USAID	ashek@usaid.gov	
17	15	Shields	Lindsey	SI - SCBI	shieldsl@si.edu	
18	16	Skorton	David	SI	??	unconfirmed
19	17	Sohlberg	Sarah	USAID	ssohlberg@usaid.gov	
20	18	Vallitutto	Marc	SI - SCBI	vallituttom@si.edu	
21	19	Waldman	Ronald	GWU	ronwaldman@email.gwu.edu	
22	20	Zimmerman	Dawn	SI - SCBI	zimmermand@si.edu	

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>;djwolking@ucdavis.edu <djwolking@ucdavis.edu>;kaleasure@ucdavis.edu <kaleasure@ucdavis.edu>;wasmith@ucdavis.edu <wasmith@ucdavis.edu>
Sent: 9/14/2018 3:53:31 PM
Subject: Fwd: Security Alert: Ethiopia

FYI

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

Begin forwarded message:

From: Marilyn Crane <mcrane@usaid.gov>
Date: September 14, 2018 at 3:53:40 PM GMT+2
To: Carrie Coslin <cosl0001@umn.edu>, Patricia Buenzle <buenz010@umn.edu>, Jeff Bender <bende002@umn.edu>, Katey Pelican <pelicank@umn.edu>, Jane Pederson <peder010@umn.edu>, "Sommers, Theresa E." <Theresa.Sommers@tufts.edu>, "Tzipori, Saul" <saul.tzipori@tufts.edu>
Cc: OHWMGT <ohwmgt@usaid.gov>
Subject: Security Alert: Ethiopia

Ethiopia - Security Alert dated 9/13/18 - **The U.S. Embassy is monitoring reports of protest and unrest throughout Addis Ababa, with police deployed in response.** These incidents may continue through the weekend with little or no warning. Expect an increased police presence and be prepared for road closures. U.S. Government personnel are advised to avoid non-essential road movements in Addis Ababa on Saturday, September 15, 2018, especially on Bole and Meskel Square Roads, and to limit movement in Addis Ababa until the end of the weekend.

--
Marilyn Crane
Senior International Higher Education Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (AID)
Telephone: (571) 551-7184
Cell Phone: (703) 474-3824
Email: mcrane@usaid.gov

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From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Andrew Clements <aclements@usaid.gov>
CC: predictmgt@usaid.gov <predictmgt@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>;Kevin N Gonzalez <kngonzalez@ucdavis.edu>;Hannah R Chale <hrchale@UCDAVIS.EDU>
Sent: 10/4/2018 3:36:48 PM
Subject: PREDICT Year 5 Equipment Purchase Request #1

Hi Andrew. Please find attached a request for authorization to purchase a freezer for IEDCR in Bangladesh. This item was not originally included in the proposal budget and now requires approval. Please let me know if you have any questions or require any additional information to proceed.

Thanks!
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

USAID | PREDICT
FROM THE AMERICAN PEOPLE

October 4, 2018
Award No. and Title: AID-OAA-A-14-00102, PREDICT-2
University of California, Davis PREDICT-2 Equipment Request

PREDICT-2 requests authorization to purchase the following equipment item to enable in-country work for the project. This item was not originally included in the approved proposal budget and require approval. Per Attachment A – Schedule of the PREDICT-2 cooperative agreement, budget revisions shall be administered in accordance with 2 CFR 200 (as of Mod. 4 dated 9/30/15), which stipulates that the inclusion of costs that require prior approval in accordance with the applicable cost principles must have prior approval from USAID. The applicable cost principles indicate that equipment with an acquisition cost of $5,000 USD or more and a useful life of more than one year require prior approval from the awarding agency to be allowable.

Country: Bangladesh
Partner/Subaward: Institute of Epidemiology, Disease Control, and Research (IEDCR)
Item: Upright Freezer -86C 28 Cubic ft.
Vendor: K2 Scientific
Geographic Code: The authorized geographic code for this purchase is 937.
Estimated Cost: $10,295.00 USD (Freezer only); Qty: 1
Solicitation and Selection: Four quotes were obtained for a -86 Ultra Low Freezer from various vendors via email solicitation, including K2 Scientific, So-Low Environmental Equipment Company, LABRepCo, and Tovatech (see attached). The K2 Scientific 28 cu. ft. -80C U80-28 upright freezer was selected, as it was the best value based on cost of freezer for the size (28 cubic ft) needed with an audible and visual alarm for high or low temperature, power failure, low battery, and door open.
Justification: PREDICT-2 is focused on the detection of potentially zoonotic viruses at the human-animal interface and had collected numerous samples from animal taxa of interest and humans at critical interfaces. Thus, through the course of this project, thousands of samples have been collected. The –80˚C freezers are obligatory for secure storage and archival of samples collected in the field and lab samples and aliquots for the study and to ensure viability of the samples for viral detection. IEDCR has been allowing the PREDICT project to store some overflow samples in their freezers to date, however, these freezers are currently full and IEDCR is working on new projects that will require the use of these freezers going forward. Additional samples cannot be stored until this freezer is purchased.
Budget Impact: Funds for this freezer are included in the Year 5 PREDICT budget for IEDCR, which is currently pending AOR approval. The need for this freezer has become very time sensitive, so this request is being submitted prior to receiving notice of Y5 budget approval.

USAID | UC DAVIS VETERINARY MEDICINE | WCS | EcoHealth Alliance | METABIOTA

K2 Scientific
401 Hawthorne Lane
Suite 110-139
Charlotte North Carolina 28204
U.S.A

Quote

 # K2Q-000864

Provided For
EcoHealth Alliance

Quote Date : June 04, 2018

Item & Description	Quantity	Price	Total
UBD 28 28 cu. ft. -60C UBD-28 upright freezer	1.00	10,295.00	10,295.00
		Sub Total	10,295.00
		Total	**$10,295.00**

Notes

Please let us know if you have any questions or concerns.

Terms & Conditions

Free dock to dock LTL shipping to the Continental 48. Please let us know if you request a lift gate, inside or white glove delivery (additional charges apply for lift gate, inside and white glove delivery).

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www.labrepco.com

To	Phone	PROPOSAL		
Emily Hagan EcoHealth Alliance 460 West 34th Street 17th floor New York, NY 10001	(212) 380-4491			
	Fax	Terms	Date	Quote No.
		NO TERMS - Credit	6/6/2018	QD94066
	Email	Needed	Sales Representative	
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Proposal Valid for	Ship Date	F.O.B.	Rep Email	
60 Days		Fact PPD	jon.emerson@labrepco.com	

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LABREPCO, Inc.
purchaseorders@labrepco.com
Fax: (215) 442-9202

Qty	Item No.	Description	Unit Price	Extension
1	MDF-U76VC-PA	Panasonic VIP® Series 25.7 Cu. Ft. (Capacity: 576 x 2" Boxes) -86°C Upright ULT Freezer (230V)	$ 10,752.00	$ 10,752.00

Specifications:
-Capacity: 25.7 cu. ft. / 728L
-Area Footprint (nominal): 9.51sq. ft.
-Door(s): 1 exterior; 2 interior (optional 4 inner doors)
-Storage Capacity:
  -576 standard 2" boxes (57,600 x 2ml vials)
  -384 standard 3" boxes (38,400 x 4ml vials)
  -3,456 standard microplates with foil tape
  -2,596 standard microplates with cover lid
-Temperature Range: -50°C to -86°C (in 1°C increments)
-Exterior Dimension: 78.3"H x 39.8"W x 34.4"F-B
-Interior Dimension: 55.1"H x 34.2"W x 23.6"F-B
-Alarm: standard
-Access Port: 2, center, upper back wall and back left chamber floor, 0.6"
-Casters: 4 (2 leveling feet on front base)
-Shelves: 3 stainless steel (4 compartments)
-Door Lock: side
-Voltage: 208-230V, 60Hz
-Net Weight: 805 lbs.

Standard Features:
-Easy-In/Easy-Out door latch for smooth, one-handed operation, positive seal against gasket. -Padlock provision standard.
-Integrated, microprocessor-based control system and LED display includes comprehensive set-point, alarm, monitoring, diagnostic and communications functions.
-Insulated and gasketed inner doors seal inside to offer additional protection and improve uniformity. Inner door latches are standard. Doors can be easily removed for defrosting.
-Front access to washable, electrostatic condenser filter for

Continued

LABREPCO, Inc. will not be responsible for freight charges, rigging or any special delivery requirements such as lift gate delivery or delivery inside a customer's facility unless noted on this quotation.

TOVATECH

Quote

Tovatech LLC
205 Rutgers St.
Maplewood, NJ 07040 U.S.
(973) 913-9734

Quote #: Emily Lab Freezer Quote 6-2014
Date: June 4, 2018
Expiration Date: July 4, 2018

To:
EcoHealth Alliance

Qty	Item Number	Description	Unit Price	Line Total (USD)
1.00	NSSUF281WWW/0	Nor-Lake Scientific Select Ultra Low Temperature Upright Freezer -86C, One Door 27.5 Cubic Ft. 115V, 60Hz	$14,800.00	$14,800.00

Shipping:

Total: $14,800.00 USD

SALESPERSON	EMAIL	PHONE	FAX
Matt Begyn	mbegyn@tovatech.com	(973) 821-3006	(973) 843-1114

Prices in USD.

SO-LOW Environmental Equipment Co., Inc.
10310 Spartan Dr., Cincinnati, Ohio 45215 USA
(513) 772-8810 e-mail: sales@so-low.com
Fax (513) 772-9578 http://www.so-low.com

JUNE 6, 2018
ECOHEALTH ALLIANCE
NEW YORK, NY

QUOTATION

UPRIGHT FREEZER

MODEL NU80-20 SO-LOW FREEZER CABINET	Model NU80-20 So-Low Freezer has a 20 cubic ft. capacity.
PLATINUM SERIES TEMPERATURE CONTROL DOOR MOUNTED WITH COLOR TOUCH SCREEN	The freezer will be equipped with a 4.3" touch screen digital control. The default screen shows both the set temperature and actual temperature of the freezer. The control has an adjustable temperature range from -40°C to -85°C, and is adjustable in 1° increments. Security features include operator audit trail and operator security levels. Control is tamper-proof.
PLATINUM SERIES TEMPERATURE RECORDER WITH VIEWABLE GRAPH AND ELECTRONIC DATA STORAGE	The 4.3" touch screen temperature control is also a paperless temperature recorder, with email & text messaging alarm notification. Temperature data will be saved on the 2GB memory and can be downloaded by USB or FTP. LAN functions also include remote access via PC or smart device.
CABINET OUTER SHELL	The cabinet is fabricated of 16-ga. steel, welded to the base providing sturdy all round construction. The cabinet has a cool gray powder coat finish. Unit is provided with heavy duty swivel casters.
CHAMBER SHELL	The chamber is constructed of 14-ga. corrosion resistant galvanized steel, zinc coated to prevent rust, providing extra life to the cabinet. Chamber walls have copper refrigerant tubes that are soldered and covered with a special aluminum foil that provides instant cooling.
OUTSIDE DIMENSIONS	Width 53", Front to Back 30¾", Height 79¾".
CHAMBER DIMENSIONS	Width 38", Front to Back 25", Height 51¼".
INSULATION CFC-FREE NEW ECOMATE FOAM	The chamber walls are sealed and insulated with five inches of the new Ecomate family of Polyurethane foams. It is approved by the EPA, SNAP, and meets current regulatory mandates.

UCDUSR0001276

SHELVES AND INNER DOORS	Located in the chamber will be four solid shelves and five inner doors with hinges. Solid shelves retain cold air in uncpened compartments when other compartments are opened. The shelves are adjustable. The dimensions of the five individual compartments are 38" x 25" x 10" high.
ALARM SYSTEM WITH RELAY	Battery operated alarm system provides an audible and visual signal in a high/low temperature alarm condition. The alarm will also signal in the event of a power failure. Also provided is an alarm silencing feature. Relay contacts are provided for remote alarm hook-up.
WARRANTY	One year Warranty on all parts and labor. All So-Low freezers are tested for seven days.
PRICE EACH	**$12,395.00 f.o.b. Cincinnati, OH.**
TEMPERATURE RECORDER NO. 100 (Optional)	7-day temperature recorder with 6" circular chart. The recorder has a battery back-up that will keep the recorder operating for approximately 24 hours after power failure. Recorder comes with 52 charts. ..Add $1,175.00 to price quoted above.
INVENTORY RACK NO. 23-12-3 (Optional)	Stainless steel storage rack 23" x 5¾" x 9-3/4" high. Includes twelve 3" high, water repellent cardboard boxes. Each box will contain a card board 81 cell divider. ..Add $80.00 to price quoted above.
INVENTORY RACK NO. 23-16-2 (Optional)	Stainless steel storage rack 23" x 5¾" x 9-3/4" high. Includes sixteen 2" high water repellent cardboard boxes. Each box will contain a card-board 81 cell divider. ..Add $95.00 to price quoted above.
	NOTE: Model NU80-28 can hold a total of 30 racks.
COLD SAFETY GLOVES NO. 1100 (Optional)	Specially insulated cryogenic protection gloves for use with ultra-cold materials. Provide protection and warmth. Mid arm length, sizes medium or large. Please specify size desired when placing order. ..Add $125.00 per pair to price quoted above.
SHIPMENT	Approximately 4 weeks from receipt of order. So-Low Environmental Equipment Co., Inc. will not be responsible for freight charges or any special delivery requirements such as liftgate delivery or delivery inside customer's facility. If special delivery is required please contact So-Low customer service.

UCDUSR0001277

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
To: Cara Chrisman <cchrisman@usaid.gov>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Eri Togami <etogami@ucdavis.edu>;Kevin Olival PhD <olival@ecohealthalliance.org>;Daniel Schar <dSchar@usaid.gov>;Anchalee Jittapai <ajittapai@usaid.gov>;Dennis Carroll <dcarroll@usaid.gov>;Siana Tackett <stackett@usaid.gov>;Jones, Melissa (USAID/Dhaka/PHE) <mejones@usaid.gov>;Mo Monica Limtanakool <mlimtanakool@usaid.gov>
Sent: 10/5/2018 1:26:38 AM
Subject: Re: Thailand National Virome Project: Mtg Attendance

This is great, thank you.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Adviser
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

On Fri, Oct 5, 2018 at 3:01 AM, Cara Chrisman <cchrisman@usaid.gov> wrote:
Hi Sudarat,

Thanks for all of this! We are having a communications person review the GVP briefer and then we'll re-share for circulation at the meeting.

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSI-ID - Social Solutions International, Inc., prime contractor

On Wed, Oct 3, 2018 at 8:07 PM Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
Dear Cara,

Thank you very much. We will adjust Dennis's session to 45 min as suggested. If you have the new GVP briefer/fact sheet in electronic file, we are happy to print out here to distribute at the launching workshop.

See you soon.

Sudarat

Sent from my mobile.

On Oct 4, 2018, at 4:05 AM, Cara Chrisman <cchrisman@usaid.gov> wrote:

Hi Sudarat,

Appreciate all these updates and the hotel suggestions!

In terms of the questions, I just spoke with Dennis and his talk will be around 20-25 minutes. In order to leave time for questions, we were thinking to block around 45 minutes. Does that work on your end? He's flexible.

We also talked about the 23rd and it sounds like the Conrad would make the most sense (people like air conditioning!). Thanks for your assistance with the reservations!

Best,
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Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSAB - Social Solutions International, Inc. prime contractor

On Wed, Oct 3, 2018 at 1:10 PM Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
The meeting is at Pullman Hotel, King Power. I suggest that you stay at Conrad or Plaza Athenee Hotel. We can go there quite easily by Sky Train and 5 minutes walk to the hotel.

Thank you for your kind offer. I think most of it will be responsible and handled by DMSC, MOH and NSTDA.

The final prep meeting to finalize the meeting agenda is on Oct 9. But it is all set from our end, I thought. How long for Dennis's talk? It is now 1 h 15 mins. Please let us know if he wants to adjust the time or prefers to fix as it is.

Nov 23 is a Thai Holiday, thus there might be the limitation to use the room at RDMA (no air- condition on the holiday). If not, I will reserve the conference room at the Conrad Hotel for 10 people during 10.00 am - 5.00 pm.

Please stay tuned.

Best regards,
Sudarat

Sent from my mobile.

On Oct 3, 2018, at 7:56 PM, Cara Chrisman <cchrisman@usaid.gov> wrote:

Hi Sudarat,

Thanks for submitting and for letting us know! We had a couple other quick questions related to the meeting:

1. Is there anything that we can help with on this end? It sounds like invitations and logistics are pretty set, but please let us know if there's anything we can do to assist.
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3. The presenters were planning to meet the day before in order to align our presentations and do further planning. Dennis recommended that we reach out to you to see if there was someone on the team who could assist in getting a room in which to meet? It would be for around 10 people and from approximately 10am to 5pm. He initially suggested the conference room at the Conrad as he'll be staying there. If that's not possible to reserve, he suggested that perhaps there might be a room at RDMA?

Thanks again,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
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2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSI-III - Social Solutions International, Inc. prime contractor

On Tue, Oct 2, 2018 at 10:41 PM Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
I did submit the list of speakers/participants from USAID HQ and GVP, PREDICT 2 Team with the total of 9 to DMSC yesterday evening.

USAID HQ

1. Dennis Carroll at dcarroll@usaid.gov

2. Cara Chrisman at cchrisman@usaid.gov

GVP, PREDICT Team

1 Jonna Mazet at jkmazet@ucdavis.edu

2. Eri Togami at etogami@ucdavis.edu

3. Kelvin Olival at olival@ecohealthalliance.org

4. Davis McIver at dmciver@metabiota.com

5. Sam Halabi at slh9@georgetown.edu

6. Alice Latinne at latinne@ecohealthalliance.org (PREDICT Liaison for Thailand)

7. Hongying Li at li@ecohealthalliance.org (PREDICT Liaison for China and is coordinating the China GVP meeting planned for the coming year)

Best regards,
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USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

---------- Forwarded message ----------
From: **Noppavan Janejai** <noppavan.j@dmsc.mail.go.th>
Date: Wed, Oct 3, 2018 at 9:33 AM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Cc: Supaporn Wacharapluesadee <sprwa@hotmail.com>

ได้รับแล้ว ขอบคุณค่ะ

Noppavan Janejai
Deputy Director
National Institute of Health, Department of Medical Sciences
88/7 Tiwanon Road, Nonthaburi 11000, Thailand

----- **ข้อความดั้งเดิม** -----
จาก: "Sudarat Damrongwatanapokin" <sdamrongwatanapokin@usaid.gov>
ถึง: "Supaporn Wacharapluesadee" <sprwa@hotmail.com>, "Noppavan Janejai" <noppavan.j@dmsc.mail.go.th>
ส่งแล้ว: อังคาร, 2 **ตุลาคม**, 2018 5:18:33 PM
เรื่อง: Fwd: Thailand National Virome Project: Mtg Attendance

Thank you for your eagle's eyes. I did correct it as the list below.
Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Adviser
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

---------- Forwarded message ----------
From: S Wacharapluesadee <spwa@hotmail.com>
Date: Tue, Oct 2, 2018 at 4:50 PM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sadarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>, Noppavan Janejai <noppavan.j@dmsc.mail.go.th>

olival@ecohealthalliance.org

แก้ไข email ของ Dr.Kevin Olival ค่ะ (ตัว g ใน org ตกไปค่ะ)

ขอบคุณค่ะ

Supaporn Wacharapluesadee, PhD

ศูนย์วิทยาศาสตร์สุขภาพโรคอุบัติใหม่ โรงพยาบาลจุฬาลงกรณ์
Thai Red Cross Emerging Infectious Diseases - Health Science Centre
WHO Collaborating Centre for Research and Training on Viral Zoonoses
King Chulalongkorn Memorial Hospital
Faculty of Medicine, Chulalongkorn University
Rama4 road, Patumwan
Bangkok, Thailand 10330
Tel 662-256 4000 ext 3561
Fax 662-652 3122

From: Sadarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Sent: Tuesday, October 2, 2018 4:43 PM
To: Noppavan Janejai
Cc: Daniel Schar; Anchalee Jatapai; Wantanee Kalpravidh; Supaporn Wacharapluesadee; Bandit Nuansrichay; Prasert Auewarakul; Monta Thammasatta; prasit.pal@mahidol.ac.th; Thanat Chookajorn; Jonna Mazet; ctogami@ucdavis.edu
Subject: Re: Thailand National Virome Project: Mtg Attendance

Dear Noppavan,

Please see below the list of speakers/participants from USAID HQ and GVP, PREDICT 2 Team with the total of 9.

USAID HQ

1. Dennis Carroll at dcarroll@usaid.gov

2. Cara Chrisman at cchrisman@usaid.gov

GVP, PREDICT Team

1.Jonna Mazet at jkmazet@ucdavis.edu

2. Eri Togami at etogami@ucdavis.edu

3. Kelvin Olival at olival@ecohealthalliance.org

4. Davis Melver at dmciver@metabiota.com

5. Sam Halabi at sfh9@georgetown.edu

6. Alice Latinne at latinne@ecohealthalliance.org (PREDICT Liaison for Thailand)

7. Hongying Li at li@ecohealthalliance.org (PREDICT Liaison for China and is coordinating the China GVP meeting planned for the coming year)

Please issue the invitation letter via e-mail address provided above.

Thank you very much.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Adviser
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

From: Andrew Clements <aclements@usaid.gov>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: PREDICTMGT <predictmgt@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>;Predict inbox <predict@ucdavis.edu>;Kevin N Gonzalez <kngonzalez@ucdavis.edu>;Hannah R Chale <hrchale@ucdavis.edu>
Sent: 10/5/2018 2:19:07 PM
Subject: Re: PREDICT Year 5 Equipment Purchase Request #1

Hi Liz,

Equipment request approved.

Andrew

Andrew Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4233
E-mail: aclements@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

On Thu, Oct 4, 2018 at 5:46 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Hi Andrew. Please find attached a request for authorization to purchase a freezer for IEDCR in Bangladesh. This item was not originally included in the proposal budget and now requires approval. Please let me know if you have any questions or require any additional information to proceed.

Thanks!

Liz

Elizabeth Leasure

One Health Institute

University of California, Davis

530-754-9034 (office)

530-304-1403 (cell)

From: Eri Togami <etogami@ucdavis.edu>
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
CC: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 10/19/2018 7:23:50 PM
Subject: RE: Thailand National Virome Project/ conference room reservation at Conrad on Oct 23, 8.30 am - 5.00 pm

Sudarat, thank you for extending the room reservation.
-Eri

From: Sudarat Damrongwatanapokin [mailto:sdamrongwatanapokin@usaid.gov]
Sent: Wednesday, October 17, 2018 9:20 PM
To: salita.panitchpakdi@conradhotels.com; BKKCLReservations@conradhotels.com
Cc: Cara Chrisman ; Jonna Mazet ; Eri Togami ; Parntep Ratanakorn ; Daniel Schar
Subject: Fwd: Thailand National Virome Project/ conference room reservation at Conrad on Oct 23, 8.30 am - 5.00 pm

Dear Khun Salita,

We would like to request the meeting room reservation extension starting from 8.30 am-5.00 pm instead of 10.00 am-5.00 pm as originally planned. There will be another guest, Dean Dr. Partep Ratanakorn, Mahidol University, who will join the meeting at 8.30-9.30 am.

Thank you very much for your kind assistance upon the request.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Adviser
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

---------- Forwarded message ----------
From: **Monica Limtanakool** <mlimtanakool@usaid.gov>
Date: Thu, Oct 4, 2018 at 11:00 AM
Subject: Re: Thailand National Virome Project/ conference room reservation at Conrad on Oct 23
To: Salita Panitchpakdi <salita.panitchpakdi@conradhotels.com>
Cc: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>

Dear Salita,

It's nice talking to you. With reference to our phone conversation, please book a meeting room that could accommodate 10 people on **Tuesday, October 23 from 10.00 am - 5.00 pm**. The room could be located in Executive Lounge area where U.S. Government in-house guests entitled for 2 hours/guest.

I'm copying Cara and Sudarat in case you may have any questions that are needed related to our request

Best Regards,

Monica Lintanakool (Mo)

Secretary, Office of Public Health (OPH)
Regional Development Mission for Asia (RDMA)
USAID | U.S. Agency for International Development
Bangkok, Thailand
Office: +66 (0)2 257 3298
USAID Cellphone: + 66 (0)98 253 1029

Official - SBU
UNCLASSIFIED

---------- Forwarded message ----------
From: **Cara Chrisman** <cchrisman@usaid.gov>
Date: Thu, Oct 4, 2018 at 4:05 AM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sadarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Eri Togami <etogami@ucdavis.edu>, Kevin Olival PhD <olival@ecohealthalliance.org>, Daniel Schar <dSchar@usaid.gov>, Anchalee Jatapai <ajatapai@usaid.gov>, Dennis Carroll <dcarroll@usaid.gov>, Siana Tackett <stackett@usaid.gov>, "Jones, Melissa (USAID/Dhaka/PHNE)" <mejones@usaid.gov>, mlimtanakool@usaid.gov

Hi Sadarat,

Appreciate all these updates and the hotel suggestions!

In terms of the questions, I just spoke with Dennis and his talk will be around 20-25 minutes. In order to leave time for questions, we were thinking to block around 45 minutes. Does that work on your end? He's flexible.

We also talked about the 23rd and it sounds like the Conrad would make the most sense (people like air conditioning!). Thanks for your assistance with the reservations!

Best,
Cara

Cara J. Chrisman, PhD
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Desk: (571) 551-7413
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GHSA-III - Social Solutions International, Inc. prime contractor

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Please stay tuned.

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1. Is there anything that we can help with on this end? It sounds like invitations and logistics are pretty set, but please let us know if there's anything we can do to assist.
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Thanks again,
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Tel: +662-257-3243, Fax:+662 -2573099

---------- Forwarded message ----------
From: **Noppavan Janejai** <noppavan.j@dmsc.mail.go.th>
Date: Wed, Oct 3, 2018 at 9:33 AM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Cc: Supaporn Wacharapluesadee <sprwa@hotmail.com>

ใช่ค่ะ ขอบคุณค่ะ

Noppavan Janejai
Deputy Director
National Institute of Health, Department of Medical Sciences
88/7 Tiwanon Road, Nonthaburi 11000, Thailand

----- **ข้อความที่ส่งต่อ** -----
จาก: "Sudarat Damrongwatanapokin" <sdamrongwatanapokin@usaid.gov>

ถึง: "Supaporn Wacharapluesadee" <spwa@hotmail.com>, "Noppavan Janejai" <noppavan.j@dmsc.mail.go.th>
ส่งแล้ว: **อังคาร**, 2 **ตุลาคม**, 2018 5:18:33 PM
เรื่อง: Fwd: Thailand National Virome Project: Mtg Attendance

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Sudarat Damrongwatanapokin, D.V.M., Ph.D.
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From: S Wacharapluesadee <spwa@hotmail.com>
Date: Tue, Oct 2, 2018 at 4:50 PM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>, Noppavan Janejai <noppavan.j@dmsc.mail.go.th>

olival@ecohealthalliance.org

แก้ไข email **ของ** Dr.Kevin Olival **ค่ะ** (**ตัว** g **ใน** org **ตกไปค่ะ**)

ขอบคุณค่ะ

Supaporn Wacharapluesadee, PhD

ศูนย์วิทยาศาสตร์สุขภาพโรคอุบัติใหม่ โรงพยาบาลจุฬาลงกรณ์
Thai Red Cross Emerging Infectious Diseases - Health Science Centre
WHO Collaborating Centre for Research and Training on Viral Zoonoses
King Chulalongkorn Memorial Hospital
Faculty of Medicine, Chulalongkorn University
Rama4 road, Patumwan
Bangkok, Thailand 10330
Tel 662-256 4000 ext 3561
Fax 662-652 3122

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Sent: Tuesday, October 2, 2018 4:43 PM
To: Noppavan Janejai
Cc: Daniel Schar; Anchalee Jatapai; Wantanee Kalpravidh; Supaporn Wacharapluesadee; Bandit Nuansrichay; Prasert Auewarakul; Meeta

Thammasatta; prasit.pal@mahidol.ac.th; Thanat Chookajorn; Jonna Mazet; etogami@ucdavis.edu
Subject: Re: Thailand National Virome Project: Mtg Attendance

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Please see below the list of speakers/participants from USAID HQ and GVP, PREDICT 2 Team with the total of 9.

USAID HQ

1. Dennis Carroll at dcarroll@usaid.gov

2. Cara Chrisman at cchrisman@usaid.gov

GVP, PREDICT Team

1.Jonna Mazet at jkmazet@ucdavis.edu

2. Eri Togami at etogami@ucdavis.edu

3. Kelvin Olival at olival@ecohealthalliance.org

4. Davis Melver at dmelver@metabiota.com

5. Sam Halabi at sfh9@georgetown.edu

6. Alice Latinne at latinne@ecohealthalliance.org (PREDICT Liaison for Thailand)

7. Hongying Li at li@ecohealthalliance.org (PREDICT Liaison for China and is coordinating the China GVP meeting planned for the coming year)

Please issue the invitation letter via e-mail address provided above.

Thank you very much.

Best regards,
Sadarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Adviser
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

From: David J Wolking <djwolking@ucdavis.edu>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: David J Wolking <djwolking@ucdavis.edu>;Brooke Genovese <bgenovese@ucdavis.edu>
Sent: 1/7/2019 3:32:11 PM
Subject: Re: Annual Report 2018 Review - thoughts for Monday

Jonna,

Here's a stab at the intro letter and a rough take at the acknowledgements.

David

On Thu, Jan 3, 2019 at 5:07 PM Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Thanks so much for the guide!
I think your ideas on the preface and acknowledgements sound great, if you want to work on something for those. I'll think about the pub section as I go through it.
Happy New Year,
Jonna

P.S. Off again tomorrow, as moving out of Stinson house to tear it down. Text if you need anything.

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A few thoughts here to help guide your review, section by section (in case you feel like skimming or skipping some entirely).

Preface: Thought it might be nice to have a letter from the Director to break up the monotony of this preface that has been the same each report (and workplan) since 2016. If OK by you, I can draft something for you to customize and sign. Might be nice to highlight the tone of the year (successful wrap up of field work, maturing capacity for our OH workforce, exciting success stories and publications, etc.) as this is likely the only thing people will read :-)

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Welcome back to the grind ;-)

David

Introduction

This year marked the 100-year anniversary of the most devastating infectious disease event in recorded human history, the 1918 influenza pandemic, which decimated our population and threatened to extinguish our species. The 1918 pandemic, estimated to have infected one third of our planet's human population, caused widespread economic, social, and political harm and further disrupted our world as we waged the first world war.

We have come a long way in pandemic prevention in 100 years through advances in science and technology that have improved our understanding of infectious diseases and strengthened our ability to detect, treat, and prevent them. Through global engagement, we have worked to improve our planet's health security through strategic investments in health systems and international cooperation. Yet the pandemic threat remains.

This year did not bring a resurgence of the influenza strain that caused the 1918 pandemic, yet as we prepared to welcome 2019, health care workers in eastern Democratic Republic of Congo rushed to combat their second Ebolavirus outbreak in year, now the second largest Ebolavirus outbreak since the 2014 outbreak in West Africa that caused massive global disruption and over 11,000 deaths. We are seeing an increase in the emergence and spread of infectious diseases as well as thriving conditions that may cause them: instability and conflict, changes in land use, natural disasters exacerbated by climate change, migrating human populations across borders and increasingly from the countryside to cities, and health systems struggling to cope with the burden of disease and dynamic challenges.

2018 was our fourth year implementing the second five-year phase of the US Agency for International Development's (USAID) PREDICT project (www.predict.global), an innovative pillar of USAID's Emerging Pandemic Threat's Program designed to tackle these challenges head-on in some of the world's most vulnerable hot-spots for disease emergence. PREDICT, which launched in 2009, is charged with building a consortium of global partners to strengthen capacity for surveillance and detection of emerging viral threats to preemptively confront them before they become pandemics. This year, our teams, using the One Health approach in 28 countries, made significant strides towards that end and towards strengthening global health security.

This year our project reached maturity, providing proof of concept for early detection of potentially deadly diseases through the discovery of a new Ebolavirus in bats in Sierra Leone and by working closely with our Government of Sierra Leone partners to design and implement a prevention and risk communication campaign in communities in Sierra Leone and across Africa where these bats reside.

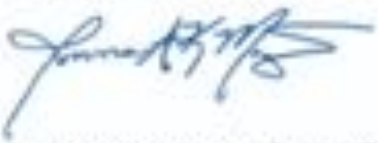
We continued to support development of the world's One Health workforce, supporting professional development and training for over 270 staff and team members from our host country partners, who this year achieved a major project milestone by completing One Health surveillance through sampling wildlife and domestic animal populations and at-risk human communities were viral spillover and spread are most likely to occur. To date, our capacity strengthening team has worked to serve over 550 health professionals, including 104 members of tomorrow's workforce, and over 300 faculty members at host country universities or research institutes. Further, we continued to support disease detection in more than 60 labs and to promote One Health laboratory networks in Africa and Asia. Forty labs now have the capability to test for known and emerging viral threats, which combined with our investments in human resources will be a lasting contribution to education, science, and health security.

Also this year, our PREDICT teams supported 10 outbreak response investigations in five countries helping partners get to the source of diseases of unknown origin and preemptively head off potential outbreaks in animal populations before they infect people. In Thailand, our PREDICT partner lab at Chulalongkorn University was requested by government partners to use our disease detection platform, optimized to screen for known and unknown viruses of bat origin, to support health evaluations for members of the Thai soccer team trapped in a cave, a widely publicized international emergency.

We also continued to invest in the science and knowledge of emerging infectious diseases, developing risk maps and models to inform policy and guide surveillance and detection efforts, and producing 39 publications (many in top tier journals such as *Nature*) and 40 evidence-based resources and policy briefs.

In this year's *2018 Annual Report*, we are proud to showcase these successes and other achievements, which reflect the hard work, talent, and dedication of a truly amazing and unique global team. In 2019, the last and final of this five-year phase, our One Health team will continue to advance the frontiers of knowledge of emerging diseases and work to create long-lasting and self-reliant platforms for disease surveillance, detection, and control.

Best regards,



Dr. Jonna A.K. Mazet, DVM, MPVM, PhD
Professor and Global Director
One Health Institute & USAID PREDICT project
University of California, Davis

PREDICT 2018 ANNUAL REPORT

This publication was prepared by the PREDICT Consortium headquartered at the One Health Institute (OHI), School of Veterinary Medicine, University of California, Davis.

www.predict.global
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Layout and design:
Eunah Cho, Justin Cox, Bridgette Smith, and David Wolking
UC Davis One Health Institute

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Special thanks to the governments of and partners in Bangladesh, Bolivia, Brazil, Cambodia, Cameroon, China, Gabon, Democratic Republic of Congo, Indonesia, Laos, Malaysia, Mexico, Nepal, Peru, Tanzania, Uganda, Republic of Congo, Rwanda, Thailand, and Vietnam. The success realized by the PREDICT project, documented herein, would not have been possible without the valuable contributions of Andrew Clements, Alisa Pereira, and Cara Chrisman.

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: David J Wolking <djwolking@ucdavis.edu>
CC: David J Wolking <djwolking@ucdavis.edu>;Brooke Genovese <bgenovese@ucdavis.edu>
Sent: 1/7/2019 6:42:32 PM
Subject: Re: Annual Report 2018 Review - thoughts for Monday

Beautifully done!
My edits attached.
Thanks very much,
J

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Editorial contributions:
Brooke Genovese, Kevin Gonzalez, Zoe Grange, Eri Togami, and Marcy Uhart

Content:
Substantively developed and contributed by editors (see above) objective leads (Simon Anthony, Peter Daszak, Leilani Francisco, Tracey Goldstein, Christine Kreuder Johnson, William Karesh, Catherine Machalaba, Kevin Olival, Karen Saylors, Woutrina Smith) and the PREDICT-2 Consortium.

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UCDUSR0001299

Introduction

This year marked the 100-year anniversary of the most devastating infectious disease event in recorded human history, the 1918 influenza pandemic, which decimated our population and continues to serve as a reminder of just how vulnerable we are as a species. As a result of the more than 50 million deaths and associated fear, panic, and loss, the 1918 pandemic caused widespread economic, social, and political harm and further disrupted our world as we waged the First World War. It is estimated to have infected up to one third of our planet's human population, similar to infection rates seen with the 2009 H1N1 influenza pandemic that began just as the PREDICT Project was being initiated.

While pandemic prevention has improved in the past 100 years, through advances in science and technology that have improved our understanding of recognized infectious diseases and strengthened our ability to detect, treat, and prevent them, our preparedness for the threat of new or unexpected diseases has not advanced comparably. Through global engagement, we have worked to improve our planet's health security through strategic investments in health systems and international cooperation. Yet the pandemic threat remains.

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promote One Health laboratory networks in Africa and Asia. Forty labs now have the capability to test for known and emerging viral threats, which combined with our investments in human resources will be a lasting contribution to education, science, and health security.

Also this year, our PREDICT teams supported 10 outbreak response investigations in five countries, helping partners get to the source of diseases of unknown origin and preemptively head off potential outbreaks in animal populations before they infect people. In Thailand, our PREDICT partner lab at Chulalongkorn University was requested by government partners to use our disease detection platform, optimized to screen for known and unknown viruses of bat origin, to support health evaluations for members of the Thai soccer team trapped in a cave, a widely publicized international emergency.

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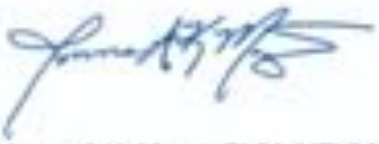
Best regards,



Jonna A.K. Mazet, DVM, MPVM, PhD
Professor and Global Director
One Health Institute & USAID PREDICT project
University of California, Davis

From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Jonna Mazet <jkmazet@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>
CC: predict Sympa List <predict@ucdavis.edu>
Sent: 1/24/2019 10:43:45 PM
Subject: RE: Restriction for Trafficking in persons.

Per the State department website, Tier 3 countries include:

TIER 3
China (PRC)
Congo, Democratic Republic of
Congo, Republic of
Guinea
South Sudan
Sudan

I'll reach out to Alisa et al for clarification, but we may also want to add this to our next SMT agenda.

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Elizabeth Leasure
Sent: Thursday, January 24, 2019 3:40 PM
To: 'Beth Edison'
Cc: predict Sympa List ; Karen Saylors ; Jonna Mazet ; David John Wolking
Subject: RE: Restriction for Trafficking in persons.

Hi Beth. Thanks for forwarding, and no, I haven't heard anything about this from any other countries. All of our Ebola funds (which are funding DRC as you know) have been obligated to the prime CoAg at this point, so perhaps we aren't impacted? If you find any additional info, please share. I'll follow up with USAID/Washington to see if they can provide any insight.

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edison <bedison@metabiota.com>
Sent: Wednesday, January 23, 2019 7:31 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: predict Sympa List <predict@ucdavis.edu>; Karen Saylors <ksaylors@metabiota.com>
Subject: Fwd: Restriction for Trafficking in persons

Hi Liz,

Charles, our CC in DRC, received the below email from the mission. What he's saying is that DRC is on the list of countries that is restricted by the TVPA act and that no new money will be allocated until these restrictions are lifted. Apparently some organizations have already received an email advising the restriction has been lifted but FAO, CBT and UC Davis are still restricted and no new money will be allocated for DRC until an email is received. We are allowed to continue operating with funds already received.

Have you heard anything about this at all? I did a brief search for a list of countries and haven't found one yet, but it's possible that other PREDICT countries might be affected as well. If I find more info, I will send it along.

Thanks,
Beth

---------- Forwarded message ---------
From: **Charles Kumakamba** <ckumakamba@metabiota.com>
Date: Wed, Jan 23, 2019 at 1:07 AM
Subject: Fwd: Restriction for Trafficking in persons.
To: Karen Saylors <ksaylors@metabiota.com>, Beth Edison <bedison@metabiota.com>

FYI!

---------- Forwarded message ---------
From: **Jean-Felly Numbi** <jnumbi@usaid.gov>
Date: mer. 23 janv. 2019 10 h 01
Subject: Restriction for Trafficking in persons.
To: Jean Pierre Kabuayi <jpkabuayi@theunion.org>, Charles Kumakamba <ckumakamba@metabiota.com>

Bonjour Jean Pierre et Charles,
Merci pour le message sur le shutdown en rapport avec la mis en oeuvre des activités sur terrain.
En effet, il ya deux situations différentes à ce sujet à savoir :
1) Le shut-down qui est le retard d'approbation du budget du gouvernement américain par le Congrès suite aux tractations entre le président Trump et les démocrates. Comme conséquence c'est le retard pour l'argent attendu cette année en cours. Cependant si votre projet a encore un solde de l'année passée dans ce cas vous continuez avec la mise en oeuvre si le plan d'action est déjà approuvé. Tous nous attendons le New Money de cette année quand le shut-down sera levé.

2) **Trafficking in Persons (TIP)** : cette restriction sous laquelle la RDC est tombée parmi tant autres pays, voir le message ci-dessous,CTB, FAO, Predict 2 Davis sont encore sous cette restriction par conséquent vos ne recevrez new money tant pas levée. Bien sûr elle sera levée mais on ne sait pas quand. La levée de cette mesure est progressive car autres projets de la RDC viennent d'être autorisées de commencer la mise en oeuvre appuyant le gouvernement. C'est la restriction suspend de faire le business avec le gouvernement concerné. Que faire? Encore une fois si vous avez de l'argent du solde de l'année passée, je vous conseillerais de continuer les activités prioritaires de cette année car on ne sait pas quand la mesure sera levée.

Merci. Je suis disponible pour toute autre information.
Jean-Felly.
---------- Forwarded message ---------
From: **Andre-Guy Soh** <asoh@usaid.gov>
Date: Wed, Dec 12, 2018 at 2:24 PM
Subject: Update Concerning Impact of Trafficking-in-Persons Legislation on USAID awards
To: Andre-Guy Soh <asoh@usaid.gov>

Dear partners,

On November 28, I informed you that the U.S. Government was in the process of clarifying the effects of

restrictions imposed by the Trafficking and Victims Protection Act of 2000 (the "TVPA") on U.S. Government activities in all Tier 3 designated countries.

We have received clearance for a limited number of awards, and have informed the organizations and contractors concerned.

If you have not received an email from USAID/DRC indicating that the U.S. Government has determined that your award is NOT COVERED by TVPA restrictions, then we are still unable to provide any assurance that additional funds will be obligated into your respective awards due to the potential application of TIP restrictions.

We understand this situation may create difficulties for program operations. While we wait for further guidance from Washington, feel free to reach out to your AOR/CORs for any questions you may have.

Regards,
AG

Andre-Guy Soh
Contracting/Agreement Officer
Office of Acquisition and Assistance (OAA) | USAID/Democratic Republic of Congo
U.S. AGENCY FOR INTERNATIONAL DEVELOPMENT
Kinshasa, Democratic Republic of Congo (DRC)
T. +(243) 81 555 4552 | M. +(243) 81 710 0655 U.S. Emb. Ext. 2408
USAID.gov | asoh@usaid.gov | @USAID

ReplyReply allForward

--

Jean-Felly Numbi
USAID-DRC TB& Infectious Disease Advisor
Office Phone #: +243 81 555 45 22
Cellular Phone #: +243 81 700 86 91

--

Beth Edison
Program Manager | Metabiota
(250)739-8987

From:	Jonna Mazet <jkmazet@ucdavis.edu>
To:	Nita Madhav <nmadhav@metabiota.com>
CC:	Dean Jamison <djamison@uw.edu>;Brooke Genovese <bgenovese@ucdavis.edu>;boppenheim@metabiota.com <boppenheim@metabiota.com>;Dennis Carroll <dcarroll@usaid.gov>;Eri Togami <etogami@ucdavis.edu>;Karen Saylors <ksaylors@metabiota.com>
Sent:	1/28/2019 5:09:05 PM
Subject:	Re: Briefing in Washington on status of GVP BCA?

That all sounds like a good plan, Nita. I think we should add Cara Chrisman from USAID, as well.
One question based on the invite list & location. We had originally discussed DC for Dennis and other stakeholders there. If Dennis (potentially Cara) is the only DC person, and he has already said that he can travel, should we consider New York or Boston or even San Francisco? If Dean will be in DC anyway, totally happy to go there. Just want to make sure strategy (location) is evolving along with participation ideas.
Once we confirm location, I assume you'd like us to get a location & logistics going, yes?
Thanks for following up.
Jonna

On Sun, Jan 27, 2019 at 8:22 PM Nita Madhav <nmadhav@metabiota.com> wrote:
Dear Brooke and Jonna,
Following up on Dean's message, I wanted to touch base on the logistics for the March 13 meeting in DC.
Ben, Dean, and I met last week to push forward on the GVP BCA work. We also firmed up the planning for the March 13th meeting in DC. Below, please find the relevant details. Please let us know any feedback.
Best regards, Nita

March 13, 2019 - Washington, DC - Proposed Meeting Logistics
Who is on the invite list?
- Ben
- Nita
- Dean
- Jonna
- Dennis (Jonna to confirm)
- Peter Daszak (if available - Karen to reach out)
- Steve Morse (if available - Ben to reach out)
- Stefano Bertozzi (if available - Dean to reach out)
- Michael Kremer (if available - Dean to reach out)
- Mukesh Chawla (if available - Ben to reach out)
- Karen or Eddy (Ben/Nita to confirm)

What is the plan?
- Presentation of powerpoint deck (revised version attached)
  - Preliminary project design
  - Spend some proper time on the epidemiological modeling and economic modeling methods to convey the concepts in some detail
  - Harvest feedback on analytical plan
  - Get sign-off on some decision-points (e.g. how we handle vaccine development)
- Discussion of national virome program pilots (Thailand & China)-- what is the status?
  - What degree of flexibility is there for countries to determine their epidemiological priorities?

Can the pilot countries focus on flu?
- Presentation of preliminary results from early exceedance probability modeling
- Discussion of pre-meeting requests to PREDICT et al. for costing data

How long should the meeting be?

- 4 hours (tentatively 1pm - 5pm), perhaps time for informal drinks afterwards
- Note: Dean mentioned that he could do as early as 10am-2pm if that works better for people.

On Thu, Jan 10, 2019 at 12:31 PM Dean Jamison <djamison@uw.edu> wrote:
Dear Brooke

I believe there has been no change to the agreement to meet in DC on March 13. I wonder how Dennis is affected by the government shutdown, though?

My own preference for the 13th is for us to begin at 2pm. And for whoever who can do so to stay on for a drink in the early evening.

Best

Dean

On Jan 10, 2019, at 10:22 AM, Brooke Genovese <bgenovese@ucdavis.edu> wrote:

Hi everyone,

I wanted to check in on the status of this trip – is there a consensus on traveling to SF or D.C.?

Thank you,
Brooke

From: Brooke Genovese <bgenovese@ucdavis.edu>
Date: Thursday, November 29, 2018 at 10:45 AM
To: "boppenheim@metabiota.com" <boppenheim@metabiota.com>, Dennis Carroll <dcarroll@usaid.gov>, Dean Jamison <djamison@uw.edu>, Nita Madhav <nmadhav@metabiota.com>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Eri Togami <etogami@ucdavis.edu>
Subject: Re: Briefing in Washington on status of GVP BCA?

Hi everyone,

I can confirm Jonna's support for a DC briefing on March 13th.
Thanks!

-Brooke

From: Jonna Mazet <jkmazet@ucdavis.edu>
Date: Thursday, November 29, 2018 at 9:29 AM
To: Brooke Genovese <bgenovese@ucdavis.edu>
Subject: Fwd: Briefing in Washington on status of GVP BCA?

---------- Forwarded message ---------
From: **Ben Oppenheim** <boppenheim@metabiota.com>
Date: Wed, Nov 28, 2018 at 11:58 PM
Subject: Re: Briefing in Washington on status of GVP BCA?
To: Dennis Carroll <dcarroll@usaid.gov>
Cc: Dean Jamison <djamison@uw.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, Nita Madhav <nmadhav@metabiota.com>

Hi Dennis and Jonna,
Nita and I can both do 13 March (or 14th, but sounds like 13 would be better for Dean).
Shall we plan on that?
all the best,
Ben

On Wed, Nov 28, 2018 at 4:19 PM Dennis Carroll <dcarroll@usaid.gov> wrote:
Dean, apologies for the tardy reply. I greatly appreciate the opportunity for scheduling the update. I can accommodate whichever dates work best for you in either DC or SF. Thanks

Dr Dennis Carroll
Director
Emerging Threats
Global Health
USAID
301-646-6235

On Nov 28, 2018, at 7:00 PM, Dean Jamison <djamison@uw.edu> wrote:

March 13 slightly better for me but either the 13th or 24th works fine.

Dean

Sent from my iPhone

On Nov 28, 2018, at 11:51 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

I could do March 13th or 14th DC.
Jonna

On Wed, Nov 28, 2018 at 11:40 AM Dean Jamison <djamison@uw.edu> wrote:
Dear Jonna, Dennis

Thanks for getting back on this.

I unfortunately have personal commitments during the 4th week of March.

I could make March 13 or 14 or 18 in DC. Alternatively I could make any day during the first week of April in SF if that works better.

Best

Dean

Sent from my iPhone

--
Ben Oppenheim, PhD
Senior Scientist
Product Development

510.501.1097

—

Nita Madhav
Vice President of Data Science
Metabiota
425 California St. #1200
San Francisco, CA 94104
Email: nmadhav@metabiota.com
Phone: +1-281-723-3025

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From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Molly Turner <turner@ecohealthalliance.org>
CC: Evelyn Luciano <luciano@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh" <karesh@ecohealthalliance.org>;predict Sympa List <predict@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 1/29/2019 9:12:27 PM
Subject: RE: Restriction for Trafficking in persons (PREDICT)

At this point, yes. We'll be discussing this on SMT and EB next week, so there may be new info or guidance at that time.

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1493 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Molly Turner
Sent: Tuesday, January 29, 2019 2:09 PM
To: Elizabeth Leasure
Cc: Evelyn Luciano ; Peter Daszak ; William B. Karesh
Subject: Re: Restriction for Trafficking in persons (PREDICT)

Thanks for the heads up, Liz. Shall we proceed as usual until we receive further guidance?

Molly

On Fri, Jan 25, 2019 at 3:28 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Hi everyone. Just a heads up that new funding obligations for countries categorized as Tier 3 with regard to the Trafficking and Victims Protection Act (TVPA) have been put on hold or restricted. Current PREDICT-2 countries that are Tier 3 include DRC, Guinea, China, and RoC. All Ebola funds have been obligated to the PREDICT cooperative agreement, so Y5 funding and activities in Ebola funded countries (DRC and Guinea) should not be impacted, as we are allowed to proceed with activities in Tier 3 countries using funds obligated to date. Future obligations, however, are on hold until the country improves their status to Tier 2 or better or an exemption is obtained. USAID is working to obtain an exemption as we speak, but additional funding for China and RoC may be impacted if those efforts prove unsuccessful. This development is especially unfortunately given the only partial obligation of our Y5 core budget, but we will do everything we can to avoid such a scenario. We will keep you posted as we are updated by USAID. If you have any questions, please let me know.

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1493 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Alisa Pereira <apereira@usaid.gov>
Sent: Friday, January 25, 2019 10:23 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Andrew Clements <aclements@usaid.gov>; Lindsay Parish <lparish@usaid.gov>; predictmgt@usaid.gov; predict Sympa List <predict@ucdavis.edu>; David John Wolking <djwolking@ucdavis.edu>; Jonna Mazet <jkmazet@ucdavis.edu>; Hannah R Chale <hrchale@UCDAVIS.EDU>
Subject: Re: Question: Restriction for Trafficking in persons (PREDICT)

Dear Liz,

You are correct. The DRC activities have been fully obligated with FY17 funds, and as such, are allowed to proceed as planned. Unfortunately, for the other countries, we are still waiting for guidance. We have submitted information on the types of activities planned within the impacted countries, but have not received an exemption to proceed once funding becomes available. We will keep you posted as information becomes available.

Thanks
Alisa

Alisa Pereira, Senior Public Health Advisor
USAID, Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-0001, Arlington, VA 22202
Phone: 202-997-9966
Email: apereira@usaid.gov

GHSI-III - Social Solutions International, Inc. prime contractor

On Fri, Jan 25, 2019 at 12:41 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Hi Andrew, Lindsay, and Alisa. We recently received an email from one of our Country Coordinators in DRC alerting us to potential funding allocation restrictions in DRC related to the Trafficking and Victims Protection Act (TVPA) and DRC's current status as a Tier 3 country. The email came from Andre-Guy Soh in the USAID/DRC OAA office and was followed up by Jean-Felly Numbi at the Mission (emails below for your reference). Can you confirm whether or not this restriction applies to the PREDICT-2 cooperative agreement? As you know, DRC is an Ebola-funded country, and all of our Ebola funds have been obligated. Since we appear to be able to continue operating with existing funds, this TVPA restriction may not have any impact on PREDICT in DRC, however there are other core-funded countries (including China and Roc) for which all funds have not yet been obligated, as we are still awaiting the obligation of the remainder of our Y5 core budget. Any guidance you can provide regarding the applicability of this restriction and any actions we should be taking to ensure compliance would be most helpful and appreciated.

Quick Google Translation from Jean-Felly Numbi's email:
Trafficking in Persons (TIP): this restriction under which the DRC fell among many other countries, see the message below. CTB, FAO, Predict 2 Davis are still under this restriction therefore you will not receive new money as long as not raised. Of course it will be up but we do not know when. The lifting of this measure is gradual because other projects of the DRC have just been authorized to start implementation by supporting the government. It's the restriction that suspends doing business with the government concerned. What to do?

Thank you,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edson <bedson@metabiota.com>
Sent: Wednesday, January 23, 2019 7:31 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>

Cc: predict Sympa List <predict@ucdavis.edu>; Karen Saylors <ksaylors@metabiota.com>
Subject: Fwd: Restriction for Trafficking in persons.

Hi Liz,

Charles, our CC in DRC, received the below email from the mission. What he's saying is that DRC is on the list of countries that is restricted by the TVPA act and that no new money will be allocated until these restrictions are lifted. Apparently some organizations have already received an email advising the restriction has been lifted but FAO, CBT and UC Davis are still restricted and no new money will be allocated for DRC until an email is received. We are allowed to continue operating with funds already received.

Have you heard anything about this at all? I did a brief search for a list of countries and haven't found one yet, but it's possible that other PREDICT countries might be affected as well. If I find more info, I will send it along.

Thanks,
Beth

---------- Forwarded message ---------
From: **Charles Kumakamba** <ckumakamba@metabiota.com>
Date: Wed, Jan 23, 2019 at 1:07 AM
Subject: Fwd: Restriction for Trafficking in persons.
To: Karen Saylors <ksaylors@metabiota.com>, Beth Edison <bedison@metabiota.com>

FYI!

---------- Forwarded message ---------
From: **Jean-Felly Numbi** <jnumbi@usaid.gov>
Date: mer. 23 janv. 2019 10 h 01
Subject: Restriction for Trafficking in persons.
To: Jean Pierre Kabuayi <jpkabuayi@theunion.org>, Charles Kumakamba <ckumakamba@metabiota.com>

Bonjour Jean Pierre et Charles,
Merci pour le message sur le shutdown en rapport avec la mis en oeuvre des activités sur terrain.
En effet, il ya deux situations différentes à ce sujet à savoir :
1) Le shut-down qui est le retard d'approbation du budget du gouvernement américain par le Congrès suite aux tractations entre le président Trump et les démocrates. Comme conséquence c'est le retard pour l'argent attendu cette année en cours. Cependant si votre projet a encore un solde de l'année passée dans ce cas vous continuez avec la mise en oeuvre si le plan d'action est déjà approuvé. Tous nous attendons le New Money de cette année quand le shut-down sera levé.

2) **Trafficking in Persons (TIP)** : cette restriction sous laquelle la RDC est tombée parmi tant autres pays, voir le message ci-dessous,CTB, FAO, Predict 2 Davis sont encore sous cette restriction par conséquent vos ne recevrez new money tant pas levée. Bien sûr elle sera levée mais on ne sait pas quand. La levée de cette mesure est progressive car autres projets de la RDC viennent d'être autorisées de commencer la mise en oeuvre appuyant le gouvernement. C'est la restriction suspend de faire le business avec le gouvernement concerné. Que faire? Encore une fois si vous avez de l'argent du solde de l'année passée, je vous conseillerais de continuer les activités prioritaires de cette année car on ne sait pas quand la mesure sera levée.

Merci. Je suis disponible pour toute autre information.
Jean-Felly.

---------- Forwarded message ---------
From: **Andre-Guy Soh** <asoh@usaid.gov>
Date: Wed, Dec 12, 2018 at 2:24 PM
Subject: Update Concerning Impact of Trafficking-in-Persons Legislation on USAID awards
To: Andre-Guy Soh <asoh@usaid.gov>

Dear partners,

On November 28, I informed you that the U.S. Government was in the process of clarifying the effects of restrictions imposed by the Trafficking and Victims Protection Act of 2000 (the "TVPA") on U.S. Government activities in all Tier 3 designated countries.

We have received clearance for a limited number of awards, and have informed the organizations and contractors concerned.

If you have not received an email from USAID/DRC indicating that the U.S. Government has determined that your award is NOT COVERED by TVPA restrictions, then we are still unable to provide any assurance that additional funds will be obligated into your respective awards due to the potential application of TIP restrictions.

We understand this situation may create difficulties for program operations. While we wait for further guidance from Washington, feel free to reach out to your AOR/CORs for any questions you may have.

Regards,
AG

Andre-Guy Soh
Contracting/Agreement Officer
Office of Acquisition and Assistance (OAA) | USAID/Democratic Republic of Congo
U.S. AGENCY FOR INTERNATIONAL DEVELOPMENT
Kinshasa, Democratic Republic of Congo (DRC)
T. +(243) 81 555 4552 | M. +(243) 81 710 0655 U.S. Emb. Ext. 2408
USAID.gov | asoh@usaid.gov | @USAID

Reply Reply all Forward

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Jean-Felly Numbi
USAID-DRC TB& Infectious Disease Advisor
Office Phone #: +243 81 555 45 22
Cellular Phone #: +243 81 700 86 91

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Beth Edison
Program Manager | Metabiota
(250)739-8987

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Molly Turner
Federal Grants Coordinator

EcoHealth Alliance Operations

EcoHealth Alliance
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New York, NY 10001

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www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Beth Edison <bedison@metabiota.com>
CC: Shaun Tse <stse@metabiota.com>;Hannah R Chale <hrchale@ucdavis.edu>;predict Sympa List <predict@ucdavis.edu>
Sent: 3/27/2019 10:52:05 PM
Subject: [predict] RE: Contract mod

Hi Beth. Please take a look at the rebudget and coming amendment for PREDICT. Basically, we're rebudgeting from Core to Ebola to zero out all transitioned countries (resolving the overdraft for the Ebola countries in the process) and moving GVP carryover to Lao PDR, the idea being that these are FY17 funds that are not subject to the TVPA restriction, and we'll use FY18 money to fund the full GVP budget. Please take a look and let me know what you think. I'll need to process the rebudget with the amendment to add funds, so Hannah will hold off on processing the amendment until you confirm everything looks okay.

The Y5 funding obligation includes 25% of your full GVP budget for Y5 (excluding BCA funds-which will come separately), the balance of your Y5 Ebola budget (so you will now have your full Ebola budget in hand inclusive of carryover), and enough Core funds to ensure that you have 25% of your core budget in hand for Y5 (inclusive of carryover). Hopefully that makes sense. Let me know if you have any questions.

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530.304.1403 (cell)
530.754.9034 (office)
Skype: ealeasure

From: Beth Edison
Sent: Thursday, February 28, 2019 10:50 AM
To: Elizabeth Leasure
Cc: Shaun Tse
Subject: Contract mod

Hi Liz,

Do you have any thoughts on when we might expect a contract mod that includes the Ebola funds and GVP? I know we'll have to wait a while for core funds.

Thanks!
Beth

--
Beth Edison
Program Manager | Metabiota
(250)739-8987

	A	B	C	D	E
1	PREDICT-2 Budget				
2	Summary by Country & Fund Source (October 2018 - September 2019)				
3		USAID Core	USAID EBOLA	USAID GVP (Core)	Cost Share
4					
5	Global	224,081	414,655	15,667	14,210
6	Administrative Management	3,983	7,239	1,261	-
7	**Asia**				
8	Lao PDR	131,137			-
9	**Asia Subtotal**	**131,137**	-	-	-
10	**Africa**				
11	Cameroon		525,530		-
12	DRC		280,611		24,300
13	**Africa Subtotal**	-	**806,141**	-	**24,300**
14					
15	**Total**	**359,201**	**1,228,035**	**16,928**	**38,510**
16					
17	**TOTAL USAID**	**$ 1,604,164**			
18	**TOTAL Cost Share**	**$ 38,510**			
19		**$ 1,642,674**			
20					
21	**Year 4 Carryover**				
22	USAID Core	399,286			
23	USAID Ebola	631,888			
24	USAID GVP	-			
25		1,031,174			
26					
27	**Total Year 5 Obligation needed**				
28	USAID Core	1,436,805			
29	USAID Ebola	1,228,035			
30	USAID GVP	67,711			
31		2,732,551			
32					
33			359,201	25% of Y5 obligation needed	
34			1,228,035	Balance of Y5 Ebola budget	
35			16,928	25% of Y5 obligation needed	

	G	H	I
1			
2			
3	**TOTAL**		
4			
5	668,614		
6	12,483		
7			
8	131,137		
9	**131,137**		
10			
11	825,530		
12	304,911		
13	**830,441**		
14			
15	**1,642,674**		
16			
17			
18			
19			
20			
21			
22			
23			
24			
25			
26			
27			
28			
29			
30			
31			
32			
33	19.56%		0.195633686
34	66.026120%		0.660261204
35	25.00%		

	A	B	C	D	E
1	**PREDICT-2 Global Year 5 Budget - METABIOTA subagreement**				
2	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID Core**	**USAID EBOLA**
3					
4	**Salaries**				
5				-	-
6	Christian Lange, Virologist	92,976	80%	43,699	23,530
7	Dave McIver, Epidemiologist	88,882	10%	5,222	2,812
8	Beth Edson, Program Manager	135,668	65%	51,808	27,897
9	Amethyst Gillis, Global QAQC Coordinator	96,819	100%	56,881	30,628
10	Tammie O'Rourke, Systems Integrator	94,525	100%	55,533	29,903
11	Karen Saylors, Director of Surveillance	218,225	45%	57,693	31,066
12	Catherine Cleary, Research Assistant, Behavioural Risk Department	77,267	40%	18,158	9,777
13	Jason Euren, Behavioural Risk Analyst	111,650	25%	16,399	8,830
14	Ashley Lucas, Global Health Nurse	100,425	30%	17,700	9,531
15	Daniel Guenther, Software Developer	80,289	100%	23,670	12,745
16	Junhua Hu, Assistant Database Administrator	63,212	13%	4,828	2,600
17	Patrick Savage, Data Quality Analyst	37,191	100%	21,850	11,765
18	Dan O'Rourke, Health Information Developer	49,395	100%	29,020	15,626
19	Eddy Rubin, Chief Science Officer and PI	170,500	40%	22,587	16,134
20	Nathan Wolfe, Executive Support	360,000	2%		
21					
22					
23	**Salaries Total**			**425,047**	**232,843**
24					
25	**Fringe Benefits**		**39.33%**		
26	Christian Lange, Virologist	36,567	80%	17,187	9,254
27	Dave McIver, Epidemiologist	34,957	10%	2,054	1,106
28	Beth Edson, Program Manager	53,358	65%	20,376	10,972
29	Amethyst Gillis, Global QAQC Coordinator	38,079	100%	22,371	12,046
30	Tammie O'Rourke, Systems Integrator	37,177	100%	21,841	11,761
31	Karen Saylors, Director of Surveillance	85,828	45%	22,691	12,218
32	Catherine Cleary, Research Assistant, Behavioural Risk Department	30,389	40%	7,141	3,845
33	Jason Euren, Behavioural Risk Analyst	43,912	25%	6,450	3,473
34	Ashley Lucas, Global Health Nurse	39,497	30%	6,961	3,748
35	Daniel Guenther, Software Developer	15,846	100%	9,309	5,013
36	Junhua Hu, Assistant Database Administrator	24,861	13%	1,899	1,022
37	Patrick Savage, Data Quality Analyst	14,627	100%	8,593	4,627
38	Dan O'Rourke, Health Information Developer	19,427	100%	11,413	6,146
39	Eddy Rubin, Chief Science Officer and PI	70,204	40%	8,884	6,345
40	Nathan Wolfe, Executive Support	141,588	2%	-	-
41	0	-	0%	-	-
42	0	-	0%	-	-
43	**Fringe Benefits Total**			**167,171**	**91,577**
44					
45	**International Travel**				

	A	B	C	D	E
46	Eddy Rubin - PREDICT	MB management	2,144	2	2,787	1,501
47	Karen Saylors - PREDICT	MB management	2,144	2	2,787	1,501
48	Tammie O'Rourke - PREDICT	MB management	1,199	4	3,117	1,679
49	Beth Edison - PREDICT	MB management	1,704	2	2,215	1,193
50	Dan O'Rourke - PREDICT]MB Management		1,199	4	3,117	1,679
51	Tammie O'Rourke - PREDICT	MB management	1,595	1	1,037	558
52	Beth Edison - PREDICT	MB management	1,595	1	1,037	558
53	Dan O'Rourke - PREDICT]MB Management		1,595	1	1,037	558
54	David McIver - PREDICT	MB management	1,595	1	1,037	558
55	David McIver - PREDICT	MB management	1,704	1	1,108	596
56	Amethyst Gillis - PREDICT Regional meeting		1,910	1	1,242	669
57	Beth Edison - PREDICT regional Meeting		2,568	1	1,669	899
58	Tammie O'Rourke- PREDICT regional meeting		2,568	1	1,669	899
59	Dan O'Rourke - PREDICT regional meeting		2,568	1	1,669	899
60	Dave McIver - PREDICT regional meeting		2,568	1	1,669	899
61	Christian Lange - PREDICT Regional Meeting		2,568	1	1,669	899
62	Jason Euren - PREDICT Regional Meeting		2,736	1	1,778	958
63	Eddy Rubin - PREDICT regional Meeting		2,736	1	1,778	958
64	Karen Saylors - PREDICT Regional Meeting		2,736	1	1,778	958
65	Outreach Meetings		5,000	1		
82						
83	**Total International Travel**				**34,202**	**18,416**
84						
85	**Contractual**					
86	Boston Children's Hospital contract				25,392	15,723
87	International Society for Infectious Diseases (ISID) subaward				28,270	15,223
88						
89	**Total Contractual**				**53,663**	**30,946**
90						
91	**Other Costs**					
92	EIDITH Maintenance Services		61,000	1	39,650	21,350
93	Placeholder for unknown EIDITH closure costs		10,000	1	6,500	3,500
94	Communications and Subscriptions		15,000	1	9,750	5,250
95	Severance (Canada Office)		57,564	1	37,417	20,147
96	**Total Other Costs**				**93,317**	**50,247**
97	**Total Direct Costs**				**773,399**	**424,029**
98	***OH Onsite***			***24.3%***	118,756	65,291
99	***OH Offsite***			***15.9%***	16,470	8,869
100	**G&A**			***26.1%***	222,803	121,764
101	***Indirect Costs on subagreements & Contracts***			***26.1%***	13,985	8,064
102	**Total Costs**				**1,145,412**	**628,017**
103						
104						
105	**to International Society for Infectious Diseases**					

	A	B	C	D	E
106	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID Core**	**USAID EBOLA**
107					
108	**Salaries**				
109	Project Manager	75,000	5%	2,438	1,313
110	Technical Specialist	74,000	5%	2,405	1,295
111	Project Director	96,000	5%	3,120	1,680
112				-	-
113	**Salaries Total**			**7,963**	**4,288**
114					
115	**Fringe Benefits**		**30.0%**		
116	Project Manager	22,500	5%	731	394
117	Technical Specialist	22,200	5%	722	389
118	Project Director	28,800	5%	936	504
119	0	-	0%	-	-
120	**Fringe Benefits Total**			**2,389**	**1,286**
121					
122	**Contractual**				
123	ProMED Associate Editors	5,795	1	3,767	2,028
124	ProMED Copy Editors	5,885	1	3,825	2,060
125	ProMED Wildlife Moderators -	11,934	1	7,757	4,177
126				-	-
127	**Total Contractual**			**15,349**	**8,265**
128					
129	**Supplies**				
130				-	-
131	**Total Supplies**			-	-
132					
133	**Other Costs**				
134	**Total Other Costs**				
135	**Total Direct Costs**			**25,700**	**13,839**
136	**Indirect Costs**		***10%***	*2,570*	*1,384*
137	**Total Costs**			**28,270**	**15,223**
138					
139	**Boston Children's Hospital**				
140	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID Core**	**USAID EBOLA**
141					
142	**Salaries**				
143	Project Coordinator	60,000	5%	1,950	1,050
144	Programmer/Software Engineer	102,000	10%	6,630	3,570
145	Front End Developer	102,000	10%	6,630	3,570
146				-	-
147	**Salaries Total**			**15,210**	**8,190**
148					

	A	B	C	D	E
149	**Fringe Benefits**		**30.6%**		
150	Project Coordinator	18,336	5%	5%	321
151	Programmer/Software Engineer	31,171	10%	2,026	1,091
152	Front End Developer	31,171	10%	2,026	1,091
153	0	-	0%	-	-
154	**Fringe Benefits Total**			**4,668**	**2,503**
155					
156	**Supplies**				
157	Amazon Web Services	4,000	1	1,400	2,520
158	**Total Supplies**			**1,400**	**2,520**
159	**Total Direct Costs**			**21,338**	**13,213**
160	***Indirect Costs***		***19%***	*4,054*	*2,510*
161	**Total Costs**			**25,392**	**15,723**
162					

	F	G	H	I	J	K	L	M
1					Core	Ebola	GVP	
2	**USAID GVP**	**Cost Share**	**Year 5 Total**		**Partial obligation**	***Balance of Y5 Budget due***	**Partial obligation**	**Total Obligation**
3								
4								
5			-					
6			**67,229**		8,549	15,536	-	24,085
7			**8,034**		1,022	1,856	-	2,878
8			**79,705**		10,135	18,419	-	28,555
9			**87,509**		11,128	20,223	-	31,351
10			**85,436**		10,864	19,744	-	30,608
11			**88,759**		11,287	20,511	-	31,798
12			**27,935**		3,552	6,456	-	10,008
13			**25,229**		3,208	5,830	-	9,038
14			**27,231**		3,463	6,293	-	9,755
15			**36,415**		4,631	8,415	-	13,046
16			**7,427**		944	1,716	-	2,661
17			**33,615**		4,275	7,768	-	12,043
18			**44,645**		5,677	10,317	-	15,994
19	25,814		**64,535**		4,419	10,652	6,453	21,525
20		6,500	**6,500**		-	-	-	-
21			-		-	-	-	-
22			-		-	-	-	-
23	**25,814**	**6,500**	**690,211**		**83,153**	**153,737**	**6,453**	**243,344**
24								
25								
26	-		**26,441**		3,362	6,110	-	9,473
27	-		**3,168**		402	730	-	1,132
28	-		**31,348**		3,986	7,244	-	11,231
29	-		**34,417**		4,377	7,954	-	12,330
30	-		**33,602**		4,273	7,765	-	12,038
31	-		**34,909**		4,439	8,067	-	12,506
32	-		**10,987**		1,397	2,539	-	3,936
33	-		**9,922**		1,262	2,293	-	3,555
34	-		**10,710**		1,362	2,475	-	3,837
35	-		**14,322**		1,821	3,310	-	5,131
36	-		**2,921**		371	675	-	1,047
37	-		**13,221**		1,681	3,055	-	4,736
38	-		**17,559**		2,233	4,058	-	6,291
39	10,153	-	**25,381**		1,738	4,190	2,538	8,466
40	-	2,559	**2,559**		-	-	-	-
41	-		-		-	-	-	-
42	-		-		-	-	-	-
43	**10,153**	**2,559**	**271,460**		**32,704**	**60,465**	**2,538**	**95,707**
44								
45								

	F	G	H	I	J	K	L	M
46			**4,288**		545	991	-	1,536
47			**4,288**		545	991	-	1,536
48			**4,796**		610	1,108	-	1,718
49			**3,408**		433	788	-	1,221
50			**4,796**		610	1,108	-	1,718
51			**1,595**		203	369	-	571
52			**1,595**		203	369	-	571
53			**1,595**		203	369	-	571
54			**1,595**		203	369	-	571
55			**1,704**		217	394	-	610
56			**1,918**		243	441	-	684
57			**2,568**		327	593	-	920
58			**2,568**		327	593	-	920
59			**2,568**		327	593	-	920
60			**2,568**		327	593	-	920
61			**2,568**		327	593	-	920
62			**2,736**		348	632	-	980
63			**2,736**		348	632	-	980
64			**2,736**		348	632	-	980
65	5,000		**5,000**		-	-	1,250	1,250
82			-		-	-	-	-
83	**5,000**	-	**57,618**		**6,691**	**12,160**	**1,250**	**20,101**
84								
85								
86			**41,116**		4,968	10,381	-	15,349
87	-	-	**43,493**		5,531	10,051	-	15,581
88			-		-	-	-	-
89	-	-	**84,609**		**10,498**	**20,432**	-	**30,931**
90								
91								
92	-		**61,000**		7,757	14,097	-	21,853
93	-		**10,000**		1,272	2,311	-	3,583
94	-		**15,000**		1,907	3,466	-	5,374
95	-		**57,564**		7,320	13,303	-	20,622
96	-	-	**143,564**		**18,256**	**33,176**	-	**51,432**
97	**40,966**	**9,067**	**1,247,462**		**151,303**	**279,970**	**10,242**	**410,584**
98	8,747	2,205	**194,999**		23,233	43,109	2,187	68,528
99	-	-	**25,339**		3,222	5,856	-	9,078
100	12,955	2,938	**360,459**		43,588	80,396	3,239	127,222
101	-	-	**22,049**		2,736	5,325	-	8,061
102	**62,669**	**14,210**	**1,850,308**		**224,081**	**414,655**	**15,667**	**623,473**
103								
104								
105					Core	Ebola	GVP	

	F	G	H	I	J	K	L	M
106	**USAID GVP**	**Cost Share**	**Year 5 Total**		**Partial obligation**	***Balance of Y5 Budget due***	**Partial obligation**	**Total Obligation**
107								
108								
109	-		**3,750**		477	867	-	1,343
110	-		**3,700**		470	855	-	1,326
111	-		**4,800**		610	1,109	-	1,720
112	-		-		-	-	-	-
113	-	-	**12,250**		**1,558**	**2,831**	-	**4,389**
114								
115								
116	-		**1,125**		143	260	-	403
117	-		**1,110**		141	257	-	398
118	-		**1,440**		183	333	-	516
119	-		-		-	-	-	-
120	-	-	**3,675**		**467**	**849**	-	**1,317**
121								
122								
123	-		**5,795**		737	1,339	-	2,076
124	-		**5,885**		748	1,360	-	2,108
125	-		**11,934**		1,518	2,758	-	4,275
126	-		-		-	-	-	-
127	-	-	**23,614**		**3,003**	**5,457**	-	**8,460**
128								
129								
130	-		-		-	-	-	-
131	-	-	-		-	-	-	-
132								
133								
134								
135	-	-	**39,539**		**5,028**	**9,137**	-	**14,165**
136	-	-	3,954		503	914	-	1,416
137	-	-	**43,493**		**5,531**	**10,051**	-	**15,581**
138								
139					Core	Ebola	GVP	
140	**USAID GVP**	**Cost Share**	**Year 5 Total**		**Partial obligation**	***Balance of Y5 Budget due***	**Partial obligation**	**Total Obligation**
141								
142								
143	-		**3,000**		381	693	-	1,075
144	-		**10,200**		1,297	2,357	-	3,654
145	-		**10,200**		1,297	2,357	-	3,654
146	-		-		-	-	-	-
147	-	-	**23,400**		**2,976**	**5,408**	-	**8,383**
148								

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	F	G	H	I	J	K	L	M
149								
150	-		**917**		117	212	-	328
151	-		**3,117**		396	720	-	1,117
152	-		**3,117**		396	720	-	1,117
153	-		-		-	-	-	-
154	-	-	**7,151**		**909**	**1,653**	-	**2,562**
155								
156								
157	-		**4,008**		290	1,664	-	1,953
158	-	-	**4,008**		**290**	**1,664**	-	**1,953**
159	-	-	**34,551**		**4,174**	**8,724**	-	**12,898**
160	-	-	6,565		793	1,658	-	2,451
161	-	-	**41,116**		**4,968**	**10,381**	-	**15,349**
162								

	A	B	C	D	E	F
1	**PREDICT-2 Administrative Management Year 5 Budget - METABIOTA subagreement**					
2	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID Core**	**USAID EBOLA**	**USAID GVP**
3						
4	**Salaries**					
5				-	-	-
6				-	-	-
7	**Salaries Total**			-	-	-
8						
9	**Fringe Benefits**		**39.33%**			
10	0	-	0%	-	-	-
11	0	-	0%	-	-	-
12	**Fringe Benefits Total**			-	-	-
13						
14	**Domestic Travel**					
15	Karen Saylors - EB/EPT meetings	1,385	2	1,801	970	-
16	Eddy Rubin - 1 RT - EB/EPT meetings	1,385	2	1,801	970	-
17	and Outreach Meetings	2,000	2			4,000
18						
19	**Total Domestic Travel**			**3,601**	**1,939**	**4,000**
20						
21	**Supplies**					
22	Computer and Office Supplies	14,310	1	9,302	5,009	-
23	Project closure costs	5,000	1	3,250	1,750	-
24	**Total Supplies**			**12,552**	**6,759**	-
25	**Total Direct Costs**			**16,153**	**8,698**	**4,000**
26	**OH Onsite**		**24.3%**			
27	**OH Offsite**		**15.9%**			
28	***G&A***		***26.1%***	4,209	2,267	1,042
29	***Indirect Costs on subagreements & Contracts***		***26.1%***			
30	**Total Costs**			**20,362**	**10,964**	**5,042**
31						
32						
33						

	G	H	I	J	K	L	M
1				Core	Ebola	GVP	
2	**Cost Share**	**Year 5 Total**		**Partial obligation**	***Balance of Y5 Budget due***	**Partial obligation**	**Total Obligation**
3							
4							
5		-		-	-	-	-
6		-		-	-	-	-
7	-	-		-	-	-	-
8							
9							
10		-		-	-	-	-
11		-		-	-	-	-
12	-	-		-	-	-	-
13							
14							
15		**2,770**		352	640	-	**992**
16		**2,770**		352	640	-	**992**
17		**4,000**		-	-	1,300	**1,000**
18		-		-	-	-	-
19	-	**9,540**		**704**	**1,280**	**1,000**	**2,985**
20							
21							
22		**14,310**		1,820	3,307	-	**5,127**
23		**5,000**		636	1,155	-	**1,791**
24	-	**19,310**		**2,455**	**4,462**	-	**6,918**
25	-	**28,850**		**3,160**	**5,743**	**1,000**	**9,903**
26				-	-	-	-
27				-	-	-	-
28	-	**7,518**		823	1,497	261	**2,581**
29		-		-	-	-	-
30	-	**36,368**		**3,983**	**7,239**	**1,261**	**12,483**
31							
32							
33							

	A	B	C	D	E
1	**subagreement**				
2	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID EBOLA**	**Cost Share**
3					
4	**Salaries**				
5	Ubald Tamoufe (Regional Director)	89,699	16%	12,972	
6	Julius Agbor (Fin & Ops Manager)	44,777	15%	6,071	
7	Arrey Roosevelt (Finance Assistant)	14,036	15%	1,933	
8	Adolphe Ngole (Customs Liaison Officer)	9,717	30%	2,635	
9	EPANE Marcel (Driver)	8,098	100%	7,319	
10	Valantine Ngum Ndze, Laboratory Director	34,272	16%	4,956	
11	NKOM Felix Ntumvi (Lab Scientist)	17,275	80%	12,491	
12	Joseph Diffo (Senior Field Ecologist)	17,275	30%	4,684	
13	Jean Michel Takuo (Field Ecologist)	11,877	30%	3,220	
14	Victorine Tuguem	15,118	30%	4,099	
15	Mbongo Beatrice	11,337	15%	1,537	
16	Beth Edison, Program Manager	135,668	5%	6,131	
17	Karen Saylors, Director of Surveillance	218,225	10%	19,724	
18	Dana Ellis, Program Coordinator	54,229	33%	16,338	
19	**Salaries Total**			**104,082**	-
20					
21	**Fringe Benefits**		**39.33%**		
22	Ubald Tamoufe (Regional Director)	89,699	16%	5,132	
23	Julius Agbor (Fin & Ops Manager)	44,777	15%	2,388	
24	Arrey Roosevelt (Finance Assistant)	14,036	15%	748	
25	Adolphe Ngole (Customs Liaison Officer)	9,717	30%	1,036	
26	EPANE Marcel (Driver)	8,098	100%	2,879	
27	Valantine Ngum Ndze, Laboratory Director	34,272	16%	1,949	
28	NKOM Felix Ntumvi (Lab Scientist)	17,275	80%	4,913	
29	Joseph Diffo (Senior Field Ecologist)	17,275	30%	1,842	
30	Jean Michel Takuo (Field Ecologist)	11,877	30%	1,267	
31	Victorine Tuguem	15,118	30%	1,612	
32	Mbongo Beatrice	11,337	15%	605	
33	Beth Edison, Program Manager	135,668	5%	2,411	
34	Karen Saylors, Director of Surveillance	218,225	10%	7,758	
35	Dana Ellis, Program Coordinator	54,229	33%	6,426	
36	**Fringe Benefits Total**			**40,935**	-
37					
38	**Domestic Travel**				
39	Hospital Final Meeting 2 sites @ 1 trips	1,100	2	2,200	
40	Women Bushmeat Sellers Sensibilisation 2 sites @ 1 trips	1,100	2	2,200	
41	Community outreach (local villages) 6 sites @ 1 trips	1,400	6	8,400	
42	One Health day 2 sites @ 1 trips	1,300	2	2,600	
43	National conference or event 5 events @ 1 trips	630	5	3,150	

	A	B	C	D	E
44	Participation at MINEPIA and MINFOF regional biannual Meeting	462	4	1,848	
45	Bat Book Pilot 3 sites @ 1 trip	860	3	2,580	
46	Extra behavioral data collection 3 sites @ 1 trips	920	3	2,760	
47				-	
48	**Total Domestic Travel**			**25,738**	-
49					
50	**International Travel**				
51	Karen Saylors - Cameroon Trip	2,926	2	5,852	
52	Jason Euren - Cameroon Trip			-	
53	Beth Edson - Cameroon Trip	3,014	1	3,014	
54	Dave McIver - Cameroon Trip	3,014	1	3,014	
55	Gov't Rep to PREDICT Final mtg	1,910	1	1,910	
56	Regional or International Conference	3,500	1	3,500	
57	**Total International Travel**			**17,290**	-
58					
59	**Contractual**				
60	Mosaic subagreement (detail below)			172,117	-
61					
62	**Total Contractual**			**172,117**	-
63					
64	**Equipment**				
65	Analytical and Precision Balance	7,718	1	7,718	
66	Ultra-Low Temperature Freezer	17,810	1	17,810	
67	**Total Equipment**			**25,528**	
68					
69	**Diagnostics**				
70	Laboratory Reagents and Consumables to complete testing for Flavi (6277)	50,574	1	50,574	
71				-	
72				-	
73	**Total Diagnostics**			**50,574**	-
74					
75	**Supplies**				
76	Office Supplies	273	12	3,270	
77	Local field and lab supplies	5,000	1	5,000	
78				-	
79	Outbreak Kits	6,480	1	6,480	
80	**Total Supplies**			**14,750**	-
81					
82	**Other Costs**				
83	Karen Saylors - SOS Insurance	850	1	850	
84	Vaccination	75	10	750	
85	Cloning	238	155	36,890	
86	Permit Renewals (MINFOF/MINRESI)	350	4	1,400	
87	Laboratory Waste Incineration	800	10	8,000	

	A	B	C	D	E
88	World Courier shipment of serology samples to USA	3,500	1	3,500	
89	DHL coupons for sample shipment	100	12	1,200	
90	Customs Clearance	3,000	1	3,000	
91	LN Plant maintenance	5,000	1	5,000	
92	Biosafety Cabinet Certification	4,606	1	4,606	
93	Workshop One Health Surveillance workforce to transfer skills and knowledge	2,500	2	5,000	
94	Lab training (One Health lab Network, Student): sharing data and protocols	2,800	3	8,400	
95	End-of-project workshop	9,000	1	9,000	
96	Sample Disposition Placeholder	15,000	1	15,000	
97	Possible consultant agreements for field staff	5,000	1	5,000	
98	Publication Costs	12,800	1	12,800	
99	Severance Costs (for staff at 100% LOE)	29,999	1	29,999	
100	**Total Other Costs**			**150,395**	-
101	**Total Direct Costs**			**601,409**	-
102	**OH Onsite**		**24.3%**	**35,268**	
103	**OH Offsite**		**15.9%**		
104	**G&A**		**26.1%**	114,412	-
105	***Indirect Costs on subagreements & Contracts***		**26.1%**	44,854	
106	**Total Costs**			**795,942**	-
107					
108	**PREDICT-2 Cameroon Year 5 Budget - MB subagreement to Mosaic**				
109	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID EBOLA**	**Cost Share**
110					
111	**Salaries**				
112	Senior Technical Advisor (Matthew LeBreton)	141,984	34.0%	48,275	
113	Country Coordinator (Moctar Mouiche)	33,688	100.0%	33,688	
114				-	
115	**Salaries Total**			**81,963**	-
116					
117					
118	**Fringe Benefits**		**35.0%**		
119	Senior Technical Advisor (Matthew LeBreton)	49,694	34.0%	16,896	
120	**Fringe Benefits local staff**		**22.0%**		
121	Country Coordinator (Moctar Mouiche)	7,411	100.0%	7,411	
122	0	-	0.0%	-	
123	**Fringe Benefits Total**			**24,307**	-
124					
125	**Domestic Travel**				
126	Senior Technical Advisor Douala	416	3	1,248	
127	Senior Technical Advisor field sites	312	3	936	
128	Country Coordinator workshops/meetings	506	6	3,036	
129	Country Coordinator field sites	294	5	1,470	

	A	B	C	D	E
130				-	
131	**Total Domestic Travel**			**6,690**	-
132					
133	**International Travel**				
134	PREDICT Meeting (CC and Tech Adviser)	2,514	2	5,028	
135				-	
136	**Total Contractual**			**5,028**	-
137					
138	**Supplies**				
139	vaccinations	50	1	50	
140	internet access	19	12	228	
141	phone costs	58	12	696	
142	office, dropbox, antivirus and carbonite software	200	1	200	
143	field supplies and research permits	750	1	750	
144	office supplies	98	12	1,176	
145	training supplies	200	1	200	
146	**Total Supplies**			**3,300**	-
147	**Total Direct Costs**			**121,288**	-
148	***Indirect Costs***		***19.00%***	*23,045*	-
149	***VAT***		***19.25%***	*27,784*	
150	**Total Costs**			**172,117**	-
151					
152					

	F	G	H
1			Ebola
2	**Year 5 Total**		***Balance of Y5 Budget due***
3			
4			
5	**12,972**		8,565
6	**6,071**		4,008
7	**1,903**		1,256
8	**2,635**		1,740
9	**7,319**		4,833
10	**4,956**		3,272
11	**12,491**		8,247
12	**4,684**		3,093
13	**3,220**		2,126
14	**4,099**		2,707
15	**1,537**		1,015
16	**6,131**		4,048
17	**19,724**		13,023
18	**16,338**		10,787
19	**104,082**		**68,721**
20			
21			
22	**5,102**		3,369
23	**2,388**		1,576
24	**748**		494
25	**1,036**		684
26	**2,879**		1,901
27	**1,949**		1,287
28	**4,913**		3,244
29	**1,842**		1,216
30	**1,267**		836
31	**1,612**		1,065
32	**605**		399
33	**2,411**		1,592
34	**7,758**		5,122
35	**6,426**		4,243
36	**60,935**		**27,028**
37			
38			
39	**2,200**		1,453
40	**2,200**		1,453
41	**8,400**		5,546
42	**2,600**		1,717
43	**3,150**		2,080

	F	G	H
44	**1,848**		1,220
45	**2,580**		1,703
46	**2,760**		1,822
47	-		-
48	**25,738**		**16,994**
49			
50			
51	**5,852**		3,864
52	-		-
53	**3,014**		1,990
54	**3,014**		1,990
55	**1,910**		1,261
56	**3,500**		2,311
57	**17,290**		**11,416**
58			
59			
60	**172,117**		113,642
61	-		-
62	**172,117**		**113,642**
63			
64			
65	**7,718**		5,096
66	**17,810**		11,759
67	**25,528**		**16,855**
68			
69			
70	**50,574**		33,392
71	-		-
72	-		-
73	**50,574**		**33,392**
74			
75			
76	**3,270**		2,159
77	**5,000**		3,301
78	-		-
79	**6,480**		4,278
80	**14,750**		**9,739**
81			
82			
83	**850**		561
84	**750**		495
85	**36,890**		24,357
86	**1,400**		924
87	**8,000**		5,282

	F	G	H
88	3,500		2,311
89	1,200		792
90	3,000		1,981
91	5,000		3,301
92	4,606		3,041
93	5,000		3,301
94	8,400		5,546
95	9,000		5,942
96	15,000		9,904
97	5,000		3,301
98	12,800		8,451
99	29,999		19,807
100	150,395		99,300
101	601,409		397,087
102	35,268		23,286
103	-		-
104	114,412		75,542
105	44,854		29,615
106	795,942		525,530
107			
108			Ebola
109	**Year 5 Total**		***Balance of Y5 Budget due***
110			
111			
112	48,275		31,874
113	33,688		22,243
114	-		-
115	81,963		54,117
116			
117			
118			
119	16,896		11,156
120			-
121	7,411		4,893
122	-		-
123	24,307		16,049
124			
125			
126	1,248		824
127	936		618
128	3,036		2,005
129	1,470		971

	F	G	H
130	-		-
131	**6,690**		**4,417**
132			
133			
134	**5,028**		3,320
135	-		-
136	**5,028**		**3,320**
137			
138			
139	**50**		33
140	**228**		151
141	**696**		460
142	**200**		132
143	**750**		495
144	**1,176**		776
145	**200**		132
146	**3,300**		**2,179**
147	**121,288**		**80,082**
148	23,045		15,216
149	27,784		18,345
150	**172,117**		**113,642**
151			
152			

	A	B	C	D
1	**PREDICT-2 DRC Year 5 Budget - METABIOTA subagreement**			
2	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID EBOLA**
3				
4	**Salaries**			
5	Charles Kamakamba, Country Coordinator	47,136	70%	29,823
6	Maria Makuwa, Lab Virol. & Assist. Accountant	37,200	15%	5,043
7	Frieda N'Kawa, Lab Technician	35,360	20%	6,392
8	Andre Berakuzu, Logistician	16,236	15%	2,201
9	Eric Mbala, Driver	13,520	30%	3,666
10	Albert Mbungu, Accountant	36,550	14%	4,625
11	Beth Edison, Program Manager	135,668	5%	6,131
12	Karen Saylors, Director of Surveillance	218,225	10%	19,724
13	Dana Ellis, Program Coordinator	54,229	33%	16,338
14	**Salaries Total**			**93,944**
15				
16	**Fringe Benefits**		**39.33%**	
17	Charles Kamakamba, Country Coordinator	47,136	70%	11,729
18	Maria Makuwa, Lab Virol. & Assist. Accountant	37,200	15%	1,984
19	Frieda N'Kawa, Lab Technician	35,360	20%	2,514
20	Andre Berakuzu, Logistician	16,236	15%	866
21	Eric Mbala, Driver	13,520	30%	1,442
22	Albert Mbungu, Accountant	36,550	14%	1,819
23	Beth Edison, Program Manager	135,668	5%	2,411
24	Karen Saylors, Director of Surveillance	218,225	10%	7,758
25	Dana Ellis, Program Coordinator	54,229	33%	6,426
26	**Fringe Benefits Total**			**36,948**
27				
28	**Domestic Travel**			
29	Communication to Sampling Sites (Kongo Central, Isongo)	1,540	1	1,540
30	Equateur follow up	7,000	1	7,000
31	**Total Domestic Travel**			**8,540**
32				
33	**International Travel**			
34	Karen Saylors - DRC Trip	4,755	1	4,755
35	Amethyst Gillis - DRC Trip	3,274	1	3,274
36				-
37	**Total International Travel**			**8,029**
38				
39	**Contractual**			
40	INRB subagreement (detail below)			31,498
41	**Total Contractual**			**31,498**
42				
43	**Equipment**			
46				-
47	**Total Equipment**			-

	A	B	C	D
48				
49	**Diagnostics**			
50	Laboratory Reagents and Consumables to complete testing for Ilavi (427)	4,602	1	4,602
52				-
53	**Total Diagnostics**			**4,602**
54				
55	**Supplies**			
56	Office supplies	2,130	1	2,130
57	Local lab supplies	3,000	1	3,000
58	Outbreak Go Kits	6,480	1	6,480
59	**Total Supplies**			**11,610**
60				
61	**Other Costs**			
62	Cloning	238	83	19,754
63	DHL Shipments	132	6	792
64	Communication	1,260	1	1,260
65	Customs Clearance	3,000	1	3,000
66	Permit Renewal	600	1	600
67	IRB Renewal	1,800	1	1,800
68	Internet	1,200	1	1,200
69	Biosafety Cabinet Certification	5,000	1	5,000
70	Grace Muyembe (Lab Intern)	500	4	1,750
71	PREDICT Completion Partner meeting	1,900	1	1,900
72	Publication costs	6,400	1	12,800
73	Severance Costs (All staff excluding Maria Makuwa)	45,281	1	45,281
74	Sample Disposition Placeholder	15,000	1	15,000
75	**Total Other Costs**			**110,137**
76	**Total Direct Costs**			**305,308**
77	**OH Onsite**		**24.3%**	**31,833**
78	**OH Offsite**		**15.9%**	
79	**G&A**		**26.1%**	**79,651**
80	***Indirect Costs on subagreements & Contracts***		**26.1%**	**8,208**
81	**Total Costs**			**425,000**
82				
118				
119	**PREDICT-2 DRC Year 5 Budget - MB subagreement to Institut National de Recherche Biomedicale (INRB)**			
120	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID EBOLA**
121				
122	**Diagnostics**			
124				-
125	**Total Diagnostics**			-
126				
127	**Other Costs**			
128	Equipment maintenance/certification	7,165	1	7,165

	A	B	C	D
129	Fuel for laboratory Backup Generator	12,000	1	12,000
130	Vehicle maintenance	10,000	1	10,000
131	Operational costs (electricity, water use, housekeeping, security, backup generator costs not covered by indirects)	7,500	3	-
132				-
133	**Total Other Costs**			**29,165**
134	**Total Direct Costs**			**29,165**
135	***Indirect Costs***		**8%**	*2,333*
136	**Total Costs**			**31,498**
137				
138				

	E	F	G	H
1				Ebola
2	**Cost Share**	**Year 5 Total**		***Balance of Y5 Budget due***
3				
4				
5		**29,823**		19,691
6		**5,043**		3,330
7		**6,392**		4,220
8		**2,201**		1,453
9		**3,666**		2,421
10		**4,625**		3,054
11		**6,131**		4,048
12		**19,724**		13,023
13		**16,338**		10,787
14	-	**93,944**		**62,027**
15				
16				
17		**11,729**		7,744
18		**1,984**		1,310
19		**2,514**		1,660
20		**866**		572
21		**1,442**		952
22		**1,819**		1,201
23		**2,411**		1,592
24		**7,758**		5,122
25		**6,426**		4,243
26	-	**36,948**		**24,395**
27				
28				
29		**1,540**		1,017
30		**7,000**		4,622
31	-	**8,540**		**5,639**
32				
33				
34		**4,755**		3,140
35		**3,274**		2,162
36		-		-
37	-	**8,029**		**5,301**
38				
39				
40	24,300	**55,798**		20,797
41	**24,300**	**55,798**		**20,797**
42				
43				-
46		-		-
47	-	-		-

	E	F	G	H
48				
49				
50		**4,602**		3,039
52		-		-
53	-	**4,602**		**3,039**
54				
55				
56		**2,130**		1,406
57		**3,000**		1,981
58		**6,480**		4,278
59	-	**11,610**		**7,666**
60				
61				
62		**19,754**		13,043
63		**792**		523
64		**1,260**		832
65		**3,000**		1,981
66		**600**		396
67		**1,800**		1,188
68		**1,200**		792
69		**5,000**		3,301
70		**forec**		1,155
71		**1,900**		1,254
72		**12,800**		8,451
73		**45,281**		29,897
74		**15,000**		9,904
75	-	**108,387**		**72,719**
76	**24,300**	**327,858**		**201,583**
77		**31,833**		21,010
78		-		-
79	-	**79,651**		52,590
80		**8,208**		5,420
81	**24,300**	**447,550**		**280,611**
82				
118				
119				Ebola
120	**Cost Share**	**Year 5 Total**		***Balance of Y5 Budget due***
121				
122				
124		-		-
125	-	-		-
126				
127				
128		**7,165**		4,731

	E	F	G	H
129		**12,000**		7,923
130		**10,000**		6,603
131	22,500	**22,500**		-
132		-		-
133	**22,500**	**51,665**		**19,257**
134	**22,500**	**51,665**		**19,257**
135	1,800	4,133		1,541
136	**24,300**	**55,798**		**20,797**
137				
138				

	A	B	C	D	E
1	**PREDICT-2 Lao PDR Year 5 Budget - METABIOTA subagreement**				
2	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID Core**	**Cost Share**
3					
4	**Salaries**				
5	Silithammavong, Soubanh, Country Coordinator	44,254	100%	39,999	
6	Viengkeo Anoana	10,095	100%	9,124	
7	Dave McIver, Epidemiologist	88,882	90%	72,302	
8	Beth Edison, Program Manager	135,668	25%	30,656	
9	Dana Ellis, Program Coordinator	54,229	33%	16,338	
10	**Salaries Total**			**168,419**	-
11					
12	**Fringe Benefits**		**39.33%**		
13	Silithammavong, Soubanh, Country Coordinator	44,254	100%	15,732	
14	Viengkeo Anoana	10,095	100%	3,589	
15	Dave McIver, Epidemiologist	88,882	90%	28,436	
16	Beth Edison, Program Manager	135,668	25%	12,057	
17	Dana Ellis, Program Coordinator	54,229	33%	6,426	
18	**Fringe Benefits Total**			**66,239**	-
19					
20	**Domestic Travel**				
21	Community Outreach trips	492	5	2,460	
22				-	
23	**Total Domestic Travel**			**2,460**	-
24					
25	**International Travel**				
26	Jason Eaves- Lao PDR Regional Trip	2,030	1	2,030	
27	Karen Saylors - Lao PDR Regional Trip	2,030	1	2,030	
28	Amethyst Gillis - Lao PDR Trip	5,199	2	10,398	
29	Dave McIver - Asia Regional Trip	2,742	3	8,226	
30	Beth Edison - Asia Regional Trip	2,742	1	2,742	
31	Country Coordinator and Gov't Rep to PREDICT Regional Meeting	2,534	2	5,068	
32	Regional or International Conference	2,534	1	2,534	
33	**Total International Travel**			**33,028**	-
34					
35	**Contractual**				
36	National Animal Health Laboratory (NAHL) subagreement (detail below)			52,556	-
37					
38	**Total Contractual**			**52,556**	-
39					
40	**Equipment**				
41	Thermocycler	**6,250**	**1**	6,250	
42	Minus 80 Freezer	18,750	1	18,750	

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	A	B	C	D	E
43			1		
44					
45	**Total Equipment**			**25,000**	-
46					
47	**Diagnostics**				
48	Laboratory Reagents and Consumables to test a second set of samples (226)	17,356	1	17,356	
49	other diagnostics	7,725	1	7,725	
50	Cloning	238	100	23,800	
51	Follow up Projects	3,731	1	3,731	
52	**Total Diagnostics**			**52,612**	-
53					
54	**Supplies**				
55	Lab Equipment < 5k	15,294	1	15,294	
56	Office Supplies	300	12	3,600	
57	Outbreak Kit	6,480	1	6,480	
58				-	
59	**Total Supplies**			**25,374**	-
60					
61	**Other Costs**				
62	David McIver SOS Insurance	850	1	850	
63	Payroll services 108/pub	15,000	1	15,000	
64	Final Gov't Communication Meeting	4,000	1	4,000	
65	Communication	1,500	1	1,500	
66	Local transportation	80	12	960	
67	DHL Shipments	100	12	1,200	
68	World Courier shipment of serology samples to USA	4,000	1	4,000	
69	Publication Costs	6,400	1	6,400	
70	Placeholder Sample Disposition	15,000	1	15,000	
71	Severance	11,008	1	11,008	
72	**Total Other Costs**			**59,918**	-
73	**Total Direct Costs**			**485,607**	-
74	**OH Onsite**		**24.3%**	**40,424**	
75	**OH Offsite**		**15.9%**	**10,882**	
76	**G&A**		**26.1%**	119,709	-
77	***Indirect Costs on subagreements & Contracts***		**26.1%**	13,696	
78	**Total Costs**			**670,317**	-
79					
80					
81	**PREDICT-2 Lao PDR Year 5 Budget - MB subagreement to NAHL**				
82	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID Core**	**Cost Share**
83					
84	**Domestic Travel**				
85	In country communication meetings	1,757	4	7,028	

	A	B	C	D	E
86				-	
87				-	
88	**Total Domestic Travel**			**7,028**	-
89					
90	**Contractual**				
91	National Centre for Laboratories and Epidemiology (NCLE) subagreement (detail below)			19,960	
92	**Total Contractual**			**19,960**	-
93					
94	**Diagnostics**				
95	Lab materials and supplies	200	3	600	
96	Sample fee	2	2,120	3,180	
97	**Total Diagnostics**			**3,780**	-
98				-	
99	**Supplies**				
100	Office supplies	100	12	1,200	
101				-	
102	**Total Supplies**			**1,200**	-
103				-	
104	**Other Costs**				
105	Health insurance for staff	600	2	1,200	
106	Data input	100	3	300	
107	Generator Fuel	50	12	600	
108	Metabiota Office Rent	1,000	12	12,000	
109	Incinerator (lab waste)	20	6	120	
110	Lab coat laundry	25	6	150	
111	Security and Garbage Disposal	50	12	600	
112	Communication	70	12	840	
113	**Total Other Costs**			**15,810**	-
114	**Total Direct Costs**			**47,778**	-
115	***Indirect Costs***		***10.00%***	2,782	-
116	***Indirect Costs on subagreements & Contracts***		***10.00%***	1,996	
117	**Total Costs**			**52,556**	-
118					
119	**PREDICT-2 Lao PDR Year 4 Budget -NAHL subagreement to NCLE**				
120	**EXPENSE DESCRIPTION**	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID Core**	**Cost Share**
121					
122	**Salaries**				
123	Dr. Onchanh Keosavanh	3,917	17%	666	
124	Dr. Bouaphan Khamphaphonggphane	3,813	23%	877	
125	Dr. Bounthanom Senglorpraseuth	3,645	23%	838	
126	Mr. Supatsone Houthonkham	3,195	23%	735	
127	**Total Salaries**			**3,116**	-
128					

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	A	B	C	D	E
129	**Domestic Travel**				
130	In Country Communication Meetings	1,757	4	7,028	
131	Serology in Na Pa Kieh	2,982	1	2,982	
132				-	
133	**Total Domestic Travel**			**10,010**	-
134					
135	**Contractual**				
136					
137	**Total Diagnostics**			-	-
138					
139	**Diagnostics**				
140	Lab consumables	180	3	539	
141	Processing fee (per sample)	2	200	300	
142	**Total Diagnostics**			**839**	-
143				-	
144	**Supplies**				
145	Office Supplies	69	12	831	
146				-	
147	**Total Supplies**			**831**	-
148				-	
149	**Other Costs**				
150	Liquid nitrogen	700	1	700	
151	Health insurance for staff	650	2	1,300	
152	Communication	100	12	1,200	
153	Waste Disposal	50	3	150	
154	**Total Other Costs**			**3,350**	-
155	**Total Direct Costs**			**18,144**	-
156	**Indirect Costs, est**		**10.00%**	1,815	-
157	**Total Costs**			**19,960**	-

	F	G	H
1			
2	**Year 5 Total**		**Partial obligation**
3			
4			
5	**39,999**		7,825
6	**9,124**		1,785
7	**72,382**		14,145
8	**30,656**		5,997
9	**16,338**		3,196
10	**168,419**		**32,948**
11			
12			
13	**15,732**		3,078
14	**3,589**		702
15	**28,436**		5,563
16	**12,057**		2,359
17	**6,426**		1,257
18	**66,239**		**12,959**
19			
20			
21	**2,460**		481
22	-		-
23	**2,460**		**481**
24			
25			
26	**2,030**		397
27	**2,030**		397
28	**10,398**		2,034
29	**8,226**		1,609
30	**2,742**		536
31	**5,068**		991
32	**2,534**		496
33	**33,028**		**6,461**
34			
35			
36	**52,556**		10,282
37	-		-
38	**52,556**		**10,282**
39			
40			
41	**6,250**		1,223
42	**18,750**		3,668

	F	G	H
43	-		-
44			-
45	**25,000**		**4,891**
46			
47			
48	**17,356**		3,395
49	**7,725**		1,511
50	**23,800**		4,656
51	**3,731**		730
52	**52,612**		**10,293**
53			
54			
55	**15,296**		2,992
56	**3,600**		704
57	**6,480**		1,268
58			-
59	**25,376**		**4,964**
60			
61			
62	**850**		166
63	**15,000**		2,935
64	**4,000**		783
65	**1,500**		293
66	**960**		188
67	**1,200**		235
68	**4,000**		783
69	**6,400**		1,252
70	**15,000**		2,935
71	**11,008**		2,154
72	**59,918**		**11,722**
73	**485,607**		**95,001**
74	**40,424**		7,908
75	**10,882**		2,129
76	**119,708**		23,419
77	**13,696**		2,679
78	**670,317**		**131,137**
79			
80			
81			
82	**Year 5 Total**		**Partial obligation**
83			
84			
85	**7,028**		1,375

	F	G	H
86	-		-
87	-		-
88	**7,028**		**1,375**
89			
90			
91	**19,960**		3,905
92	**19,960**		**3,905**
93			
94			
95	**600**		117
96	**3,180**		622
97	**3,780**		**739**
98			
99			
100	**1,200**		235
101	-		-
102	**1,200**		**235**
103			
104			
105	**1,200**		235
106	**300**		59
107	**600**		117
108	**12,000**		2,348
109	**120**		23
110	**150**		29
111	**600**		117
112	**840**		164
113	**15,810**		**3,093**
114	**47,778**		**9,347**
115	*2,782.80*		544
116	*1,996*		390
117	**52,556**		**10,282**
118			
119			
120	**Year 4 Total**		**Partial obligation**
121			
122			
123	**666**		130
124	**877**		172
125	**838**		164
126	**735**		144
127	**3,116**		**610**
128			

	F	G	H
129			
130	**7,028**		1,375
131	**2,982**		583
132	-		-
133	**10,010**		**1,958**
134			
135			
136	-		
137	-		-
138			
139			
140	**539**		105
141	**300**		59
142	**839**		**164**
143			
144			
145	**831**		163
146	-		-
147	**831**		**163**
148			
149			
150	**700**		137
151	**1,300**		254
152	**1,200**		235
153	**150**		29
154	**3,350**		**655**
155	**18,146**		**3,550**
156	*1,815*		355
157	**19,960**		**3,905**

PREDICT-2 Budget Summary by Country & Fund Source (October 2018 - September 2019)					
	USAID Core	USAID EBOLA	USAID GVP (Core)	Cost Share	TOTAL
Global	224,081	414,655	15,667	14,210	668,614
Administrative Management	3,983	7,239	1,261	-	12,483
Asia					
Lao PDR	131,137			-	131,137
Asia Subtotal	**131,137**	-	-	-	**131,137**
Africa					
Cameroon		525,530		-	525,530
DRC		280,611		24,300	304,911
Africa Subtotal	-	**806,141**	-	**24,300**	**830,441**
Total	**359,201**	**1,228,035**	**16,928**	**38,510**	**1,642,674**

TOTAL USAID	**$**	**1,604,164**
TOTAL Cost Share	**$**	**38,510**
	$	**1,642,674**

Year 4 Carryover

USAID Core	399,286
USAID Ebola	631,888
USAID GVP	-
	1,031,174

Total Year 5 Obligation needed

USAID Core	1,436,805
USAID Ebola	1,228,035
USAID GVP	67,711
	2,732,551

PREDICT-2 Global Year 5 Budget - METABIOTA subagreement

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID Core	USAID EBOLA	USAID GVP	Cost Share	Year 5 Total	Core: Partial obligation	Ebola: Balance of Y5 Budget due	GVP: Partial obligation	Total Obligation
Salaries											
			-	-			-				
Christian Lange, Virologist	92,976	80%	43,699	23,536			**67,229**	8,549	15,536	-	24,085
Jane McIver, Epidemiologist	89,082	09%	5,222	2,812			**8,034**	1,022	1,856	-	2,878
Beth Edison, Program Manager	135,648	65%	51,888	27,897			**79,785**	10,131	18,419	-	28,555
Amethyst Gillis, Global QAQC Coordinator	96,819	100%	56,681	30,628			**87,309**	11,128	20,223	-	31,351
Tammie O'Rourke, Systems Integrator	94,525	100%	55,333	29,903			**85,436**	10,864	19,744	-	30,608
Karen Saylors, Director of Surveillance	208,225	45%	57,693	31,066			**88,759**	11,287	20,511	-	31,798
Catherine Cleary, Research Assistant, Behavioural Risk Dy	77,267	40%	18,158	9,777			**27,935**	3,552	6,456	-	10,008
Jason Kwon, Behavioural Risk Analyst	111,458	25%	14,399	8,850			**25,229**	3,208	5,830	-	9,038
Ashley Lucas, Global Health Nurse	100,425	30%	17,760	9,531			**27,231**	3,463	6,293	-	9,755
Daniel Gunnlier, Software Developer	60,289	100%	23,670	12,745			**36,415**	4,631	8,415	-	13,046
Joshua Hu, Assistant Database Administrator	63,212	15%	4,828	2,600			**7,427**	944	1,716	-	2,661
Patrick Savage, Data Quality Analyst	37,191	100%	21,850	11,765			**33,615**	4,275	7,768	-	12,043
Dan O'Rourke, Health Information Developer	89,295	100%	29,029	15,629			**44,645**	5,677	10,317	-	15,994
Eddy Rubin, Chief Science Officer and PI	170,500	40%	22,587	16,134	25,814		**64,535**	4,419	10,652	6,433	21,525
Nathan Wolfe, Executive Support	360,000	2%				6,500	**6,500**	-	-	-	-
							-	-	-	-	-
							-	-	-	-	-
Salaries Total			**425,067**	**232,843**	**25,814**	**6,500**	**690,221**	**83,553**	**153,727**	**6,433**	**243,344**
Fringe Benefits		**39.33%**									
Christian Lange, Virologist	36,567	80%	17,187	9,254	-		**26,441**	3,362	6,110	-	9,473
Jane McIver, Epidemiologist	34,957	09%	2,054	1,106	-		**3,160**	402	730	-	1,132
Beth Edison, Program Manager	53,358	65%	20,376	10,972	-		**31,348**	3,986	7,244	-	11,231
Amethyst Gillis, Global QAQC Coordinator	38,079	100%	22,371	12,046	-		**34,417**	4,377	7,954	-	12,330
Tammie O'Rourke, Systems Integrator	37,177	100%	21,841	11,761	-		**33,602**	4,273	7,765	-	12,038
Karen Saylors, Director of Surveillance	85,038	45%	22,691	12,218	-		**34,909**	4,439	8,067	-	12,506
Catherine Cleary, Research Assistant, Behavioural Risk Department	30,389	40%	7,141	3,845	-		**10,987**	1,397	2,539	-	3,936
Jason Kwon, Behavioural Risk Analyst	43,913	25%	6,450	3,473	-		**9,922**	1,262	2,293	-	3,555
Ashley Lucas, Global Health Nurse	39,497	30%	6,961	3,748	-		**10,710**	1,362	2,475	-	3,837
Daniel Gunnlier, Software Developer	15,846	100%	9,309	5,013	-		**14,322**	1,821	3,310	-	5,131
Joshua Hu, Assistant Database Administrator	24,861	15%	1,899	1,022	-		**2,921**	371	675	-	1,047
Patrick Savage, Data Quality Analyst	14,627	100%	8,593	4,627	-		**13,221**	1,681	3,055	-	4,736
Dan O'Rourke, Health Information Developer	19,427	100%	11,413	6,146	-		**17,559**	2,233	4,058	-	6,291
Eddy Rubin, Chief Science Officer and PI	70,294	40%	8,884	6,345	10,153	-	**25,381**	1,738	4,390	2,538	8,466
Nathan Wolfe, Executive Support	141,588	2%	-	-	-	2,559	**2,559**	-	-	-	-
0	-	0%	-	-	-		-	-	-	-	-
0	-	0%	-	-	-		-	-	-	-	-
Fringe Benefits Total			**167,171**	**91,577**	**10,153**	**2,559**	**271,460**	**32,709**	**60,465**	**2,538**	**95,707**
International Travel											
Eddy Rubin - PREDICT	MB management	2,144	2	2,787	1,501		**4,288**	541	991	-	1,536
Karen Saylors - PREDICT	MB management	2,144	2	2,787	1,501		**4,288**	541	991	-	1,536
Tammie O'Rourke - PREDICT	MB management	1,199	4	3,117	1,679		**4,796**	610	1,108	-	1,718

Beth Edison - PREDICT	WB management	1,784	2	2,215	1,193			**3,408**	433	788	-	1,221
Dan O'Rourke - PREDICT/MB Management		1,199	4	3,117	1,679			**4,796**	433	1,338	-	1,710
Tasnime O'Rourke - PREDICT	MB management	1,595	1	1,037	558			**1,595**	203	369	-	571
Beth Edison - PREDICT	WB management	1,595	1	1,037	558			**1,595**	203	369	-	571
Dan O'Rourke - PREDICT/MB Management		1,595	1	1,037	558			**1,595**	203	369	-	571
David McIver - PREDICT	MB management	1,595	1	1,037	558			**1,595**	203	369	-	571
David McIver - PREDICT	MB management	1,784	1	1,168	596			**1,784**	217	394	-	610
Amethyst Gillis - PREDICT Regional meeting		1,910	1	1,242	669			**1,910**	243	443	-	684
Beth Edison - PREDICT regional Meeting		2,568	1	1,669	899			**2,568**	327	593	-	920
Tasnime O'Rourke- PREDICT regional meeting		2,568	1	1,669	899			**2,568**	327	593	-	920
Dan O'Rourke - PREDICT regional meeting		2,568	1	1,669	899			**2,568**	327	593	-	920
Dana McIver - PREDICT regional meeting		2,568	1	1,669	899			**2,568**	327	593	-	920
Christine Lange - PREDICT Regional Meeting		2,568	1	1,669	899			**2,568**	327	593	-	920
Jason Evans - PREDICT Regional Meeting		2,736	1	1,778	958			**2,736**	348	632	-	980
Eddy Rukin - PREDICT regional Meeting		2,736	1	1,778	958			**2,736**	348	632	-	980
Karen Saylors - PREDICT Regional Meeting		2,736	1	1,778	958			**2,736**	348	632	-	980
Outreach Meetings		5,000	1			5,000		**5,000**	-	-	1,250	1,250
								-	-	-	-	-
Total International Travel				**34,202**	**18,436**	**5,000**	**-**	**57,638**	**6,691**	**12,160**	**1,250**	**20,101**
Contractual												
Boston Children's Hospital contract				25,392	15,723			**41,116**	4,960	10,301	-	15,349
International Society for Infectious Diseases (ISID) subaward				28,279	15,221	-	-	**43,499**	5,531	10,051	-	15,581
								-	-	-	-	-
Total Contractual				**53,665**	**30,946**	**-**	**-**	**84,609**	**10,490**	**20,352**	**-**	**30,931**
Other Costs												
USAID Maintenance Services		61,000	1	39,650	21,350	-		**61,000**	7,757	14,097	-	21,853
Placeholder for unknown USAID closure costs		10,000	1	6,500	3,500	-		**10,000**	1,272	2,311	-	3,583
Communications and Subscriptions		15,000	1	9,750	5,250	-		**15,000**	1,907	3,466	-	5,374
Severance (Canada Office)		37,564	1	37,417	20,147	-		**57,564**	7,320	13,303	-	20,622
Total Other Costs				**93,317**	**50,247**	**-**	**-**	**143,564**	**18,256**	**33,176**	**-**	**51,432**
Total Direct Costs				**773,399**	**424,029**	**68,966**	**9,067**	**1,247,462**	**151,503**	**279,970**	**10,242**	**410,594**
G&A Onsite			**24.3%**	118,756	65,291	8,747	2,205	**194,999**	23,233	43,329	2,187	68,528
G&A Offsite			**15.9%**	16,470	8,869	-	-	**25,339**	3,222	5,856	-	9,078
G&A			**26.1%**	222,863	115,764	12,955	3,958	**340,459**	43,589	80,396	3,239	127,223
Indirect Costs on subagreements & Contracts			**26.1%**	13,985	8,064	-	-	**22,049**	2,734	5,325	-	8,061
Total Costs				**1,145,472**	**628,017**	**61,669**	**14,230**	**1,830,308**	**224,281**	**414,615**	**15,667**	**623,473**

PREDICT 2 Global Year 5 Budget - MB subagreement to International Society for Infectious Diseases (ISID)

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID Core	USAID EBOLA	USAID GVP	Cost Share	Year 5 Total	Core: Period obligation	Ebola: Balance of FY5 Budget due	GVP: Period obligation	Total Obligation
Salaries											
Project Manager	75,000	3%	2,438	1,313	-		**3,750**	477	867	-	1,343

Technical Specialist	74,000	5%	2,405	1,295	-		**3,700**	470	855	-	1,326
Project Director	96,000	5%	3,120	1,680	-		**4,800**	610	1,109	-	1,720
			-	-	-		-	-	-	-	-
Salaries Total			**7,963**	**4,288**	-	-	**12,250**	**1,558**	**2,811**	-	**4,369**
Fringe Benefits		**30.8%**									
Project Manager	22,580	5%	731	394	-		**1,125**	143	260	-	403
Technical Specialist	22,200	5%	722	389	-		**1,110**	141	257	-	398
Project Director	28,800	5%	936	504	-		**1,440**	183	333	-	516
0	-	0%	-	-	-		-	-	-	-	-
Fringe Benefits Total			**2,389**	**1,286**	-	-	**3,675**	**467**	**849**	-	**1,317**
Contractual											
ProMED Associate Editors	5,795	1	3,767	2,028	-		**5,795**	737	1,339	-	2,076
ProMED Copy Editors	5,885	1	3,825	2,060	-		**5,885**	748	1,360	-	2,109
ProMED Wildlife Moderators	11,934	1	7,757	4,177	-		**11,934**	1,518	2,758	-	4,275
			-	-	-		-	-	-	-	-
Total Contractual			**15,349**	**8,265**	-	-	**23,614**	**3,003**	**5,457**	-	**8,460**
Supplies											
			-	-	-		-	-	-	-	-
Total Supplies			-	-	-	-	-	-	-	-	-
Other Costs											
Total Other Costs											
Total Direct Costs			**25,700**	**13,839**	-	-	**39,539**	**5,028**	**9,117**	-	**14,145**
Indirect Costs		**8%**	2,570	1,384	-	-	3,954	503	914	-	1,416
Total Costs			**28,270**	**15,223**	-	-	**43,493**	**5,531**	**10,031**	-	**15,561**

PROJECT 2 Global Year 5 Budget - MB contract with Boston Children's Hospital

								Core	Ebola	GVP	
EXPENSE DESCRIPTION	**UNIT COST / ANNUAL RATE**	**UNIT # / LOE %**	**USAID-Core**	**USAID EBOLA**	**USAID GVP**	**Cost Share**	**Year 1 Total**	**Partial obligation**	**Balance of Y1 Budget due**	**Partial obligation**	**Total Obligation**
Salaries											
Project Coordinator	60,000	5%	1,950	1,050	-		**3,000**	385	693	-	1,075
Programmer/Software Engineer	182,000	10%	4,630	3,570	-		**08,200**	1,297	2,357	-	3,654
Front End Developer	182,000	10%	4,630	3,570	-		**08,200**	1,297	2,357	-	3,654
			-	-	-		-	-	-	-	-
Salaries Total			**15,210**	**8,190**	-	-	**23,400**	**2,976**	**5,408**	-	**8,383**
Fringe Benefits		**30.6%**									
Project Coordinator	18,336	5%	596	321	-		**917**	117	212	-	328
Programmer/Software Engineer	33,171	10%	2,026	1,091	-		**3,117**	396	720	-	1,117
Front End Developer	33,171	10%	2,026	1,091	-		**3,117**	396	720	-	1,117
0	-	0%	-	-	-		-	-	-	-	-
Fringe Benefits Total			**4,648**	**2,503**	-	-	**7,151**	**909**	**1,653**	-	**2,562**

Supplies												
Amazon Web Services	4,000	1	3,480	2,520	-		**4,000**	290	1,664	-	1,953
Total Supplies			**3,480**	**2,520**	**-**	**-**	**4,000**	**290**	**1,664**	**-**	**1,953**
Total Direct Costs			**21,330**	**13,213**	-	-	**34,551**	**6,174**	**8,724**	-	**12,898**
Indirect Costs		**19%**	*4,054*	*2,510*	-	-	*6,565*	703	1,658	-	2,453
Total Costs			**25,392**	**15,723**	**-**	**-**	**41,116**	**6,968**	**10,381**	**-**	**15,349**

PREDICT-2 Administrative Management Year 5 Budget - METABIOTA subagreement

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID Core	USAID EBOLA	USAID GVP	Cost Share	Year 5 Total	Core Partial obligation	Ebola Balance of FY Budget due	GVP Partial obligation	Total Obligation
Salaries			-	-	-		-	-	-	-	-
			-	-	-		-	-	-	-	-
Salaries Total			-	-	-	-	-	-	-	-	-
Fringe Benefits		**39.33%**									
0	-	0%	-	-	-		-	-	-	-	-
0	-	0%	-	-	-		-	-	-	-	-
Fringe Benefits Total			-	-	-	-	-	-	-	-	-
Domestic Travel											
Karen Saylors - EB/EPT meetings	1,385	2	1,801	970	-		**2,770**	352	640	-	**992**
Eddy Rubio - 1 RT - EB/EPT meetings	1,385	2	1,801	970	-		**2,770**	352	640	-	**992**
and Outreach Meetings	2,000	2			4,000		**4,000**	-	-	1,000	**1,000**
							-	-	-	-	-
Total Domestic Travel			**3,601**	**1,939**	**4,000**	-	**9,540**	**704**	**1,280**	**1,000**	**2,985**
Supplies											
Computer and Office Supplies	14,310	1	9,302	5,009	-		**14,310**	1,820	3,307	-	**5,127**
Project closure costs	5,000	1	3,250	1,750			**5,000**	636	1,155	-	**1,791**
Total Supplies			**12,552**	**6,759**	-	-	**19,310**	**2,455**	**4,462**	-	**6,918**
Total Direct Costs			**16,153**	**8,698**	**4,000**	-	**28,850**	**3,160**	**5,743**	**1,000**	**9,903**
OH Onsite		**24.3%**						-	-	-	-
OH Offsite		**15.9%**						-	-	-	-
G&A		**26.1%**	4,209	2,267	1,042	-	7,518	823	1,497	261	**2,581**
Indirect Costs on subagreements & Contracts		**26.1%**					-	-	-	-	-
Total Costs			**20,362**	**10,964**	**5,042**	-	**36,368**	**3,983**	**7,239**	**1,261**	**12,483**

PREDICT-2 Cameroon Year 5 Budget - METABIOTA subagreement

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID EBOLA	Cost Share	Year 5 Total
Salaries					
Ubald Tamoufe (Regional Director)	89,699	16%	12,972		**12,972**
Julius Agbor (Fin & Ops Manager)	44,777	15%	6,071		**6,071**
Arrey Roosevelt (Finance Assistant)	14,036	15%	1,903		**1,903**
Adolphe Ngole (Customs Liaison Officer)	9,717	30%	2,635		**2,635**
EPANE Marcel (Driver)	8,098	100%	7,319		**7,319**
Valantine Ngum Ndze, Laboratory Director	34,272	16%	4,956		**4,956**
NKOM Felix Ntumvi (Lab Scientist)	17,275	80%	12,491		**12,491**
Joseph Diffo (Senior Field Ecologist)	17,275	30%	4,684		**4,684**
Jean Michel Takuo (Field Ecologist)	11,877	30%	3,220		**3,220**
Victorine Toguem	15,118	30%	4,099		**4,099**
Mbongo Beatrice	11,337	15%	1,537		**1,537**
Beth Edison, Program Manager	135,668	5%	6,131		**6,131**
Karen Saylors, Director of Surveillance	218,225	10%	19,724		**19,724**
Dana Ellis, Program Coordinator	54,229	33%	16,338		**16,338**
Salaries Total			**104,082**	-	**104,082**
Fringe Benefits		**39.33%**			
Ubald Tamoufe (Regional Director)	89,699	16%	5,102		**5,102**
Julius Agbor (Fin & Ops Manager)	44,777	15%	2,388		**2,388**
Arrey Roosevelt (Finance Assistant)	14,036	15%	748		**748**
Adolphe Ngole (Customs Liaison Officer)	9,717	30%	1,036		**1,036**
EPANE Marcel (Driver)	8,098	100%	2,879		**2,879**
Valantine Ngum Ndze, Laboratory Director	34,272	16%	1,949		**1,949**
NKOM Felix Ntumvi (Lab Scientist)	17,275	80%	4,913		**4,913**
Joseph Diffo (Senior Field Ecologist)	17,275	30%	1,842		**1,842**
Jean Michel Takuo (Field Ecologist)	11,877	30%	1,267		**1,267**
Victorine Toguem	15,118	30%	1,612		**1,612**
Mbongo Beatrice	11,337	15%	605		**605**
Beth Edison, Program Manager	135,668	5%	2,411		**2,411**
Karen Saylors, Director of Surveillance	218,225	10%	7,758		**7,758**
Dana Ellis, Program Coordinator	54,229	33%	6,426		**6,426**
Fringe Benefits Total			**40,935**	-	**40,935**
Domestic Travel					
Hospital Final Meeting 2 sites @ 1 trips	1,100	2	2,200		**2,200**
Women Bushmeat Sellers Sensibilisation 2 sites @ 1 trips	1,100	2	2,200		**2,200**
Community outreach (local villages) 6 sites @ 1 trips	1,400	6	8,400		**8,400**
One Health day 2 sites @ 1 trips	1,300	2	2,600		**2,600**
National conference or event 5 events @ 1 trips	630	5	3,150		**3,150**
Participation at MINEPIA and MINFOF regional biannual Meeting	462	4	1,848		**1,848**
Bat Book Pilot 3 sites @ 1 trip	860	3	2,580		**2,580**
Extra behavioral data collection 3 sites @ 1 trips	920	3	2,760		**2,760**
			-		-

Total Domestic Travel			**25,738**	-	**25,738**
International Travel					
Karen Saylors - Cameroon Trip	2,926	2	5,852		**5,852**
Jason Euren - Cameroon Trip			-		-
Beth Edison - Cameroon Trip	3,014	1	3,014		**3,014**
Dave McIver - Cameroon Trip	3,014	1	3,014		**3,014**
Gov't Rep to PREDICT Final mtg	1,910	1	1,910		**1,910**
Regional or International Conference	3,500	1	3,500		**3,500**
Total International Travel			**17,290**	-	**17,290**
Contractual					
Mosaic subagreement (detail below)			172,117	-	**172,117**
					-
Total Contractual			**172,117**	-	**172,117**
Equipment					
Analytical and Precision Balance	7,718	1	7,718		**7,718**
Ultra-Low Temperature Freezer	17,810	1	17,810		**17,810**
Total Equipment			**25,528**		**25,528**
Diagnostics					
Laboratory Reagents and Consumables to complete testing for Flavi (6277)	50,574	1	50,574		**50,574**
			-		-
			-		-
Total Diagnostics			**50,574**	-	**50,574**
Supplies					
Office Supplies	273	12	3,270		**3,270**
Local field and lab supplies	5,000	1	5,000		**5,000**
			-		-
Outbreak Kits	6,480	1	6,480		**6,480**
Total Supplies			**14,750**	-	**14,750**
Other Costs					
Karen Saylors - SOS Insurance	850	1	850		**850**
Vaccination	75	10	750		**750**
Cloning	238	155	36,890		**36,890**
Permit Renewals (MINFOF/MINRESI)	350	4	1,400		**1,400**
Laboratory Waste Incineration	800	10	8,000		**8,000**
World Courier shipment of serology samples to USA	3,500	1	3,500		**3,500**
DHL coupons for sample shipment	100	12	1,200		**1,200**
Customs Clearance	3,000	1	3,000		**3,000**
LN Plant maintenance	5,000	1	5,000		**5,000**
Biosafety Cabinet Certification	4,606	1	4,606		**4,606**
Workshop One Health Surveillance workforce to transfer skills and knowledge	2,500	2	5,000		**5,000**

Lab training (One Health lab Network, Student): sharing data and protocols	2,800	3	8,400		**8,400**
End-of-project workshop	9,000	1	9,000		**9,000**
Sample Disposition Placeholder	15,000	1	15,000		**15,000**
Possible consultant agreements for field staff	5,000	1	5,000		**5,000**
Publication Costs	12,800	1	12,800		**12,800**
Severance Costs (for staff at 100% LOE)	29,999	1	29,999		**29,999**
Total Other Costs			**150,395**	-	**150,395**
Total Direct Costs			**601,409**	-	**601,409**
OH Onsite		**24.3%**	**35,268**		**35,268**
OH Offsite		**15.9%**			-
G&A		**26.1%**	114,412	-	**114,412**
Indirect Costs on subagreements & Contracts		**26.1%**	44,854		**44,854**
Total Costs			**795,942**	-	**795,942**

PREDICT-2 Cameroon Year 5 Budget - MII subagreement to Mosaic

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID EBOLA	Cost Share	Year 5 Total
Salaries					
Senior Technical Advisor (Matthew LeBreton)	141,984	34.0%	48,275		**48,275**
Country Coordinator (Moctar Mosiche)	33,688	100.0%	33,688		**33,688**
			-		-
Salaries Total			**81,963**	-	**81,963**
Fringe Benefits		**35.0%**			
Senior Technical Advisor (Matthew LeBreton)	49,694	34.0%	16,896		**16,896**
Fringe Benefits local staff		**22.0%**			
Country Coordinator (Moctar Mosiche)	7,411	100.0%	7,411		**7,411**
0	-	0.0%	-		-
Fringe Benefits Total			**24,307**	-	**24,307**
Domestic Travel					
Senior Technical Advisor Douala	416	3	1,248		**1,248**
Senior Technical Advisor field sites	312	3	936		**936**
Country Coordinator workshops/meetings	506	6	3,036		**3,036**
Country Coordinator field sites	294	5	1,470		**1,470**
			-		-
Total Domestic Travel			**6,690**	-	**6,690**
International Travel					
PREDICT Meeting (CC and Tech Advisor)	2,514	2	5,028		**5,028**
			-		-
Total Contractual			**5,028**	-	**5,028**
Supplies					
vaccinations	50	1	50		**50**
internet access	19	12	228		**228**

phone costs	58	12	696		**696**
office, dropbox, antivirus and carbonite software	200	1	200		**200**
field supplies and research permits	750	1	750		**750**
office supplies	98	12	1,176		**1,176**
training supplies	200	1	200		**200**
Total Supplies			**3,300**	-	**3,300**
Total Direct Costs			**121,288**	-	**121,288**
Indirect Costs		**19.00%**	*23,045*	-	*23,045*
VAT		**19.25%**	*27,784*		*27,784*
Total Costs			**172,117**	-	**172,117**

PREDICT-2 DRC Year 5 Budget - METABIOTA subagreement

Ebola

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID EBOLA	Cost Share	Year 5 Total	Balance of FY Budget due
Salaries						
Charles Kumakamba, Country Coordinator	47,136	70%	29,823		29,823	19,691
Maria Makowa, Lab Virol. & Assist. Accountant	37,500	15%	5,943		5,943	3,330
Frieda N'Kawa, Lab Technician	35,360	20%	6,392		6,392	4,220
Andre Bimakawu, Logistician	16,234	15%	2,201		2,201	1,403
Eric Mbala, Driver	13,520	30%	3,666		3,666	2,421
Albert Mbunga, Accountant	36,350	18%	6,625		6,625	3,958
Berh Edison, Program Manager	135,668	5%	6,131		6,131	4,048
Karen Saylors, Director of Surveillance	218,225	10%	19,724		19,724	13,023
Dana Ellis, Program Coordinator	54,229	33%	16,338		16,338	10,787
Salaries Total			**93,944**	-	**93,944**	**62,827**
Fringe Benefits		**31.32%**				
Charles Kumakamba, Country Coordinator	47,136	70%	11,729		11,729	7,744
Maria Makowa, Lab Virol. & Assist. Accountant	37,500	15%	1,984		1,984	1,310
Frieda N'Kawa, Lab Technician	35,360	20%	2,516		2,516	1,660
Andre Bimakawu, Logistician	16,234	15%	866		866	572
Eric Mbala, Driver	13,520	30%	1,442		1,442	952
Albert Mbunga, Accountant	36,350	18%	1,819		1,819	1,201
Berh Edison, Program Manager	135,668	5%	2,411		2,411	1,592
Karen Saylors, Director of Surveillance	218,225	10%	7,758		7,758	5,121
Dana Ellis, Program Coordinator	54,229	33%	6,426		6,426	4,243
Fringe Benefits Total			**36,948**	-	**36,948**	**24,395**
Domestic Travel						
Communication to Sampling Sites (Kongo Central, Isongo)	1,540	1	1,540		1,540	1,017
Equateur follow up	7,000	1	7,000		7,000	4,622
Total Domestic Travel			**8,540**	-	**8,540**	**5,639**
International Travel						
Karen Saylors - DRC Trip	4,755	1	4,755		4,755	3,140
Amethyst Ellis - DRC Trip	3,274	1	3,274		3,274	2,162
			-		-	-
Total International Travel			**8,029**	-	**8,029**	**5,301**
Contractual						
VHHI subagreement (detail below)			31,498	24,300	55,798	36,797
Total Contractual			**31,498**	**24,300**	**55,798**	**36,797**
Equipment						-
			-	-	-	-
Total Equipment			-	-	-	-
Diagnostics						
Laboratory Reagents and Consumables to complete testing for Flavi (427)	4,602	1	4,602		4,602	3,039
			-		-	-
Total Diagnostics			**4,602**	-	**4,602**	**3,039**
Supplies						
Office supplies	2,130	1	2,130		2,130	1,406
Local lab supplies	3,000	1	3,000		3,000	1,981
Outbreak Go Kits	6,480	1	6,480		6,480	4,278
Total Supplies			**11,610**	-	**11,610**	**7,666**
Other Costs						
Cleaning	150	83	19,754		19,754	13,043
DHL Shipments	132	6	792		792	523
Communication	1,260	1	1,260		1,260	832
Customs Clearance	3,000	1	3,000		3,000	1,981
Permit Renewal	600	1	600		600	396
IRB Renewal	1,800	1	1,800		1,800	1,188
Internet	1,200	1	1,200		1,200	792
Biosafety Cabinet Certification	5,000	1	5,000		5,000	3,301
Grace Mayembe (Lab Intern)	500	4	1,750		1,750	1,155

PREDICT Completion Partner meeting	1,900	1	1,900		1,900	1,254
Publication costs	6,400	2	12,800		12,800	8,451
Severance Costs (All staff excluding Wafula Mukanesi)	45,281	1	45,281		45,281	29,897
Sample Disposition Placeholder	15,000	1	15,000		15,000	9,904
Total Other Costs			**159,337**	**-**	**106,307**	**72,729**
Total Direct Costs			**385,308**	**24,300**	**327,858**	**201,583**
IDI Onsite		**24.3%**	**31,833**		**31,833**	21,018
IDI Offsite		**15.9%**			-	-
G&A		**24.3%**	**79,651**	-	**79,651**	52,590
Indirect Costs on subagreements & Contracts		**24.3%**	**8,308**		**8,308**	5,420
Total Costs			**625,000**	**24,300**	**447,550**	**280,611**

PREDICT-2 DRC Year 5 Budget - NRI subagreement to Institut National de Recherche Biomedicale (INRB)

Check

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID EBOLA	Cost Share	Year 5 Total	*Balance of Y5 Budget due*
Diagnostics			-	-	-	-
Total Diagnostics			-	-	-	-
Other Costs						
Equipment maintenance/certification	7,165	1	7,165		7,165	4,731
Fuel for laboratory Backup Generator	12,000	1	12,000		12,000	7,923
Vehicle maintenance	10,000	1	10,000		10,000	6,602
Operational costs (electricity, water use, housekeeping, security, backup generator costs not covered by indirects)	7,500	3	-	22,500	22,500	-
			-		-	-
Total Other Costs			**29,165**	**22,500**	**51,665**	**19,257**
Total Direct Costs			29,165	22,500	51,665	19,257
Indirect Costs		**8%**	*2,333*	*1,800*	*4,133*	*1,541*
Total Costs			**31,498**	**24,300**	**55,798**	**20,797**

PREDICT-2 Lao PDR Year 5 Budget - METABIOTA subagreement

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID Core	Cost Share	Year 5 Total	Partial obligation
Salaries						
Sithammavong, Souhaeh, Country Coordinator	44,254	100%	39,999		**39,999**	7,825
Vongkeo Assana	10,095	100%	9,124		**9,124**	1,785
Dove McIver, Epidemiologist	88,882	90%	72,302		**72,302**	14,145
Beth Edison, Program Manager	135,668	25%	30,656		**30,656**	5,997
Dana Ellis, Program Coordinator	54,229	33%	16,338		**16,338**	3,196
Salaries Total			**168,419**	-	**168,419**	**32,948**
Fringe Benefits		**39.33%**				
Sithammavong, Souhaeh, Country Coordinator	44,254	100%	15,732		**15,732**	3,078
Vongkeo Assana	10,095	100%	3,589		**3,589**	702
Dove McIver, Epidemiologist	88,882	90%	28,436		**28,436**	5,563
Beth Edison, Program Manager	135,668	25%	12,057		**12,057**	2,359
Dana Ellis, Program Coordinator	54,229	33%	6,426		**6,426**	1,257
Fringe Benefits Total			**66,239**	-	**66,239**	**12,959**
Domestic Travel						
Community Outreach trips	892	5	2,460		**2,460**	481
			-		-	-
Total Domestic Travel			**2,460**	-	**2,460**	**481**
International Travel						
Jason Eaton- Lao PDR Regional Trip	2,030	1	2,030		**2,030**	397
Karen Saylors - Lao PDR Regional Trip	2,030	1	2,030		**2,030**	397
Amethyst Gillis - Lao PDR Trip	5,199	2	10,398		**10,398**	2,034
Dove McIver - Asia Regional Trip	2,742	3	8,226		**8,226**	1,609
Beth Edison - Asia Regional Trip	2,742	1	2,742		**2,742**	536
Country Coordinator and Gov't Rep to PREDICT Regional Meeting	2,534	2	5,068		**5,068**	991
Regional or International Conference	2,534	1	2,534		**2,534**	496
Total International Travel			**33,028**	-	**33,028**	**6,461**
Contractual						
National Animal Health Laboratory (NAHL) subagreement (detail below)			52,556	-	**52,556**	10,282
					-	-
Total Contractual			**52,556**	-	**52,556**	**10,282**
Equipment						
Thermocycler	**6,250**	**1**	6,250		**6,250**	1,223
Minus 80 Freezer	18,750	1	18,750		**18,750**	3,668
		1			-	-
						-
Total Equipment			**25,000**	-	**25,000**	**4,891**
Diagnostics						
Laboratory Reagents and Consumables to test a second set of samples (226)	17,356	1	17,356		**17,356**	3,395
other diagnostics	7,725	1	7,725		**7,725**	1,511
Cloning	238	100	23,800		**23,800**	4,656
Follow up Projects	3,731	1	3,731		**3,731**	730
Total Diagnostics			**52,612**	-	**52,612**	**10,293**
Supplies						
Lab Equipment < 5k	15,294	**1**	15,294		**15,294**	2,992
Office Supplies	300	12	3,600		**3,600**	704
Outbreak Kit	6,480	1	6,480		**6,480**	1,268

			-			-
Total Supplies			**25,374**	-	**25,374**	**4,964**
Other Costs						
David McIver SOS Insurance	850	1	850		**850**	166
Payroll services 108jab	15,000	1	15,000		**15,000**	2,935
Final Gov't Communication Meeting	4,000	1	4,000		**4,000**	783
Communication	1,500	1	1,500		**1,500**	293
Local transportation	80	12	960		**960**	188
DHL Shipments	100	12	1,200		**1,200**	235
World Courier shipment of serology samples to USA	4,000	1	4,000		**4,000**	783
Publication Costs	6,400	1	6,400		**6,400**	1,252
Placeholder Sample Disposition	15,000	1	15,000		**15,000**	2,935
Severance	11,000	1	11,000		**11,000**	2,154
Total Other Costs			**59,938**	-	**59,938**	**11,722**
Total Direct Costs			**485,607**	-	**485,607**	**95,001**
OH Onsite		**24.3%**	**60,424**		**60,424**	7,908
OH Offsite		**15.9%**	**10,882**		**10,882**	2,129
G&A		**26.1%**	119,708	-	**119,708**	23,419
Indirect Costs on subagreements & Contracts		**26.1%**	13,696		**13,696**	2,679
Total Costs			**670,317**	-	**670,317**	**131,137**

PREDICT-2 Lao PDR Year 5 Budget - MB subagreement to NAHL

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID Core	Cost Share	Year 5 Total	Partial obligation
Domestic Travel						
In country communication meetings	3,757	4	7,028		**7,028**	1,375
			-		-	-
			-		-	-
Total Domestic Travel			**7,028**	-	**7,028**	**1,375**
Contractual						
National Centre for Laboratories and Epidemiology (NCLE) subagreement (detail below)			19,960		**19,960**	3,905
Total Contractual			**19,960**	-	**19,960**	**3,905**
Diagnostics						
Lab materials and supplies	200	3	600		**600**	117
Sample fee	2	2,120	3,180		**3,180**	622
Total Diagnostics			**3,780**	-	**3,780**	**739**
			-			
Supplies						
Office supplies	100	12	1,200		**1,200**	235
			-		-	-
Total Supplies			**1,200**	-	**1,200**	**235**
			-			
Other Costs						
Health insurance for staff	600	2	1,200		**1,200**	235
Data input	100	3	300		**300**	59
Generator Fuel	50	12	600		**600**	117
Metabiota Office Rent	1,000	12	12,000		**12,000**	2,348
Incinerator (lab waste)	20	6	120		**120**	23
Lab coat laundry	25	6	150		**150**	29
Security and Garbage Disposal	50	12	600		**600**	117
Communication	70	12	840		**840**	164
Total Other Costs			**15,810**	-	**15,810**	**3,093**
Total Direct Costs			**47,778**	-	**47,778**	**9,347**

Indirect Costs		*10.00%*	*2,782*	-	*2,781.80*	544
Indirect Costs on subagreements & Contracts		*10.00%*	*1,996*		*1,996*	390
Total Costs			**52,556**	-	**52,556**	**10,282**

PREDICT-2 Lao PDR Year 4 Budget -NAHL subagreement to NCLE

EXPENSE DESCRIPTION	UNIT COST / ANNUAL RATE	UNIT # / LOE %	USAID Core	Cost Share	Year 4 Total	Partial obligation
Salaries						
Dr. Onchanh Keesuvanh	3,917	17%	666		**666**	130
Dr. Boauphan Khamphaphongphane	3,813	23%	877		**877**	172
Dr. Bounthanom Sengkooprasouth	3,645	23%	838		**838**	164
Mr. Supatsone Houthonkham	3,195	23%	735		**735**	144
Total Salaries			**3,116**	-	**3,116**	**610**
Domestic Travel						
In Country Communication Meetings	1,757	4	7,028		**7,028**	1,375
Serology in Na Pa Kieb	2,982	1	2,982		**2,982**	583
			-		-	-
Total Domestic Travel			**10,010**	-	**10,010**	**1,958**
Contractual						
					-	
Total Diagnostics			-	-	-	-
Diagnostics						
Lab consumables	180	3	539		**539**	105
Processing fee (per sample)	2	200	300		**300**	59
Total Diagnostics			**839**	-	**839**	**164**
			-			
Supplies						
Office Supplies	69	12	831		**831**	163
			-		-	-
Total Supplies			**831**	-	**831**	**163**
			-			
Other Costs						
Liquid nitrogen	700	1	700		**700**	137
Health insurance for staff	650	2	1,300		**1,300**	254
Communication	100	12	1,200		**1,200**	235
Waste Disposal	50	3	150		**150**	29
Total Other Costs			**3,350**	-	**3,350**	**655**
Total Direct Costs			**18,146**	-	**18,146**	**3,550**
Indirect Costs, est		*10.00%*	*1,815*	-	*1,815*	355
Total Costs			**19,960**	-	**19,960**	**3,905**

	A	B	C	D
1	**Budget**			
2	**Reporting Period:**	September 2018		
4	**Total Costs**	**Total**		
5	*Salaries*	80,246.87		
6	*Fringe*	29,851.84		
7	*Equipment*	41,897.48		
8	*Domestic Travel*	3,196.04		
9	*Foreign Travel*	8,136.94		
10	*Services*	112,104.80		
11	*Diagnostics*	-		
12	*Supplies*	22,071.72		
13	*Other*	13,093.50		
14	***Total Direct Costs***	310,599.19		
15	*Indirect*	74,071.71		
16	**Total Costs**	384,670.90		
18	**Global (Ebola) Year 4**	**Total**		
19	*Salaries*	23,600.60		
20	*Fringe*	8,779.42		
21	*Equipment*	-		
22	*Domestic Travel*	-		
23	*Foreign Travel*	726.69	OK	
24	*Services*	28,138.64		
25	*Diagnostics*	-		
26	*Supplies*	-		
27	*Other*	866.74		
28	***Total Direct Costs***	62,112.08		
29	*Indirect*	15,967.52	26%	
30	**Total Global (Ebola)**	78,079.60		
32	**Global (Core) Year 4**	**Total**		
33	*Salaries*	15,262.56		
34	*Fringe*	5,677.67		
35	*Equipment*	-		
36	*Domestic Travel*	-		
37	*Foreign Travel*	426.78	OK	
38	*Services*	16,525.87		
39	*Diagnostics*	-		
40	*Supplies*	-		
41	*Other*	509.03		
42	***Total Direct Costs***	38,401.92		
43	*Indirect*	10,281.74	27%	
44	**Total Global (Core)**	48,683.66		
45				

	A	B	C	D
46	**Global (GVP) Year 4**	**Total**		
47	*Salaries*	2,380.00		
48	*Fringe*	885.36		
49	*Equipment*	-		
50	*Domestic Travel*	-		
51	*Foreign Travel*	-		
52	*Services*	-		
53	*Diagnostics*	-		
54	*Supplies*	-		
55	*Other*	-		
56	***Total Direct Costs***	3,265.36		
57	*Indirect*	1,534.72	47%	
58	**Total Global (GVP)**	4,800.08		
59				
60	**Admin Mgt (Ebola) Year 4**	**Total**		
61	*Salaries*	-		
62	*Fringe*	-		
63	*Equipment*	-		
64	*Domestic Travel*	-		
65	*Foreign Travel*	-		
66	*Services*	-		
67	*Diagnostics*	-		
68	*Supplies*	-		
69	*Other*	-		
70	***Total Direct Costs***	-		
71	*Indirect*	-		
72	**Total Admin Mgt (Ebola) Year 4**	-		
73				
74	**Admin Mgt (Core) Year 4**	**Total**		
75	*Salaries*	-		
76	*Fringe*	-		
77	*Equipment*	-		
78	*Domestic Travel*	-		
79	*Foreign Travel*	-		
80	*Services*	-		
81	*Diagnostics*	-		
82	*Supplies*	-		
83	*Other*	-		
84	***Total Direct Costs***	-		
85	*Indirect*	-		
86	**Total Admin Mgt (Core)Year 4**	-		

	A	B	C	D
87				
88	**Admin Mgt (GVP) Year 4**	**Total**		
89	*Salaries*	-		
90	*Fringe*	-		
91	*Equipment*	-		
92	*Domestic Travel*	-		
93	*Foreign Travel*	-		
94	*Services*	-		
95	*Diagnostics*	-		
96	*Supplies*	-		
97	*Other*	-		
98	***Total Direct Costs***	-		
99	*Indirect*	-		
100	**Total Admin Mgt (GVP)Year 4**	-		
101				
102	**Cameroon Year 4**	**Total**		
103	*Salaries*	16,515.77		
104	*Fringe*	6,143.87		
105	*Equipment*	13,766.71	OK	
106	*Domestic Travel*	2,547.79		
107	*Foreign Travel*	-		
108	*Services*	13,609.00		
109	*Diagnostics*	-		
110	*Supplies*	9,043.20		
111	*Other*	5,606.84		
112	***Total Direct Costs***	67,233.18		
113	*Indirect*	18,733.01	28%	
114	**Total Cameroon Year 4**	85,966.19		
115				
116	**DRC Year 4**	**Total**		
117	*Salaries*	9,583.83		
118	*Fringe*	3,565.18		
119	*Equipment*	13,555.91	OK	
120	*Domestic Travel*	446.39		
121	*Foreign Travel*	-		
122	*Services*	15,781.04		
123	*Diagnostics*	-		
124	*Supplies*	282.02		
125	*Other*	4,405.02		
126	***Total Direct Costs***	47,619.39		
127	*Indirect*	9,063.91	23%	
128	**Total DRC Year 4**	56,683.31		
129				

	A	B	C	D
130	**Lao PDR Year 4**	**Total**		
131	*Salaries*	12,904.11		
132	*Fringe*	4,800.33		
133	*Equipment*	14,574.86	OK	
134	*Domestic Travel*	201.86		
135	*Foreign Travel*	6,983.47	OK	
136	*Services*	38,050.26		
137	*Diagnostics*	-		
138	*Supplies*	12,746.50		
139	*Other*	1,705.87		
140	***Total Direct Costs***	91,967.26		
141	*Indirect*	18,490.81	20%	
142	**Total Lao PDR Year 4**	110,458.06		
143				
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8	Total Core		
9	163,941.80		
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11	Total Ebola		
12	220,729.09		
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18	Full	Lim	EHP
19	3,371.51	842.88	1,685.76
20	1,254.20	313.55	627.10
21	-	-	-
22	-	-	-
23	103.81	25.95	51.91
24	4,019.81	1,004.95	2,009.90
25	-	-	-
26	-	-	-
27	123.82	30.95	61.91
28			
29	2,281.07	570.27	1,140.54
30	11,154.23	2,788.56	5,577.11
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	A	B	C	D
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2	REBUDGET OF CARRYOVER FUNDS FROM CORE TO EBOLA			
3				
4	**Metabiota PREDICT-2 Year 4 Budget Summary** as of 9/30/2018			
5	**all formulas, do not manually enter*			
6	**Total Costs**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended (includes lingering spending for transition countries)**
7	*Salaries*	(245,966)	1,541,809	1,196,064
8	*Fringe*	(91,501)	573,553	444,936
9	*Equipment*	491,066	111,096	41,897
10	*Domestic Travel*	145,961	162,674	68,302
11	*Foreign Travel*	(328,465)	192,332	131,021
12	*Services*	1,499,398	570,937	469,092
13	*Diagnostics*	(131,678)	339,713	298,153
14	*Supplies*	88,267	59,840	105,702
15	*Other*	(722,287)	216,416	300,236
16	***Total Direct Costs***	704,794	3,768,370	3,055,402
17	*Indirect*	(654,108)	1,544,575	1,277,055
18	**Total Costs**	50,686	5,312,945	4,332,457
19				
20	**Global (Ebola) Year 4**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
21	Salaries	123,831	395,159	321,135

	A	B	C	D
22	*Fringe*	46,065	146,999	119,462
23	*Equipment*	-	-	-
24	*Domestic Travel*	(1,447)	-	1,331
25	*Foreign Travel*	(75,893)	36,062	22,196
26	*Services*	136,358	78,174	80,412
27	*Diagnostics*	-	-	-
28	*Supplies*	(1,793)	-	617
29	*Other*	(54,220)	37,219	39,864
30	***Total Direct Costs***	172,900	693,612	585,017
31	*Indirect*	(21,423)	311,463	251,970
32	**Total Global (Ebola)**	**151,477**	**1,005,075**	**836,987**
33				
34	**Global (Core) Year 4**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
35	*Salaries*	57,755	226,669	205,356
36	*Fringe*	21,485	84,321	76,392
37	*Equipment*	-	-	-
38	*Domestic Travel*	(850)	-	782
39	*Foreign Travel*	(38,277)	24,841	13,036
40	*Services*	39,693	45,911	47,226
41	*Diagnostics*	-	-	-
42	*Supplies*	(1,053)	-	362
43	*Other*	(31,207)	21,859	23,412
44	***Total Direct Costs***	47,547	403,601	366,566
45	*Indirect*	(15,448)	181,157	158,785
46	**Total Global (Core)**	**32,099**	**584,758**	**525,351**
47				
48	**Global (GVP) Year 4**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
49	*Salaries*	(2,074)	54,209	32,807
50	*Fringe*	(771)	20,166	12,204
51	*Equipment*	-	-	-
52	*Domestic Travel*	-	-	329
53	*Foreign Travel*	7,007	20,000	7,502
54	*Services*	-	-	-
55	*Diagnostics*	-	-	-
56	*Supplies*	-	-	-
57	*Other*	-	-	-
58	***Total Direct Costs***	4,162	94,375	52,841
59	*Indirect*	1,956	44,356	24,835
60	**Total Global (GVP)**	**6,118**	**138,731**	**77,676**

	A	B	C	D
61				
62	**Admin Mgt (Ebola) Year 4**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
63	*Salaries*	(41,219)	22,204	5,407
64	*Fringe*	(15,333)	8,260	2,011
65	*Equipment*	-	-	-
66	*Domestic Travel*	18,812	2,394	3,408
67	*Foreign Travel*	-	-	(216)
68	*Services*	24,418	-	-
69	*Diagnostics*	-	-	-
70	*Supplies*	13,197	6,426	3,484
71	*Other*	9,601	-	813
72	***Total Direct Costs***	9,477	39,283	14,907
73	*Indirect*	(7,022)	18,463	7,006
74	**Total Admin Mgt (Ebola)**	**2,456**	**57,746**	**21,913**
75				
76	**Admin Mgt (Core) Year 4**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
77	*Salaries*	(24,207)	13,040	3,176
78	*Fringe*	(9,005)	4,851	1,181
79	*Equipment*	-	-	-
80	*Domestic Travel*	11,048	1,406	2,001
81	*Foreign Travel*	-	-	(127)
82	*Services*	14,341	-	-
83	*Diagnostics*	-	-	-
84	*Supplies*	7,751	3,774	2,046
85	*Other*	5,639	-	477
86	***Total Direct Costs***	5,566	23,071	8,755
87	*Indirect*	(4,124)	10,843	4,115
88	**Total Admin Mgt (Core)**	**1,443**	**33,915**	**12,870**
89				
90	**Admin Mgt (GVP) Year 4**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
91	*Salaries*	-	-	-
92	*Fringe*	-	-	-
93	*Equipment*	-	-	-
94	*Domestic Travel*	3,469	10,000	1,040
95	*Foreign Travel*	-	-	1,532
96	*Services*	-	-	-
97	*Diagnostics*	-	-	-

	A	B	C	D
98	*Supplies*	-	-	-
99	*Other*	-	-	-
100	***Total Direct Costs***	3,469	10,000	2,572
101	*Indirect*	1,630	4,700	1,209
102	**Total Admin Mgt (GVP)**	**5,100**	**14,700**	**3,780**
103				
104	**Cameroon Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
105	*Salaries*	(50,736)	284,468	226,921
106	*Fringe*	(18,874)	105,822	84,415
107	*Equipment*	7,773	61,548	13,767
108	*Domestic Travel*	62,901	86,826	44,262
109	*Foreign Travel*	(48,504)	37,459	4,649
110	*Services*	208,604	256,566	148,848
111	*Diagnostics*	(59,486)	115,291	207,046
112	*Supplies*	8,224	26,945	60,268
113	*Other*	(75,253)	31,865	63,492
114	***Total Direct Costs***	34,648	1,006,790	853,668
115	*Indirect*	(67,564)	341,229	336,545
116	**Total Cameroon Year 4**	**(52,916)**	**1,348,019**	**1,190,213**
117				
118	**DRC Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
119	*Salaries*	(155,940)	377,108	230,614
120	*Fringe*	(58,010)	140,284	85,788
121	*Equipment*	48,429	34,048	13,556
122	*Domestic Travel*	5,635	40,228	10,124
123	*Foreign Travel*	(84,653)	43,262	23,960
124	*Services*	323,586	72,824	43,449
125	*Diagnostics*	51,570	157,204	58,897
126	*Supplies*	19,802	20,295	12,526
127	*Other*	(96,502)	76,890	66,076
128	***Total Direct Costs***	53,919	962,143	544,990
129	*Indirect*	(163,040)	425,620	244,943
130	**Total DRC Year 4**	**(109,121)**	**1,387,763**	**789,932**
131				
132	**Lao PDR Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
133	*Salaries*	(16,700)	168,954	140,080
134	*Fringe*	(6,213)	62,851	52,110

	A	B	C	D
135	*Equipment*	(20,558)	15,500	14,575
136	*Domestic Travel*	27,086	21,820	4,930
137	*Foreign Travel*	(45,560)	30,708	46,739
138	*Services*	173,916	117,461	71,322
139	*Diagnostics*	(67,742)	67,218	32,209
140	*Supplies*	30,064	2,400	27,513
141	*Other*	36,277	48,583	26,145
142	***Total Direct Costs***	110,571	535,495	415,623
143	*Indirect*	(17,697)	206,743	165,206
144	**Total Lao PDR Year 4**	**92,875**	**742,238**	**580,829**
145				
146			*Total Core*	*Total Ebola*
147	FORMER METABIOTA COUNTRIES (NO Y4 BUDGET)		*833,877*	*(912,720)*
148	**China Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
149	*Salaries*	-	-	-
150	*Fringe*	-	-	-
151	*Equipment*	-	-	-
152	*Domestic Travel*	12,374	-	-
153	*Foreign Travel*	(23,190)	-	-
154	*Services*	165,924	-	-
155	*Diagnostics*	-	-	-
156	*Supplies*	4,876	-	-
157	*Other*	74,569	-	-
158	***Total Direct Costs***	234,554	-	-
159	*Indirect*	25,084	-	-
160	**Total China Year 4**	**259,637**	-	-
161				
162	**CDI Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
163	*Salaries*	42,464	-	-
164	*Fringe*	15,797	-	-
165	*Equipment*	177,986	-	-
166	*Domestic Travel*	29,611	-	-
167	*Foreign Travel*	(17,411)	-	-
168	*Services*	61,624	-	34,145
169	*Diagnostics*	(7,690)	-	-
170	*Supplies*	36,407	-	-
171	*Other*	(86,156)	-	-
172	***Total Direct Costs***	252,633	-	34,145

	A	B	C	D
175	*Indirect*	26,913	-	6,773
176	**Total CDI Year 4**	**279,546**	**-**	**40,918**
175				
176	**Guinea Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
177	*Salaries*	(23,103)	-	15,909
178	*Fringe*	(8,594)	-	5,918
179	*Equipment*	(30,830)	-	-
180	*Domestic Travel*	(15,432)	-	229
181	*Foreign Travel*	(30,511)	-	9,040
182	*Services*	94,926	-	3,369
183	*Diagnostics*	32,514	-	-
184	*Supplies*	(96,382)	-	-
185	*Other*	(134,666)	-	10,557
186	***Total Direct Costs***	(212,079)	-	45,023
187	*Indirect*	(109,123)	-	21,161
188	**Total Guinea Year 4**	**(321,202)**	**-**	**66,183**
189				
190	**Indonesia Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
191	*Salaries*	-	-	-
192	*Fringe*	-	-	-
193	*Equipment*	-	-	-
194	*Domestic Travel*	-	-	-
195	*Foreign Travel*	29,578	-	-
196	*Services*	278,977	-	40,320
197	*Diagnostics*	-	-	-
198	*Supplies*	-	-	-
199	*Other*	958	-	-
200	***Total Direct Costs***	309,513	-	40,320
201	*Indirect*	14,352	-	11,750
202	**Total Indonesia Year 4**	**323,865**	**-**	**52,070**
203				
204	**RoC Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
205	*Salaries*	(18,775)	-	-
206	*Fringe*	(6,984)	-	-
207	*Equipment*	166,406	-	-
208	*Domestic Travel*	(1,403)	-	(133)
209	*Foreign Travel*	25,689	-	(84)

	A	B	C	D
210	*Services*	67,741	-	-
211	*Diagnostics*	8,947	-	-
212	*Supplies*	43,361	-	(104)
213	*Other*	(51,998)	-	(2,726)
214	***Total Direct Costs***	232,985	-	(3,047)
215	*Indirect*	17,390	-	(1,432)
216	**Total RoC Year 4**	**250,374**	-	**(4,479)**
217				
218	**Sierra Leone Year 4 Budget**	**Year 3 Carryover**	**Y4 Budgeted**	**Expended**
219	*Salaries*	(137,263)	-	14,660
220	*Fringe*	(51,063)	-	5,454
221	*Equipment*	141,860	-	-
222	*Domestic Travel*	(5,844)	-	-
223	*Foreign Travel*	(26,740)	-	2,794
224	*Services*	(90,710)	-	-
225	*Diagnostics*	(89,792)	-	-
226	*Supplies*	23,811	-	(1,012)
227	*Other*	(319,331)	-	72,126
228	***Total Direct Costs***	(555,072)	-	94,022
229	*Indirect*	(315,992)	-	44,190
230	**Total Sierra Leone Year 4**	**(871,064)**	-	**138,212**
231				
232				

	E	F	G	H	I	J
1		Totals after Rebudget	Core	399,286		
2			Ebola	631,888		
3			GVP	-		
4				***1,031,174***		
5						
6	**Available to Spend**			**Carryover balance after rebudget**		
7	99,779			(9,897)		
8	37,117			(3,682)		
9	560,265			104,842		
10	240,333			225,533		
11	(267,154)			(124,320)		
12	1,601,243			928,097		
13	(90,118)			(34,097)		
14	42,405			33,041		
15	(806,107)			(93,151)		
16	1,417,762			1,026,366		
17	(386,588)			4,808		
18	1,031,174			1,031,174		
19						
20	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
21	197,854		(197,854)	-		

	E	F	G	H	I	J
22	73,602		(73,602)	-		
23	-		-	-		
24	(2,778)		2,778	-		
25	(62,028)		62,028	-		
26	134,119		(134,119)	-		
27	-		-	-		
28	(2,409)		2,409	-		
29	(56,865)		56,865	-		
30	281,495		(281,495)	-		
31	38,071		(38,071)	-		
32	**319,565**		**(319,565)**	-		
33						
34	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
35	79,068		(79,068)	-		
36	29,413		(29,413)	-		
37	-		-	-		
38	(1,632)		1,632	-		
39	(26,471)		26,471	-		
40	38,378		(38,378)	-		
41	-		-	-		
42	(1,415)		1,415	-		
43	(32,760)		59,511	26,751		
44	84,582		(57,831)	26,751		
45	6,924		5,649	12,573		
46	**91,506**		**(52,182)**	**39,323**		
47						
48	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
49	19,329		(19,329)	-		
50	7,190		(7,190)	-		
51	-		-	-		
52	(329)		329	-		
53	19,506		(19,506)	-		
54	-		-	-		
55	-		-	-		
56	-		-	-		
57	-		-	-		
58	45,696		(45,696)	-		
59	21,477		(21,477)	-		
60	**67,173**		**(67,173)**	-		

	E	F	G	H	I	J
61						
62	**Available to Spend**			**Carryover balance after rebudget**		
63	(24,422)			(24,422)		
64	(9,085)			(9,085)		
65	-			-		
66	17,798			17,798		
67	216			216		
68	24,418			24,418		
69	-			-		
70	16,139			16,139		
71	8,789			8,789		
72	33,854			33,854		
73	4,435			4,435		
74	**38,289**			**38,289**		
75						
76	**Available to Spend**			**Carryover balance after rebudget**		
77	(14,342)			(14,342)		
78	(5,335)			(5,335)		
79	-			-		
80	10,453			10,453		
81	127			127		
82	14,341			14,341		
83	-			-		
84	9,478			9,478		
85	5,162			5,162		
86	19,883			19,883		
87	2,605			2,605		
88	**22,487**			**22,487**		
89						
90	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
91	-		-	-		
92	-		-	-		
93	-		-	-		
94	12,429		(12,429)	-		
95	(1,532)		1,532	-		
96	-		-	-		
97	-		-	-		

	E	F	G	H	I	J
98	-		-	-		
99	-		-	-		
100	10,897		(10,897)	-		
101	5,122		(5,122)	-		
102	**16,019**		**(16,019)**	-		
103						
104	**Available to Spend**			**Carryover balance after rebudget**		
105	6,810			6,810		
106	2,533			2,533		
107	55,555			55,555		
108	105,465			105,465		
109	(15,695)			(15,695)		
110	316,322			316,322		
111	(151,241)			(151,241)		
112	(25,099)			(25,099)		
113	(106,880)			(106,880)		
114	187,770			187,770		
115	(82,880)			(82,880)		
116	**104,890**			**104,890**		
117						
118	**Available to Spend**			**Carryover balance after rebudget**		
119	(9,446)			(9,446)		
120	(3,514)			(3,514)		
121	68,921			68,921		
122	35,740			35,740		
123	(65,351)			(65,351)		
124	352,962			352,962		
125	149,877			149,877		
126	27,571			27,571		
127	(85,688)			(85,688)		
128	471,072			471,072		
129	17,637			17,637		
130	**488,709**			**488,709**		
131						
132	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
133	12,175		19,329	31,504		
134	4,529		7,190	11,719		

	E	F	G	H	I	J
135	(19,633)		-	(19,633)		
136	43,976		12,101	56,076		
137	(61,591)		17,974	(43,617)		
138	220,054		-	220,054		
139	(32,733)		-	(32,733)		
140	4,951		-	4,951		
141	58,715		-	58,715		
142	230,443		56,594	287,037		
143	23,840		26,598	50,439		
144	**254,284**		**83,192**	**337,476**		
145						
146	*TOTAL*					
147	*(78,843)*					
148	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
149	-		-	-		
150	-		-	-		
151	-		-	-		
152	12,374		(12,374)	-		
153	(23,190)		23,190	-		
154	165,924		(165,924)	-		
155	-		-	-		
156	4,876		(4,876)	-		
157	74,569		(74,569)	-		
158	234,554		(234,554)	-		
159	25,084		(25,084)	-		
160	**259,637**		**(259,637)**	-		
161						
162	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
163	42,464		(42,464)	-		
164	15,797		(15,797)	-		
165	177,986		(177,986)	-		
166	29,611		(29,611)	-		
167	(17,411)		17,411	-		
168	27,479		(27,479)	-		
169	(7,690)		7,690	-		
170	36,407		(36,407)	-		
171	(86,156)		86,156	-		
172	218,488		(218,488)	-		

	E	F	G	H	I	J
175	20,140		(20,140)	-		
176	**238,628**		**(238,628)**	-		
175						
176	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
177	(39,012)		39,012	-		
178	(14,513)		14,513	-		
179	(30,830)		30,830	-		
180	(15,661)		15,661	-		
181	(39,551)		39,551	-		
182	91,557		(91,557)	-		
183	32,514		(32,514)	-		
184	(96,382)		96,382	-		
185	(145,223)		145,223	-		
186	(257,101)		257,101	-		
187	(130,283)		130,283	-		
188	**(387,385)**		**387,385**	-		
189						
190	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
191	-		-	-		
192	-		-	-		
193	-		-	-		
194	-		-	-		
195	29,578		(29,578)	-		
196	238,656		(238,656)	-		
197	-		-	-		
198	-		-	-		
199	958		(958)	-		
200	269,193		(269,193)	-		
201	2,602		(2,602)	-		
202	**271,795**		**(271,795)**	-		
203						
204	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
205	(18,775)		18,775	-		
206	(6,984)		6,984	-		
207	166,406		(166,406)	-		
208	(1,270)		1,270	-		
209	25,773		(25,773)	-		

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210	67,741		(67,741)	-		
211	8,947		(8,947)	-		
212	43,465		(43,465)	-		
213	(49,272)		49,272	-		
214	236,031		(236,031)	-		
215	18,822		(18,822)	-		
216	**254,853**		**(254,853)**	-		
217						
218	**Available to Spend**		**Rebudget**	**Carryover balance after rebudget**		
219	(151,924)		151,924	-		
220	(56,517)		56,517	-		
221	141,860		(141,860)	-		
222	(5,844)		5,844	-		
223	(29,534)		29,534	-		
224	(90,710)		90,710	-		
225	(89,792)		89,792	-		
226	24,823		(24,823)	-		
227	(391,457)		391,457	-		
228	(649,094)		649,094	-		
229	(360,183)		360,183	-		
230	**(1,009,277)**		**1,009,277**	-		
231						
232						

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5			TRANSITION COUNTRIES	
6	**End Balances Y4 (Core) - China, Indonesia, RoC**	**Global (Core) End Balance Y4**	**End Balances Y4 (Ebola) - CDI, Guinea, Sierra Leone**	**Global (Ebola) End Balance Y4**
7	(18,775)	79,068	(148,472)	197,854
8	(6,984)	29,413	(55,232)	73,602
9	166,406	-	289,016	-
10	11,104	(1,632)	8,105	(2,778)
11	32,161	(26,471)	(86,497)	(62,028)
12	472,321	38,378	28,326	134,119
13	8,947	-	(64,968)	-
14	48,341	(1,415)	(35,152)	(2,409)
15	26,256	(32,760)	(622,836)	(56,865)
16	739,778	84,582	(687,708)	281,496
17	46,507	6,924	(470,325)	38,071
18	786,285	91,506	(1,158,033)	319,565
19			TRANSITION COUNTRIES	
20	**Country Rebudget (Core) - China, Indonesia, RoC**	**Global Rebudget (Core)**	**Country Rebudget (Ebola) - CDI, Guinea, Sierra Leone**	**Global Rebudget (Ebola)**
21	18,775	(79,068)	148,472	(197,854)

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22	6,984	(29,413)	55,232	(73,602)
23	(166,406)	-	(289,016)	-
24	(11,104)	1,632	(8,105)	2,778
25	(32,161)	26,471	86,497	62,028
26	(472,321)	(38,378)	(28,326)	(134,119)
27	(8,947)	-	64,968	-
28	(48,341)	1,415	35,152	2,409
29	(26,256)	59,511	622,836	56,865
30	(739,778)	(57,831)	687,708	(281,495)
31	(46,507)	5,649	470,325	(38,071)
32	(786,285)	(52,182)	1,158,033	(319,565)
33				
34	**Total Core**	**(838,468)**	**Total Ebola**	**838,468**
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5			TRANSITION COUNTRIES		
6	**TOTAL**		**Y3 Carryover (Core) - China, Indonesia, RoC**	**Y3 Carryover (Ebola) - CDI, Guinea, Sierra Leone**	**TOTAL**
7	***109,676***		(18,775)	(117,902)	***(136,677)***
8	***40,799***		(6,984)	(43,860)	***(50,845)***
9	***455,423***		166,406	289,016	***455,423***
10	***14,800***		10,971	8,335	***19,306***
11	***(142,835)***		32,077	(74,663)	***(42,586)***
12	***673,145***		512,642	65,840	***578,482***
13	***(56,020)***		8,947	(64,968)	***(56,020)***
14	***9,365***		48,238	(36,164)	***12,074***
15	***(686,205)***		23,530	(540,153)	***(516,623)***
16	***418,147***		777,052	(514,518)	***262,534***
17	***(378,823)***		56,825	(398,202)	***(341,376)***
18	***39,323***		833,877	(912,720)	***(78,843)***
19					
20	**TOTAL**				
21	***(109,676)***				

	O	P	Q	R	S
22	*(40,799)*				
23	*(455,423)*				
24	*(14,800)*				
25	*142,835*				
26	*(673,145)*				
27	*56,020*				
28	*(9,365)*				
29	*712,955*				
30	*(391,396)*				
31	*391,396*				
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	A	B	C	D	E	F
1	**Year 4 Budget**		**63%**			
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	123,831	395,159	518,989	321,135	40,408.52
5	*Fringe*	46,065	146,999	193,064	119,462	15,031.97
6	*Equipment*	0	-	-	-	
7	*Domestic Travel*	(1,447)	-	(1,447)	1,331	
8	*Foreign Travel*	(75,893)	36,062	(39,832)	22,196	399.84
9	*Services*	136,358	78,174	214,531	80,412	
10	*Diagnostics*	0	-	-	-	
11	*Supplies*	(1,793)	-	(1,793)	617	
12	*Other*	(54,220)	37,219	(17,001)	39,864	9,096.60
13	***Total Direct Costs***	**172,900**	***693,612***	***866,512***	***585,017***	***64,937***
14	*Indirect*	(21,423)	*311,463*	*290,040*	*251,970*	30,520.36
15	**Total Costs**	**151,477**	**1,005,075**	**1,156,552**	**836,987**	**95,457**
16	**Carryover amount from September 2017 invoice*					
17						
18						
19						
20						
21						

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2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	38,423.64	30,786.09	22,481.32	18,679.26	21,770.22	21,158.97	25,610.28
5	14,293.59	11,452.43	8,363.05	6,948.68	8,098.52	7,871.14	9,527.02
6							
7		25.20	(62.72)	(53.90)			104.48
8	553.94	4,548.67	3,152.39	4,597.26	1,471.69	5,182.54	962.23
9			7,895.95	-			44,377.36
10							
11		616.64					
12	2,175.60	973.93	6,824.32	2,349.95	3,902.35	5,418.66	2,688.90
13	***55,447***	***48,403***	***48,654.31***	***32,521.25***	***35,242.77***	***39,631.31***	***83,260.27***
14	26,059.98	22,749.39	22,867.52	15,284.99	16,564.10	18,626.72	29,368.87
15	**81,507**	**71,152**	**71,521.83**	**47,806.24**	**51,806.88**	**58,258.03**	**112,629.14**
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3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4	28,128.78	26,449.01	23,638.30	23,600.60			
5	10,463.91	9,839.03	8,793.45	8,779.42			
6							
7	932.29	386.02					
8	610.61			726.69			
9				28,138.64			
10							
11							
12	2,797.07	1,949.46	820.80	866.74			
13	***42,932.67***	***38,623.52***	***33,252.54***	***62,112.08***	-	-	-
14	20,178.35	18,153.06	15,628.70	15,967.52			
15	**63,111.02**	**56,776.58**	**48,881.24**	**78,079.60**	-	-	-
16							
17							
18							
19							
20							
21							

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3	**Funds Available**
4	197,854
5	73,602
6	-
7	(2,778)
8	(62,028)
9	134,119
10	-
11	(2,409)
12	(56,865)
13	***281,495***
14	38,071
15	**319,565**
16	
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20	
21	

	A	B	C	D	E	F
1	**4 Budget**		**37%**			
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	57,755	226,669	284,424	205,356	23,731.99
5	*Fringe*	21,485	84,321	105,806	76,392	8,828.30
6	*Equipment*	0	-	-	-	
7	*Domestic Travel*	(850)	-	(850)	782	
8	*Foreign Travel*	(38,277)	24,841	(13,436)	13,036	234.82
9	*Services*	39,693	45,911	85,604	47,226	
10	*Diagnostics*	0	-	-	-	
11	*Supplies*	(1,053)	-	(1,053)	362	
12	*Other*	(31,207)	21,859	(9,348)	23,412	5,342.44
13	***Total Direct Costs***	**47,547**	**403,601**	***451,148***	***366,566***	***38,138***
14	*Indirect*	(15,448)	181,157	165,709	158,785	17,924.65
15	**Total Costs**	**32,099**	**584,758**	**616,857**	**525,351**	**56,062**
16	**Carryover amount from September 2017 invoice*					
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18						
19						

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3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	22,566.26	18,080.72	15,427.15	12,675.10	14,350.47	13,753.73	17,033.71
5	8,394.65	6,726.03	5,738.90	4,715.14	5,338.37	5,116.39	6,336.54
6							
7		14.80	(36.84)	(31.66)			61.36
8	325.33	2,671.44	1,851.41	2,699.98	864.32	3,043.72	559.25
9			4,637.30	-			26,062.89
10							
11		362.16					
12	1,277.56	571.99	4,007.93	1,380.13	2,291.85	3,182.39	1,579.19
13	***32,564***	***28,427***	***31,625.85***	***21,438.69***	***22,845.02***	***25,096.22***	***51,632.94***
14	15,304.99	13,360.75	14,864.15	10,076.18	10,737.16	11,795.22	18,533.39
15	**47,869**	**41,788**	**46,490.01**	**31,514.87**	**33,582.18**	**36,891.45**	**70,166.34**
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3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4	18,639.57	17,545.67	16,289.03	15,262.56			
5	6,933.92	6,526.99	6,059.52	5,677.67			
6							
7	547.54	226.71					
8	358.62			426.78			
9				16,525.87			
10							
11							
12	1,642.73	1,144.92	482.05	509.03			
13	***28,122.37***	***25,444.29***	***22,830.60***	***38,401.92***	-	-	-
14	13,217.51	11,958.82	10,730.36	10,281.74			
15	**41,339.88**	**37,403.11**	**33,560.99**	**48,683.66**	-	-	-
16							
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18							
19							

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3	**Funds Available**
4	79,068
5	29,413
6	-
7	(1,632)
8	(26,471)
9	38,378
10	-
11	(1,415)
12	(32,760)
13	***84,582***
14	6,924
15	**91,506**
16	
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	A	B	C	D	E	F
1	**4 Budget**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(2,074)	54,209	52,135	32,807	1,925.00
5	*Fringe*	(771)	20,166	19,394	12,204	716.10
6	*Equipment*	0		-	-	
7	*Domestic Travel*	0		-	329	326.60
8	*Foreign Travel*	7,007	20,000	27,007	7,502	3,299.47
9	*Services*	0		-	-	
10	*Diagnostics*	0		-	-	
11	*Supplies*	0		-	-	
12	*Other*	0		-	-	
13	***Total Direct Costs***	**4,162**	**94,375**	**98,537**	**52,841**	**6,267**
14	*Indirect*	1,956	44,356	46,312	24,835	2,945.57
15	**Total Costs**	**6,118**	**138,731**	**144,849**	**77,676**	**9,213**
16	**Carryover amount from September 2017 invoice*					
17						
18						
19						

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3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	733.44	8,380.27	4,811	2,082.50	2,082.50	2,082.50	2,082.50
5	272.84	3,117.46	1,789.54	774.69	774.69	774.69	774.69
6							
7	2.00						
8				2,146.00		1,346.76	
9							
10							
11							
12							
13	***1,008***	***11,498***	***6,600***	***5,003.27***	***2,857.19***	***4,203.95***	***2,857.19***
14	473.89	5,403.93	3,102.06	2,351.54	1,342.88	1,975.86	1,342.88
15	**1,482**	**16,902**	**9,702**	**7,354.81**	**4,200.07**	**6,179.81**	**4,200.07**
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19							

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3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4	2,082.50	2,082.50	2,082.50	2,380.00			
5	774.69	774.69	774.69	885.36			
6							
7							
8	619.20		90.00				
9							
10							
11							
12							
13	***3,476.39***	***2,857.19***	***2,947.19***	***3,265.36***	-	-	-
14	1,633.90	1,342.88	1,385.18	1,534.72			
15	**5,110.29**	**4,200.07**	**4,332.37**	**4,800.08**	-	-	-
16							
17							
18							
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3	**Funds Available**
4	19,329
5	7,190
6	-
7	(329)
8	19,506
9	-
10	-
11	-
12	-
13	**45,696**
14	21,477
15	**67,173**
16	
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	A	B	C	D	E	F
1	**Management**				**63%**	
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(41,219)	22,204	(19,015)	5,407	2,135.94
5	*Fringe*	(15,333)	8,260	(7,074)	2,011	794.57
6	*Equipment*	0	-	-	-	
7	*Domestic Travel*	18,812	2,394	21,206	3,408	1,191.66
8	*Foreign Travel*	0	-	-	(216)	
9	*Services*	24,418		24,418	-	
10	*Diagnostics*	0	-	-	-	
11	*Supplies*	13,197	6,426	19,623	3,484	
12	*Other*	9,601		9,601	813	21.16
13	***Total Direct Costs***	**9,477**	***39,283***	***48,761***	***14,907***	***4,143***
14	*Indirect*	(7,022)	*18,463*	*11,441*	7,006	1,947.36
15	**Total Costs**	**2,456**	**57,746**	**60,202**	**21,913**	**6,091**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	761.00	1,118.63	1,082	309			
5	283.09	416.13	402.61	115.00			
6							
7		710.05				271.72	473.53
8		6.35				58.43	(293.31)
9							
10							
11	34.11	45.98	10				3,197.62
12	22.20	1.27				78.93	643.49
13	***1,100***	***2,298***	***1,495***	***424***	**-**	***409.08***	***4,021.33***
14	517.19	1,080.25	702.66	199.35	-	192.27	1,890.03
15	**1,618**	**3,379**	**2,198**	**624**	**-**	**601.34**	**5,911.36**
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7		21.42	739.17				
8			12.70				
9							
10							
11	76.46	119.91					
12		45.54					
13	***76.46***	***186.87***	***751.87***	-	-	-	-
14	35.93	87.83	353.38	-			
15	**112.39**	**274.70**	**1,105.25**	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	(24,422)
5	(9,085)
6	-
7	17,798
8	216
9	24,418
10	-
11	16,139
12	8,789
13	***33,854***
14	4,435
15	**38,289**
16	

	A	B	C	D	E	F
1	**Management**				**37%**	
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(24,207)	13,040	(11,167)	3,176	1,254.44
5	*Fringe*	(9,005)	4,851	(4,154)	1,181	466.65
6	*Equipment*	0	-	-	-	
7	*Domestic Travel*	11,048	1,406	12,454	2,001	699.87
8	*Foreign Travel*	0	-	-	(127)	
9	*Services*	14,341		14,341	-	
10	*Diagnostics*	0	-	-	-	
11	*Supplies*	7,751	3,774	11,525	2,046	
12	*Other*	5,639		5,639	477	12.43
13	***Total Direct Costs***	***5,566***	***23,071***	***28,637***	***8,755***	***2,433***
14	*Indirect*	(4,124)	*10,843*	*6,720*	4,115	1,143.69
15	**Total Costs**	**1,443**	**33,915**	**35,357**	**12,870**	**3,577**
16	**Carryover amount from September 2017 invoice*					
17						
18						
19						
20						
21						

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	446.93	656.98	636	182			
5	166.26	244.40	236.45	67.54			
6							
7		417.02				159.58	278.10
8		3.73				34.32	(172.26)
9							
10							
11	20.04	27.01	6				1,877.97
12	13.04	0.75				46.35	377.93
13	***646***	***1,350***	***878***	***249***	**-**	***240.25***	***2,361.74***
14	303.75	634.45	412.67	117.08	-	112.92	1,110.02
15	**950**	**1,984**	**1,291**	**366**	**-**	**353.17**	**3,471.75**
16							
17							
18							
19							
20							
21							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7		12.58	434.12				
8			7.46				
9							
10							
11	44.90	70.42					
12		26.75					
13	***44.90***	***109.75***	***441.58***	-	-	-	-
14	21.10	51.58	207.54	-			
15	**66.01**	**161.33**	**649.12**	-	-	-	-
16							
17							
18							
19							
20							
21							

	U
1	
2	
3	**Funds Available**
4	(14,342)
5	(5,335)
6	-
7	10,453
8	127
9	14,341
10	-
11	9,478
12	5,162
13	**19,883**
14	2,605
15	**22,487**
16	
17	
18	
19	
20	
21	

	A	B	C	D	E	F
1	**Management**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	0	-	-	-	
5	*Fringe*	0	-	-	-	
6	*Equipment*	0		-	-	
7	*Domestic Travel*	3,469	10,000	13,469	1,040	322.68
8	*Foreign Travel*	0		-	1,532	
9	*Services*	0		-	-	
10	*Diagnostics*	0		-	-	
11	*Supplies*	0		-	-	
12	*Other*	0		-	-	
13	***Total Direct Costs***	***3,469***	***10,000***	***13,469***	***2,572***	***323***
14	*Indirect*	1,630	4,700	6,330	1,209	151.66
15	**Total Costs**	**5,100**	**14,700**	**19,800**	**3,780**	**474**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4							
5							
6							
7	361.15	183.46					
8						1,531.96	
9							
10							
11							
12							
13	**361**	**183**	-	-	-	**1,531.96**	-
14	169.74	86.23	-	-	-	720.02	-
15	**531**	**270**	-	-	-	**2,251.98**	-
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7			172.50				
8							
9							
10							
11							
12							
13	-	-	**172.50**	-	-	-	-
14	-	-	81.08	-			
15	-	-	**253.58**	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	-
5	-
6	-
7	12,429
8	(1,532)
9	-
10	-
11	-
12	-
13	**10,897**
14	5,122
15	**16,019**
16	

	A	B	C	D	E	F
1	**Budget**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(50,736)	284,468	233,731	226,921	19,635.29
5	*Fringe*	(18,874)	105,822	86,948	84,415	7,304.33
6	*Equipment*	7,773	61,548	69,321	13,767	
7	*Domestic Travel*	62,901	86,826	149,727	44,262	3,370.10
8	*Foreign Travel*	(48,504)	37,459	(11,045)	4,649	2,692.93
9	*Services*	208,604	256,566	465,170	148,848	10,158.86
10	*Diagnostics*	(59,486)	115,291	55,805	207,046	53,618.42
11	*Supplies*	8,224	26,945	35,169	60,268	2,284.13
12	*Other*	(75,253)	31,865	(43,388)	63,492	3,441.08
13	***Total Direct Costs***	***34,648***	***1,006,790***	***1,041,438***	***853,668***	***102,505***
14	*Indirect*	(87,564)	341,229	253,665	336,545	48,177.41
15	**Total Costs**	**(52,916)**	**1,348,019**	**1,295,103**	**1,190,213**	**150,683**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	22,036.59	19,376.80	28,256.14	17,214.30	19,704.29	16,507.73	18,192.98
5	8,197.61	7,208.17	10,511.28	6,403.72	7,330.00	6,140.88	6,767.79
6							
7	2,068.18	8,147.09	7,426.36	4,136.01	1,655.71	732.91	7,215.86
8	141.57		1,183.61	327.67		1,003.35	
9	9,736.93	11,314.16	10,393.44	5,594.12	19,768.86	10,986.48	15,789.77
10	1,812.81	10,436.39	2,910.09	57,816.44	5,735.63	20,717.43	20,654.64
11	678.37		226.84			581.78	
12	3,473.23	10,605.05	6,368.09	5,829.31	2,792.28	1,150.64	5,196.20
13	***48,145***	***67,088***	***67,296***	***97,321.57***	***56,986.77***	***57,821.20***	***73,817.24***
14	22,628.29	31,531.20	23,825.46	43,111.90	17,492.42	22,012.32	27,272.91
15	**70,774**	**98,619**	**91,121**	**140,433.47**	**74,479.18**	**79,833.51**	**101,090.15**
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4	16,518.33	16,621.36	16,341.80	16,515.77			
5	6,144.82	6,183.15	6,079.15	6,143.87			
6				13,766.71			
7	1,770.12	4,252.46		79			
8		(700.01)					
9		17,260.11		00			
10	33,344.27						
11	78.49	13,692.64	33,682.79	9,043.20			
12	5,593.60	5,917.91	7,497.42	5,606.84			
13	**63,449.63**	**63,227.62**	**88,776.89**	**67,233.18**	-	-	-
14	29,821.33	21,604.73	30,333.97	18,733.01			
15	**93,270.95**	**84,832.34**	**119,110.86**	**85,966.19**	-	-	-
16							

Apple:
Hotel refund due to duplicate charge by error (paid in April during reserving the room, but

	U
1	
2	
3	**Funds Available**
4	6,810
5	2,533
6	55,555
7	105,465
8	(15,695)
9	316,322
10	(151,241)
11	(25,099)
12	(106,880)
13	***187,770***
14	(82,880)
15	**104,890**
16	

	A	B	C	D	E	F
1	**Republic of Congo**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(155,940)	377,108	221,168	230,614	23,287.95
5	*Fringe*	(56,010)	140,284	82,274	85,788	8,663.12
6	*Equipment*	48,429	34,048	82,477	13,556	
7	*Domestic Travel*	5,635	40,228	45,863	10,124	164.85
8	*Foreign Travel*	(84,653)	43,262	(41,391)	23,960	102.75
9	*Services*	323,586	72,824	396,411	43,449	(4,500.00)
10	*Diagnostics*	51,570	157,204	208,774	58,897	15,299.32
11	*Supplies*	19,802	20,295	40,097	12,526	
12	*Other*	(96,502)	76,890	(19,612)	66,076	3,776.80
13	***Total Direct Costs***	***53,919***	***962,143***	***1,016,062***	***544,990***	***46,795***
14	*Indirect*	(163,040)	425,620	262,580	244,943	24,108.55
15	**Total Costs**	**(109,121)**	**1,387,763**	**1,278,642**	**789,932**	**70,903**
16	**Carryover amount from September 2017 invoice*					
17						

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	24,216.68	21,404.89	24,682.33	19,200.48	19,247.86	18,278.80	18,043.83
5	9,008.60	7,962.62	9,181.83	7,142.58	7,160.20	6,799.71	6,712.30
6							
7	90.00	1,510.00	25.00	90.00	235.00	575.00	2,204.96
8	2,424.61	3,105.27	2,130.20	732.96		1,003.35	988.42
9	3,103.92	2,040.00	3,616.46	1,420.00	620.00	620.00	620.00
10	515.04	2,127.61				27,160.31	4,577.49
11	470.00		545.00	99.71	95.44		
12	1,114.24	4,676.42	4,649.06	5,106.59	5,813.63	5,121.90	4,925.42
13	***40,943***	***42,827***	***44,829.90***	***33,792.34***	***33,172.13***	***59,559.07***	***38,072.42***
14	19,243.25	20,128.60	21,070.05	15,882.40	15,590.90	27,992.76	17,894.04
15	**60,186**	**62,955**	**65,899.95**	**49,674.74**	**48,763.04**	**87,551.84**	**55,966.46**
16							
17							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4	18,529.71	18,804.03	15,333.27	9,583.83			
5	6,893.05	6,995.10	5,703.98	3,565.18			
6				13,555.91			
7	2,620.00	1,960.00	202.44	446.39			
8	8,978.07	4,388.80	105.75				
9	620.00	620.00	18,887.12	15,781.04			
10	5,171.14	4,046.52					
11			11,033.88	282.02			
12	3,897.76	10,003.25	12,585.74	4,405.02			
13	***46,709.73***	***46,817.70***	***63,852.18***	***47,619.39***	-	-	-
14	21,953.57	22,004.32	30,010.52	9,063.91			
15	**68,663.31**	**68,822.02**	**93,862.70**	**56,683.31**	-	-	-
16							
17							

	U
1	
2	
3	**Funds Available**
4	(9,446)
5	(3,514)
6	68,921
7	35,740
8	(65,351)
9	352,962
10	149,877
11	27,571
12	(85,688)
13	***471,072***
14	17,637
15	**488,709**
16	
17	

	A	B	C	D	E	F
1	**Budget**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(16,700)	168,954	152,255	140,080	11,422.06
5	*Fringe*	(6,213)	62,851	56,638	52,110	4,249.01
6	*Equipment*	(20,558)	15,500	(5,058)	14,575	
7	*Domestic Travel*	27,086	21,820	48,906	4,930	
8	*Foreign Travel*	(45,560)	30,708	(14,852)	46,739	1,479.04
9	*Services*	173,916	117,461	291,376	71,322	12,000.00
10	*Diagnostics*	(67,742)	67,218	(524)	32,209	
11	*Supplies*	30,064	2,400	32,464	27,513	
12	*Other*	36,277	48,583	84,860	26,145	3,151.89
13	***Total Direct Costs***	***110,571***	***535,495***	***646,066***	***415,623***	***32,302***
14	*Indirect*	(17,697)	206,743	189,046	165,206	15,181.94
15	**Total Costs**	**92,875**	**742,238**	**835,113**	**580,829**	**47,484**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4	15,124.88	3,170.96	20,017.05	3,569.52	13,871.16	8,271.88	8,657.28
5	5,626.46	1,179.60	7,446.34	1,327.86	5,160.07	3,077.14	3,220.51
6							
7	1,501.27	49.72	1,677.67		915.12		
8	8,962.48	7,426.09		1,465.84	2,338.43	1,934.35	153.77
9	1,821.05	3,116.36	718.72	4,120.20			11,495.73
10	67.51					17,246.72	
11		65.34		4,020.38		-	
12	2,729.13	105.63	962.54	211.26	2,927.15	2,858.41	
13	***35,833***	***15,114***	***30,822.32***	***14,715.06***	***25,211.93***	***33,388.50***	
14	16,841.40	7,103.44	14,486.49	6,916.08	11,849.61	15,692.59	2,263.10
15	**52,674**	**22,217**	**45,308.81**	**21,631.14**	**37,061.54**	**49,081.09**	**18,573.92**
16							

Apple:
We initially cha
$17,246.72 ag
Supplies in Apr
caught the cat

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4	10,164.02	13,298.75	19,607.87	12,904.11			
5	3,781.02	4,947.14	7,294.13	4,800.33			
6				14,574.86			
7			584.84	201.86			
8	2,267.03	10,297.97	3,430.55	6,983.47			
9				38,050.26			
10	[illegible].13						
11	rged inst t. Beth ing error	.29	10,662.61	12,746.50			
12		.65 2,337.12	4,151.60	1,705.87			
13	[illegible]**11**	**30,880.98**	**45,731.60**	**91,967.26**	-	-	-
14	20,372.67	14,514.06	21,493.85	18,490.81			
15	**63,718.77**	**45,395.03**	**67,225.45**	**110,458.06**	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	12,175
5	4,529
6	(19,633)
7	43,976
8	(61,591)
9	220,054
10	(32,733)
11	4,951
12	58,715
13	**230,443**
14	23,840
15	**254,284**
16	

	A	B	C	D	E	F
1	**Budget**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	-		-	-	
5	*Fringe*	-		-	-	
6	*Equipment*	-		-	-	
7	*Domestic Travel*	12,374		12,374	-	
8	*Foreign Travel*	(23,190)		(23,190)	-	
9	*Services*	165,924		165,924	-	
10	*Diagnostics*	-		-	-	
11	*Supplies*	4,876		4,876	-	
12	*Other*	74,569		74,569	-	
13	***Total Direct Costs***	***234,554***	-	***234,554***	-	-
14	*Indirect*	25,084		25,084	-	
15	**Total Costs**	**259,637**	-	**259,637**	-	-
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4							
5							
6							
7							
8							
9							
10							
11							
12							
13	-	-	-	-	-	-	-
14							
15	-	-	-	-	-	-	-
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7							
8							
9							
10							
11							
12							
13	-	-	-	-	-	-	-
14							
15	-	-	-	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	-
5	-
6	-
7	12,374
8	(23,190)
9	165,924
10	-
11	4,876
12	74,569
13	**234,554**
14	25,084
15	**259,637**
16	

	A	B	C	D	E	F
1	[redacted] (transitioned to					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	42,464		42,464	-	
5	*Fringe*	15,797		15,797	-	
6	*Equipment*	177,986		177,986	-	
7	*Domestic Travel*	29,611		29,611	-	
8	*Foreign Travel*	(17,411)		(17,411)	-	
9	*Services*	61,624		61,624	34,145	40,735.07
10	*Diagnostics*	(7,690)		(7,690)	-	
11	*Supplies*	36,407		36,407	-	
12	*Other*	(86,156)		(86,156)	-	
13	***Total Direct Costs***	***252,633***	**-**	***252,633***	***34,145***	***40,735***
14	*Indirect*	26,913		26,913	6,773	9,870.00
15	**Total Costs**	**279,546**	**-**	**279,546**	**40,918**	**50,605**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4							
5							
6							
7							
8							
9	(21,000.00)				14,064.25		345.75
10							
11							
12							
13	***(21,000.00)***	-	-	-	***14,064.25***	-	***345.75***
14	(9,870.00)				6,610.20	-	162.50
15	**(30,870.00)**	-	-	-	**20,674.45**	-	**508.25**
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7							
8							
9							
10							
11							
12							
13	-	-	-	-	-	-	-
14							
15	-	-	-	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	42,464
5	15,797
6	177,986
7	29,611
8	(17,411)
9	27,479
10	(7,690)
11	36,407
12	(86,156)
13	***218,488***
14	20,140
15	**238,628**
16	

	A	B	C	D	E	F
1	**Budget**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(23,103)		(23,103)	15,909	15,909.08
5	*Fringe*	(8,594)		(8,594)	5,918	5,918.18
6	*Equipment*	(30,830)		(30,830)	-	
7	*Domestic Travel*	(15,432)		(15,432)	229	229.15
8	*Foreign Travel*	(30,511)		(30,511)	9,040	9,040.05
9	*Services*	94,926		94,926	3,369	
10	*Diagnostics*	32,514		32,514	-	
11	*Supplies*	(96,382)		(96,382)	-	
12	*Other*	(134,666)		(134,666)	10,557	10,557.09
13	***Total Direct Costs***	***(212,079)***	**-**	***(212,079)***	***45,023***	***41,654***
14	*Indirect*	*(109,123)*		*(109,123)*	21,161	19,577.17
15	**Total Costs**	**(321,202)**	**-**	**(321,202)**	**66,183**	**61,231**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4							
5							
6							
7							
8							
9							3,368.97
10							
11							
12							
13	-	-	-	-	-	-	**3,368.97**
14							1,583.42
15	-	-	-	-	-	-	**4,952.39**
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7							
8							
9							
10							
11							
12							
13	-	-	-	-	-	-	-
14							
15	-	-	-	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	(39,012)
5	(14,513)
6	(30,830)
7	(15,661)
8	(39,551)
9	91,557
10	32,514
11	(96,382)
12	(145,223)
13	***(257,101)***
14	(130,283)
15	**(387,385)**
16	

	A	B	C	D	E	F
1	**Budget**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	-		-	-	
5	*Fringe*	-		-	-	
6	*Equipment*	-		-	-	
7	*Domestic Travel*	-		-	-	
8	*Foreign Travel*	29,578		29,578	-	
9	*Services*	278,977		278,977	40,320	(37,878.00)
10	*Diagnostics*	-		-	-	
11	*Supplies*	-		-	-	
12	*Other*	958		958	-	
13	***Total Direct Costs***	***309,513***	**-**	***309,513***	***40,320***	***(37,878)***
14	*Indirect*	14,352		14,352	11,750	
15	**Total Costs**	**323,865**	**-**	**323,865**	**52,070**	**(37,878)**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4							
5							
6							
7							
8							
9			17,419	60,779			
10							
11							
12							
13	-	-	**17,419**	**60,779**	-	-	-
14			8,187	3,563			
15	-	-	**25,606**	**64,342**	-	-	-
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7							
8							
9							
10							
11							
12							
13	-	-	-	-	-	-	-
14							
15	-	-	-	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	-
5	-
6	-
7	-
8	29,578
9	238,656
10	-
11	-
12	958
13	**269,193**
14	2,602
15	**271,795**
16	

	A	B	C	D	E	F
1	[redacted] (transitioned to					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(18,775)		(18,775)	-	
5	*Fringe*	(6,984)		(6,984)	-	
6	*Equipment*	166,406		166,406	-	
7	*Domestic Travel*	(1,403)		(1,403)	(133)	
8	*Foreign Travel*	25,689		25,689	(84)	
9	*Services*	67,741		67,741	-	
10	*Diagnostics*	8,947		8,947	-	
11	*Supplies*	43,361		43,361	(104)	
12	*Other*	(51,998)		(51,998)	(2,726)	
13	***Total Direct Costs***	***232,985***	**-**	***232,985***	***(3,047)***	**-**
14	*Indirect*	*17,390*		*17,390*	(1,432)	
15	**Total Costs**	**250,374**	**-**	**250,374**	**(4,479)**	**-**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4							
5							
6							
7	(133.46)						
8	(83.53)						
9							
10							
11	(103.50)						
12	(2,726.23)						
13	***(3,047)***	-	-	-	-	-	-
14	(1,431.96)						
15	**(4,479)**	-	-	-	-	-	-
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7							
8							
9							
10							
11							
12							
13	-	-	-	-	-	-	-
14							
15	-	-	-	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	(18,775)
5	(6,984)
6	166,406
7	(1,270)
8	25,773
9	67,741
10	8,947
11	43,465
12	(49,272)
13	**236,031**
14	18,822
15	**254,853**
16	

	A	B	C	D	E	F
1	**4 Budget**					
2						
3	**Total Costs**	**Carry-forward from Year 3**	**Year 4 Budget**	**Total Available Y4**	**Yr to Date Total Spent**	**Total Oct 17**
4	*Salaries*	(137,263)		(137,263)	14,660	14,660.28
5	*Fringe*	(51,063)		(51,063)	5,454	5,453.62
6	*Equipment*	141,860		141,860	-	
7	*Domestic Travel*	(5,844)		(5,844)	-	
8	*Foreign Travel*	(26,740)		(26,740)	2,794	2,873.96
9	*Services*	(90,710)		(90,710)	-	
10	*Diagnostics*	(89,792)		(89,792)	-	
11	*Supplies*	23,811		23,811	(1,012)	
12	*Other*	(319,331)		(319,331)	72,126	74,970.51
13	***Total Direct Costs***	***(555,072)***	**-**	***(555,072)***	***94,022***	***97,958***
14	*Indirect*	(315,992)		(315,992)	44,190	46,040.43
15	**Total Costs**	**(871,064)**	**-**	**(871,064)**	**138,212**	**143,999**
16	**Carryover amount from September 2017 invoice*					

	G	H	I	J	K	L	M
1							
2							
3	**Total Nov 17**	**Total Dec 17**	**Total Jan 18**	**Total Feb 18**	**Total Mar 18**	**Total Apr 18**	**Total May 18**
4							
5							
6							
7							
8	(80.20)						
9							
10							
11	(1,011.55)						
12	(7,156.20)	862.31		1,724.57	862.31	862.30	
13	***(8,248)***	***862***	**-**	***1,724.57***	***862.31***	***862.30***	**-**
14	(3,876.54)	405.29	-	810.55	405.29	405.28	
15	**(12,124)**	**1,268**	**-**	**2,535.12**	**1,267.60**	**1,267.58**	**-**
16							

	N	O	P	Q	R	S	T
1							
2							
3	**Total Jun 18**	**Total Jul 18**	**Total Aug 18**	**Total Sep 18**	**Total Oct 18**	**Total Nov 18**	**Total Dec 18**
4							
5							
6							
7							
8							
9							
10							
11							
12							
13	-	-	-	-	-	-	-
14							
15	-	-	-	-	-	-	-
16							

	U
1	
2	
3	**Funds Available**
4	(151,924)
5	(56,517)
6	141,860
7	(5,844)
8	(29,534)
9	(90,710)
10	(89,792)
11	24,823
12	(391,457)
13	**(649,094)**
14	(360,183)
15	**(1,009,277)**
16	

Totals after Rebudget		
	Core	399,286
	Ebola	631,888
	GVP	-
		1,031,174

REBUDGET OF CARRYOVER FUNDS FROM CORE TO EBOLA

Metabiota PREDICT-2 Year 4 Budget Summary as of 9/30/2018

*all formulas, do not manually enter

Total Costs	Year 3 Carryover	Y4 Budgeted	Expended (includes lingering spending for transition countries)	Available to Spend	Carryover balance after rebudget
Salaries	(245,906)	1,541,809	1,196,084	99,779	(9,89*)
Fringe	(91,501)	573,553	444,936	37,117	(3,682)
Equipment	491,066	111,096	41,897	560,265	504,842
Domestic Travel	145,961	162,674	68,302	240,333	225,533
Foreign Travel	(326,465)	192,332	131,021	(267,154)	(124,320)
Services	1,499,398	570,937	469,092	1,601,243	829,097
Diagnostics	(131,679)	339,713	298,153	(90,118)	(34,097)
Supplies	66,267	59,849	105,702	42,405	33,041
Other	(722,267)	216,416	300,236	(806,107)	(93,151)
Total Direct Costs	704,794	3,768,379	3,355,402	1,417,762	1,026,366
Indirect	(504,106)	1,544,575	1,277,055	(389,586)	4,808
Total Costs	90,686	5,312,948	4,332,457	1,031,174	1,031,174

Global (Ebola) Year 4	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	123,831	395,159	321,135	197,854	(197,854)	-
Fringe	46,045	146,999	119,462	73,602	(73,602)	-
Equipment	-	-	-	-	-	-
Domestic Travel	(1,447)	-	1,331	(2,778)	2,778	-
Foreign Travel	(75,893)	36,082	22,196	(62,028)	62,028	-
Services	136,356	78,174	80,412	134,119	(134,119)	-
Diagnostics	-	-	-	-	-	-
Supplies	(1,793)	-	617	(2,409)	2,409	-
Other	(54,220)	37,219	38,804	(56,805)	16,805	-
Total Direct Costs	172,909	693,632	583,957	281,495	(281,495)	-
Indirect	(21,423)	311,463	251,970	38,071	(38,071)	-
Total Global (Ebola)	**151,477**	**1,005,675**	**835,967**	**319,565**	**(319,565)**	**-**

Global (Core) Year 4	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	57,755	226,969	205,306	79,064	(79,064)	-
Fringe	21,485	84,321	76,392	29,413	(25,413)	-
Equipment	-	-	-	-	-	-
Domestic Travel	(850)	-	782	(1,632)	1,632	-
Foreign Travel	(38,277)	24,841	13,036	(26,471)	26,471	-
Services	39,693	45,811	47,226	38,378	(38,378)	-
Diagnostics	-	-	-	-	-	-
Supplies	(1,053)	-	362	(1,415)	1,403	-
Other	(31,207)	21,859	23,412	(32,760)	19,121	(6,751)
Total Direct Costs	47,547	403,801	366,506	84,582	(97,831)	(26,751)
Indirect	(15,448)	181,157	158,785	6,924	5,449	12,373
Total Global (Core)	**32,099**	**584,758**	**525,291**	**91,506**	**(92,182)**	**39,123**

Global (GVP) Year 4	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	(2,074)	54,209	32,807	19,329	(19,329)	-
Fringe	(771)	20,168	12,204	7,190	(7,190)	-
Equipment	-	-	-	-	-	-
Domestic Travel	-	-	329	(329)	329	-
Foreign Travel	7,007	26,809	7,552	19,506	(19,506)	-
Services	-	-	-	-	-	-
Diagnostics	-	-	-	-	-	-
Supplies	-	-	-	-	-	-
Other	-	-	-	-	-	-

Total Direct Costs	4,162	94,375	52,841	45,696	(45,696)	-
Indirect	1,956	44,356	24,835	21,477	(21,477)	-
Total Global (GVP)	**6,118**	**138,731**	**77,676**	**67,173**	**(67,173)**	**-**

Admin Mgt (Ebola) Year 4	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Carryover balance after rebudget
Salaries	(41,219)	22,204	5,407	(24,422)	(24,422)
Fringe	(15,333)	8,260	2,011	(9,060)	(9,060)
Equipment	-	-	-	-	-
Domestic Travel	18,812	2,394	3,408	17,798	17,798
Foreign Travel	-	-	(216)	216	216
Services	24,418	-	-	24,418	24,418
Diagnostics	-	-	-	-	-
Supplies	13,197	6,426	3,484	16,139	16,139
Other	9,001	-	813	8,789	8,789
Total Direct Costs	9,477	39,283	14,907	33,854	33,854
Indirect	(7,022)	16,463	7,006	4,435	4,435
Total Admin Mgt (Ebola)	**2,456**	**57,746**	**21,913**	**38,289**	**38,289**

Admin Mgt (Core) Year 4	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Carryover balance after rebudget
Salaries	(24,207)	13,040	3,176	(14,342)	(14,342)
Fringe	(9,005)	4,851	1,181	(5,335)	(5,335)
Equipment	-	-	-	-	-
Domestic Travel	11,048	1,406	2,001	10,453	10,453
Foreign Travel	-	-	(127)	127	127
Services	14,341	-	-	14,341	14,341
Diagnostics	-	-	-	-	-
Supplies	7,751	3,774	2,046	9,478	9,478
Other	5,639	-	477	5,162	5,162
Total Direct Costs	5,566	23,071	8,755	19,883	19,883
Indirect	(4,124)	10,843	4,115	2,605	2,605
Total Admin Mgt (Core)	**1,443**	**33,915**	**12,870**	**22,487**	**22,487**

Admin Mgt (GVP) Year 4	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	-	-	-	-	-	-
Fringe	-	-	-	-	-	-
Equipment	-	-	-	-	-	-
Domestic Travel	3,469	10,000	1,040	12,429	(12,429)	-
Foreign Travel	-	-	1,532	(1,532)	1,532	-
Services	-	-	-	-	-	-
Diagnostics	-	-	-	-	-	-
Supplies	-	-	-	-	-	-
Other	-	-	-	-	-	-
Total Direct Costs	3,469	10,000	2,572	10,897	(10,897)	-
Indirect	1,630	4,708	1,209	5,122	(5,122)	-
Total Admin Mgt (GVP)	**5,100**	**14,708**	**3,780**	**16,019**	**(16,019)**	**-**

Cameroon Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Carryover balance after rebudget
Salaries	(30,736)	264,468	226,921	6,810	6,810
Fringe	(18,874)	105,822	84,415	2,533	2,533
Equipment	7,773	61,548	13,767	55,555	55,555
Domestic Travel	62,901	86,826	44,262	105,465	105,465
Foreign Travel	(46,504)	37,459	4,649	(15,695)	(15,695)
Services	206,604	256,566	148,848	316,322	316,322
Diagnostics	(59,486)	115,291	207,046	(151,241)	(151,241)
Supplies	8,224	26,945	60,268	(25,099)	(25,099)
Other	(75,253)	31,865	63,492	(106,880)	(106,880)
Total Direct Costs	34,648	1,006,790	853,668	187,770	187,770
Indirect	(87,584)	341,229	336,545	(82,900)	(82,900)
Total Cameroon Year 4	**(52,936)**	**1,348,019**	**1,190,213**	**104,890**	**104,890**

DRC Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Carryover balance after rebudget
Salaries	(100,940)	377,108	230,614	(9,446)	(9,446)
Fringe	(58,010)	140,284	85,788	(3,514)	(3,514)
Equipment	48,429	34,048	13,556	68,921	68,921
Domestic Travel	5,835	40,228	10,124	35,740	35,740
Foreign Travel	(56,853)	43,262	23,960	(65,351)	(65,351)
Services	323,586	72,824	43,449	352,962	352,962
Diagnostics	51,570	157,204	58,897	149,877	149,877
Supplies	19,802	20,295	12,526	27,571	27,571
Other	(96,502)	76,896	56,078	(85,684)	(85,684)
Total Direct Costs	**33,919**	**962,143**	**544,990**	**471,072**	**471,072**
Indirect	(163,040)	425,820	244,943	17,837	17,837
Total DRC Year 4	**(109,121)**	**1,387,763**	**789,932**	**488,709**	**488,709**

Lao PDR Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	(16,700)	168,954	140,080	12,175	19,329	31,504
Fringe	(6,213)	62,851	52,110	4,529	7,190	11,719
Equipment	(20,556)	15,506	14,575	(19,633)	-	(19,633)
Domestic Travel	27,086	21,829	4,930	43,976	12,593	56,676
Foreign Travel	(45,560)	30,708	48,739	(61,591)	17,974	(43,617)
Services	173,918	117,461	71,322	220,054	-	220,054
Diagnostics	(67,742)	67,218	32,209	(32,733)	-	(32,733)
Supplies	30,064	2,400	27,513	4,951	-	4,951
Other	36,277	48,593	26,145	58,715	-	58,721
Total Direct Costs	**110,571**	**535,495**	**415,623**	**330,443**	**56,094**	**287,237**
Indirect	(17,697)	206,743	165,206	23,840	26,598	50,439
Total Lao PDR Year 4	**92,875**	**742,238**	**580,829**	**354,284**	**83,192**	**337,476**

FORMER METABOTA COUNTRIES (NO Y4 BUDGET)	Total Core	Total Gheda	TOTAL
	833,677	(833,720)	(78,843)

China Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	-	-	-	-	-	-
Fringe	-	-	-	-	-	-
Equipment	-	-	-	-	-	-
Domestic Travel	12,374	-	-	12,374	(12,374)	-
Foreign Travel	(23,190)	-	-	(23,190)	23,190	-
Services	165,824	-	-	165,824	(165,824)	-
Diagnostics	-	-	-	-	-	-
Supplies	4,876	-	-	4,876	(4,876)	-
Other	74,569	-	-	74,569	(74,569)	-
Total Direct Costs	**234,554**	**-**	**-**	**234,554**	**(234,554)**	**-**
Indirect	25,084	-	-	25,084	(25,084)	-
Total China Year 4	**259,637**	**-**	**-**	**259,637**	**(259,637)**	**-**

CDI Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	42,464	-	-	42,464	(42,464)	-
Fringe	15,797	-	-	15,797	(15,797)	-
Equipment	177,986	-	-	177,986	(177,986)	-
Domestic Travel	29,611	-	-	29,611	(29,611)	-
Foreign Travel	(17,411)	-	-	(17,411)	17,411	-
Services	61,624	-	34,145	27,479	(27,479)	-
Diagnostics	(7,690)	-	-	(7,690)	7,690	-
Supplies	36,407	-	-	36,407	(36,407)	-
Other	(86,156)	-	-	(86,156)	86,156	-
Total Direct Costs	**252,633**	**-**	**34,145**	**218,488**	**(218,488)**	**-**
Indirect	26,913	-	6,773	20,140	(20,140)	-
Total CDI Year 4	**279,546**	**-**	**40,918**	**238,628**	**(238,628)**	**-**

Guinea Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	(23,193)	-	15,909	(39,012)	39,012	-
Fringe	(8,594)	-	5,918	(14,513)	14,513	-
Equipment	(30,830)	-	-	(30,830)	30,830	-
Domestic Travel	(15,432)	-	229	(15,661)	15,661	-
Foreign Travel	(30,511)	-	9,040	(39,551)	39,551	-
Services	94,928	-	3,369	91,557	(91,557)	-
Diagnostics	32,514	-	-	32,514	(32,514)	-
Supplies	(96,362)	-	-	(96,362)	96,362	-
Other	(134,666)	-	10,557	(145,223)	145,223	-
Total Direct Costs	**(212,076)**	**-**	**45,023**	**(257,101)**	**257,101**	**-**
Indirect	(109,123)	-	21,161	(130,283)	130,283	-
Total Guinea Year 4	**(321,200)**	**-**	**66,183**	**(387,385)**	**387,385**	**-**

Indonesia Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	-	-	-	-	-	-
Fringe	-	-	-	-	-	-
Equipment	-	-	-	-	-	-
Domestic Travel	-	-	-	-	-	-
Foreign Travel	29,576	-	-	29,576	(29,576)	-
Services	278,977	-	40,320	238,656	(238,656)	-
Diagnostics	-	-	-	-	-	-
Supplies	-	-	-	-	-	-
Other	958	-	-	958	(958)	-
Total Direct Costs	**309,510**	**-**	**40,320**	**269,190**	**(269,190)**	**-**
Indirect	14,352	-	11,750	2,602	(2,602)	-
Total Indonesia Year 4	**323,865**	**-**	**52,070**	**271,795**	**(271,795)**	**-**

RoC Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	(18,775)	-	-	(18,775)	18,775	-
Fringe	(6,964)	-	-	(6,964)	6,964	-
Equipment	166,406	-	-	166,406	(166,406)	-
Domestic Travel	(1,403)	-	(133)	(1,270)	1,270	-
Foreign Travel	25,689	-	(84)	25,773	(25,773)	-
Services	67,741	-	-	67,741	(67,741)	-
Diagnostics	8,947	-	-	8,947	(8,947)	-
Supplies	43,361	-	(104)	43,465	(43,465)	-
Other	(51,996)	-	(2,726)	(49,272)	49,272	-
Total Direct Costs	**232,986**	**-**	**(3,047)**	**236,033**	**(236,033)**	**-**
Indirect	17,390	-	(1,432)	18,822	(18,822)	-
Total RoC Year 4	**250,374**	**-**	**(4,479)**	**254,853**	**(254,853)**	**-**

Sierra Leone Year 4 Budget	Year 3 Carryover	Y4 Budgeted	Expended	Available to Spend	Rebudget	Carryover balance after rebudget
Salaries	(137,260)	-	14,660	(151,924)	151,924	-
Fringe	(51,063)	-	5,454	(56,517)	56,517	-
Equipment	141,860	-	-	141,860	(141,860)	-
Domestic Travel	(5,844)	-	-	(5,844)	5,844	-
Foreign Travel	(26,740)	-	2,794	(29,534)	29,534	-
Services	(90,710)	-	-	(90,710)	90,710	-
Diagnostics	(89,792)	-	-	(89,792)	89,792	-
Supplies	23,811	-	(1,012)	24,823	(24,823)	-
Other	(319,331)	-	72,126	(391,457)	391,457	-
Total Direct Costs	**(555,072)**	**-**	**94,022**	**(649,094)**	**649,094**	**-**
Indirect	(315,992)	-	44,190	(360,183)	360,183	-
Total Sierra Leone Year 4	**(871,064)**	**-**	**138,212**	**(1,009,277)**	**1,009,277**	**-**

From:	William B. Karesh <karesh@ecohealthalliance.org>
To:	Beth Edison <bedison@metabiota.com>;David Wolking <djwolking@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
CC:	Amanda Andre <amanda.andre@ecohealthalliance.org>;Catherine Machalaba <cmachalaba@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>
Sent:	4/26/2019 7:53:08 PM
Subject:	Regrets for Vancouver

Hi Folks,

Unfortunately, I'm going to have to miss our Vancouver meeting but Catherine will be there to represent the efforts.

I had been hoping to avoid needing to be at the GHSA Steering Group quarterly meeting on Tuesday and Wednesday, but as last head of delegation and lead on a task force, they want me to be there to help keep things moving forward.

I'll miss seeing everyone.

BK

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Executive Vice President for Health and Policy

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President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From:	Andrew Clements <aclements@usaid.gov>
To:	<undisclosed-recipients:>
BCC:	jkmazet@ucdavis.edu
Sent:	5/28/2019 11:28:33 AM
Subject:	May 28, 2019 Emerging Pandemic Threat update

Summary: 22 poultry outbreaks and 667 human infections with 10 pathogens (various avian influenza viruses, Ebola, Lassa, MERS-CoV, and monkey pox) were reported by 10 countries between April 28 and May 27, 2019. These outbreaks/infections occurred between March 2017 and May 2019.

Specific pathogens and countries affected:

H5N1/Asia High Pathogenicity Avian Influenza (HPAI) – 2 new poultry outbreaks and 1 human infection (Nepal, Vietnam) [First-ever human infection in Nepal]

A total of 23,852 bird outbreaks (more than 250 million birds affected) and 881 human infections (52% average case fatality rate) have been reported by 67 countries since 1997.

Viral pedigree: Influenza A sub-type H5N1/Asia HPAI was first detected in 1996 and has since donated genetic segments to many new influenza A HPAI viruses (including several below). Influenza A viruses have caused four pandemics since 1918.

H5N2/Asia HPAI – 6 new poultry outbreaks (China)

A total of 913 bird outbreaks (7.2 million birds affected) have been reported by 1 country since virus first detected in 2012; no human infections reported to date.

Viral pedigree: Influenza A sub-type H5N2/Asia HPAI is related to H5N1/Asia HPAI (see above).

H5N2 Low Pathogenicity Avian Influenza (LPAI) – 6 new poultry outbreaks (China)

A total of 265 bird events (4.1 million birds affected) have been reported by 17 countries since 2006; no human infections reported to date.

Viral pedigree: no information available.

H7N3 HPAI – 7 new poultry outbreaks (Mexico)

A total of 159 bird outbreaks (more than 23.4 million birds affected) have been reported by 1 country between 2012 and 2019. 5 human infections (0% average case fatality rate) have been reported by 3 countries between 2004 and 2012.

H7N7 LPAI – 1 new poultry outbreak (China)

A total of 61 bird events (627,545 birds affected) have been reported by 9 countries since 2009; no human infections reported to date.

Viral pedigree: no information available.

H9N2 LPAI – 1 new human infection (Oman)

A total of 51 human infections (2% average case fatality rate) have been reported by 4 countries since 1999.

Viral pedigree: No information available on this influenza A sub-type H9N2 LPAI virus.

Ebola/Zaire – 499 new confirmed and probable human cases (DR Congo) [This outbreak is the largest ever reported in DR Congo (now exceeding 1,800 cases) and the 2nd largest Ebola outbreak ever reported in any country/region. The current number of deaths (1,241) is greater than the individual totals for avian influenza (1997-2019), Lassa (2000-2019), Marburg (1967-2019), MERS-CoV (2012-2019), Monkeypox (1970-2019), Nipah (1998-2019), and SARS (2002-2003)]

At least 33,009^ human infections (43% average case fatality rate) with all Ebola viruses have been reported by 18 countries between 1976 and 2019. *^ Total includes confirmed, probable, and suspected cases.*

Viral pedigree: the Central African Ebola/Zaire virus has caused 16 outbreaks with 3,382 human infections (72%

average case fatality rate) in 4 countries since first being detected in 1976.

Lassa – 32 new confirmed and probable human cases (Liberia, Nigeria)

At least 3,738^ human infections (22% average case fatality rate) have been reported by 16 countries since 2000. *^ Total includes confirmed, probable, and suspected cases.*

MERS-CoV – 11 new confirmed human cases (Saudi Arabia) [There have been more MERS-CoV cases in the first 4 months of 2019 than in all of 2018.]

A total of 36 camel outbreaks and at least 2,439 confirmed human infections (35% average case fatality rate) have been reported by 27 countries since virus first detected in 2012.

Viral pedigree: MERS-CoV is in the beta-coronavirus family which also includes the SARS virus which caused a pandemic in 2003 with more than 8,000 human infections (10% average case fatality rate) in 27 countries.

Monkeypox – 123 new confirmed human cases (Nigeria, Singapore*) [First-ever reported case in Singapore]

At least 4,003^ human infections (2% average case fatality rate) have been reported by 15 countries since 1970. *^ Total includes confirmed, probable, and suspected cases. * Imported from Nigeria.*

Viral pedigree: Monkeypox is in the orthopox viral family which also includes the smallpox virus that was a worldwide scourge before it was eradicated in 1980.

à Next update on/about June 24, 2019

Data sources:

http://www.who.int/csr/don/en/
http://www.who.int/influenza/human_animal_interface/en/
http://www.afro.who.int/en/clusters-a-programmes/whe/outbreaks-and-other-emergencies-updates.html
http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/WI
http://empres-i.fao.org/eipws3g/
https://www.cdc.gov/flu/weekly/index.htm
https://www.moh.gov.sa/en/CCC/events/national/Pages/2019.aspx
http://newsletters.afro.who.int/outbreak-dashboards/p36fck/gcoy1ggvybnlogp?email=true
http://www.chp.gov.hk/en/index.html
https://www.moh.gov.om/en/-/---951
https://www.dhakatribune.com/health/2019/03/03/death-of-5-in-thakurgaon-linked-to-nipah-virus

About the USAID Emerging Pandemic Threats update: first started in 2005 with a focus on H5N1 avian influenza, this monthly update was expanded in 2012 to include other zoonotic pathogens with pandemic potential. The update brings together information on both human and animal infectious disease outbreaks involving viruses having known or potential ability to infect and spread directly from human to human without vectors such as insects, water, or food. The current mailing list includes readers from USAID (Washington and missions in 22 countries in Africa, Asia, and the Middle East), other US Government Departments/Agencies (including HHS, CDC, NIH, USDA, Department of Defense, Department of Interior, State Department), international organizations (FAO, IFRC, OIE,WHO), universities, and NGOs.

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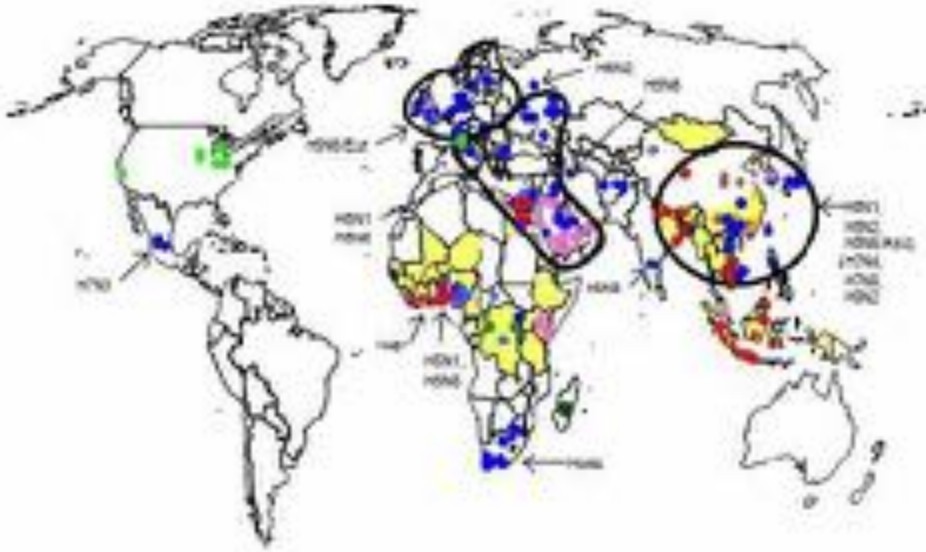
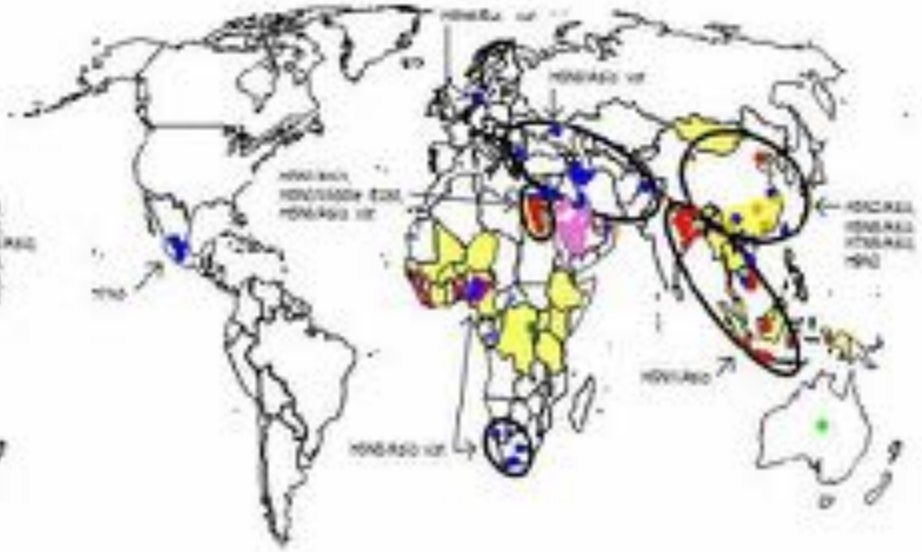
For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

Detection of Specific Pathogens with Potential to Infect and Directly Spread among Humans^

Nov 2017-Oct 2018



Nov 2018-Oct 2019



- = H5N1/Asian lineage HPAI* (poultry, wild birds, humans)
- = H7N9 LPAI/Asia** (poultry, wild birds, or humans)
- = other HPAI or LPAI (humans)
- = other HPAI including H5N1/Eur lineage, H5N1/NA lineage (poultry, wild birds)
- = H1N1v, H1N2v, and H3N2v swine influenza (humans)
- = Middle East Respiratory Syndrome-Coronavirus (humans or animals)
- = Ebola (humans)
- = Marburg (humans)
- = Lassa (humans)
- = Nipah (humans)
- = monkeypox (primates, humans)
- = plague (humans)

Sources = OIE, WHO, CDC, Ministry of Agriculture/FAO (Egypt, Indonesia), and IEDCR (Bangladesh) reports between 11/1/17 and 5/27/19. ^ While these reports reflect known infections with these viruses, there may be additional viral circulation in these and other countries that is not detected due to limitations in surveillance and/or detection. All of these viruses are from viral families with at least one member that is capable of infecting people and spreading directly from person to person without using food, water or insects as vectors. *Highly-pathogenic avian influenza. ** Low-pathogenicity avian influenza. ▭ = countries (including eastern/southeastern China, northeastern India, and most of Indonesia) using USAID avian influenza, Ebola, or other emerging pandemic threats funding between FY2017 and FY2019 for prevention, detection, and response. ★ = location where a new virus first detected.

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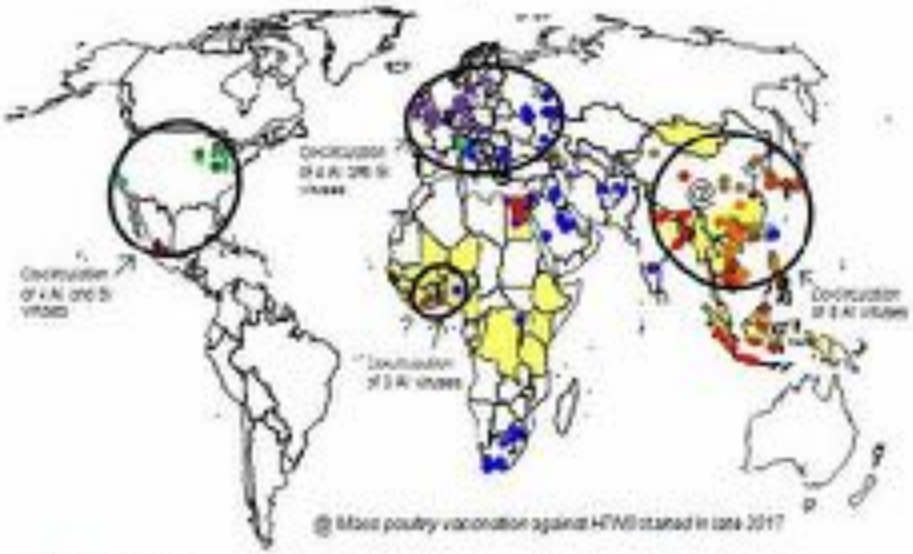
Global Health/Emerging Threats Division

UCDUSR0001467

Recent Detection of Avian and Swine Influenza Viruses in Animals and Humans^

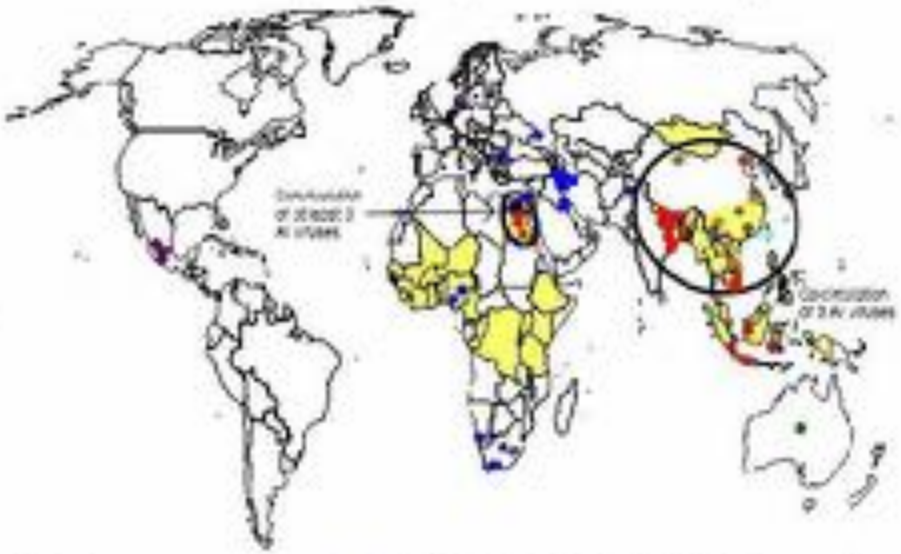
Nov 2017-Oct 2018

→ *737 bird outbreaks and 35 human infections with 16 AI/SI sub-types/variants (9 of which are zoonotic)*



Nov 2018-Oct 2019

→ *180 bird outbreaks and 5 human infections with 8 AI/SI sub-types/variants (4 of which are zoonotic)*



- = H5N1/Asia HPAI* (P, WB, H)
- = H5N1/Europe HPAI (P, WB, H)
- = H5N2/Asia HPAI (P, WB)
- = H5N2/Eurasia HPAI (P)
- = H5N2/Middle East HPAI (P)
- = H5N5 HPAI (P, WB)
- = H5N6/Asia HPAI (P, WB, H)
- = H5N6/Asia HPAI variant (P, WB)
- = H5N6/Europe HPAI (P, WB)
- = H5N6/Europe variant HPAI (P, WB)
- = H7N2 (P, H)
- = H7N3 HPAI (P)
- = H5N8/Asia variant HPAI lineage (P, WB)
- = H7N4 LPAI** (H)
- = H7N9/Asia HPAI or LPAI (P, WB, H)
- = H7N9/N. America (P)
- = H3N2 LPAI (P, H)
- = H1N1v SI (H)
- = H1N2v SI (H)
- = H3N2v SI (H)
- ○ = first-ever detector of new virus

Sources = OIE, WHO, CDC, and Ministry of Agriculture/FAO (Egypt, Indonesia) reports between 11/1/17 and 5/27/19. ^ While these reports reflect known infections with animal influenza viruses, there may be additional viral circulation in these and other countries that is not detected due to limitations in surveillance and/or detection. * Highly-pathogenic avian influenza (in chickens). ** Low-pathogenicity avian influenza (in chickens). ☐ = countries (including eastern/southeastern China, northeastern India, and most of Indonesia) using USAID avian influenza, Ebola, or other emerging pandemic threats funding between FY2017 and FY2019 for prevention, detection, and response. P = poultry; WB = wild birds; H = humans; F = feline.

USAID
FROM THE AMERICAN PEOPLE
Global Health/Emerging Threats Division

UCDUSR0001468

From: Andrew Clements <aclements@usaid.gov>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;predictmgt@usaid.gov <predictmgt@usaid.gov>;predict Sympa List <predict@ucdavis.edu>
Sent: 5/29/2019 6:38:34 PM
Subject: Re: [predict] Fwd: VAT Exemption for USAID/Egypt for PREDICT-2

Mission says they hope to have an answer the second week of June.

For now keep doing what you're doing until told otherwise. If your waiver expired then stop doing what it allowed you to do until told otherwise.

For the millionth time (and probably not the last), my apologies for our inept agency.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

From: Jon Epstein <epstein@ecohealthalliance.org>
To: Andrew Clements <AClements@usaid.gov>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Dr VAN KERKHOVE, Maria <vankerkhovem@who.int>
Sent: 6/3/2019 5:31:19 PM
Subject: Re: Nipah Virus Case Yet To Be Confirmed, Says Kerala Minister, 52 Under Surveillance

Thanks, I saw that and am following the news. If it turns out to be a confirmed case, hopefully there will be some information as to how he was infected.
Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
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On Mon, Jun 3, 2019, 11:59 AM Andrew Clements <aclements@usaid.gov> wrote:
FYI

https://www.ndtv.com/india-news/nipah-virus-case-yet-to-be-confirmed-says-kerala-minister-52-under-surveillance-2047246

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Senior Scientific Advisor
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From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Andrew Clements <aclements@usaid.gov>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;David J Wolking <djwolk@gmail.com>
Sent: 6/21/2019 7:06:31 PM
Subject: RE: Update

Excellent! Thanks for keeping us posted, Andrew. Fingers and toes still crossed!

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Andrew Clements
Sent: Friday, June 21, 2019 12:01 PM
To: Elizabeth Leasure
Cc: Jonna Mazet ; David J Wolking
Subject: Re: Update

It's now with OAA so getting closer with more than two hours to go

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
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On Jun 21, 2019, at 1:07 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Fingers-crossed! Toes, too!

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Andrew Clements <aclements@usaid.gov>
Sent: Friday, June 21, 2019 10:03 AM
To: Jonna Mazet <jkmazet@ucdavis.edu>; David J Wolking <djwolk@gmail.com>; Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Subject: Update

Things moving on the funding front. May be possible for it to be completed by COB today if the stars are aligned and everyone's fingers are crossed.

Will keep you posted.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
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Mobile phone: 1-571-345-4253

Email: acfements@usaid.gov

From: William B. Karesh <karesh@ecohealthalliance.org>
To: David Wolking <djwolking@ucdavis.edu>
CC: Matthew LeBreton <mlebreton@mosaic.om>;Peter Daszak <daszak@ecohealthalliance.org>;Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Kirsten Gilardi <kvgilardi@ucdavis.edu>;Sarah Olson <solson@wcs.org>;Brian Bird <bhbird@ucdavis.edu>;Tierra Smiley Evans <tsmevans@ucdavis.edu>;Terra Kelly <trkelly@ucdavis.edu>;Jon Epstein <epstein@ecohealthalliance.org>;sja2127@cumc.columbia.edu <sja2127@cumc.columbia.edu>;David Molver <dmolver@metabiota.com>;Christian Lange <clange@metabiota.com>;Catherine Machalaba <machalaba@ecohealthalliance.org>;Patrick Dawson <dawson@ecohealthalliance.org>;Suzan Murray <MurrayS@si.edu>;Chris Johnson <ckjohnson@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;Kevin Olival <olival@ecohealthalliance.org>;Marcela Uhart <muhart@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 6/28/2019 4:12:54 PM
Subject: Re: PREDICT Pubs and USAID Open Data Requirements

Hi David and Marcy,

Was there any decisions made on the ones listed as "debatable" or is that up to us?

BK

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Executive Vice President for Health and Policy

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www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On Jun 28, 2019, at 11:13 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi there,

Following up on our previous request, we are now writing to ask that you **complete the task of making your data from papers published during P2 publicly available within 30 days. For ease of tracking, we have decided to set the deadline for July 31, 2019.**

As a reminder, attached is an inventory of all publications during the applicable Period of Performance (P2 data or P1 and P2 data for pubs happening since updating the Uniform Guidance, October 2015 and beyond), categorized based on whether they have raw data publicly available (see the attached workbook).

We acknowledge that some of you have contacted us since our previous email noting specific details of your papers on the inventory (e.g. date of publication prior to October 2015, project funded by sources other than PREDICT, etc). We hope your questions were clarified, and please disregard your this message if you have already complied or this request does not apply to you.

For all others, we ask that you please submit your data to a public data repository such as Dryad https://datadryad.org/ (a platform that emerged as a priority on EB), Zenodo https://zenodo.org/ or USAID's own platform, the Data Development Library (DDL). If you don't have a strong preference for a platform, we ask that you default to Dryad.

Once you have uploaded the data, we ask that you send us (David and Marcy) the DOI and link, so we can follow up and track this in our publications database and for reporting to USAID.

Keep in mind that for ALL future P2 publications, your raw data should be made public by the time of public release (e.g., publication). Please be prepared to act on this important new requirement going forward.

Thanks and please send us your data upload confirmation in an email with DOI and link by July 31, 2019.

Best,

David and Marcy

On Wed, May 8, 2019 at 1:53 PM David J Wolking <djwolking@ucdavis.edu> wrote:

Hi there,

As many of you are aware from our multiple PREDICT Executive Board discussions, PREDICT is required to make our data publicly available within 30 days of public release (e.g., publication). To aid in the process, Marcy put a ton of energy into compiling an inventory of all publications during the applicable Period of Performance (P2 data or P1 and P2 data for pubs happening since updating the Uniform Guidance, October 2015 and beyond), and then categorized publications in terms of them having raw data publicly available (see attached workbook).

If you are being contacted, one or more of your papers doesn't meet the criteria for publicly available.

To reach compliance, our Executive Board came to the consensus that data can be submitted to a public data repository such as Dryad https://datadryad.org/ (a platform that emerged as a priority on EB), Zenodo https://zenodo.org/ or USAID's own platform, the Data Development Library (DDL). If you don't have a strong preference for a platform, we ask that you default to Dryad.

Please make plans to communicate with any relevant co-authors and be ready to submit your data, as you will receive official notice regarding compliance in the coming days.

Thanks!

David and Marcy

Marcela Uhart, Med. Vet.

Director Latin America Program

One Health Institute

School of Veterinary Medicine

University of California, Davis

Address: Los Alerces 3376, Puerto Madryn

Chubut (9120), Argentina

Phone: +54 9280 4696332

Email: muhart@ucdavis.edu

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>;Elizabeth Leasure <eaileasure@UCDAVIS.EDU>
CC: Jon Epstein <epstein@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>;Emily Hagan <hagan@ecohealthalliance.org>
Sent: 8/23/2019 7:37:53 PM
Subject: RE: Impact of potential budget reduction, Bangladesh, Indonesia, India

Sorry – forgot to copy you Liz…

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: Peter Daszak
Sent: Friday, August 23, 2019 3:07 PM
To: Jonna Mazet
Cc: Jon Epstein; Evelyn Luciano; Emily Hagan
Subject: Impact of potential budget reduction, Bangladesh, Indonesia, India
Importance: High

Hi Jonna – attached are some initial thoughts on how this would impact our work. Here they are in bullet form in case you're working from a phone…

Impacts of reduced funding for following countries: 23rd August 2019

India

- Complete final testing results would not be made available.
- We would be unable to conduct final reporting with recommendations to government and stakeholders.

Indonesia

- Community engagement and final reporting to government and stakeholders would have to be halted.
- The Country Coordinator and in-country teams from Institut Pertanian Bogor-Primate Research Center and Eijkman Institute would not be able to attend the final PREDICT All-country Meeting in Indonesia planned for September. This would be a huge loss because they are the country host of the closeout meeting.

Bangladesh

- Unable to complete uploading of data into EIDITH and meeting PREDICT requirement for data

sharing and for final round of interpretation for reporting to government partners.
- Unable to meet PREDICT IRB requirement of results sharing with communities.
- Data analysis for PREDICT risk assessments and economic assessment during final meetings with government partners and stakeholders would not be disseminated.
- Unable to attend the PREDICT All-country Meeting in Bali, Indonesia for the culmination of 10 years of PREDICT.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

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UCDUSR0001478

From: Dennis Carroll <dcarroll008@gmail.com>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Cara Chrisman <cchrisman@usaid.gov>;Eddy Rubin <erubin@metabiota.com>;Eri Togami <etogami@ucdavis.edu>;Nathan Wolfe <nwolfe@metabiota.com>;Peter Daszak <daszak@ecohealthalliance.org>;Samtha Maher <maher@ecohealthalliance.org>
Sent: 12/19/2019 3:57:21 PM
Subject: Re: 100&Change Top-Rated Proposals

Congratulations!!! Well done. Great to see the process is truly open to "bold" thinking ☺

d

On Thu, Dec 19, 2019 at 11:25 AM Jonna Mazet <jkmazet@ucdavis.edu> wrote:
We made it up another wrung of the ladder & looks like they will include us in fundraising activities, irrespective of our winning the final award or not. Keep positive thoughts!
Happy Holidays,
Jonna

---------- Forwarded message ---------
From: **MacArthur Foundation** <communications@email-macfound.org>
Date: Tue, Dec 17, 2019 at 12:51 PM
Subject: 100&Change Top-Rated Proposals
To: <jkmazet@ucdavis.edu>

View Online »



Dear Applicant,

As one of the highest-ranked applicants to *100&Change*, your proposal is eligible* to be included in the Bold Solutions Network, an online repository of the top-rated proposals from the competition. Lever for Change, an affiliate of the MacArthur Foundation, will showcase top-scoring proposals that emerge from *100&Change* and other competitions it manages to connect applicants to philanthropists interested in funding social change.

Part of Lever for Change's inspiration for launching the Bold Solutions Network is the additional $419 million in funding that has been unlocked to date to support bold solutions by applicants in the inaugural *100&Change* competition. Organizations included in the Bold Solutions Network will also have access to valuable learning programs and will be eligible for technical support opportunities in the coming months.

In order to be featured in the Bold Solutions Network, which will launch in February 2020, eligible organizations are required to create and submit a two-page overview of the project outlined in your proposal. Lever for Change will host a webinar on creating these factsheets on **January 8th at 9:30 a.m. CST**. The webinar will provide you with all necessary guidelines, deadlines, and best practices for successfully profiling your work.

Join us for the webinar.
The Best Way to Influence Potential Donors? Fact-Filled Factsheets

— Register Now —

We look forward to helping you generate positive exposure and attention for your ideas.

Best,
100&Change and Lever for Change Teams

"Your proposal is undergoing a domain specific technical review from an expert in your field. Selected proposals will advance to the next round of the competition and be featured in the Bold Solutions Network.



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--
Dr Dennis Carroll
Global Virome Project, Core Team
Senior Fellow, Scowcroft Institute of International Affairs at the Bush School of Government and Public Service, Texas A&M University
Counselor and Advisor to the Faculty of Tropical Medicine at Mahidol University

mobile: 202-999-6144
email: dcarroll808@gmail.com

From: Nathan Wolfe <nwolfe@metabiota.com>
To: Dennis Carroll <dcarroll008@gmail.com>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Cara Chrisman <cchrisman@usaid.gov>;Eddy Rubin <erubin@metabiota.com>;Eri Togami <etogami@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Samtha Maher <maher@ecohealthalliance.org>
Sent: 12/19/2019 6:22:05 PM
Subject: Re: 100&Change Top-Rated Proposals

Wonderful news. And very hard to get this far in these kinds of competitions. well done.

On Thu, Dec 19, 2019 at 8:57 AM Dennis Carroll <dcarroll008@gmail.com> wrote:
Congratulations!!! Well done. Great to see the process is truly open to "bold" thinking

d

On Thu, Dec 19, 2019 at 11:25 AM Jonna Mazet <jkmazet@ucdavis.edu> wrote:
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--
Dr Dennis Carroll
Global Virome Project, Core Team
Senior Fellow, Scowcroft Institute of International Affairs at the Bush School of Government and Public Service, Texas A&M University
Counselor and Advisor to the Faculty of Tropical Medicine at Mahidol University

mobile: 202-999-6144
email: dcarroll808@gmail.com

From:	Brandon Minto <bjminto@UCDAVIS.EDU>
To:	Karl M Engelbach <kmengelbach@ucdavis.edu>
CC:	Mary Radford <maradford@ucdavis.edu>;John Pascoe <jrpascoe@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>;Matthew Blake <mblake@ucdavis.edu>;Michael Dale Lairmore <mdlairmore@ucdavis.edu>;Mabel Salon <masalon@ucdavis.edu>;Lori Hubbard <lahubbard@ucdavis.edu>;Lisa Kay Chance Berriz <lkchance@ucdavis.edu>
Sent:	2/4/2020 5:29:54 PM
Subject:	FW: Feinstein to USAID: Reinstate Pandemic Prevention Program

Good morning, Karl –

I want to flag the below for you and thank you and the Chancellor, as well as Jonna and the VetMed team, for the extremely quick turnaround on the Global Health Security letter to Senator Feinstein. She is now a leading advocate for the continuation of the USAID PREDICT zoonotic disease discovery surveillance and forecasting program; and as a senior member of Senate Appropriations that is impactful. PREDICT is an incredibly important program for Global Health Security and has brought over $200 million to UC Davis over the last ten years.

Thanks again, all, for the great work!

Sincerely,

Brandon

Brandon Minto
Director, Federal Government Relations
University of California, Davis
Office of the Chancellor
Government and Community Relations
202 Cousteau Pl. Ste. 240 | Davis, CA 95618

Phone: (530) 754-2246
Fax: (530) 754-2026
Cell: (530) 750-9080

Email: bjminto@ucdavis.edu
Web: http://gcr.ucdavis.edu/

From: Fuentes, Andrew (Feinstein)
Sent: Tuesday, February 4, 2020 10:17 AM
To: Brandon Minto
Cc: Thomson, Deborah (Feinstein)
Subject: FW: Feinstein to USAID: Reinstate Pandemic Prevention Program

Hi Brandon – Quickly wanted to flag the Senator's letter on PREDICT that was sent to USAID today. We're hopeful that the program can continue.

-Andrew

Andrew Fuentes
Legislative Assistant
U.S. Senator Dianne Feinstein
331 Hart | (202) 224 - 3841
Website | Twitter | Facebook | YouTube

From: Feinstein Press <Feinstein_press@feinstein.senate.gov>

Sent: Tuesday, February 4, 2020 1:11 PM
Subject: Feinstein to USAID: Reinstate Pandemic Prevention Program

NEWS FROM DIANNE FEINSTEIN
UNITED STATES SENATOR FOR CALIFORNIA
www.feinstein.senate.gov

For Immediate Release
February 4, 2020

Contact: Anthony Rivera-Rodriguez
(202) 224-9629

Feinstein to USAID: Reinstate Pandemic Prevention Program

Washington—Senator Dianne Feinstein (D-Calif.) today called on the U.S. Agency for International Development (USAID) to reinstate the PREDICT zoonotic disease surveillance and forecasting program. PREDICT is a program that proactively searches for pathogens with the potential to cause pandemics in order to prevent their spread from animals to humans. USAID canceled the program last year.

"Since 2009, PREDICT has led to the discovery of nearly 1,000 new viruses, including coronaviruses similar to what has caused the outbreak in Wuhan, China. For example, in 2018, a new Ebola strain found in healthy bats was discovered in Sierra Leone and was the first Ebola strain to be discovered before an outbreak in humans occurred," Senator Feinstein wrote.

Feinstein continued: **"The current deadly viral outbreak and its quick appearance in the United States make clear that PREDICT's contributions to zoonotic disease surveillance and forecasting must continue. We simply cannot afford to go backwards and jeopardize the success we've seen over the last ten years."**

Full text the letter follows:

February 4, 2020

Mr. Mark Green
Administrator
United States Agency for International Development
2231 Crystal Drive
Arlington, VA 22202

Dear Administrator Green:

In light of the deeply concerning coronavirus outbreak in China, which has now led to several cases in California, I write to ask that you reverse your decision last year to shut down the U.S. Agency for International Development's (USAID) PREDICT zoonotic disease surveillance and forecasting program.

Since 2009, PREDICT has led to the discovery of nearly 1,000 new viruses, including coronaviruses similar to what has caused the outbreak in Wuhan, China. For example, in

2018, a new Ebola strain found in healthy bats was discovered in Sierra Leone and was the first Ebola strain to be discovered before an outbreak in humans occurred. Its discovery will help Sierra Leone and neighboring countries update their diagnostics to ensure they can detect all known Ebola viruses and reduce the risk of exposure.

PREDICT has even helped inform preparedness and response efforts being used to combat the current coronavirus outbreak. Specifically, research supported by PREDICT led to the discovery of several SARS-like coronaviruses related to the new virus in Wuhan, including viruses in bats that could be transmitted directly to people. This research has helped inform the scientific community about the possibility of animal-to-human interaction being a risk factor in the current outbreak. Even more, PREDICT trained and equipped public health professionals in several countries that are now supporting the diagnosis of the virus and other efforts to control outbreak.

The current deadly viral outbreak and its quick appearance in the United States make clear that PREDICT's contributions to zoonotic disease surveillance and forecasting must continue. We simply cannot afford to go backwards and jeopardize the success we've seen over the last ten years. I urge you to reinstate the PREDICT program, and I look forward to working with you on this critical issue.

Sincerely,

Dianne Feinstein
United States Senator

###

UCDJS#00001487

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Thomson, Deborah (Feinstein) <Deborah_Thomson@feinstein.senate.gov>
CC: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Sent: 2/4/2020 6:04:12 PM
Subject: Re: FW: Feinstein to USAID: Reinstate Pandemic Prevention Program

Amazing -- thank you so much!
Jonna

Jonna AK Mazet, DVM, MPVM, PhD
Professor of Epidemiology & Disease Ecology
Executive Director, One Health Institute
Director, One Health Workforce – Next Generation of USAID Emerging Threats Division
Director Emeritus, PREDICT Project of USAID Emerging Threats Division

School of Veterinary Medicine
University of California, Davis
onehealthinstitute.net

Institute for Global Health Sciences
University of California, San Francisco
https://globalhealthsciences.ucsf.edu/

For scheduling and logistical issues, please contact:
Ms. Mary Radford
maradford@ucdavis.edu
+1-530-752-3830

On Tue, Feb 4, 2020 at 10:16 AM Thomson, Deborah (Feinstein) <Deborah_Thomson@feinstein.senate.gov> wrote:

From: Feinstein Press <Feinstein_press@feinstein.senate.gov>
Sent: Tuesday, February 4, 2020 1:11 PM
Subject: Feinstein to USAID: Reinstate Pandemic Prevention Program

NEWS FROM DIANNE FEINSTEIN
UNITED STATES SENATOR FOR CALIFORNIA
www.feinstein.senate.gov

For Immediate Release — Contact: Anthony Rivera-Rodriguez

February 4, 2020 — (202) 224-9629

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Sincerely,

Dianne Feinstein

United States Senator

###

From: Candace Gibson <candaceg@uwo.ca>
To: djwolking@ucdavis.edu <djwolking@ucdavis.edu>;jkmazet@ucdavis.edu" <jkmazet@ucdavis.edu>
Sent: 7/31/2020 3:23:29 PM
Subject: Book Chapter - the Nature of Pandemics

Dear Drs. Wolking and Mazet -

First my sincere apologies for the long delay in communication and information about the status of the F&T book, The Nature of Pandemics for which you contributed a chapter. We had a number of personal and professional issues arise that have delayed the publication but the publisher is still (now more than ever due to COVID) interested in publishing it.

Second, thank you for your wonderful contribution on the description of PREDICT, its evolution and its activities. I have attached the edited version; there were few edits required and primarily the need to convert the footnotes to full references in the APA style.
We started to put these into the correct text citation and reference listing style (alphabetical, nut numbered) but realized you probably can do this much more quickly through your reference manager software. If not please let me know and we can take care of that conversion.
A reminder that the publisher is only going to be using grey-scale for printing of the photos/figures - so you may need to adjust some of the figures submitted (or point to the full color maps on a web site?).

Francis & Taylor will try to get this published before the end of the year but that now means a rapid turn-around. Could you please get revisions and any updates you feel are appropriate back to us in 3 weeks.
I'm not sure how you want to handle updates - this is currently a wonderful description of a comprehensive monitoring program that includes some excellent examples and the emphasis on One Health approaches couldn't be more timely.

Thank you both for your patience and for your excellent work.

Sincerely,

Candace Gibson, PhD, CHIM
Professor, Pathology & Laboratory Medicine
Acting Vice Dean, Basic Medical Sciences
Schulich School of Medicine & Dentistry,
Western University
London, ON
N6A 5C1

Tel: 989-909-0097

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Anthony, S.J., C.K. Johnson, D.J. Greig, S. Kramer, X. Che, H. Wells, A.L. Hicks, D.O. Joly, N.D. Wolfe, P. Daszak, W. Karesh, W.I. Lipkin, S.S. Morse, PREDICT Consortium, J.A.K. Mazet, and T. Goldstein (2017). Global patterns in coronavirus diversity. Virus Evolution 3(1):vex012. DOI: 10.1093/ve/vex012.

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The PREDICT Project: a transdisciplinary case study in partnerships for pandemic prevention

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> Go out on a limb. That's where the fruit is. - *Jimmy Carter*

First emergence

The day was relatively normal for staff at the Amani Health Centre, a few children presenting with fevers, some cases of dysentery, and the week's excitement still hovered around the big accident on the main road to the neighboring province. Thankfully the 12 individuals treated from the accident were on the mend. In fact, it was a slow day, a good time to update the clinic registry and manage some routine administrative tasks.

In the afternoon, an older woman from a nearby village, a trader at the local market, arrived with a high fever and muscle pain and was admitted. Staff provided fluids and NSAIDs (pain reliever and anti-inflammatory drugs), and the patient appeared to improve. But when the Chief Medical Officer returned the next day, he learned the woman had passed away overnight. Sickness and death were not unusual in this community, a relatively isolated rural area where livelihoods were hard earned from the land in the shadows of the nearby forest and mountains. Since the woman lived nearby, clinic staff sent a messenger to the family on bicycle with the news. When he returned, the messenger informed them that two others in the woman's household were also ill, one of them a child who was vomiting and both with fevers. Clinic staff made arrangements to bring the two to the clinic where they too received fluids and supportive care.

Meanwhile, the neighboring Safi Health Centre also began to receive unusually high volumes of febrile cases. After a long dry season, the onset of rains had been particularly intense, which had a big impact on the mosquito population that was a constant buzz in the local soundscape even in normal conditions. With mosquitoes comes malaria, and Safi staff attributed the onslaught of febrile cases to the beginning of malaria season. Plans were made to acquire more anti-malarial drugs, additional bed nets to prevent transmission from one patient to another, and another thermometer as the clinic had only one working device, a glass and mercury tube left over from the old missionary hospital.

Over the next two weeks, more than 60 patients with fevers were admitted to the clinics, and staff were rapidly overwhelmed, trying to balance outpatient units, pediatric and maternal health needs, and what was increasingly being recognized as some sort of outbreak. Reports were

shared with ministry officials, and samples were collected for testing at the national lab, but because the area was so remote, transporting the samples would take time not to mention any subsequent diagnosis and development of response plans. In short, help was not on the way, at least not when it was needed most.

Because clinic staff lacked the ability to conduct tests onsite or provide effective treatment, they shifted focus to alleviating suffering. Each clinic's lab, a small room with a single microscope used primarily to look for *Plasmodium* (the protozoa that causes malarial disease), had been transformed into a disinfection space where staff did their best to sterilize equipment and gear in buckets of chlorine bleach to prevent patient-to-patient transmission and hospital-acquired infections. Despite these precautions and due to a lack of personal protective equipment (staff burned through the inventory of gloves, masks, and other gear as they responded to the unusually high patient volume), two nurses at the Safi Health Centre had already fallen ill, as had the Amani's clinic administrative assistant. Remaining staff and available community health workers were now working around the clock. New patients kept arriving even as others were leaving, wrapped in cloth and destined for burial. The situation was near disaster.

Fast forward 30 days and life at Amani and Safi was once again quiet, but it was no longer peaceful. Disaster had been averted on a national and international level but at great cost to the affected area. The "mystery disease" as community elders described it, had taken a severe toll. Though a national response unit eventually arrived, by that time more than a quarter of villagers in the area were infected and around 30% did not recover, a disproportionate number of them children, leaving an eerie silence in areas formerly vibrant with laughter and play. Those who

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dared talk about the disease with the response team's investigators said it simply moved on to other villages like a wildfire, that it was a punishment for sins or mistreatment of ancestral spirits, or that it was a curse. The only thing they could agree on was that it was gone.

This story is fictional but not at all uncommon. Since 2000, there have been many dozens of reports of viral hemorrhagic fevers, nearly all of them from Sub-Saharan Africa and from remote areas marginalized from infrastructure and health services (WHO, 2018) [1]. Many are immediately suspected to be known and often deadly diseases like Ebola, Yellow Fever, or Lassa Fever, while others are branded "mystery" or "strange" diseases, elusive to detection unless or until they are identified by state-of-the-art molecular laboratories often on a distant continent from where the emerging disease was observed. In the media, stories of these events appear and vanish almost as quickly as some of the outbreaks themselves, but their mystery remains.

In this modern, technological age, should this scenario be the status quo? Why don't we have the ability to identify where and how these new diseases will emerge? How can a pathogen appear so swiftly, wreak such havoc, and then just slip away, often without being identified for preparation of future prevention and control measures? How did Ebola, for example, go regionally undetected and suddenly emerge from the forests of West Africa to cause such destruction after being known and expected in neighboring areas for decades? Can you prepare for or prevent something you do not understand? Can we predict when and where a deadly pathogen might appear and be prepared for the potentiality?

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In response to these questions, the United States Agency of International Development (USAID) boldly launched the Emerging Pandemic Threats (EPT) program in 2009. The program is a follow on from USAID's Pandemic Influenza and Other Emerging Threats activities, initiated in 2005 to strengthen the capacities of over 50 countries for monitoring the spread of highly pathogenic avian influenza among wild bird populations, domestic poultry, and people; to help countries rapidly and effectively contain avian influenza viruses; and to support operational capacities in the event a pandemic influenza virus emerged (USAID, 2016)[2]. But a key distinction of the current EPT program is the emphasis on early detection and response to infectious diseases of any viral origin, with an intense focus on potentially high-consequence animal viruses, or zoonotic disease threats. The initiating aim of EPT was to strengthen capacities of developing countries to prevent, detect, and control infectious diseases. In short, EPT was conceived as a suite of science and development projects that look into the unknown and help prepare the world's most vulnerable states for hidden disaster.

Behind the curtain

Why would the leading international development agency from the world's largest contributor to overseas development assistance invest in a program focused on emerging zoonotic disease threats? The answer is in the numbers. The majority of emerging infectious diseases (EIDs) are zoonotic or are diseases that are shared between animals and people (Jones et al., 2006)[3]. These diseases result in millions of deaths each year, and the economic losses from a single outbreak can amount to tens of billions of dollars, as evidenced by SARS (Lee & McKibbon, 2004; World Bank, 2012). Zoonotic diseases are caused by pathogens that can infect different species, often

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nimble actors and frequently viruses, which comprise 25-44% of emerging and re-emerging pathogens (Jones et al, 2006; Taylor, Latham, & Woodhouse, 2001). Viruses are particularly well suited for emergence, especially RNA viruses that can rapidly evolve to infect and replicate in new host species, as evidenced by the HIV/AIDS pandemic (35 million deaths as of 2012) (Morens, Folkers, & Fauci, 2008; Fauci & Folkers, 2012) and the 1918 influenza pandemic (50 million deaths), two of the most devastating global pandemics in recorded history.

Detecting the agent responsible for an emerging disease event is one battle (the "what"), but the greater challenge lies in identifying the underlying drivers for its emergence (the "how" and "why"). While the global health community recognizes the threat posed by EIDs and their significance, there remains a limited understanding of the drivers for emergence and spread of zoonotic pathogens from animals to people (Murray & Daszak, 2013). So far, four domains have gained acceptance[10,11,12]:

1. Genetic and biological factors of pathogens and affected hosts
2. Physical and environmental factors, such as weather
3. Ecological factors, such as biodiversity and land-use change
4. Social, political, and economic factors, such as poverty, health infrastructure, and interconnectivity in our globalized marketplace.

In reality, an emerging disease event could be triggered by any combination of the domains above, as they dynamically interact often creating perfect conditions for a viral storm. One study by Jones et al.[3] (2006) that analyzed over 300 EID events occurring between 1940 and 2004 revealed that more than 70% of emerging zoonotic pathogens originated in wildlife and that the

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incidence of EID events stemming from wildlife pathogens has increased significantly over time. Clearly wildlife have an important role, but they are the character actors in a play where humans take center stage. It is ironic that despite the urbanization and digitization of human society, we as a species are getting increasingly intimate with nature, but perhaps not in a manner best for our long-term survival.

When it comes to risk for disease emergence, wildlife hosts are not a homogenous group, as different species and certain taxonomic groups are known to be richer sources of zoonotic pathogens than others[13]. Among the taxonomic groups assessed to date, zoonotic viruses have been most commonly detected in bats, birds, non-human primates, rodents, our carnivore friends, and ungulates – hoofed animals[14,15,16,17]. However, these animals are not to blame for their "risky" nature, as the mechanisms for viral spillover from wildlife tend to be induced by human behaviors, such as encroaching into or degrading wildlife habitat for agriculture or deliberately seeking contact with wild animals for direct economic gain, as illustrated by wildlife trade. To minimize risks of disease emergence, it appears we need to balance political, social, economic, health, and conservation goals, a tall order considering the pressures confronting our species and planet as we approach a projected population of 9.7 billion by 2050[18].

An approach seeking to address these myriad challenges is One Health. The One Health approach recognizes the value of comparative medicine and the critical role that environmental, ecological, and social factors play in the health of people and animals[19]. Because of the complexity of factors that can be involved in infectious disease emergence, there is a need to incorporate diverse expertise and a cooperative approach to the design of response and

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mitigation strategies. The One Health approach can enable multidisciplinary cooperation, encouraging the global community to come together to address the risks posed by pandemics, one of our species greatest threats. Though it may appear to be another grand challenge, investing in One Health to catalyze the development of a global consortium and harness diverse skills and expertise to innovatively address emerging infectious disease threats is what USAID's EPT program aspired to do.

Through EPT, USAID heeded the call to invest in a paradigm shift away from the conventional, reactive approach to EIDs and towards a proactive, predictive approach for early detection, prevention, and timely control[20,21]. Because infrastructure improvements and technological advances, such as information technologies, risk modeling, and molecular detection, have continued to dramatically and rapidly improve our ability to identify pathogens (including new viruses) and identify high-risk interfaces for disease transmission, we now have the best chance in history to reduce the threat from zoonotic viruses and to effectively mitigate the risks that an outbreak becomes a pandemic. USAID EPT's PREDICT Project provided an opportunity to develop a strategic framework and to nurture the partnerships necessary to put the One Health approach into action and work towards this new paradigm for pandemic risk reduction, while also strengthening capacity and health systems in areas at highest risk for viral emergence. PREDICT's challenge was multifaceted: build the cooperative global and local partnerships required for a truly multidisciplinary One Health approach; develop appropriate technologies for rapid detection of emerging viral threats and for assessing risks of spillover and spread from animals to people; and transfer those technologies along with the skills and capacity to deploy

them to the lower and middle income countries considered most vulnerable and at-risk in our global health system.

It takes a village

In the realm of emerging infectious diseases, there is considerable global expertise, but no one expert can handle the complexity of all the factors involved. Efficient and appropriate prevention and response is best achieved through a team-driven enterprise, where relationships and partnerships are critical to success. In bidding for and later establishing PREDICT, five key partners joined together in 2008 to build a One Health consortium: the University of California, Davis' One Health Institute, part of the world's top-ranked School of Veterinary Medicine; EcoHealth Alliance (formerly the Wildlife Trust), a non-governmental organization and long-time advocate of ecosystem health and conservation medicine; Metabiota, Inc. (formerly Global Viral), a respected company with a history of success hunting microbes in the forests of Central Africa and beyond; the Wildlife Conservation Society (WCS), an international NGO with revered field veterinary and conservation medicine programs; and the Smithsonian Institution, the world's largest museum, education, and research complex. PREDICT, funded by USAID on a five-year timeline, was first charged with building an evidence base for zoonotic disease emergence from wildlife across countries in Africa, Asia, and Latin America that would inform capacity strengthening initiatives for EID mitigation, control, and prevention. The project was initially designed to tackle five main objectives:

1. Strengthening zoonotic disease surveillance systems in areas considered "hotspots" for spillover and spread

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2. Improving viral detection and discovery by developing laboratory and outbreak response capacity
3. Characterizing high-risk human-animal interfaces and drivers of viral emergence
4. Optimizing predictive models for disease emergence and spread
5. Developing cutting edge tools for information management and communications that cultivate open data sharing and encourage a more integrated global approach to EIDs

<FIGURE 1. MAP OF PREDICT COUNTRIES (2009 – 2019) HERE>

PREDICT's consortium model leveraged the expertise and assets of each organization along with their networks of global partnerships required for swift implementation. PREDICT is managed through a central hub based at the UC Davis One Health Institute but is coordinated through an executive board with representation from all partners and a senior management team in cooperation with USAID. The consortium has established seven operational teams, all cross-pollinated with expertise to encourage a diversity of thought and perspectives in project design and implementation from the global to country level: 1) an operations team for overall project management and implementation; 2) a capacity strengthening team focused on developing the tools, skills, and One Health workforce needed to get the job done; 3) a surveillance team charged with designing the strategy for sampling; 4) a viral detection and discovery team tasked with developing and introducing appropriate tools and technologies for use in labs around the world; 5) an information management team to create data collection tools and to host and manage project data; 6) an epidemiology team; and 7) a modeling and analytics team to draw insight and advance predictive models for viral emergence and spread. By design, no teams were

mutually exclusive, and partners worked in an iterative feedback loop with information flows helping to strengthen each team's focus, as insights from the epidemiology and modeling and analytics teams were used to help refine and focus the surveillance approach, then later as the project matured, vital findings served to launch new investigations and inquiries into new areas. At the country level, all consortium partners provided leadership for project implementation with local implementing partners, including government ministries, research institutes, universities, and non-governmental organizations.

> "Rather than become the project's *bete noire*, its diversities and complexities have become its source of strength and innovation." – Dr. Dennis Carroll, Director of the Emerging Threats Program, USAID.

With a diversity of expertise, opinions, and perspectives, a consortium model is naturally time-intensive and requires a democratic organizational structure and diplomatic membership dedicated to a shared cause and ideology to succeed. PREDICT's partners were unified by a shared commitment to the One Health approach and to advancing the goals of development, health, and conservation in addressing emerging disease threats. This shared commitment enabled the consortium to move quickly from development of strategies and plans to launch of activities in target countries due to the partnership's extensive global network of collaborators.

To find the needle, first find the haystack

The first phase of PREDICT activities (2009-2014) was implemented in Africa (Cameroon, Gabon, Republic of Congo, Tanzania, Uganda and Rwanda), Asia (Bangladesh, Cambodia, China, Indonesia, Laos, Malaysia, Nepal, Thailand, Viet Nam), and Latin America (Bolivia, Brazil, Columbia, Mexico, and Peru). The sheer extent and scale of the project's zoonotic disease surveillance and capacity strengthening activities were unprecedented, as partners worked to target investments and activities at areas most at-risk for viral spillover from wildlife to people.

To identify these areas, PREDICT worked to develop partnerships with government ministries, scientific institutions, local organizations, and community-level stakeholders, cultivating multisectoral cooperation and deepening the understanding of risk. Surveillance activities were targeted in geographic areas identified as emerging infectious disease hotspots[3], due to high wildlife biodiversity and pressure on habitats by encroaching anthropogenic activities. Teams also worked with in-country partners to further assess surveillance locations using the available evidence base, observational methods, and standardized site evaluation criteria. This approach allowed us to hone in on animal-human interfaces promoting zoonotic transmission, such as locations where a diversity of wildlife species and their pathogens come into contact with people or their domestic animals, as seen with the emergence of SARS in wildlife markets in China, or areas where hunting, butchering, and handling of wild non-human primates is common as occurred with Ebola and HIV/AIDS.

Risk-based surveillance

"PREDICT, the world's largest effort to track down emerging zoonotic diseases[22]." – Karl Gruber, *Nature Ecology & Evolution*

In its first five-year phase, PREDICT effectively engaged 59 government ministries and hundreds of scientific institutions, local organizations, and other stakeholders in planning and implementation. At this scale, a daunting challenge was standardizing project activities across all participating countries to produce comparable data for global insight. To that end, PREDICT established standardized surveillance criteria applicable to contexts as diverse as densely populated, informal urban settlements and slums in South Asia and rural communities near fragmented forests in Central Africa. Just as with PREDICT's overarching strategy, the criteria hinged on three distinct elements of risk: 1) the taxonomic groups from which zoonotic viral threats are most likely to spillover; 2) the human-animal contact interface(s) at which spillover could occur; and 3) the most likely specimen types associated with potential pathogen transmission at each interface and the likely subsequent infection pathways.

On the wild side

When attempting to target hosts for a risk-based zoonotic disease surveillance strategy, how do you decide what species to sample? Numerous wildlife species are known to harbor dangerous pathogens and are considered to be high-risk potential reservoirs for zoonotic threats. In fact, there are some demographic, ecologic, and behavioral characteristics associated with particular taxonomic groups that have been suggested to affect the likelihood of them serving as reservoirs for zoonotic pathogens[13,15,16,23]. For example, bats have been identified as the reservoir for Marburg virus in Central Africa, for Nipah and Hendra paramyxoviruses across Asia, and as important reservoirs for coronaviruses worldwide[24]. Based on a combination of evolutionary and biological characteristics, we know bats harbor an abundance of viral diversity, and their ability

to fly long distances and rapidly disperse provide bats with frequent opportunities for viral transmission to other wildlife, people, and domestic animals[14,15,25].

To maximize viral detection potential, PREDICT focused surveillance on high-risk taxa, such as bats, as well as other groups with documented evidence of being the source of viral spillover to people. To confirm the integrity of this strategy and further inform our surveillance approach, PREDICT completed multiple studies, including a peer-reviewed literature-based network analysis focusing on animal hosts linked to spillover of all zoonotic viruses[26]. That analysis confirmed that the vast majority of zoonotic viruses recognized to date would have been detected through targeted surveillance focusing on just three taxonomic groups – bats, non-human primates, and rodents. With a few exceptions (notably the wildlife trade interface), PREDICT's surveillance strategy was directed towards these groups in geographic hotspots for disease emergence[3], from Indonesia in the Far East to Peru's Amazon in the West. Capacity strengthening efforts were directed towards the design of detailed biosafety and sampling protocols and trainings for field surveillance teams in methods for safe live capture, handling, sampling, and release of these animals with field implementation of animal sampling following soon thereafter.

Wherever they may roam

PREDICT's second surveillance criterion, standardizing high-risk human and animal interfaces for viral transmission, was established to allow the investigation and ranking of risk for pathogen transmission. PREDICT teams targeted key taxonomic groups in the wild at areas with differing levels and types of land use changes, such as fragmented forest lands or areas cleared for cultivation or extractive industry activities, at high-risk interfaces, such as animal value chains

(e.g., hunted animals, bushmeat market and restaurants, and the wildlife trade); in areas with ecotourism; and habitats in or near human dwellings, crop lands, and grazing areas. Standardized data collection tools enabled comparison of data across sites, countries, and regions and enabled further refinement of surveillance strategies in an iterative feedback loop across PREDICT's surveillance, viral detection, information management, and modeling and analytics teams.

<FIGURE 2 -INSIDE THE HUMAN-ANIMAL INTERFACE HERE>

Pathways of emergence

We established PREDICT's targeting of surveillance activities on select taxonomic groups of wildlife and more narrowly focused efforts on high-risk interfaces where viral spillover could occur. But when sampling animals, how do you determine what specimens should be collected for viral testing? In a perfect world with no limits on resources or project timelines, the answer is any and all available specimens. But in a fast-moving development project, where information and insight are needed as quickly as possible to help refine surveillance plans and achieve project objectives, tough decisions must be made. In addition to the effort put into targeting taxonomic groups and identifying high-risk interfaces and surveillance sites, we also worked to identify the most likely specimen types for viral spillover at each particular interface and PREDICT teams initially selected specimens for viral testing based on likely route of transmission. For example, if sampling hunted non-human primates, blood was prioritized due to probability for direct contact and consumption. In a peri-domestic setting, where rodents were sampled around houses or in agricultural fields, feces and oral swabs were prioritized as the most likely routes for human exposure were theough contamination with excreta and saliva. As such, PREDICT strived not only to test a standardized set of samples uniformly across all countries, but also to match these

sample types and specimens to specific risks of the most common routes of exposure across interfaces. Over time, data collected in the field were paired with results from partner labs and analyzed at the global level to determine which specimen types were most likely to yield positive findings across each targeted viral group. These findings then helped optimize selection of specimen types using an evidence base directly related to PREDICT's sampling and detection platforms.

The viral detection paradox

The linchpin of a project designed around understanding viral emergence is without question the laboratory. PREDICT's surveillance strategy emphasized detection of viral shedding from wildlife and evaluation of spillover risk, requiring the development of novel and sophisticated molecular viral detection techniques. With recent technological advances reducing costs and improving the accessibility of viral discovery platforms, such as next generation sequencing, that enable the identification of the full genome, PREDICT's options for innovation appeared endless. However, as a USAID project, PREDICT's overarching goal was, and remains, capacity strengthening to improve surveillance and detection systems in some of the world's most vulnerable and low resource settings. The viral detection and discovery strategy, therefore, faced a paradox: advancing cutting-edge technologies for improved detection of new viruses while ensuring that these same cutting-edge techniques were readily transferrable, adoptable, and implementable in real-world laboratory settings in all participating countries. These settings also varied considerably. For example, at the start of the project, PREDICT's partner lab at the Institut Pasteur in Cambodia was much more advanced and ready-made for molecular viral

identification both in terms of infrastructure and human resources than our similarly-motivated but under-resourced partner lab at the Sokoine University of Agriculture in Tanzania. To compensate for the disparity in existing infrastructure and capabilities, PREDICT adapted a strategy rooted in basic molecular techniques using consensus-based polymerase chain reaction (cPCR) with project-generated universal controls and primers targeting genes at the viral family level instead of individual viruses[27]. This strategy was rapidly implementable in almost any laboratory setting that had existing capacity for PCR testing yet expanded the focus of a lab's testing from often only a single pathogen to a potentially endless range of viral diversity. Beyond innovative, this strategy was also extremely cost effective, as labs with limited resources would be able to screen samples for both known and new viral threats at the same time and produce specific, high-resolution data. By combining cPCR with high-throughput sequencing (HTS) where available as a complement to capture any viral diversity missed by cPCR, PREDICT created an approach with high sensitivity and broad reactivity that could detect viruses at low levels while simultaneously casting a broad net[28].

This strategy was coupled with an intensive capacity strengthening plan designed to bolster lab infrastructure and capabilities for implementation, as well as shore up biosafety and biosecurity, cold chain, and data management. By 2014, a total of 32 PREDICT partner labs had been successfully integrated into the project's global viral detection network, either through the active screening of samples using project techniques or receiving training in preparation for launch of activities.

<FIGURE 3A AND B. COMPARISON OF VIRAL TESTING CAPACITIES AT ONSET AND END OF P-1 – HERE>

Rich in data

At scale, PREDICT's One Health surveillance and viral detection activities generate enormous volumes of data. For perspective, every surveillance site characterized for suitability of field activities yields multiple data fields capturing geospatial, ecologic, environmental, and anthropogenic information; each animal sampled yields on average eight specimen tubes all with unique IDs; at the lab, each prioritized specimen, for example an oral swab, is further processed into a minimum of five tubes during RNA extraction and viral family testing; final PCR products sent for sequencing yield additional data including bioinformatic-rich information; and viral findings, following interpretation, result in reports forwarded to host country government partners for approval and public release with sequences ultimately shared with GenBank[29].

As a project committed to open data, one PREDICT challenge was to develop an information management system capable of capturing and storing all of this data, synthesizing and aggregating the diversity of data to enable meaningful analytics, and designing a universal user interface addressing the needs of all consortium partners from New York to Nepal. For project's working with emerging infectious disease data, the challenge is intensified: sample and all associated risk factor data must be easily identifiable and linked, as well as available for further analysis in case needs arise to evaluate a virus's role in an outbreak. Incorporation of human data complicates things even further, as identities and privacies must be strictly protected.

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Data collection and management

PREDICT's information management system grew out of the USAID and US Centers for Disease Control and Prevention's Global Animal Information System (GAINS), initially established to track avian influenza in wild birds. For PREDICT's goals, GAINS was adapted and redesigned into the Emerging Infectious Disease Information and Technology Hub (EIDITH), a flexible platform that could collect and integrate standardized data from field surveillance activities along with public information sources, and provide mechanisms for data input, management, and visualization.

Project data along with publicly available information, such as disease alerts from ProMED and HealthMap, were monitored in real-time by PREDICT epidemiologists and our in-country teams in a continual effort to refine and improve targeted surveillance and to provide real-time information on potential zoonotic disease threats to stakeholders and decision makers.

Knowledge dissemination

PREDICT data, once approved for public release by host country government partners, are openly shared with the public through easily accessible channels. Field surveillance and viral testing data are georeferenced and hosted by HealthMap on a site dedicated to PREDICT and emerging zoonotic disease threats[30]. By integrating data visualizations of EID hotspots[2] with overlays of PREDICT data and real-time disease alerts from HealthMap's system, this platform provides decision makers with a toolkit for evaluating known and emerging disease risks. PREDICT's viral sequence data is also open to the public on a dedicated National Center for

Biotechnology Information (NCBI) Bioproject, a collective repository for our viral findings facilitating further analysis and research[29].

<FIGURE 4. SCREENSHOT OF HEALTHMAP SITE DATA.PREDICT.GLOBAL HERE>

Source site? Need permissions for use ?

Predicting the next pandemic

For a project entitled PREDICT by USAID, there are major expectations for advancing the knowledge, technologies, and tools to improve the world's ability to forecast when and where the next pandemic could emerge. Building on the expertise of consortium members, already pushing the boundaries of knowledge on the drivers of disease emergence and spatial and temporal patterns of spillover, PREDICT developed and applied cutting edge analytical techniques to characterize risk of emerging infectious diseases, focusing on emerging viral threats from wildlife. The goals were twofold: 1) to design more efficient, effective, and targeted disease surveillance, prevention, and control strategies, and 2) to identify critical areas for future research.

By drawing on the wealth of data generated by the project, along with publicly available information and additional data sources, PREDICT's modeling and laboratory teams worked to update forecasts for risks of novel disease emergence from wildlife and create new hotspots maps; explored high-risk interfaces for disease emergence and spread; contributed to an online repository of disease emergence events and information (EIDR); investigated the relationships

between hosts, pathogens, and phylogeny; analyzed viral diversity to estimate the numbers of undiscovered viruses in mammals and generate "viral discovery" curves to help establish data-driven sampling targets for surveillance teams; assessed pandemic risks from transmission pathways and global travel and trade; developed strategies to rank zoonotic potential of newly discovered viruses; and worked to quantify the economic impacts of EIDs.

<FIGURE 5. VIRAL DISCOVERY CURVE HERE>

Legend?

Proof of concept: early detection of Ebolavirus in the Democratic Republic of Congo

On August 11, 2014, in the village of Ikanamongo in the Democratic Republic of Congo's Equateur Province, a woman with symptoms of a hemorrhagic fever died of unknown causes. By August 18th, officials in the capital city of Kinshasa had received reports of 24 suspected cases in nearby villages. Meanwhile, the African and international community were struggling to respond to the Ebola virus disease outbreak in West Africa, a growing pandemic which threatened to spread throughout the region and potentially cripple national health systems. The Democratic Republic of Congo, a country with a long history of Ebola virus disease outbreaks and home to the river after which Ebola virus was first named in 1976[31], had sent experienced national virology staff to West Africa to support response efforts. In their absence, the PREDICT laboratory was requested to conduct diagnostic testing for a disease of unknown origin. Using the project's viral detection platform and screening for viruses at the family level, Ebolavirus was confirmed on August 23, 2014, one day after samples were received at the lab from the national response team. The early detection of the virus helped catalyze and enable rapid

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enactment of disease control and containment measures including quarantine, dispatch of a mobile laboratory for rapid onsite detection, and contact tracing, among others. In this situation, where national staff were mobilized in response to another pandemic threat, PREDICT's early detection and diagnostic expertise were pivotal in limiting the spread of the outbreak and preventing the virus from spreading into an uncontrollable disaster as was happening in neighboring West Africa, where detection capabilities and health system were ill prepared to respond and where public trust in the system was deficient.

Local relevance, global impact

As a USAID-funded development project, one of PREDICT's primary challenges was to explore the feasibility for strengthening systems for surveillance and detection of zoonotic disease threats of wildlife origin in at-risk areas, which are often remote, rural areas marginalized from improved infrastructure. To evaluate impact and proof of concept, we tracked the ability of participating countries to safely and effectively collect, transport, test, and report viral findings from samples collected from these challenging locations and from targeted species of wild animals. In addition, we worked with our teams around the world to identify interfaces and human behaviors associated with increased risk of viral spillover and to explore the zoonotic potential of the viruses, aiming towards identification of potential risk mitigation strategies. At the end of PREDICT's first phase in 2014, all participating countries had safely collected and tested wildlife samples from targeted taxonomic groups and secured approval from host country governments for public release of findings, a major success yielding a wealth of data that

continues to catalyze efforts for understanding risk and forecasting viral emergence from wildlife to this day.

Building a One Health workforce

To date, PREDICT has engaged government, NGO, technical, and local community partners and trained over 3,300 individuals from ministry officials to physicians and veterinarians, students, and local community members. Our trainings focused on the broad scope of PREDICT activities and were organized around the One Health approach, bridging disciplinary divides and encouraging cross training in the diversity of skills required for safe and effective zoonotic disease surveillance and viral detection. Additionally, to develop the capabilities required for sample processing and viral detection in partner laboratories, PREDICT has engaged, equipped, supplied, and/or trained staff in 60 diagnostic laboratories around the world, transferring the knowledge and skills required for detecting known and newly emerging viral threats.

PREDICT's capacity strengthening effort is likely the world's most comprehensive to date, emphasizing on-the-job skills required to mobilize a One Health workforce. Through the project, our staff and collaborators were provided the opportunity to learn new skills put them to work each day - from sample collection to testing and through the analytical process required to characterize and understand risk. As a result, project staff were recognized by host country governments and requested to serve on national task forces and to provide technical and expert assistance for numerous high-profile disease investigation and response efforts, including H7N9 influenza A, Nipah Virus, MERS, and multiple Ebola virus disease outbreaks. Our partner labs continue to serve as resources for disease detection and are contributing to national systems and global health security.

Surveillance for pandemic prevention

PREDICT's surveillance strategy was inherently risky. The aim after all was to systematically sample healthy animals from high-risk taxonomic groups and then to test specimens based on likely disease transmission pathways to humans using a newly developed viral detection platform. A worthy challenge further compounded by the need to simultaneously develop the capabilities of field and lab teams in 36 participating countries to conduct the work in a coordinated manner. Did this risk-based strategy pay off?

<FIGURE 6. DATA INFOGRAPHIC (PREDICT LIFE OF PROJECT 2009-2017) HERE >

Our trained field teams, in collaboration with local partners safely and humanely sampled more than 74,000 non-human primates, bats, rodents, and other wild animals (including animals from the bushmeat value chain and wildlife trade), livestock and domestic animals, and people at high-risk interfaces where viral spillover and spread were most likely to occur. In addition, to further evaluate risk for spillover and potential viral sharing between wildlife and people, PREDICT designed and launched pilot human disease surveillance efforts in 24 countries in Africa and Asia.

Using our low-cost viral detection platform in just the first five years of the project, technicians conducted over 420,000 tests yielding 6,787 positive results and detecting 1,002 unique viruses in wild animals and 34 viruses in our human pilot efforts[28]. These 984 unique viruses, which include 820 newly discovered viruses (82%) and 182 known viruses (18%) represent the most thorough and systematic viral detection and discovery effort to date, as our project detected more

viruses in just five years than the total number of viruses previously recognized in mammals by the International Committee on Taxonomy of viruses (ICTV)[28].

<TABLE 1. VIRUSES DETECTED AND DISCOVERED IN FIRST PHASE OF PREDICT BY TAXA HERE>

Through our commitment to open data, all viral genetic sequences are being deposited into GenBank database for public access, while georeferenced animal sampling data along with positive viral findings are also displayed in HealthMap with associated metadata to enable informed decision making on risk[29,30].

Risk-based intelligence to prevent pandemic threats

Beyond generation of valuable data, PREDICT synthesized information from field surveillance, viral findings, and other data sources to advance the evidence base on risks for viral spillover and spread and disease emergence. Through innovative modeling and analytical techniques, we revisited temporal and spatial patterns of disease emergence to design an updated "hotspots" map, providing a refined projection of global EID risk[28]. In addition, project epidemiologists shed light on spillover properties of pandemic viruses with high host plasticity[34]; explored evolutionary dynamics and global diversity of influenza A viruses[32] and the global biogeography of human infectious diseases[35]; identified non-random patterns in viral diversity[36]; evaluated how best to target transmission pathways for emerging disease threats in surveillance and control programs[31]; identified bats as the evolutionary source of Middle East Respiratory Syndrome (MERS) coronavirus[26]; identified global patterns of coronavirus diversity[24]; and conducted

numerous assessments and investigations of EID risks at specific human-wildlife interfaces at the country level[17,30,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58].

Additionally, PREDICT developed "viral discovery curves" to estimate how many undiscovered viruses might exist in a targeted population and the subsequent sample size needed to maximize viral discovery[24], a critical and long-lasting contribution to the global health and surveillance communities, as this knowledge removes uncertainty when planning surveillance for emerging viral threats. To date, PREDICT work has led to the publication of over 160 peer-reviewed, scientific manuscripts, many in top-tier journals such as *Nature*, the *Proceedings of the National Academies of Science*, *The Lancet*, *Emerging Infectious Diseases*, and *mBio*.

Our work is far from complete. Ongoing analyses continue to yield valuable information on viral traits, host species, and risks for transmission and geographic spread of pathogens around our planet. Further, we are working to explore the human behaviors associated with transmission risk to identify potential risk mitigation options and intervention strategies. Our One Health surveillance and viral detection platforms, strengthened from years of training and on-the-job experience, are contributing to national health systems and playing key roles in rapid disease detection and response. Our consortium model, which brings together some of the brightest minds and innovative scientists in the field of emerging diseases, has proven itself a model for large-scale global initiatives and is a success story for the One Health approach to solving transdisciplinary problems. As a testament to PREDICT's success, USAID's Emerging Pandemic Threats program awarded a five-year continuation of the project to the consortium in

2014, enabling our efforts to promote global health and seek innovative solutions for preventing and controlling emerging disease threats to carry on into the future.

The Road Ahead

The first phase of PREDICT helped to illustrate that the time is right for a more proactive paradigm that allows for the use of knowledge on what diseases might be emerging and the development of interventions to prevent or at least control the pathogens at their source. The World Bank estimates that from 1997 to 2009, at least $80 billion US was spent responding to just six outbreaks of deadly zoonotic diseases, caused by viruses shared between people and animals[1]. The lives lost and financial implications of the West African Ebola outbreak illustrate the potential for impacts even more dramatic and devastating. Through further application of One Health approaches, these economic and human losses could be drastically reduced, as the public health community drives surveillance and interventions upstream and predicts the risk from these diseases before they emerge.

In our second phase (2014-2019), PREDICT has further honed its strategy to focus on places where environments and market systems are changing in ways that are conducive to the spillover of viruses from animals to people. Working on the ground with our local teams, which include health professionals, scientists, educators, social scientists, and ministry officials, we are identifying specific risk behaviors and associated areas posing the highest risk for exposure to disease, detecting and better characterizing pathogens of known epidemic and unknown pandemic potential, identifying significant animal reservoirs and amplification hosts of zoonotic

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viruses, and providing information needed to efficiently design and target intervention strategies at human behaviors that facilitate disease emergence and amplification. In addition, we are using a highly targeted approach to identify the biological and ecological drivers and host-pathogen dynamics by conducting standardized biological surveillance for pathogens shared by people and animals and characterizing behavioral risk in rapid and dramatically changing landscapes under circumstances that bring at-risk and immunologically naïve individuals into contact with potential spillover organisms along a continuum from rural pastoral settings to urban landscapes with large-scale animal production systems.

Human behaviors and practices are key risk components for pathogen spillover, amplification, and spread. We are now characterizing the type and frequency of contact among people, domestic animals, and potential wildlife reservoirs and investigating the correlation of specific human behaviors and zoonotic disease risk across sites to more deeply understand the behavioral mechanisms involved in the high-risk pathogen transmission pathways. By employing this strategy, the world can get one step closer to identifying potential control points and behavior change options. Combining quantitative and qualitative research methods allows PREDICT teams to identify and monitor behaviors, attitudes, practices, and socio-cultural norms and conditions that facilitate animal-human and animal-animal contact. Integration of data from biological surveillance in people and animals, behavioral risk characterization, and economic and anthropologic studies using advanced informational technologies and a dynamic analytical framework can then help to target potential interventions and inform policy development.

In addition, the project is preparing a skilled One Health workforce to be in a constant state of preparedness for contributing substantively to outbreak response, including assistance with identifying animal reservoirs involved in outbreaks of human disease. Outbreak response synergies result from strong ministerial linkages and academic and research institutional collaborations, as well as close coordination with international organizations and response partners. Where identifiable, the costs of disease outbreak response and control measures are being compared to costs of implementation of One Health strategies to calculate and demonstrate potential savings from prevention obtained through One Health approaches and advanced preparedness rather than responsive action after disease emergence.

Even with these advances, are we closer to being able to predict which viruses will be the sources of future outbreaks and under which circumstances? This critical question is currently being addressed through a collaborative approach throughout the global infectious disease expert community. By combining findings from PREDICT, the health community at large, and expert opinion, we are developing a dynamic risk ranking platform that, for the first time, focuses not only on viral characteristics, but also on the holistic circumstances of detected viruses, their ecology and epidemiology. By developing a publicly-available, risk ranking calculator that can be scientifically crowd-sourced and rigorously improved over time, the PREDICT team aims to provide a tool to the global health community that will help to put the vast viral diversity being discovered into a relative risk perspective to help inform decision making.

Dreaming of an Even Better Future

Is it feasible, that within the coming decade we could be aware of all the existing viruses that have zoonotic potential and the ecological characteristics and epidemiological circumstances that make some more risky to adverse health outcomes than others? PREDICT, on a relatively small scale, has proven that this audacious goal is achievable. A new world-wide initiative, the Global Virome Project (GVP)[39], aims to do just that. Endorsed by a growing cadre of world leaders in technology, health, and economics, the GVP recognizes that rapid advances in science and a corresponding revolution in technologies allow us to foresee a world where the impact of future pandemics can be minimized. The GVP aims at achieving this vision through core principles that embrace an international scope, while fostering local ownership; promote equitable access to data and benefits; foster transparency; assist countries in building their national capabilities for prevention, detection, and response for emerging viral threats on an unprecedented, global scale; and foster global ownership through an international alliance. Embracing these principles, the alliance may be able to do what has yet to be done – end the pandemic era by detecting and identifying nearly all potential zoonotic viral threats; characterizing the host ranges and geographic distributions; prioritizing high-risk viruses for further surveillance, research, and mitigation development; and strengthening global surveillance networks through local capacity enhancements.

First emergence revisited

How could the knowledge and tools from PREDICT and other modern technologies for disease prevention, detection, and control change our current approach to preparedness and response? What if the Amani and Safi Health Centers were in a country where an integrated One Health

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approach to surveillance, early detection, and response was adopted widely from the community to national levels, and where existing knowledge about emerging disease threats was factored into preparedness and response plans. How might a mystery disease outbreak unfold then?

Imagine the scene, clinic staff at the Amani Health Centre admit a new patient, an elderly man complaining of diarrhea, fever, headache, and muscle pains. After taking his temperature and providing pain relief and anti-inflammatory medication, a nurse serves the man tea, conducts a rapid diagnostic test for malaria, and as she waits for the results, engages in conversation designed to capture background information on the man, his occupation, his family's recent medical history, and a few other questions exploring behaviors and practices the nurse knows have been associated with diseases in the region, such as contact with livestock and wild animals and a few other topics learned during sensitization training for emerging infectious diseases. She learns that he is a fisherman by trade from the neighboring district but that he has been living at a fishing camp near the river for the past month. At home, the man is involved in several other activities to earn a living, growing mangos, raising pigs, and occasionally working as a builder. He first fell ill a few days ago. By now, the rapid test is complete, and it is negative for malaria, triggering the standard protocol for a fever of unknown origin. Clinic staff admit the man to the inpatient unit and collect additional samples: blood, an oropharyngeal swab, and they provide containers for urine and stool. The samples are preserved in liquid nitrogen immediately for pathogen detection and the patient is continuously monitored. Plans are made with health authorities through the established electronic surveillance system to transport his samples to the district's Disease Investigation Centre for testing. Over the next 48 hours, the samples undergo testing for known, endemic diseases fitting the man's case definition, as well as viruses yet to be

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known in the area at the viral family level. Within the same 48 hours, another 12 individuals arrive at Amani with similar symptoms, and though several test positive for malaria the Chief Medical Officer sounds the alarm. This is an outbreak. He contacts the Ministry of Health's Department of Epidemiology who reviews the information, requests the man's test results, and enacts preliminary response measures. The Outbreak Response Task Force is put on standby.

The next day, staff at the neighboring Safi Health Centre also report multiple cases with similar symptoms. The task force is convened and preparations made to launch further control and enact pre-organized protocols for the investigation. The man's samples, as well as those from additional patients which have been arriving daily at the district's Disease Investigation Centre, have not yielded positive results for most suspected and known threats: Yellow Fever, dengue, Ebola, Marburg, Crimean Congo Hemorrhagic Fever, and Lassa, but they are showing preliminary positive results for a novel paramyxovirus. The national lab prepares to receive the processed positive samples for rapid genetic sequencing. At this point, the task force has shared the first situation report, and the international community has been notified about the event.

Meanwhile, the task force's field investigation team, a multisectoral One Health crew constantly in a state of readiness, arrives in the area. The team includes medical doctors, nurses, social workers, veterinarians, and epidemiologists, as well as a technician who is busy setting up a mobile lab for onsite testing. They engage with clinic staff, rapidly implement disease control measures, and the social workers begin interviewing patients and their families, collecting information that might yield a clue to the outbreak's spark. Several accounts from Amani lead back to the index case, the elderly man from the fishing camp, and the ecological investigation

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team departs to begin sampling local wildlife and livestock around the camp and surrounding area, conducting interviews, and characterizing potential environmental and ecological risks that may be involved in a viral spillover event. Social workers, after mobilizing community health workers, launch an outreach and information campaign in the villages aimed at awareness of the situation as an outbreak and promoting potential prevention and safety measures based on best practices for prevention and control of a range of threats and designed to minimize contact with the sick and limit spread of the disease outside the area.

At the national lab, technicians have partially sequenced the paramyxovirus. Virologists conclude that the viral sequence is closely related to Nipah virus, not yet known to occur and cause disease on the African continent. Positive samples are shipped overnight to the lab's collaborating center of excellence in the region to sequence the full genome. Within days, the world becomes aware of a new virus, all occurring simultaneously with control measures, rather than suffering delays at the disease recognition, diagnosis, and response preparation steps.

Back in the villages, the number of suspected cases has increased among the growing list of patient contacts, but thanks to limits on movements in and out of households and between villages, outreach about potential transmission pathways of viral-origin fevers, information on disease control practices, and careful biosecurity measures at the health centres, there seems to be no evidence that the disease is spreading. The outbreak is under control with handfuls, rather than hundreds of people impacted. Soon enough, with no new cases appearing and the few remaining patients receiving treatment and improving, the response team begins to prepare for the trip home.

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Results from the ecological investigation are then received from the Central Veterinary Lab. Multiple rodent samples collected from the fishing camp also tested positive for the paramyxovirus, and results from full genome sequencing show agreement between the viruses detected in animals and the strain causing disease in people. In short, this virus is zoonotic and very recently jumped the species divide.

The task force convenes again to discuss the findings and to prepare for longer-term surveillance, prevention, and control. The virus is added to the priority zoonotic disease list, neighboring countries are put on alert. A more in-depth and targeted strategy and outreach campaign is developed focusing on rodent and human interactions, and the behaviors and practices that may be linked to risk of transmission. New tests targeting the virus' genes are in development, as are serologic tests to determine if this virus has spilled over before and where. Through an international network of partners and collaborators, plans are launched to refine surveillance around the suspected rodent reservoir, a common species of mouse with a specialized riparian niche. The world is on watch, and the affected communities, as well as those identified as potential hotspots are made aware and ready to immediately report cases to rapidly reduce the impacts of the next emergence disease event. The global community builds a knowledge base of prediction, prevention, and control measures around the new viral threat and we march one step closer to the end of the pandemic era.

Works Cited

There are no sources in the current document.

All citations/footnotes need to be converted to references according to APA style.

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From: Candace Gibson <candaceg@uwo.ca>
To: djwolking@ucdavis.edu <djwolking@ucdavis.edu>;jkmazet@ucdavis.edu" <jkmazet@ucdavis.edu>
Sent: 9/20/2020 8:27:44 PM
Subject: RE: Book Chapter - the Nature of Pandemics

Dear Drs. Wolking and Mazet -

Hope you are both well. How are the edits/changes/updates to the book chapter. We are ready to go to press and finalizing all chapters this week.

Let me know if you need any help and when you could send along the revised version of the chapter.

Thanks very much,

Candace

From: Candace Gibson
Sent: Friday, July 31, 2020 11:23 AM
To: djwolking@ucdavis.edu; jkmazet@ucdavis.edu
Subject: Book Chapter - the Nature of Pandemics

Dear Drs. Wolking and Mazet -

First my sincere apologies for the long delay in communication and information about the status of the F&T book, The Nature of Pandemics for which you contributed a chapter. We had a number of personal and professional issues arise that have delayed the publication but the publisher is still (now more than ever due to COVID) interested in publishing it.

Second, thank you for your wonderful contribution on the description of PREDICT, its evolution and its activities. I have attached the edited version; there were few edits required and primarily the need to convert the footnotes to full references in the APA style.
We started to put these into the correct text citation and reference listing style (alphabetical, nut numbered) but realized you probably can do this much more quickly through your reference manager software. If not please let me know and we can take care of that conversion.
A reminder that the publisher is only going to be using grey-scale for printing of the photos/figures - so you may need to adjust some of the figures submitted (or point to the full color maps on a web site?).

Francis & Taylor will try to get this published before the end of the year but that now means a rapid turn-around. Could you please get revisions and any updates you feel are appropriate back to us in 3 weeks.
I'm not sure how you want to handle updates - this is currently a wonderful description of a comprehensive monitoring program that includes some excellent examples and the emphasis on One Health approaches couldn't be more timely.

Thank you both for your patience and for your excellent work.

Sincerely,

Candace Gibson, PhD, CHIM
Professor, Pathology & Laboratory Medicine
Acting Vice Dean, Basic Medical Sciences
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From:	Dennis Carroll <dcarroll@usaid.gov>
To:	Eddy Rubin <erubin@metabiota.com>
CC:	Elizabeth S Chase <eschase@ucdavis.edu>;Jonna Mazet <jonna.mazet@gmail.com>;Cara Chrisman <cchrisman@usaid.gov>;Nathan Wolfe <nwolfe@metabiota.com>;Taylor Einicki <teinicki@metabiota.com>
Sent:	1/6/2017 8:13:31 PM
Subject:	Re: Planning GVP does San Francisco

Thanks Eddy and all for pulling this together. Should be fun!

d

On Fri, Jan 6, 2017 at 3:20 PM, Eddy Rubin <erubin@metabiota.com> wrote:

The most recent dance card. BioHub and Science Philanthropy have confirmed. Robert Mann, Metabiota's CEO, has graciously offered to host a fine dining experience for all involved at his house the evening of the 25th. We still have the morning of the 25th open and we need the number of people that will be attending dinner the 25th

24th

Dennis Arrives in SF ~10 gets picked up at airport drive to Palo Alto

1:00-2:00 meeting at the Science Philanthropy Alliance in Palo

3:00-5:00 meeting at Stanford with BioHub South

25th

2:00-4:00 meeting at Illumina Mission Bay

6:00 Dinner hosted at Robert Mann's house in SF

26th

All day meeting at Metabiota planning China

--

Dr. Dennis Carroll
Director, Emerging Threats Program
Bureau for Global Health
U.S. Agency for International Development

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From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 2/8/2017 3:55:14 PM
Subject: FYI for today's EB call

From: Karen Saylors [mailto:ksaylors@metabiota.com]
Sent: Wednesday, February 08, 2017 3:08 AM
To: Elizabeth Leasure
Cc: David John Wolking; Eddy Rubin
Subject: Re: PREDICT EB Agenda for call tomorrow (February 8, 2017) from 9-11AM PST/12-2PM EST

Hi Liz.
I am in flight on my way to Cote d'Ivoire during the call, and Eddy will just be getting off a plane from China at that time, so we have asked Damien to give our updates. I've sent him notes on the DRC outbreak, a Sierra Leone dog die-off, my Behavioral update, and an EHP update (which I also sent to Brian), so I think he should be covered, but please let me know if there are questions or follow-up items for us.

Thanks!
Karen

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
Date: Tuesday, February 7, 2017 at 9:26 AM
To: David John Wolking <djwolking@ucdavis.edu>, Amanda Fine <afine@wcs.org>, Brian Bird <brianhbird1@gmail.com>, Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, Damien Joly <djoly@metabiota.com>, Eddy Rubin <erubin@metabiota.com>, Jon <epstein@ecohealthalliance.org>, Karen Saylors <ksaylors@metabiota.com>, "Murray, Suzan" <MurrayS@si.edu>, Peter Daszak <daszak@ecohealthalliance.org>, Jonna Mazet <jkmazet@UCDAVIS.EDU>, Woutrina A Smith <wasmith@UCDAVIS.EDU>, Sarah Olson <solson@wcs.org>, Simon Anthony <sja2127@columbia.edu>, Tracey Goldstein <tgoldstein@UCDAVIS.EDU>, William Karesh <karesh@ecohealthalliance.org>
Cc: Taylor Ehnicki <tehnicki@metabiota.com>, Molly Turner <turner@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>, Amanda Fuchs <fuchs@ecohealthalliance.org>, Ava Sullivan <sullivan@ecohealthalliance.org>, Celina Roy <croy@metabiota.com>, Emma Lane <lane@ecohealthalliance.org>, Evelyn Luciano <luciano@ecohealthalliance.org>, Megan M Doyle <mmdoyle@UCDAVIS.EDU>
Subject: PREDICT EB Agenda for call tomorrow (February 8, 2017) from 9-11AM PST/12-2PM EST

Hi everyone. Please find below and attached the agenda for tomorrow's EB call at the regular time. Talk to you soon.

Thanks,
Liz

Executive Board Meeting

Wednesday, February 8, 2017

9:00am PST/12:00pm EST

#800-444-2801, Access code 5151894

International Dial-in number: 310-765-4820 (toll charges apply)

Agenda

1. **Management team and admin updates**
   - USAID team news
   - Save the date: Regional Jam in Mainz, Germany – May 23-24
   - Meeting with USAID to discuss PREDICT's role in GHSA
   - Outbreak reporting coordination and communications

2. **Outbreak updates (AI - Bangladesh, Uganda, & Cambodia, animal die-off in DRC, others?) - All**

3. **Mission communications round-up (All)**
    a. **Senegal**
    b. **Liberia**
    c. **Viet Nam**
    d. **RoC**
    e. **Kenya**
    f. **Other countries/regions**
4. **EPT partner coordination updates (Billy)**

5. **Operations Team updates:**
    Surveillance (Chris)

    Lab (Tracey & Simon)

    Behavior (Karen)

    M&A (Peter)
    Capacity (Woutrina)

    IM (Damien)

    EHP (Brian, Jon, Karen/Eddy)

6. **Global Virome Project update (Jonna/Peter/Eddy)**

7. **Other recent meeting updates?**
    ? Zoonotic Disease Prioritization Workshop meetings
    ? Others?

Standing Items:
Publications and ResearchGate update, ...
Related grant proposals or conferences?

Elizabeth Leasure
One Health Institute
University of California, Davis
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From: Andrew Clements <aclements@usaid.gov>
To: ghdunitmaillistusaid@usaid.gov <ghdunitmaillistusaid@usaid.gov>;Subhash (FAORAP) Morzaria <Subhash.Morzaria@fao.org>;Sophie.VonDobschuetz@fao.org <Sophie.VonDobschuetz@fao.org>;Gwenaelle.Dauphin@fao.org <Gwenaelle.Dauphin@fao.org>;Juan (AGAH) (Juan.Lubroth@fao.org) Lubroth <Juan.Lubroth@fao.org>;William Karesh <Karesh@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;daszak@ecohealthalliance.org <daszak@ecohealthalliance.org>;zhangw@who.int <zhangw@who.int>;samaang@who.int <samaang@who.int>;A. Danielle (CDC/OID/NCIRD) Iuliano <aoi0@cdc.gov>;Daniel Schar (RDMA/OPH) <dSchar@usaid.gov>;Sudarat Damrongwatanapokin (RDMA/OPH) <sDamrongwatanapokin@usaid.gov>;Lisa Kramer (Nairobi/EA/RHH) <lkramer@usaid.gov>
Sent: 2/24/2017 1:14:26 PM
Subject: France is Killing All of Its Ducks. Here's Why | UN Dispatch

FYI

http://www.undispatch.com/france-just-killed-ducks-heres/

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
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From:	Elizabeth Leasure <ealeasure@ucdavis.edu>
To:	PREDICTMGT <predictmgt@usaid.gov>
CC:	Jonna Mazet <jkmazet@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Katherine Leasure <kaleasure@ucdavis.edu>
Sent:	2/27/2017 10:37:46 PM
Subject:	PREDICT International Travel Requests

Please find below international travel requests for your review and approval. Please let me know if you have any questions. Thanks!!

1. Gillis (USA, Canada): $2,088 airfare/$341 (San Francisco), $221 (Nanaimo) max daily per diems
2. Epstein (Malaysia, Thailand): $1,079 airfare/$140 (Sabah), $246 (Bangkok) max daily per diems
3. Keatts (Cambodia): $2,500 airfare/$236 (Phnom Penh) max daily per diems
4. McIver (Laos, China): $1,168 airfare/$212 (Vientiane), $407 (Guangzhou) max daily per diems
5. Ross (Italy): $2,000 airfare/$471 (Rome) max daily per diem
6. Li (China): $3,625 airfare/$377 (Beijing), $241 (Kunming), $407 (Guangzhou), $241 (Wuhan) max daily per diems
7. Karesh (Italy): $7,000 airfare (*business class required to accommodate medical need*)/$471 (Rome) max daily per diems

Travel requests:

1. Metabiota would like to request travel approval for Amethyst Gillis to travel from Yaoundé, Cameroon to San Francisco, CA, USA from March 17 to April 1, 2017 for meetings to discuss PREDICT Year 3 workflow. From San Francisco, California, USA, she will travel to Nanaimo, BC, Canada from April 2-4, 2017 for meetings to discuss all aspects of the PREDICT program. **Amethyst Gillis will take a personal holiday from April 4– 7, 2017, during which time she will be covering her own expenses.*

Trip purpose: USA – Ms. Gillis will meet with Eddy Rubin, Robert Mann and Karen Saylors to discuss PREDICT Year 3 workflow. Canada – Ms. Gillis will meet with the PREDICT team members, Regional Coordinators, and Program Manager and the IM team to discuss all aspects of the PREDICT program.

2. EcoHealth Alliance would like to request travel approval for Dr. Jonathan Epstein to travel from New York, NY, USA to Sabah, Malaysia from March 18-20, 2017 to meet with the PREDICT-2 Country Coordinator for Malaysia. From Sabah, Malaysia, he will travel to Bangkok, Thailand from March 21-22, 2017 to meet with the Regional Development Mission in Asia (RDMA).

Trip purpose: Malaysia - Dr. Epstein will meet with Country Coordinator, Tom Hughes, and government partners to discuss PREDICT-2 activities and this year's workplan. Thailand - He will then travel to Bangkok for an informational outbrief regarding the countries of which he is the PREDICT-2 Regional Lead.

3. UC Davis would like to request travel approval for Dr. Lucy Keatts to travel from St. Thomas, US Virgin Islands to Phnom Penh, Cambodia from April 29 to May 7, 2017 to participate in coordination meetings and field surveillance in support of the PREDICT Country Coordinator for Cambodia.

Trip purpose: Dr. Keatts will travel to Cambodia to meet with government and non-governmental partners regarding coordination of PREDICT-2 sampling activities, and will oversee and offer technical guidance for the concurrent sampling of human, livestock, and wildlife planned for May 1-5, 2017 in a bat guano farming community in Kampong Cham Province.

4. Metabiota would like to request travel approval for Dr. David McIver to travel from Nanaimo, British Columbia, Canada to Vientiane, Laos from March 24-30, 2017 to meet with in country partners to discuss laboratory output, program management, and the development of human surveillance. From Vientiane, Laos, he will travel to Guangzhou, China from March 30 to April 1, 2017 to meet with program partners and implementing hospitals.

Trip purpose: Laos – In Vientiane, Dr. McIver will work with principle collaborators at both the National Animal Health Laboratory and the National Centre for Laboratory and Epidemiology to discuss issues

surrounding laboratory services, communication and collaboration strategy, and preparations for the commencement of human surveillance in Lao PDR. China – In Guangzhou, Dr. McIver will meet with key implementing partners at the Guangdong Center for Disease Control and the Guangdong Institute of Public Health to discuss the ongoing recruitment of participants in two hospitals in Guangdong province. Furthermore, he will be visiting the Tungwah Hospital, in Dongguan, to assess participant enrollment and discuss strategies for increasing enrollment, as well as balancing the enrollment of children and adults.

5. EcoHealth Alliance would like to request travel approval for Dr. Noam Ross to travel from New York, NY, USA to Rome, Italy from March 27-30, 2017 to collaborate with Ugo Pica Ciamarra at the Food and Agriculture Organization (FAO).

Trip purpose: Dr. Ross will work with Mr. Pica Ciamarra on the Africa Sustainable Livestock 2050 dynamic modeling.

6. EcoHealth Alliance would like to request travel approval for Hongying Li to travel from New York, NY USA to Beijing, Kunming, Guangzhou, and Wuhan, China from April 3 to May 31, 2017 for field coordination work and meetings with in-country partners in China.

Trip purpose: Hongying Li will be meeting with partners in Beijing for PREDICT surveillance work, and to work with local field coordinator, Dr. Guangjian Zhu, to assist the field work in Yunnan and Guangdong provinces. She will also meet with China Country Coordinator, Dr. Zhengli Shi, at Wuhan Institute of Virology for project updates and planning.

7. EcoHealth Alliance would like to request travel approval for Dr. William Karesh to travel from New York, NY, USA to Rome, Italy from March 29-31, 2017 to develop strategic partnerships.

Trip purpose: This trip is part of Dr. Karesh's role as the Head of Technical Activity for Wildlife and as a member of the OFFLU Steering Committee. As EPT Liaison, it is important for Dr. Karesh to continue to promote and optimize collaborations of PREDICT-2 objectives and OIE activities and engage on influenza initiatives to promote global health security. The meeting will be attended by experts currently generating influenza surveillance data and research activities in avian and swine. Economy class travel and per diem expenses will be covered by OIE.

From: Cara Chrisman <cchrisman@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>
CC: Dennis Carroll <dcarroll@usaid.gov>;Brooke Watson <watson@ecohealthalliance.org>;Elizabeth S Chase <eschase@ucdavis.edu>
Sent: 3/2/2017 9:24:51 PM
Subject: Earth BioGenome Project (EBP)

Hi All,

You may be more familiar with this than me, but given how often we are questioned about other projects along the same lines as the GVP (particularly the Microbiome), wanted to make sure you had all seen this article in Science about the Earth BioGenome Project (EBP).

Some highlights:

- Goal = sequence all life on earth
- 1st step = focusing on eukaryotes for about $4.8B in 10yrs
- Not yet funded
- Came up with vision 2 yrs ago
- Presented at BioGenomics 2017
- Also draw parallels to the HGP & generating new technologies
- Will build on: Genome 10K Project, which seeks to sequence 10,000 vertebrate genomes, one from each genus; i5K, an effort to decipher 5000 arthropods; and B10K, which expects to generate genomes for all 10,500 bird species.
- Commitments from BGI (china) and Wellcome Trust Sanger for sequencing

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (AID)

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From: Megan M Doyle <mmdoyle@ucdavis.edu>
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>;Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>;David John Wolking <djwolking@UCDAVIS.EDU>;Jonna Mazet <jkmazet@UCDAVIS.EDU>
Sent: 3/3/2017 11:46:07 PM
Subject: RE: P2 activities

Hi Chris et al.,
Incorporated Liz's edits with some of my edits (in red). I didn't include the EHA China stuff from the body of the email below – think we have enough info in there for China, but up to you Chris.

Have a nice weekend all!
Megan

From: Elizabeth Leasure
Sent: Friday, March 03, 2017 4:16 PM
To: Christine Kreuder Johnson ; Megan M Doyle ; David John Wolking ; Jonna Mazet
Subject: RE: P2 activities

Hi there. All of my additions (Ghana and Metabiota only) are in red text, but I wasn't quite sure how to add the information below from EHA for China (so I'll leave that to you *J*).

1) Yunnan Institute of Endemic Diseases Control and Prevention, PREDICT Human behavior risks surveillance partner, Dr. Yunzhi Zhang
2) Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, PREDICT laboratory partner, Dr. Fu Gao

Elizabeth Leasure
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From: Christine Kreuder Johnson
Sent: Friday, March 03, 2017 3:38 PM
To: Megan M Doyle; David John Wolking; Jonna Mazet; Elizabeth Leasure
Subject: P2 activities

Hi all –
Tracker looking good to me. Only # of outbreaks is pending - I think we should just delete that for now (until we get this sorted in EIDITH (or we could just add in data from the M&E).
Does anyone want to take a look to make sure our terminology isn't too confusing?
Liz, Thanks in advance for any updates you have.
Megan and I are doing one more doublecheck.
/dkj

	A	B	C	D
1	Country	# Site/Events Characterized to date	Site Characterization-Risk Interfaces Characterized	# Wild Animals Sampled to date
2	**Bangladesh**	68/106	animal production; crop production; dwellings and temporary settlements; market and value chain; natural areas; outbreak investigation; zoos and sanctuaries	6705
3	**Cambodia**	3/10	animal production; crop production; extractive industry; market and value chain	2528
4	**Cameroon**	16/33	crop production; dwellings and temporary settlements; market and value chain; natural areas; wildlife restaurant; zoos and sanctuaries	1388
5	**China**	18/39	crop production; dwellings and temporary settlements; human hospital; natural areas	542
6	**DR Congo**	27/42	crop production; dwellings and temporary settlements; extractive industry; market and value chain; natural areas; outbreak investigation; wildlife restaurant; zoos and sanctuaries; human hospital	377

	A	B	C	D
7	**Egypt**	6/12	animal production; market and value chain; natural areas	301
8	**Ethiopia**	2/5	animal production; crop production; dwellings and temporary settlements; market and value chain; natural areas	data entry ongoing (estimated n=221)
9	**Ghana**	2/2	animal production; crop production; dwellings and temporary settlements; market and value chain; natural areas	89
10	**Guinea**	1/1	animal production; crop production; market and value chain; natural areas; outbreak investigation	data entry ongoing (estimated n=141)
11	**India**	0/0		subaward pending
12	**Indonesia**	10/12	market and value chain; natural areas	data entry ongoing (estimated n=581)
13	**Ivory Coast**	data entry ongoing	data entry ongoing	data entry ongoing (estimated n=136)
14	**Jordan**	4/9	animal production; crop production; natural areas	209
15	**Kenya**	1/1	animal production; market and value chain	data entry ongoing (estimated n=135)

	A	B	C	D
16	**Lao PDR**	2/8	dwellings and temporary settlements; market and value chain	310
17	**Liberia**	5/7	extractive industry; natural areas	454
18	**Malaysia, Peninsular**	10/12	dwellings and temporary settlements	63
19	**Malaysia, Sabah**	38/67	crop production; dwellings and temporary settlements; natural areas; wildlife restaurant; zoos and sanctuaries	531
20	**Mongolia**	20/22	natural areas	1202
21	**Myanmar**	3/3	dwellings and temporary settlements; natural areas	176
22	**Nepal**	7/27	animal production; crop production; dwellings and temporary settlements; market and value chain; natural areas	639
23	**Republic of Congo**	5/5	animal production; crop production; dwellings and temporary settlements; extractive industry	346
24	**Rwanda**	13/26	crop production; dwellings and temporary settlements; natural areas	580
25	**Senegal**	outbreak approved recently		0
26	**Sierra Leone**	40/56	animal production; crop production; dwellings and temporary settlements; human hospital; market and value chain; natural areas; outbreak investigation	1814

UCDUSR0001556

	A	B	C	D
27	**Tanzania**	6/8	animal production; crop production; extractive industry	556
28	**Thailand**	17/31	dwellings and temporary settlements; market and value chain; natural areas	840
29	**Uganda**	8/21	animal production; crop production; dwellings and temporary settlements; extractive industry; human hospital; market and value chain; natural areas; zoos and sanctuaries	236
30	**Vietnam**	30/37	animal production; market and value chain; outbreak investigation; wildlife restaurant; zoos and sanctuaries	145

UCDUSR0001557

	E	F	G	H	I
1	**Wildlife Taxa Sampled (n)**	**# Domestic Animals Sampled to date**	**Domestic Species Sampled (n)**	**# Human Questionnaires to date**	**Human Questionnaire Risk Characterized**
2	rodents/shrews(214); bats(368); non-human primates(5676); birds(447)	453	poultry/other fowl(312); goats/sheep(44); camels(90); cattle/buffalo(6); dogs(1)	IRB planning phase	
3	rodents/shrews(666); bats(1857); birds(5)	1390 (sampling supported by FAO)	poultry/other fowl(806); goats/sheep(25); swine(179); cattle/buffalo(304); horses(5); dogs(61); cats(10)	219	Animal Production or Abattoir(85); Crop Production(100); Human Hospital or Clinic (11); Hunter(4); Market & Value Chain(16); Wildlife Restaurant(2); Zoos & Sanctuaries(1)
4	rodents/shrews(736); bats(427); non-human primates(128); carnivores(37); ungulates(21); pangolins(39)	not planned	not planned	local IRB pending	
5	bats(542)	in planning phase with FAO	in planning phase with FAO	33; subcontract with hospital in development	data entry ongoing, Health Professional(1); Human Hospital or Clinic (32)
6	rodents/shrews(76); bats(238); non-human primates(63)	24	poultry/other fowl(7); goats/sheep(16); swine(1)	data entry ongoing (n=31 individuals); subcontract with hospital in development	data entry ongoing

	E	F	G	H	I
7	bats(301)	sampling supported by FAO	sampling supported by FAO	data entry ongoing (estimated n=300 individuals)	Animal Production or Abattoir(77); Crop Production(4); Market & Value Chain(62)
8	bats(93); non-human primates(128)	sampling initiated by FAO	sampling initiated by FAO	planning phase	
9	rodents/shrews(15); bats(5); non-human primates(69)	not planned	not planned	IRB approval pending; subcontracts with clinics (2) in exploratory phase	
10	rodents/shrews(29); bats(112)	data entry ongoing (estimated n=193)	goats/sheep(177); swine(6); dogs(10)	local IRB pending	
11	planning phase	planning phase	planning phase	planning phase	
12	rodents/shrews(59); bats(522)	sampling supported by FAO	sampling supported by FAO	local IRB pending	
13	bats (120); birds(12); and rodents/shrews(4)	not planned	not planned	IRB approved	
14	bats(209)	sampling supported by FAO	sampling supported by FAO	planning phase	
15	bats(50); non-human primates(69); rodents(16)	43	camels(43)	local IRB pending	

	E	F	G	H	I
16	rodents/shrews(247); bats(63)	sampling supported by FAO	sampling supported by FAO	local IRB pending; subaward in development; subcontract with hospital in development	
17	bats(454)	planning phase	planning phase	local IRB pending	
18	rodents/shrews(15); bats(20); non-human primates(27); carnivores(1)	164	poultry/other fowl(77); dogs(87)	data entry ongoing	
19	rodents/shrews(104); bats(291); non-human primates(58); carnivores(36); ungulates(1); pangolins(41)	not planned	not planned	not planned	
20	birds(1202)	not planned	not planned	not planned	
21	bats(112); non-human primates(59); rodents/shrews(5)	in planning phase with FAO	in planning phase with FAO	local IRB pending	
22	rodents/shrews(157); bats(43); non-human primates(485); birds(154)	sampling supported by FAO	sampling supported by FAO	440	
23	rodents/shrews(145); bats(200); carnivores(1)	not planned	not planned	IRB approved	
24	rodents/shrews(75); bats(412); non-human primates(93)	not planned	not planned	47	
25		not planned	not planned	local IRB approved	
26	rodents/shrews(317); bats(1487); non-human primates(10)	2306	goats/sheep(970); swine(1011); dogs(320); cats(5)	local IRB pending	

	E	F	G	H	I
27	rodents/shrews(185); bats(371)	sampling initiated by FAO	sampling initiated by FAO	20	Animal Production or Abattoir(11); Crop Production(17); Health Professional(2); Hunter(3); Market & Value Chain(3)
28	rodents/shrews(174); bats(507); non-human primates(159)	sampling supported by FAO	sampling supported by FAO	IRB pending	
29	rodents/shrews(57); bats(65); non-human primates(114)	80	camels(80)	15	(15); Animal Production or Abattoir(1); Crop Production(2)
30	rodents/shrews(30); non-human primates(6); birds(3); carnivores(7); ungulates(3); pangolins(96)	185 (animals sampled by FAO)	swine(185)	local IRB pending	

	J	K	L	M	N	O	P
1	**# Humans Sampled to date**	**Ethnographic Interviews to date**	**# Focus Groups to date**	**# Focus Group Participants to date**	**# Outbreak Investigations to date**	**# Wild Animals Tested to date**	**# Domestic Animals Tested to date**
2	IRB planning phase	73	4	32	44 (associated with total 2 outbreaks)	testing initiated; data entry in progress	testing initiated; data entry in progress
3	data entry ongoing (estimated n=106)	not planned	not planned	not planned	0	512	0
4	local IRB pending	111	9	101	0	801	0
5	data entry ongoing (estimated n=33 individuals); subcontract with hospital in development	154	6	47	0	542	0
6	data entry ongoing (n=31 individuals); Eastern DRC pending AD/AOR approval; subcontract with hospital in development	124	8	53	4	data entry ongoing (estimated n=255)	24

	J	K	L	M	N	O	P
7	data entry ongoing (estimated n=300 individuals)	not planned	not planned	not planned	0	data entry ongoing (estimated n=250)	0
8	planning phase	not planned	not planned	not planned	0	in exploratory phase for animal testing	0
9	local IRB pending; subcontracts with hospitals (2) in development	not planned	not planned	not planned	0	0	0
10	not planned	local IRB pending	local IRB pending	local IRB pending	1	subaward for testing in development	subaward for testing in development
11	planning phase	not planned	not planned	not planned	0	subaward pending	subaward pending
12	local IRB pending	47	1	36	0	0	0
13	IRB approved	0	0	0	0	0	0
14	planning phase	n/a	n/a	n/a	0	0	0
15	local IRB pending	n/a	n/a	n/a	0	0	0

	J	K	L	M	N	O	P
16	local IRB pending; subaward in development; subcontract with hospital in development	local IRB pending	local IRB pending	local IRB pending	0	153	0
17	not planned	local IRB pending	local IRB pending	local IRB pending	0	75	0
18	data entry ongoing (estimated 150 individuals)	n/a	n/a	n/a	0	105	416
19	not planned	n/a	n/a	n/a	0	67	0
20	not planned	n/a	n/a	n/a	0	testing initiated	0
21	local IRB pending	n/a	n/a	n/a	0	subaward for testing in development	0
22	436	40	3	32	0	420	0
23	IRB approved	6	0	0	0	143	0
24	47; subaward for second site pending AO/AOR approval	n/a	n/a	n/a	0	92	0
25	local IRB approved	n/a	n/a	n/a	0	subaward for testing in development	0
26	not planned	0	0	0	1	3	0

	J	K	L	M	N	O	P
27	IRB approved; subaward in development	20	2	20	0	75	0
28	IRB pending	n/a	n/a	n/a	0	516	0
29	12	48	4	40	0	68	80
30	local IRB pending	2	1	3	5	0	185

	Q
1	# Humans Tested to date
2	
3	0
4	0
5	6
6	0

	Q
7	data entry ongoing (n=136)
8	0
9	0
10	subaward for testing in developmen 1
11	subaward pending
12	0
13	0
14	0
15	0

	Q
16	subaward for human testing in developmen t
17	0
18	0
19	0
20	0
21	0
22	0
23	0
24	0
25	0
26	0

	Q
27	0
28	0
29	subaward for new testing partner in developmen t
30	0

	A	B	C	D
1	**Country**	**# Site/Events Characterized Currently in Staging**	**Site Characterization-Risk Interfaces Characterized**	**# Wild Animals Sampled Currently in Staging**
2	**Bangladesh**	9/13	animal production; market and value chain; outbreak investigation	0
3	**Cambodia**	1/1	market and value chain	91
4	**Cameroon**	2/2	dwellings and temporary settlements; zoos and sanctuaries	140
5	**DR Congo**	7/7	human hospital	0
6	**Egypt**	5/5	animal production; market and value chain	0
7	**Indonesia**	2/2	market and value chain; natural areas	124
8	**Jordan**	4/4	natural areas	78
9	**Liberia**	1/1	extractive industry	44
10	**Malaysia, Sabah**	4/9	crop production; natural areas	191
11	**Myanmar**	2/2	zoos and sanctuaries	55
12	**Nepal**	1/1	animal production; crop production; dwellings and temporary settlements	50

	A	B	C	D
13	**Rwanda**	2/3	human hospital; natural areas	43
14	**Sierra Leone**	2/2	dwellings and temporary settlements; natural areas	40
15	**Uganda**	1/1	animal production; crop production; dwellings and temporary settlements	24
16	**Vietnam**	1/1	zoos and sanctuaries	8

	E	F	G	H
1	Wildlife Taxa Sampled (n)	# Domestic Animals Sampled Currently in Staging	Domestic Species Sampled (n)	# Human Questionnaires Currently in Staging
2		117	poultry/other fowl(117)	0
3	birds(4); rodents/shrews (87)	358	cats(1); cattle/buffalo(59); dogs(14); goats/sheep(10); poultry/other fowl(168); swine(104)	0
4	bats(25); non-human primates(6); rodents/shrews (109)	0		0
5		0		0
6		0		0
7	bats(111); rodents/shrews (13)	0		0
8	bats(78)	0		0
9	bats(44)	0		0
10	bats(160); carnivores(1); rodents/shrews (30)	0		0
11	non-human primates(50); rodents/shrews (5)	0		0
12	rodents/shrews (50)	0		0

	E	F	G	H
13	bats(43)	0		0
14	bats(21); rodents/shrews (19)	0		0
15	rodents/shrews (24)	0		0
16	pangolins(8)	0		0

	I	J	K	L	M
1	# Humans Sampled Currently in Staging	Human Questionnaire Risk Characterized	# Ethnographic Interviews to date	# Focus Group Participants	# Outbreak Investigations Currently in Staging
2	0	NULL	N/A	N/A	13
3	0	NULL	N/A	N/A	0
4	0	NULL	N/A	N/A	0
5	0	NULL	N/A	N/A	0
6	0	NULL	N/A	N/A	0
7	0	NULL	N/A	N/A	0
8	0	NULL	N/A	N/A	0
9	0	NULL	N/A	N/A	0
10	0	NULL	N/A	N/A	0
11	0	NULL	N/A	N/A	0
12	0	NULL	N/A	N/A	0

	I	J	K	L	M
13	0	NULL	N/A	N/A	0
14	0	NULL	N/A	N/A	0
15	0	NULL	N/A	N/A	0
16	0	NULL	N/A	N/A	0

	N	O	P
1	# Wild Animals Tested Currently in Staging	# Domestic Animals Tested Currently in Staging	# Humans Tested Curently in Staging
2	0	0	0
3	0	0	0
4	55	0	0
5	0	0	0
6	0	0	0
7	0	0	0
8	0	0	0
9	0	0	0
10	13	0	0
11	0	0	0
12	77	0	0

	N	O	P
13	0	0	0
14	0	0	0
15	0	0	0
16	0	0	0

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
CC: Megan M Doyle <mmdoyle@ucdavis.edu>;Elizabeth Leasure <ealeasure@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>
Sent: 3/4/2017 12:57:25 AM
Subject: Re: P2 activities

Sounds good to me -- thanks to all!
Have a nice weekend,
J

On Fri, Mar 3, 2017 at 5:32 PM, Christine Kreuder Johnson <ckjohnson@ucdavis.edu> wrote:

Thanks to you all -

Looking it over one last time and if I don't hear any concerns, I'll send it over to USAID shortly.

/ckj

From: Megan M Doyle <mmdoyle@UCDAVIS.EDU>
Date: Friday, March 3, 2017 at 4:46 PM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>, Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, David John Wolking <djwolking@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: P2 activities

Hi Chris et al.,

Incorporated Liz's edits with some of my edits (in red). I didn't include the EHA China stuff from the body of the email below -- think we have enough info in there for China, but up to you Chris.

Have a nice weekend all!

Megan

From: Elizabeth Leasure
Sent: Friday, March 03, 2017 4:16 PM
To: Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>; Megan M Doyle <mmdoyle@UCDAVIS.EDU>; David John Wolking <djwolking@ucdavis.edu>; Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: P2 activities

Hi there. All of my additions (Ghana and Metabiota only) are in red text, but I wasn't quite sure how to add the information below from EHA for China (so I'll leave that to you J).

1) Yunnan Institute of Endemic Diseases Control and Prevention, PREDICT Human behavior risks surveillance partner, Dr. Yunzhi Zhang
2) Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, PREDICT laboratory partner, Dr. Fu Gao

Elizabeth Leasure

One Health Institute

University of California, Davis

530-754-9034 (office)

530-304-1403 (cell)

From: Christine Kreuder Johnson
Sent: Friday, March 03, 2017 3:36 PM
To: Megan M Doyle; David John Wolking; Jonna Mazet; Elizabeth Leasure
Subject: P2 activities

Hi all –

Tracker looking good to me. Only # of outbreaks is pending - I think we should just delete that for now (until we get this sorted in EIDITH (or we could just add in data from the M&E).

Does anyone want to take a look to make sure our terminology isn't too confusing?

Liz, Thanks in advance for any updates you have.

Megan and I are doing one more doublecheck.

/ckj

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
To: Jon Epstein <epstein@ecohealthalliance.org>
CC: Dan Schar <dschar@usaid.gov>;Clements, Andrew(ANE/TS) <AClements@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 3/8/2017 12:49:34 AM
Subject: Re: China_ 2017 Country implementation plan

Thanks Jon.

I think we will need to get the updated communication instruction from P2. Hope Jonna can sort it out and provide us the instruction/ guideline on communication channel to avoid confusion in the future. Will forward you the advice from Metabiota when we sent the request for Lao CIP.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

On Wed, Mar 8, 2017 at 6:57 AM, Jon Epstein <jepstein@ecohealthalliance.org> wrote:
Hi Sudarat,
I hope you're well. Thanks for sending the CIP request. We'll have this to you on the 8th. Just a gentle reminder, as EHA is the primary implementing partner for PREDICT China, please send future communications to us (Zhengli, Hongying, and me!). We'll update the CIP with project information from both EHA's and Metabiota's activities. I just want to avoid any confusion from parallel requests.

Many thanks! I look forward to seeing you soon.

Cheers,
Jon

On Thu, Mar 2, 2017 at 3:38 AM, Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
Dear PREDICT China team,

Attachment is a draft CIP for China. Please provide update including timeline for the planned activities. And if some activities are missed, please include them in. Please update and submit 2017 to us by March 8, COB.

Thank you very much.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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web: ecohealthalliance.org

Twitter:

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Andrew Clements <aclements@usaid.gov>
CC: Alisa Pereira <apereira@usaid.gov>;Tracey Goldstein <tgoldstein@ucdavis.edu>
Sent: 3/8/2017 7:21:19 PM
Subject: Re: SL ? -- liquid nitrogen plant

Thank you very much,
J

On Wed, Mar 8, 2017 at 8:17 AM, Andrew Clements <aclements@usaid.gov> wrote:
just communicated the request to the mission. will let you know if there's any push back. if so, i'm prepared to counter it.

On Wed, Mar 8, 2017 at 5:08 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Thanks, David is working on the LN2 update.
Please note the request in the other chain for a hold on the Ambassador or anyone else briefing the President until March 15 (possibly earlier if they give us the green light). If that is not acceptable from USAID standpoint, we need to inform the team and ministries.
Thanks,
J

On Wed, Mar 8, 2017 at 5:23 AM, Alisa Pereira <apereira@usaid.gov> wrote:
Dear Jonna and team,

This morning we had a call with the Mission in SL about the finding. They had several questions. We offered up the opportunity to have a call with PREDICT HQ to answer those questions. We are going to wait until they brief the Ambassador to determine if there are additional questions from that briefing that need to be addressed.

In the meantime, they asked about the liquid nitrogen plant. Would you please let us know the status of the replacement of the liquid nitrogen plant?

Thanks
alisa

202-712-5221
202-997-9966
apereira@usaid.gov

predictmgt+unsubscribe@usaid.gov
predictmgt@usaid.gov
https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/CAO5tDrHWPkyMeW5MDgVaBXL2Uc74HmrCZCi4mY--qerUTS8EoA%40mail.gmail.com

1.571.345.4241
a[redacted]@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: David McIver <dmciver@metabiota.com>
CC: Cate Best <cbest@metabiota.com>;Karen Saylors <ksaylors@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Beth Edison <bedison@metabiota.com>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 3/17/2017 4:07:48 PM
Subject: [predict] RE: [3.7.17] PREDICT International Travel Requests

Hi Dave. I wouldn't go to any trouble or incur additional costs to rearrange your trip to for a meeting on the 24th. My suggestion would be to reach out to Andrew to see if you can schedule something that fits within your existing itinerary.

Thanks,
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: David McIver [mailto:dmciver@metabiota.com]
Sent: Friday, March 17, 2017 8:54 AM
To: Elizabeth Leasure
Cc: Cate Best; Karen Saylors; Eddy Rubin; Beth Edison
Subject: Re: [3.7.17] PREDICT International Travel Requests

Hi Liz,

Thanks very much for forwarding along this information. I wasn't planning to leave Canada until the 24th, but if we can arrange it so that I can be in Vientiane in time to meet with Andrew, I would be happy to do so.

Thank you!

Dave

—
David McIver, PhD
PREDICT Asia Regional Coordinator | Epidemiologist
Metabiota

e: dmciver@metabiota.com
c: +1 778-269-2965

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On Mar 16, 2017, at 3:52 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Hi Cate. Dave's trip below has been approved. Please note the email below from Andy Corwin at the Lao PDR Mission. He has a question and would like to schedule a meeting, if possible, while Dave is there.

Thanks,
Liz

Elizabeth Leasure

One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Corwin, Andrew L [mailto:CorwinAL@state.gov]
Sent: Tuesday, March 14, 2017 8:11 PM
To: Louis Duthil, Cassandra (GH/SDI); Kongchay, Vongsaiya
Cc: Pereira, Alisa (GH/HIDN); Clements, Andrew (GH/HIDN); Gillette, Shana (BFS); Elizabeth Leasure; David John Wolking; Huerta, Alexandria I; Martz, Robin (USAID); Schar, Daniel (RDMA/OPH)
Subject: RE: [3.7.17] PREDICT International Travel Requests

Dear Cassandra,

I will be in Vientiane during that period, but Khonchay will be in Bangkok for most of that time – although possibly we could all meet on Friday, 24 March 2017. It would be great if we could all meet, but understand if scheduling issues preclude such.

I would welcome the opportunity to speak with David, and learn in more detail of projected project activities. Also, and if scheduling permits, I would benefit from joining David during his discussions with NCLE and NAHL. Are there plans to convene any meetings during his visit with both human and animal health sectors, together?

Best regards,

Andy

Andrew L Corwin
Health Program Manager
USAID /Lao People's Democratic Republic (PDR)
Tel: 856.21.487305
Cell: 856.20.55521249
Email: corwinal@state.gov

On Wed, Mar 8, 2017 at 3:23 AM, Cassandra Louis Duthil <clouisduthil@usaid.gov> wrote:

Hello teams
RDMA and Laos,

the following travel approval requests have

come in from
PREDICT
. We appreciate your concurrence and welcome any questions you may have. *Please note: All travelers should be prepared to provide an in/out brief*

during the duration of their travel.

4.
Metabiota would like to request travel approval for

Dr. David McIver to travel from Nanaimo, British Columbia, Canada to

Vientiane, Laos from March 24-30, 2017 to meet with in country partners to discuss laboratory output, program management, and the development of human surveillance.

From Vientiane, Laos, he will travel to Guangzhou, China from March 30 to April 1, 2017 to

meet with program partners and implementing hospitals.

Trip purpose: Laos – In Vientiane, Dr. McIver will work with principle collaborators at both the National Animal Health Laboratory and the National Centre for Laboratory and Epidemiology to discuss issues surrounding

laboratory services, communication and collaboration strategy, and preparations for the commencement of human surveillance in Lao PDR.

China – In Guangzhou, Dr. McIver will meet with key implementing partners at the Guangdong Center for Disease Control and the Guangdong Institute of Public Health to discuss the ongoing recruitment of participants in two hospitals in Guangdong province.

Furthermore, he will be visiting the Tungwah Hospital, in Dongguan, to assess participant enrollment and discuss strategies for increasing enrollment, as well as balancing the enrollment of children and adults.

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Woutrina Smith <wasmith@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>
CC: Brian Bird <bhbird@ucdavis.edu>;Elizabeth Leasure <ealeasure@ucdavis.edu>;Elizabeth VanWormer <liz.vanwormer@unl.edu>
Sent: 4/20/2017 4:21:46 AM
Subject: Re: TZ grants - Request for NCE and Annual Meeting

I agree, let's separate them out if we can.
NCE and date-setting for in-country meeting (maybe September) now. If she [presses, you can say that we are sorting out major administrative issues with Metabiota at the moment that we wouldn't want to complicate or color our relationship on these projects going forward. Then we attempt to discuss options with Mary when we can separately before moving forward.
There should be some opportunities, or I can just ask her for a meeting when you all have ideas prepared for a discussion of options with her.
Sound okay?
J

On Wed, Apr 19, 2017 at 4:59 PM, Woutrina Smith <wasmith@ucdavis.edu> wrote:
I suggest we deal with the two issues separately. Falgu just asked us to provide her the time of extension and justification, so let's give her that by email to pass up the food chain, and also give the blessing to delay Mary's visit to fall amidst the busy schedules. Those are the highest priority communications and in the context of us all being so busy right now, it may take some time to schedule any follow up calls and meetings, which is fine. Other aspects of MB need time to play out before we address partnership directly for future DTRA work. Wout

---

On Apr 19, 2017, at 3:23 PM, Brian Bird <bhbird@ucdavis.edu> wrote:

Makes most sense to me to just be straight forward. Tell MB that we would like to pursue the NCE with them and that we've valued their help in managing the project, but that we'll be striking it out on our own on the next grants moving forward. We might want to have a call with them to help smooth the blow?

And communicate the same to Mary and her team (probably after the NCE is put in and hopefully approved?) so that they are aware.

Perhaps that's not very savvy, but at least it's clean and simple.

-b

aka "bull in china shop"?

From: David J Wolking <djwolking@ucdavis.edu>
Date: Wednesday, April 19, 2017 at 12:36 PM
To: "Prof. Woutrina Smith" <wasmith@ucdavis.edu>, Brian Bird <bhbird@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Cc: Elizabeth Leasure <ealeasure@ucdavis.edu>, Elizabeth VanWormer <liz.vanwormer@unl.edu>
Subject: Re: TZ grants - Request for NCE and Annual Meeting

This is timely and getting tricky with the NCE mixed in with the annual meeting and future collabs angle. The last call I had with Falgu about the equipment process was pretty awkward thanks to that future directions conversation and I simply deflected that one. But without any connections with Mary or the DTRA team directly how should we plan the diplomatic approach for: 1) pass through via MB for the NCE proposal and 2) working around MB to explore future projects?

I'm not responding until we're on the same page here with strategy as Falgu often cold calls me by phone or Skype...

David

On Wed, Apr 19, 2017 at 9:32 AM, Falgunee K. Parekh <fparekh@metabiota.com> wrote:

Hi All,

Now that the Year 3 funds have been released and the equipment purchase has been approved, I think it is a good time to discuss the Request for No Cost Extension (NCE). Currently the Period of Performance is set to end around August 5, 2017. How much additional time do you think we need? I know that we have previously discussed 6 months, but would 9 months be more appropriate to account for variations in seasonality and any potential delays in sample collection and analysis? Please let me know what would work best for you and also provide a justification for that amount of time that we can present to DTRA.

Also, I spoke with Mary briefly about the annual meeting. The earliest that she could be available for in-country meetings is end of July/beginning of August. She would prefer to see some preliminary results at the annual meeting, so if we need to delay to the fall then that is fine. Can you please let me know when you may have some preliminary results ready to present, and when would be a good time to have in-country meetings?

Finally, Mary seems very supportive of us pursuing follow-on work. This would be done through the normal BAA process, however prior to submitting an abstract we can have preliminary conversations to discuss potential concepts. Please send any potential research concepts that you may be interested in pursuing that would be reasonable follow-ons to the current projects. I would like to set up a meeting in the next few weeks to discuss potential concepts so that we can begin those conversations with Mary. As you may recall with these current grants, the process can take some time with DTRA, so now is the right time to start planning for the follow-on. Thanks.

Falgunee

Falgunee K. Parekh, MPH, PhD

Staff Scientist, Epidemiology

Metabiota, Inc.

Tel: 301.676.1919 | Email: fparekh@metabiota | skype: falguneep

metabiota.com

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From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>
Sent: 5/8/2017 8:53:29 PM
Subject: Fwd: primer for Tuesday's call

---------- Forwarded message ----------
From: **Eddy Rubin** <erubin@metabiota.com>
Date: Mon, Apr 17, 2017 at 4:31 PM
Subject: primer for Tuesday's call
To: Jonna Mazet <jonna.mazet@gmail.com>

Dear Jonna,

Look forward to chatting tomorrow. Just so you know how we are thinking and the directions we plan to go, I have included some material. Below is what we view would be the optimal Metabiota/ PREDICT Country by Country game plan going forward. This is similar to what I briefly mentioned to you when we were in DC for CUGH.

We are also working on a Sample and Data Quality Risk and Corrective Action plan which I will get to you before this Friday. I think with focus and putting in place the structures and QA and QC activities described in this document we can correct the sample/data quality/ safety… issues. We have also developed a Sierra Leone Data Report which will be completed in the next day or so. This report offers an overview of the SL data situation and includes: What happened with our data? How is our data being corrected? How will future data problems be *avoided*?

With regard to Tuesday's 9:00 AM call. I believe that it might be useful to have Karen participate on the call as she has a deep perspective on Metabiota's on the ground activities in all our countries though I defer to your decision on who should be on the call.

Best,

Eddy

Overview of Country-by-Country Game Plan

We are developing a **Sample and Data Quality Risks and Corrective Action** process, which includes new quality control checks and training plans in the following domains: 1) Animal field sampling (biosecurity, data capture, QC) refresher training; 2) Data Quality Control procedure of data from field to EIDITH; 3) lab sample quality, monitoring and analysis plan. This will be submitted to Davis upon completion (estimated timeline Wed, April 19th)

Metabiota is recommending focus on key country operations with unique field presence and discontinuation of management of China, Indonesia and ROC.

Metabiota proposes the following realignments:

Countries to be discontinued or for narrowed focus:

China : According to our analysis of the associated EIDITH data on those individuals enrolled from Dongguan and Shunto hospitals, approximately 40% of the enrolled population has lifetime animal exposure, specifically: 20% handle live animals, 31% raise live animals 13% share a water source with animals, 21% have animals in the dwelling, 20% cook or handle live animals, 13% slaughter animals, and 23% hunter or trapped.

Based on this analysis, it does not seem that this level of exposure warrants continuing work in China. If Davis concurs, Metabiota will cease operations at our two hospitals in China.

Indonesia : Metabiota will cease operations and plans for hospital surveillance will be transferred to EHA.

Republic of Congo (RoC): MII will continue behavioral data collection in Brazzaville markets with the objective of collecting qualitative and questionnaire data in 5 bushmeat markets and restaurants. Karen has submitted an update on DRC/ROC Bushmeat market work and proposed work plan for ROC (April 14, 2017). We have ceased animal sampling and any syndromic surveillance in RoC. *Discussion points with Davis: 1) Davis to assume management of RoC*

Focus Countries:

Cameroon : We will keep leadership and maintain program in Cameroon, and conduct lab and data quality retraining within the next 3 months. After centralized training, we will deploy field specialists from Cameroon to other sites : Jean Michel (bat sampling specialist), Matthew LeBreton (wildlife ecologist) and Dr. Moctar Mouiche (wildlife vet) for field trainings in other countries.

Cote d'Ivoire: Continue operations working with Institute Pasteur de Cote d'Ivoire (IPCI) and LANADA partners but do not build out separate PREDICT lab space within IPCI.

Democratic Republic of Congo (DRC): We have ceased compensation to Prof Muyembe since December 2016 and are adjusting the subcontract with INRB accordingly. We will cut the second site of Buta after our April data collection trip and will provide retraining within the next quarter. (Re-training calendar to follow by Wed, April 19th)

Guinea : Per the retraining schedule, send Dr. Moctar and Jean Michel for intensive field sampling, data QC, and biosafety training refresher, with JM to stay for 2 weeks for intensive bat sampling. Put MOU in place with Ministry partners. Frantz will be fully retrained in all of SOPS training refreshers and will travel to Guinea every other month for field supervision.

Laos : We will continue operations and maintain program in Laos, and conduct lab and data quality retraining within the next 3 months. In late April, we will send the Laos team to Indonesia for lab training.

Sierra Leone : Team will immediately go through upgraded retraining, post quality control assessment and with a new supervision plan in place. We have assigned Jason (Data Quality and Implementation Manager) to assist Aiah, James and Frantz in data cleanup. We have suspended field sampling work in SL until this training and recertification is complete. 1) Per the **Sample and Data Quality Risks and Corrective Action plan,** we will complete data cleanup. 2) Davis to approve new data QC plan and field lab biosafety plans, and 3) staff biosafety training refresher will be completed before restarting field sampling. Frantz Jean Louis will be fully trained in all of these SOPS/training refreshers and to travel to SL every other month for field supervision.

Animal sample shipment: Metabiota will ship confirmatory samples to CDC in April and remaining wildlife samples to Davis once data verification is finalized.

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: predict@ucdavis.edu <predict@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;Brian Bird <bhbird@ucdavis.edu>;Corina Monagin <cmonagin@gmail.com>
Sent: 5/12/2017 4:15:31 AM
Subject: Fwd: Summary of Wednesday discussion

FYI -- we will discuss tomorrow in UCD Predict all staff,
J

---------- Forwarded message ----------
From: **Jonna Mazet** <jkmazet@ucdavis.edu>
Date: Thu, May 11, 2017 at 9:14 PM
Subject: Re: Summary of Wednesday discussion
To: Eddy Rubin <erubin@metabiota.com>
Cc: Karen Saylors <ksaylors@metabiota.com>

Thanks very much, Eddy,
This summary aligns perfectly with our discussion and reflects the current plan.
Conferring with our team, USAID, and EHA (next week). To help us with the remaining planning pieces and smooth transitions.
I received word from Andrew and USAID contracts that we can assume MB subawards without restarting the DC review process, so that will be useful.
More soon,
Jonna

On Thu, May 11, 2017 at 4:48 PM, Eddy Rubin <erubin@metabiota.com> wrote:

Jonna

This is a quick summary from what we took from yesterday's conversation to make sure we're starting from the same page:

1. Metabiota will continue to manage:

a) PREDICT Information Management EIDITH activities.

b) Cameroon, DRC and Laos. Christian should travel to Cameroon and DRC for lab and staff capacity assessment.

2. For Sierra Leone and Guinea we work with the UC Davis team to make a transition to UC Davis management. We will need further guidance on how this would work contractually/administratively.

a) you'd like a list of the SL staff and responsibilities

b) we should notify field sampling staff that they will not be going back into the field anytime soon, due to budget reductions and shift in scope.

3. Indonesia and China we will work with EcoHealthAlliance to transfer our human activities once Davis gives us the word.

a) In China, we will work to finish lab analysis, but all human syndromic surveillance has been stopped.

b) For Indo, we may have a silent transition in country, as our sub with Eijkman is necessary to the project, and questions have been submitted to USAID, so we are on standby.

4. Côte d'Ivoire and ROC these countries will continue with a limited scope until further USAID decisions are made.

a) In ROC we will continue behavioral surveillance. ITAs have been submitted for behavioral consultants to travel to DRC for training and supervision by Ashley; Karen and Prime to travel to the region in June for behavioral supervision and discussions with the Mission.

b) In CIV, the idea is to scale back to GHSA training model, but meanwhile we will continue animal sampling (LANADA) and human behavioral work (IPCI). Plan to cancel/suppress syndromic surveillance, but need to discuss the plan on how to manage lab analysis of animal samples and equipment that is in country; this discussion will occur among our team early next week and we will get you a plan/suggestions. Cancel the ITA for Ashley and Frantz.

We will provide you with more details and suggestions of possible next steps and issues with a particular focus on Sierra Leone and Guinea by mid next week, as well as a list of issues that will need some attention in the transition, per discussions with our field teams. We will continue our activities as is in all our counties for the time being.

Eddy and Karen

From: Kevin Olival, PhD <olival@ecohealthalliance.org>
To: Andrew Clements <aclements@usaid.gov>
CC: Dr. Jonna Mazet <jkmazet@ucdavis.edu>;Alisa Pereira <apereira@usaid.gov>;Shana Gillette <sgillette@usaid.gov>;Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh" <karesh@ecohealthalliance.org>;Alison Andre <andre@ecohealthalliance.org>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 6/3/2017 2:05:45 PM
Subject: Re: DRC and ROC

Dear Andrew,

Sorry for chiming in late here. I was in Thailand at the end of last week and met with Dan and Sudarat at RDMA. I did briefly and informally mention to both of them the transition in China and Indonesia. Andrew, it would be great if you could let them know formally.

Please let me know if you have any questions.

Thank you,
Kevin

Kevin J. Olival, PhD
Associate Vice President for Research

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On Jun 3, 2017, at 2:23 AM, Andrew Clements <aclements@usaid.gov> wrote:

Thanks. Safe travels.

Once I've notified the USAID staff in ROC, RDMA, and Indonesia, I will let you all know so you can follow up with the Mission staff if they have additional questions.

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jun 2, 2017, at 9:56 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Hi Andrew,
No transition in DRC at the moment. We are hopeful that all will remain stable with Metabiota there.
RoC will transition to EcoHealth Alliance, with Billy as global lead. He and Karen are discussing scope, but

we will at least retain market behavior work and staff. If resources allow and science justifies, we may also sample upstream to address the new highway and possibility of change of risk in value chain with easier transportation.

EcoHealth was already lead partner in Indonesia and China, so they are managing the communication as usual and will or have informed that Metabiota is phasing out. Billy, Kevin, and Peter copied to make sure.

On my way toTanzania now,
J

On Thu, Jun 1, 2017 at 1:44 PM, Andrew Clements <aclements@usaid.gov> wrote:
Can you remind me what the transition plans are for DRC and ROC? Who would be the new implementing partners? Who would be the new country backstops? Etc.

Also, have the missions been notified of the proposed management changes for Indonesia and China? Any other countries where I need to notify missions (already covered CDI, SL, Guinea)?

Thanks!

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Alisa Pereira <apereira@usaid.gov>;Shana Gillette <sgillette@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>;Brooke Genovese <bgenovese@ucdavis.edu>;Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>;Brian Bird <bhbird@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>
Sent: 6/4/2017 7:24:36 AM
Subject: Re: DRC and ROC

Thanks. I'm waiting to her back regarding true day/time for a phone call.

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jun 3, 2017, at 9:53 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Thanks (& sorry for anything I missed while in the air.), but are we good to go to schedule with Guinea Mission -- they're asking for more info.
Have a good weekend,
Jonna

On Saturday, June 3, 2017, Andrew Clements <aclements@usaid.gov> wrote:
Thanks. Safe travels.

Once I've notified the USAID staff in ROC, RDMA, and Indonesia, I will let you all know so you can follow up with the Mission staff if they have additional questions.

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jun 2, 2017, at 9:56 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Hi Andrew,
No transition in DRC at the moment. We are hopeful that all will remain stable with Metabiota there.
RoC will transition to EcoHealth Alliance, with Billy as global lead. He and Karen are discussing scope, but we will at least retain market behavior work and staff. If resources allow and science justifies, we may also sample upstream to address the new highway and possibility of change of risk in value chain with easier transportation.

EcoHealth was already lead partner in Indonesia and China, so they are managing the communication as usual and will or have informed that Metabiota is phasing out. Billy, Kevin, and Peter copied to make sure.

On my way toTanzania now,
J

On Thu, Jun 1, 2017 at 1:44 PM, Andrew Clements <aclements@usaid.gov> wrote:
Can you remind me what the transition plans are for DRC and ROC? Who would be the new implementing partners? Who would be the new country backstops? Etc.

Also, have the missions been notified of the proposed management changes for Indonesia and China? Any other countries where I need to notify missions (already covered CDI, SL, Guinea)?

Thanks!

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

From: Andrew Clements <aclements@usaid.gov>
To: William B. Karesh <karesh@ecohealthalliance.org>
CC: Kevin Olival, PhD <olival@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;David Wolking <djwolking@ucdavis.edu>;Alisa Pereira <apereira@usaid.gov>;Shana Gillette <sgillette@usaid.gov>
Sent: 6/5/2017 4:15:29 PM
Subject: Re: PREDICT management changes in China

Thanks

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jun 5, 2017, at 4:42 PM, William B. Karesh <karesh@ecohealthalliance.org> wrote:

No Changes for Laos. Metabiota still working there as planned.

BK

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
460 West 34th Street - 17th Floor
New York, NY 10001 USA

+1.212.380.4463 (direct)
+1.212.380.4466 (fax)
www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On Jun 5, 2017, at 8:56 AM, Andrew Clements <aclements@usaid.gov> wrote:

Question from RDMA: any changes in Laos?

Andrew P. Clements, Ph.D.
Senior Scientific Adviser

Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jun 5, 2017, at 1:54 PM, Andrew Clements <aclements@usaid.gov> wrote:

RDMA Mission notified as well.

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

Begin forwarded message:

From: Andrew Clements <aclements@usaid.gov>
Date: June 5, 2017 at 1:48:52 PM GMT+2
To: "Daniel Schar (RDMA/OPH)" <dSchar@usaid.gov>, "Sudarat Damrongwatanapokin (RDMA/OPH)" <sDamrongwatanapokin@usaid.gov>
Cc: Alisa Pereira <apereira@usaid.gov>, Shana Gillette <sgillette@usaid.gov>
Subject: PREDICT management changes in China

Hi Sudarat and Dan,

I'm writing to let you know that PREDICT is undergoing some internal management changes in a few countries, including China. As a result, the role of Metabiota will be decreased and the role of EcoHealth Alliance will increase. We hope the impact will be minor and expect that any changes will not greatly alter PREDICT's interactions with the GOPRC, local partners, local PREDICT staff, and the Mission. While changes in the middle of a project are not ideal, PREDICT felt that this change was necessary to make sure it could deliver the expected results.

At this point, I do not know if PREDICT has mentioned this transition to its in-country staff and partners so please do not share this information until PREDICT has had a chance to do so.

PREDICT is available for a phone call with you to discuss the transition plan in more detail and answer any questions you have.

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>
CC: Brian Bird <bhbird@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 6/5/2017 4:45:26 PM
Subject: RE: Guinea VHF sub award and employee questions

Sure, see attached.

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Corina Grigorescu Monagin
Sent: Monday, June 05, 2017 9:34 AM
To: Elizabeth Leasure
Cc: Brian Bird; Jonna Mazet
Subject: Re: Guinea VHF sub award and employee questions

Hi Liz,

They have their DUNS but most likely have not registered (99.9% likely)...do you have any guiding documents that I can pass onto the CC for this? I've never done it myself so have limited advice to provide. They are most likely going to need extreme hand-holding.

Thanks
corina

From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Date: Monday, June 5, 2017 at 3:42 PM
To: Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
Cc: Brian Bird <bhbird@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: Guinea VHF sub award and employee questions

One thing you could do is confirm that their SAM.gov registration is complete. The last info I have is that it was in progress, but it will need to be complete and current in order for UCD to send out the subaward for VHF signature.

We'll also need to finalize the SOW and budget for the period May 15-Sept 30, 2017. Were the SOW and budget in the approved request that I sent you okay, or do you think a revision is required?

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Corina Grigorescu Monagin
Sent: Wednesday, May 31, 2017 11:42 PM
To: Elizabeth Leasure
Cc: Brian Bird; Jonna Mazet
Subject: Re: Guinea VHF sub award and employee questions

Thanks Liz. One of this first things on my list is to assess the feasibility and timeframe of moving the staff to the subaward. It's a government lab so I'm not sure what the process will be to include individuals underneath that award, as well as individuals who are not based in Conakry where the lab is. I hope to have some information soon.

I'm also not sure if we are mandated to use a payroll company (as you are in China – your memory is correct :). I will also find that out as well.

With the current mechanism, current contracts with MB and Footprint cover the following:

- CC and Field Coordinator – end of August 2017
- PA – end of July 2017
- 11 field staff in Conakry – end of June 2017
- 11 field staff in N'Zérékoré – end of July 2017 (I extended these individuals for 2 months because this area is critical to our workplan and it gives us more time for transition).

In terms of setting up the subaward with the VHL lab, what are the next steps? I know I need to clarify the staffing issue and whether that should be included but is there anything else I can be doing in the meantime to assist?

Regards,
corina

From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Date: Wednesday, May 31, 2017 at 10:48 PM
To: Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
Cc: Brian Bird <bhbird@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: Guinea VHF sub award and employee questions

Yes, ideally we would just move forward with UCD issuing a subaward to the lab in Guinea rather than having MB put a subaward in place only to have it end and be replaced by a UCD-issued subaward. Less paperwork and (hopefully) less confusing for the in-country staff.

I have no issues with Metabiota purchasing fuel cards to contribute to the cost of running the generator for sample storage while we get the subaward in place.

For the staffing, are we required to use an outside payroll company like Footprint to facilitate payroll payments in Guinea? I know Metabiota has been using a similar payroll firm in China, but I believe they are required to due to Chinese law (if my memory serves). It is much cleaner (and less expensive without the 18% fee) to just hire the in-country staff through the subaward once it is established (unless there is a very good reason to do otherwise). To avoid a break in service for in-country staff, however, I think we have no choice but to continue to pay them through the current mechanism (meaning through MB to Footprint) until the UCD subaward is in place and hiring (or individual contracting) through the subrecipient can occur.

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Corina Grigorescu Monagin
Sent: Tuesday, May 30, 2017 2:27 PM
To: Elizabeth Leasure
Cc: Brian Bird; Jonna Mazet
Subject: Guinea VHF sub award and employee questions

Hi Liz,

I've started the transition of Guinea and have had a few phone calls with the Metabiota team. A couple of questions for you.

MB has not signed the sub award with the VHF lab. I'm thinking that you do not want them to proceed and that it would be initially signed with UCD? If so, I would like to authorize MB to pay for fuel cards to contribute to the cost of the generator (where our freezer and samples are stored) until we can get the sub award in

place. Please advise.

In terms of the staff – all employees (contractual field staff and full time PREDICT) are paid through a payroll company "Footprint". They charge a fee of approximately 18% on all costs. I am getting a full list of staff, salary, location and contract terms and we will have to decide how to proceed. I know the ideal would be to put them all under the subcontract but I honestly don't know the possibility or length of time it will take to put in place. While I figure out our options and timeframe - Do you want to continue with Footprint or another option?

I'm sure you have tons of questions – I'm available in the afternoons (PST) when I'm back at the hotel so let me know if it's easier to talk.

Thanks
Corina

SAM
SYSTEM FOR AWARD MANAGEMENT

Quick Start Guide For New Grantee Registration

Helpful Information

What is an Entity?
In SAM, your company / business / organization is referred to as an "Entity." You register your entity to do business with the U.S. Federal government by completing the registration process in SAM.

SAM is the official **free, government-operated website** – there is NO charge to register or maintain your entity registration record in SAM.

What do I need to get started?

DUNS Number
You need a Data Universal Numbering System (DUNS) number to register your entity in SAM. DUNS numbers are unique for each physical location you are registering.

If you do not have one, you can request a DUNS number for **free** to do business with the U.S. Federal government by visiting Dun & Bradstreet (D&B) at http://fedgov.dnb.com/webform
It takes no more than 1-2 business days to obtain a DUNS number.

Taxpayer Identification Number
You need your entity's Taxpayer ID Number (TIN) and taxpayer name (as it appears on your most recent tax return). Foreign entities that do not pay employees within the U.S. do not need to provide a TIN. Your TIN is usually your Employer Identification Number (EIN) assigned by the Internal Revenue Service (IRS).

Sole proprietors may use their Social Security Number (SSN) assigned by the Social Security Administration (SSA) as their TIN, but are strongly encouraged to obtain a free EIN from the IRS by visiting: http://www.irs.gov/Businesses/Small-Businesses-&-Self-Employed/How-to-Apply-for-an-EIN
Allow approximately two weeks before your new EIN is ready for use when registering in SAM.

Steps for Registering

1. Type www.sam.gov in your Internet browser address bar.
2. Create a SAM Individual User Account (be sure to validate your e-mail address), then Login.
3. Select "Register New Entity" under "Register/Update Entity" on your "My SAM" page.
4. Select your type of Entity. Definitions are in the Glossary to the right.
5. If you are registering in SAM.gov so you can apply for a Federal financial assistance opportunity on Grants.gov, and are not interested in pursuing Federal contracts, you will have a much shorter registration path. To chose this "grants only" path:
   - Select "No" to "Do you wish to bid on contracts?"
   - Select "Yes" to "Do you want to be eligible for grants and other federal assistance?"
6. Complete the "Core Data" pages:
   - Validate your DUNS information.
   - Enter Business Information (TIN, etc.) This page is also where you create your Marketing Partner Identification Number (MPIN). Write the MPIN down as it will serve as a password for you in other government systems. You will need it for your Grants.gov registration.
   - Enter your CAGE code if you have one, but remember, CAGE codes are tied to DUNS numbers and cannot be reused. Don't worry if you don't have a CAGE code for the DUNS number you are registering; one will be assigned to you after your registration is submitted. Foreign registrants must enter their NCAGE code before proceeding.
   - Enter General Information (business types, organization structure, etc.) about your entity.
   - Provide your entity's Financial Information, i.e. U.S. bank Electronic Funds Transfer (EFT) information for Federal government payment purposes. Foreign entities do not need to provide EFT information.
   - Answer the Executive Compensation questions.
   - Answer the Proceedings Details questions.
7. Complete the "Points of Contact" pages:
   - Your Electronic Business POC is integral to your Grants.gov registration and application process. Your Government POC will be used by other government systems, such as CAGE, when they contact you. List someone with direct knowledge of this registration for both of those POCs.
8. Make sure to hit [Submit] after your final review. You will get a Congratulations message on the screen. If you do not see this message, you have not submitted your registration.
   - There are two external validation steps, one with the IRS and another with CAGE, after you submit. You will receive an email from SAM.gov when your registration is active.

Please give yourself plenty of time before your grant application submission deadline. Allow up to 7-10 business days after you submit before your registration is active in SAM, then an additional 24 hours for Grants.gov to recognize your information.

For help registering in SAM, contact the supporting Federal Service Desk (FSD) at https://www.fsd.gov/

IAE

From: Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: Brian Bird <bhbird@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 6/5/2017 4:51:41 PM
Subject: Re: Guinea VHF sub award and employee questions

Great – I will get on that. Also – the team are "open" to the idea of being paid through the subaward. Next step is to propose this to subawardee…

More soon.

Thanks
corina

From: Elizabeth Leasure
Date: Monday, June 5, 2017 at 4:45 PM
To: Corina Grigorescu Monagin
Cc: Brian Bird , Jonna Mazet
Subject: RE: Guinea VHF sub award and employee questions

Sure, see attached.

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Corina Grigorescu Monagin
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Cc: Brian Bird; Jonna Mazet
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530-304-1403 (cell)

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corina

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Date: Wednesday, May 31, 2017 at 10:48 PM
To: Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
Cc: Brian Bird <bhbird@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
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Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Corina Grigorescu Monagin
Sent: Tuesday, May 30, 2017 2:27 PM
To: Elizabeth Leasure
Cc: Brian Bird; Jonna Mazet
Subject: Guinea VHF sub award and employee questions

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Thanks
Corina

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Molly Turner <turner@ecohealthalliance.org>
CC: Ava Sullivan <sullivan@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 6/7/2017 5:42:20 PM
Subject: [predict] RE: Budget templates for P2 CoAg ceiling increase (due 6-14-17)

Hi Molly. Please also note that costs for the M&A team and One Health Approaches (Billy and Catherine's piece of the workplan) need to go on core funds only per guidance received from USAID when budgeting last year, so please keep that in mind as your putting these budgets together. The distribution of Global costs in the templates should already reflect this (since we took this into account when finalizing the Y3 budget, and the Y3 budget was used to create the Y4 and Y5 templates you received), but I just wanted to remind you of this fact. Let me know if you have any questions.

Thanks!
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Elizabeth Leasure
Sent: Tuesday, June 06, 2017 10:56 AM
To: Elizabeth Leasure; Molly Turner
Cc: Ava Sullivan; Evelyn Luciano; Peter Daszak; predict@ucdavis.edu
Subject: RE: Budget templates for P2 CoAg ceiling increase (due 6-14-17)

As promised, please find attached the justification draft document for you to revise. Let me know if you have any questions.

Happy budgeting!
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: predict-request@ucdavis.edu [mailto:predict-request@ucdavis.edu] **On Behalf Of** Elizabeth Leasure
Sent: Saturday, June 03, 2017 6:41 PM
To: Molly Turner
Cc: Ava Sullivan; Evelyn Luciano; Peter Daszak; predict@ucdavis.edu
Subject: [predict] Budget templates for P2 CoAg ceiling increase (due 6-14-17)
Importance: High

Hi Molly. As you are probably now aware, USAID has requested that we submit budgets and justifications to process an increase to the ceiling of the prime agreement, which is required in order for USAID to obligate additional funding (core and EHP) for Years 4 and 5, as we are now just $3M below the current $100M ceiling. These budgets are intended to facilitate the ceiling increase only, and do not reflect a commitment or guarantee that the funds budgeted will be received. We will still have to go through our regular budget development/approval process for Y4 later this summer, so keep that in mind as you're pulling these budgets together. This budgeting exercise (while tedious), does give us the opportunity to obtain prior approval for multiple new subawards and subcontracts at one time, as the AO has confirmed that any subawards/subcontracts included in the budgets submitted will be considered officially approved. To capitalize on this, we will need to make sure that all new subawards and subcontracts anticipated through the end of the

project in 2019 are included in the detailed budgets and justifications. This means that new subrecipients and subcontractors need to be identified by name in the detailed budgets/justifications, and a scope of work for each new subaward/subcontract needs to be provided (as noted below).

In order to fulfil USAID's request and meet the submission deadline, **please submit the following items to me by COB on Wednesday, June 14th**:

1. ***Detailed budget for the balance of unspent Y3 funds*** (Excel budget template attached). Targets included on the "Summary by Country" worksheet are based on approved budgets less expenditures to date (through the April 2017 invoice). These targets DO NOT include additional funding for Y3 costs anticipated for the transitions in China, Indonesia, RoC, and Cote d'Ivoire (CDI), but please budget for these costs anyway (knowing you will exceed the stated targets). Cost share target is based on the revised Y3 cost share budget (submitted by Molly 6/2) less the Y3 cost share reported to date (Q1-Q2).
2. ***Detailed budget for Y4*** (Excel budget template attached). Targets include $1.5M for EHP (inclusive of the diagnostic budget for Columbia that has previously flowed through UCD) and $320K for GVP, as well as additional funds for in-country costs associated with activities in China, Indonesia, RoC, and CDI that are being taken over from Metabiota. If you anticipate needing to hire additional support staff to manage CDI and RoC, please include those additional costs in your budget (you can go a bit over the targets if you're factoring in such costs). If you would prefer Columbia's diagnostic budget for EHP to continue to flow through the UCD mechanism, please reduce the EHP budget target accordingly. Cost share target of $339K is based on the 5-year EHA cost share commitment ($1,136,846) less cost share reported and committed for Y1-Y3 ($458,793; assumes total Y3 commitment is met) divided evenly between Y4 and Y5 ($1,136,846 - $458,793 = $678,053/2 years = $339,026/year).
3. ***Detailed budget for Y5*** (Excel template attached). Targets include $1M for EHP (inclusive of diagnostic budget for Columbia that has previously flowed through UCD), as well as additional funds for in-country costs associated with activities in China, Indonesia, and RoC that are being taken over from Metabiota. The Ebola target does not currently include any funds for CDI, as the remainder of the non-EHP funds are included in the Y4 Ebola target; any costs you budget for CDI in Y5 will come from the Ebola target in Y4 (which is fine, just keep that in mind). If you anticipate needing to hire additional support staff to manage CDI and RoC, please include those additional costs in your budget (you can go a bit over the targets if you're factoring in such costs). If you would prefer Columbia's diagnostic budget for EHP to continue to flow through the UCD mechanism, please reduce the EHP budget target accordingly. Cost share target of $339K is based on the 5-year EHA cost share commitment (see explanation in #4 above).
4. **Budget justifications for detailed budgets #1-3 above**. Rather than have you start from scratch, we are going to pull language from the final cost application narrative for the P2 proposal and ask you to simply update it to align with the budgets noted above. The draft budget justification documents for you to revise will be sent to you in a separate email, and you will receive them no later than COB PDT Tuesday, June 6th.
5. **Scopes of work for any new subcontracts or subawards** included detailed budgets #1-3 above.
6. **A copy of your organization's current negotiated indirect cost rate agreement.**

My apologies for the very long (and probably confusing) email. I'd like to speak by phone (once you've had a chance to read through all of this) to make sure that we're on the same page and everything is clear. Perhaps sometime on Monday? I'm free any time after 10 am PDT, so please let me know what will work for you.

Thanks!!
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From:	Cara Chrisman <cchrisman@usaid.gov>
To:	Jonna Mazet <jkmazet@ucdavis.edu>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Peter Daszak <daszak@ecohealthalliance.org>;Brooke Watson <watson@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>
CC:	Dennis Carroll <dcarroll@usaid.gov>
Sent:	6/7/2017 6:40:25 PM
Subject:	6/8 GVP Meeting - Agenda & Materials

Hi All,

Looking forward to speaking with some of you tomorrow during our regular call. We've taken a stab at the first set of countries/sites for Ph 1 (see below), based on where P-2 has relationships, where the GVP has been socialized, etc. and look forward to discussing more, as well as determining the impact on the percent yield with an updated list of sites.

Additionally, please find attached for your feedback both an updated pitch deck and a list of priority outreach to meet with and share our updated pitch (still being updated with additional contact names).

Please let us know if you have any additional items and we look forward to discussing!

Best,
Cara

Agenda

- Pitch Deck Feedback
- Phase 1 country list
- Outreach Plan
- AOB

Country/Site List

- Brazil (1st 2 sites)
- Costa Rica (1 site)
- Cameroon (3 sites)
- Kenya/Uganda (1 site)
- Uganda/DRC/Rwanda (1 site)
- Thailand (1 site)
- Vietnam (4 sites)
- China (2 sites)
- Indonesia (2 sites)
- Colombia (3 sites)

Total = 20 sites and 10-16 countries (3 Americas, 4 Asia, 3-6 Africa)

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health

U.S. Agency for International Development (AID)

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E-mail: cchrismen@usaid.gov

UCDJSR0001611

	A	B	C
1	**GVP Outreach**		
2	**Institution/Individual**	**Contact**	**Date**
3			
4			
5	Rockefeller - Raj		
6	Hemsley Charitable Trust		
7	Bloomburg		
8	Columbia University		
9	David Nabarro		
10	Laurie Garrett		
11	Yale University		
12	Boston University		
13	Harvard University		
14	Skoll Global Threats		
15	Science Philanthropy		
16	BioHub		
17	Richard Feachem		
18	Harvey Feinberg		
19	Michael McCullough		
20	Dean Jamison		
21	Illumina		
22	BM Gates		
23	Paul Allen/Vulcan		
24	University of Washington		
25	Chatham House		
26	London School		
27	CEPI		
28	Wellcome Trust		
29	Institute Pasteur		
30	Merieux Foundation	Guy Vernet	
31	OIE		
32	UNESCO	Dr Casimiro Vizzini	
33	Peggy Hamburg		
34	DTRA		
35	NSC		
36	OSTP		
37	NIH/NIAID/Fogarty	Tony Fauci, Roger Glass	
38	HHS/ASPR	Maria-Julia Marinissen	
39	Franca Jones - NAMRU		
40	Bush/Scowcroft	Andrew Natsios	
41	Costa Rica/Academy of Science	Roman Macaya Hayes, Pedro Leon	
42	Dan Janzen/Upenn		
43	IDRC		

The Global Virome Project



GLOBAL VIROME PROJECT

We are not prepared for the Dual Threats Posed by Emerging Infectious Diseases



The world is facing an increasing dual threat from

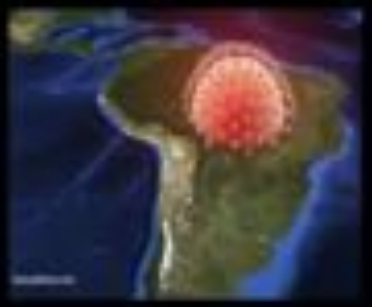
- the natural emergence of deadly infectious pathogens, and
- the accidental &/or intentional release of their laboratory-enhanced variants

The risks posed by these dual threats are outpacing our ability to develop effective and timely countermeasures

There is an urgent need to be able to prepare our responses in ADVANCE of any future threats – natural and lab-enhanced

GLOBAL VIROME PROJECT

The Global Virome Project



The Global Virome Project (GVP) is a ten year global partnership to better prepare the world for these dual threats, by:

- Developing a global database of virtually all of the planet's naturally-occurring viral threats
- Transforming the world of emerging diseases into a data-rich field – driving the advanced development of countermeasures, against all future threats, and
- Enabling rapid detection of natural and laboratory-enhanced threats

GLOBAL VIROME PROJECT

GVP Builds a Comprehensive Viral Database



GLOBAL VIROME PROJECT

Enhanced Public Health "Tool Box"

Naturally-Occurring Viruses

Ability to target high impact interventions to PREVENT "spillover" at high-risk animal-human interface

Targeted surveillance enables early DETECTION and effective RESPONSE to future spillover" events



Laboratory-Enhanced Viruses

Ability to rapidly recognize a lab-enhanced virus against the Viral Atlas database on viral ecology and genomic sequence

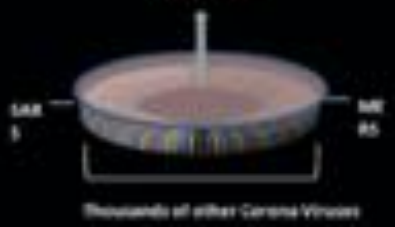
Advanced development of "broad spectrum" countermeasures for natural and laboratory-enhanced "high risk" viruses

GLOBAL VIROME PROJECT

Impact 1: Development of Broad Countermeasures

Converting Virology into a data-rich field

Universal Corona Virus Vaccine



GVP will enable the comparative analysis of thousands of members of each viral family and the advanced development of next generation countermeasures that are broadly effective – rather than against individual viruses (*e.g.* MERS, SARS)

GLOBAL VIROME PROJECT

Impact 2: Pandemic/Epidemic Prevention

Drive Targeted, High-Impact Risk Mitigation

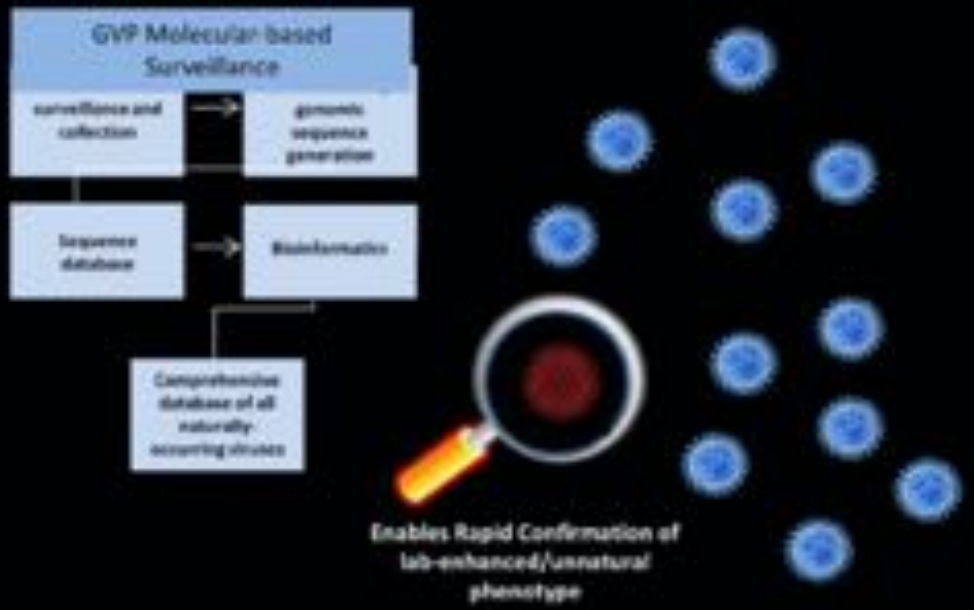


Minimizing the Risk of Spillover

GVP
will enable through detailed characterization of every virus's ecologic profile – spanning host range, geographic distribution, and epidemiology – the identification of viruses that pose the greatest potential threat and the targeting of measures to prevent spillover

GLOBAL VIROME PROJECT

Impact 3: The rapid identification of laboratory-modified viruses

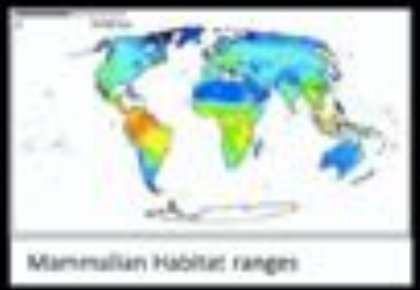


GLOBAL VIROME PROJECT

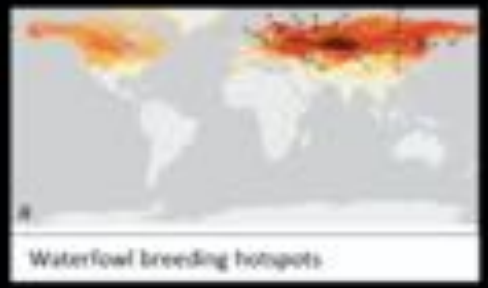
UCDUSR0001620

GVP: Get to the Source

Mammals and water fowl are viral reservoirs



Mammalian Habitat ranges

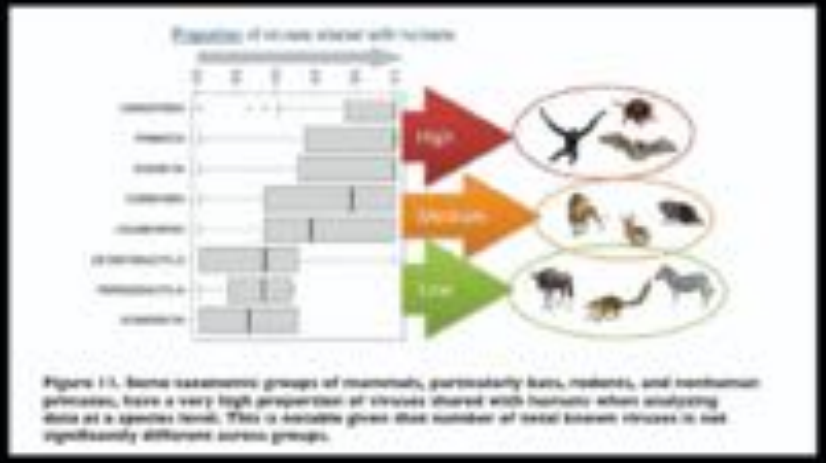


Waterfowl breeding hotspots

GLOBAL VIROME PROJECT

UCDUSR0001621

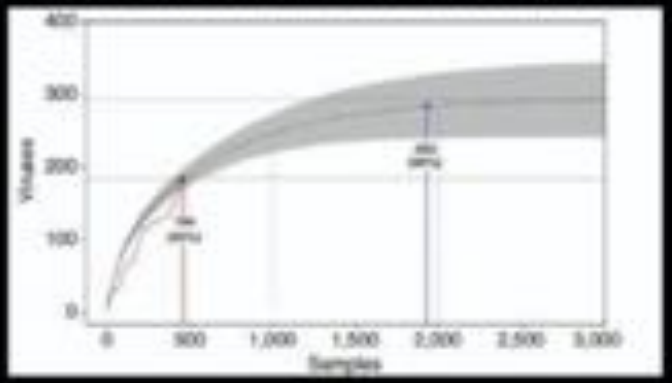
Feasibility: Targeting "High Risk" Species



GLOBAL VIROME PROJECT

Feasibility: Extrapolating Number of Samples

Discovery Curves Show the Number of Samples Required

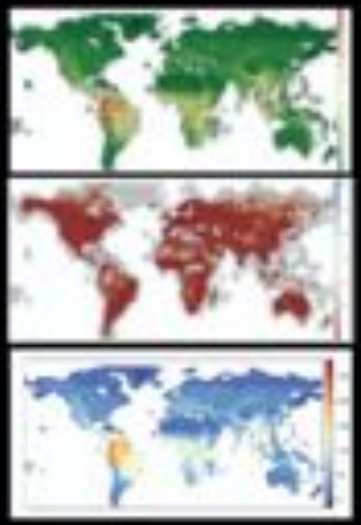


- PREDICT research has demonstrated that far fewer samples than previously expected are required to identify the most threatening viruses
- These viral discovery curve studies provide a roadmap to sampling needs for GVP

GLOBAL VIROME PROJECT

UCDUSR0001623

Approach: Prioritizing Sites for GVP Sampling



Maximize:

- Mammalian biodiversity
- Uniqueness of diversity in field sites
- Zoonotic viral yield

Minimize:

- Access costs of field work
- Overlap between sample sites

Predicting Zoonotic Risk:

- o predict zoonotic risk:
- Order and habitat range size
- Human population in habitat range
- Urban/rural human population ratio
- Human population density
- Zoogeographic region of habitat

GLOBAL VIROME PROJECT

UCDUSR0001624

Approach: Zeroing In on Sampling Sites



Selection Process:

- A **minimal** number of **efficient, high-diversity** sample units were selected from a global grid
- Each sample unit covers 20,000 km^2



Sampling Units Selected:

- 108 Sampling Units (SU) selected
- 3 Phases proposed for sample collection covering: 20, 30, and 58 SUs
- Total cost: $757,800,000

GLOBAL VIROME PROJECT

UCDUSR0001625

The Global Virome: Site Selection

Over 10 years, will target: 68.5% of global mammalian viruses, by sampling 63.5% of global mammalian diversity, to find **70% of potential zoonoses**



- Phase 1: 20 SUs, 1227 mammals, $275.4M
- Phase 2: 30 SUs, 739 mammals,
- [redacted]58 SUs, 1013 mammals, $289.6M

GLOBAL VIROME PROJECT

UCDUSR0001626

Site Selection: Country List by Phase

Phase 1	# sites	Phase 2	# sites	Phase 3	# sites
[redacted]	1	[redacted]	1	[redacted]	1

Site Selection: Summary and Costs

Over 10 years	Number of Sampling Units	Number of Species Selected	Percentage of Virus Selected	Zoonoses Selected	Laboratory Cost (US$ million)	Sample Collection cost (US$ million)	Total cost (US$ million)
Phase 1	20	1,227	33%	33%	$30,000,000	$245,400,000	$275,400,000
Phase 2	30	734	16%	16%	$45,000,000	$147,800,000	$192,800,000
Phase 3	58	1,013	20%	21%	$87,000,000	$202,600,000	$289,600,000
Total	**108**	**2,979**	**83%**	**70%**	**$162,000,000**	**$595,800,000**	**$757,800,000**

+

Water birds	50	740			$75,000,000	$148,070,000	$223,070,000
Total	**213**	**3791**	**84%**	**85%**	**$237,000,000**	**$743,870,000**	**$980,870,000**

NOTE: Estimated costs are at the high end of expected costs as they do not factor in capacities and operational platforms that already exist within each SU, nor do they factor in advances in diagnostic and/or sampling technologies – which together will greatly reduce both operational costs and time

GLOBAL VIROME PROJECT

The Global Virome Project: In Practice

- Optimal targeting: 10 years, 70% of likely zoonoses, ~$757M – will enable the fast tracking of a high impact "tool box" for preventing, detecting, and responding to dual threats.
- The modeling strategy is not wholly prescriptive – many other sites could potentially contribute to the GVP without significantly increasing costs.
- Using host factors, we can further optimize **within** chosen sampling units to decide which species to target first.
- The models can be used as a monitoring tool to verify predictions about:
  - Saturation rate of viral curves
  - Rate of sample acquisition across various sites
  - Analytical approaches (modeling and lab-based) to assess zoonotic potential of discovered viruses and whether site selection is delivering a higher rate of zoonotic discovery

GLOBAL VIROME PROJECT

UCDUSR0001629

Global Virome Project

Business Plan

GVP: Core Principles

The GVP is committed to achieving its goals through core principles that:

- Embrace an international scope, while fostering local ownership
- Promote equitable access to data and benefits
- Foster transparency
- Build national capabilities for "prevention, detection and response" for emerging viral threats
- Foster global ownership through an international alliance

GLOBAL VIROME PROJECT

GVP: The Way Forward

Planned Launch: January 29, 2018 at Prince Mahidol Awards Conference (PMAC)

Field Operations Initiated:

- First quarter, 2018
  - Launch "first wave" of 5-10 Phase 1 countries
- End of 2018
  - Launch "second wave" of remaining 10-15 Phase 1 countries

Organizational Format: International not-for-profit NGO

- Central Headquarters *(to be determined)*
- Director *(to be recruited)*
- Secretariat *(to be recruited)*
- Advisory Board *(to be recruited)*
- Task-specific working groups

Financial Requirements: $75-90 million per year over 10 years

- Covers:
  - Management, Coordination, Oversight, and Reporting
  - Country operations
  - Data and Sample Management

GLOBAL VIROME PROJECT

UCDUSR0001632

GVP: Support Options

Financial:

- Direct financial support to the GVP NGO:
  - HQ costs (oversight, coordination, standardization, working groups)
  - Data and sample management
  - Technical and operational backstopping of country operations
- Direct financial support to in-country operations

In-kind:

- Contribution of in-country platforms/systems for sample collection or laboratory analysis
- Commodities – sample collection, transport, and storage; laboratory supplies; analytics
- Technical and operational expertise

GLOBAL VIROME PROJECT

UCDUSR0001633

GVP: The "Start-Up" Team



GLOBAL VIROME PROJECT

GVP: Start-Up Team Responsibilities

Core Group:

- Provide leadership and strategic thinking for the GVP – overseeing the transition from the "Start-up" phase to the Launch
- Perform outreach to external stakeholders
- Handle day-to-day operations of the GVP and organize regular convenings of the SC

Steering Committee:

- Serve as an advisory group to the development of principles and strategies for the planning and launch of the GVP
- Assess progress and provide feedback on the scope and products of the Working Groups
- Provide additional outreach and advocacy for GVP

Working Groups:

- Develop guidance relevant to their respective Thematic Area:
    - Governance: Advise on ethical, legal, & social issues, as well as partnerships
    - Implementation: Operationalize protocols specific to sample collection and analysis
    - Science & Technology: Identify & develop standards and protocols for sample collection and analysis

GLOBAL VIROME PROJECT

UCDUSR0001635

GVP: Start-Up to Launch - Time Line



GLOBAL VIBOME PROJECT

UCDUSR0001636

GVP: Start-Up Partners

Operational Support:

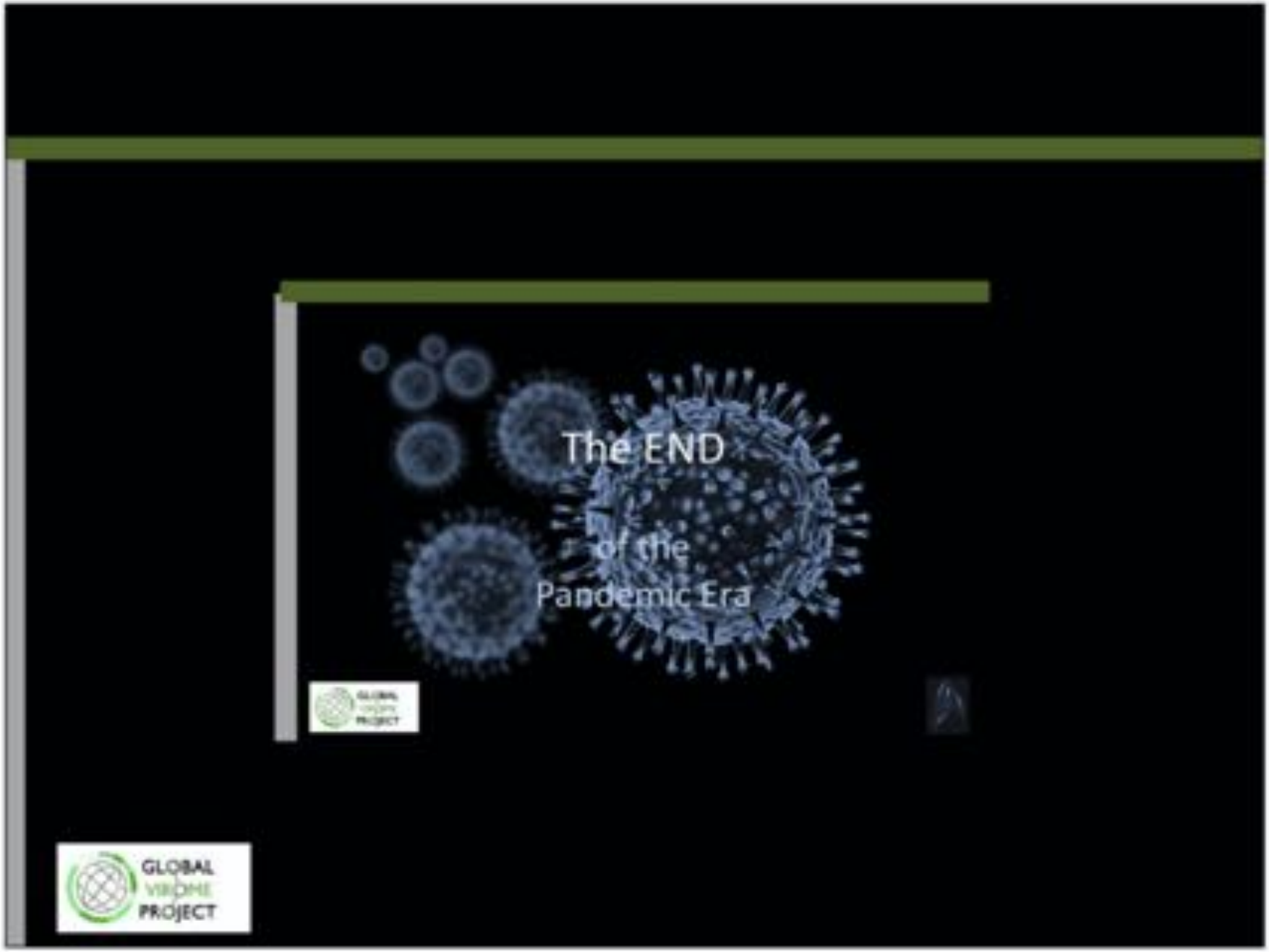
- **"Proof of Concept" – USAID, $130 million (2009-2016)**
- **Ongoing "Start-Up" phase – USAID, $3 million (2016-2017)**

Start-Up Partners:



GLOBAL VIROME PROJECT

UCDUSR0001637



UCDUSR0001638

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Cara Chrisman <cchrisman@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Brooke Watson <watson@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>
CC: Dennis Carroll <dcarroll@usaid.gov>
Sent: 6/7/2017 6:46:11 PM
Subject: RE: 6/8 GVP Meeting - Agenda & Materials

Sorry all – I won't be able to make the call tomorrow….

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

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+1.212.380.4465 (fax)
www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Wednesday, June 7, 2017 2:40 PM
To: Jonna Mazet; Nathan Wolfe; Eddy Rubin; Peter Daszak; Brooke Watson; Eri Togami
Cc: Dennis Carroll
Subject: 6/8 GVP Meeting - Agenda & Materials

Hi All,

Looking forward to speaking with some of you tomorrow during our regular call. We've taken a stab at the first set of countries/sites for Ph 1 (see below), based on where P-2 has relationships, where the GVP has been socialized, etc. and look forward to discussing more, as well as determining the impact on the percent yield with an updated list of sites.

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Cara

Agenda

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Cara J. Chrisman, PhD
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Emerging Threats Division
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Bureau for Global Health
U.S. Agency for International Development (AID)

Desk: (202) 712-1161
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

From: Beth Edison <bedison@metabiota.com>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: Eddy Rubin <erubin@metabiota.com>;Karen Saylors <ksaylors@metabiota.com>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 6/16/2017 3:46:51 PM
Subject: [predict] Re: Budget templates for P2 CoAg ceiling increase (due 6-14-17)

Hi Liz,

No, Metabiota does not have a new NICRA in place yet however it is being actively worked on and we are on track to submit our 2017 provisional rates for DCMA approval at the end of June.

Thanks,
Beth

Beth Edison
Program Manager, PREDICT | Metabiota
email: bedison@metabiota.com
mobile: (1)250-739-8987
skype: bethany.edison

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From: Elizabeth Leasure
Date: Thursday, June 15, 2017 at 9:24 AM
To: Beth Edison
Cc: Eddy Rubin , Karen Saylors , "predict@ucdavis.edu"
Subject: RE: Budget templates for P2 CoAg ceiling increase (due 6-14-17)

Does Metabiota have a new NICRA in place yet? It's been almost 3 years now, so I'm a little shocked the new NICRA hasn't been finalized yet.

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Beth Edison [mailto:bedison@metabiota.com]
Sent: Wednesday, June 14, 2017 5:26 PM
To: Elizabeth Leasure
Cc: Eddy Rubin; Karen Saylors; predict@ucdavis.edu
Subject: Re: Budget templates for P2 CoAg ceiling increase (due 6-14-17)

Hi Liz,

Attached are our draft budgets for the remainder of Year 3 and Years 4 & 5.

I tried to include as many real costs as possible associated with our wind down in our transitioning countries. You may notice a lot of supply costs –these are items that were ordered before being advised of the transition. I have informed the new country leads which supplies are in inventory and what is en route so they can include that in their budgeting/planning.

We have had so many changes since the beginning of PREDICT 2 the budget narrative is taking longer than

I had anticipated. I will have the remaining documents to you tomorrow. My apologies.

As we discussed, I'll be available to sort out the Core/Ebola funding issue or any other concerns you have.

Thank you,
Beth

Beth Edison
Program Manager, PREDICT | Metabiota
email: bedison@metabiota.com
mobile: (1)250-739-8987
skype: bethany.edison

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From: Elizabeth Leasure <ealeasure@ucdavis.edu>
Date: Sunday, June 4, 2017 at 12:10 PM
To: Beth Edison <bedison@metabiota.com>
Cc: Eddy Rubin <erubin@metabiota.com>, Karen Saylors <ksaylors@metabiota.com>, "predict@ucdavis.edu" <predict@ucdavis.edu>
Subject: Budget templates for P2 CoAg ceiling increase (due 6-14-17)

Hi Beth. As you are probably now aware, USAID has requested that we submit budgets and justifications to process an increase to the ceiling of the prime agreement, which is required in order for USAID to obligate additional funding (core and EHP) for Years 4 and 5, as we are now just $3M below the current $100M ceiling. These budgets are intended to facilitate the ceiling increase only, and do not reflect a commitment or guarantee that the funds budgeted will be received. We will still have to go through our regular budget development/approval process for Y4 later this summer, so keep that in mind as you're pulling these budgets together. This budgeting exercise (while tedious), does give us the opportunity to obtain prior approval for multiple new subawards and subcontracts at one time, as the AO has confirmed that any subawards/subcontracts included in the budgets submitted will be considered officially approved. To capitalize on this, we will need to make sure that all new subawards and subcontracts anticipated through the end of the project in 2019 are included in the detailed budgets and justifications. This means that new subrecipients and subcontractors need to be identified by name in the detailed budgets/justifications, and a scope of work for each new subaward/subcontract needs to be provided (as noted below).

In order to fulfil USAID's request and meet the submission deadline, **please submit the following items to me by COB on Wednesday, June 14th**:

1. ***Detailed budget for the balance of unspent Y3 funds*** (Excel budget template attached). Targets included on the "Summary by Country" worksheet are based on approved budgets less expenditures to date (through the April 2017 invoice). These targets DO NOT include a reduction in funding related to the transitions in China, Indonesia, RoC, Cote d'Ivoire (CDI), Guinea, and Sierra Leone, but please make sure that the budgets for these countries are reflective of the transition plans agreed to with EHA and UCD. Cost share target is zero because the Y3 commitment was met per the certifications received for Q1 and Q2.
2. ***Detailed budget for Y4*** (Excel budget template attached). Targets include $90K for GVP, as well as a reduction in funding representative of in-country costs associated with activities in China, Indonesia, RoC, CDI, Guinea, and Sierra Leone that are being taken over by other partners. Cost share target of $106K is based on the 5-year Metabiota cost share commitment ($733,118) less cost share reported for Y1-Y3 ($520,396) divided evenly between Y4 and Y5 ($733,118 - $520,396 = $212,722/2 years = $106,361/year).
3. ***Detailed budget for Y5*** (Excel template attached). Core target reflects reduction in funding representative of in-country costs associated with activites in China, Indonesia, RoC, CDI, Guinea, and Sierra Leone being taken over by other partners. The Ebola target is zero, as the remainder of

the non-EHP funds are included in the Y4 Ebola target. Cost share target of $106K is based on the 5-year Metabiota cost share commitment (see explanation in #4 above).

4. **Budget justifications for detailed budgets #1-3 above**. Rather than have you start from scratch, we are going to pull language from the final cost application narrative for the P2 proposal and ask you to simply update it to align with the budgets noted above. The draft budget justification documents for you to revise will be sent to you in a separate email, and you will receive them no later than COB PDT Tuesday, June 6th.
5. **Scopes of work for any new subcontracts or subawards** included detailed budgets #1-3 above.
6. **A copy of your organization's current negotiated indirect cost rate agreement.** Please also submit copies of subrecipient NICRA's (if applicable). If any of your foreign subrecipients use an indirect cost rate greater than the standard 10% MTDC deminimis rate allowed by the Uniform Guidance (UG), please submit supporting documentation to confirm that the rate used was reviewed by your organization and deemed appropriate in accordance with the UG.

My apologies for the very long (and probably confusing) email. I'd like to speak by phone (once you've had a chance to read through all of this) to make sure that we're on the same page and everything is clear. Perhaps sometime on Monday? I'm free any time after 10 am PDT, so please let me know what will work for you.

Thanks!!
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Eddy Rubin <erubin@metabiota.com>
Sent: 6/26/2017 2:32:14 AM
Subject: Re: Karen on Mgt call to discuss transitions in CIV, ROC, Indonesia, China, Guinea, & SL

Hi Eddy,
Sounds fine to me.
Speak to you all tomorrow,
Jonna

On Sun, Jun 25, 2017 at 8:15 AM, Eddy Rubin <erubin@metabiota.com> wrote:

Hi Jonna,

With regards to Monday's Management call with USAID. One of the important discussion items is about Mission communications and challenges with the transitions in CIV, ROC, Indonesia, China, Guinea, & SL . Karen has been intimately involved with these. I wonder whether it would be good for her to participate on the call so she can directly communicate where things are and plans for going forward, rather than things being filtered through me?

Eddy

From:	Katherine Leasure <kaleasure@ucdavis.edu>
To:	'PREDICTMGT' <predictmgt@usaid.gov>
CC:	'Predict inbox' <predict@ucdavis.edu>;'Jonna Mazet' <jkmazet@ucdavis.edu>
Sent:	6/28/2017 10:53:52 PM
Subject:	PREDICT International Travel Requests

Please find below international travel requests for your review and approval. Please let me know if you have any questions. Thanks!!

1. Monagin (Guinea): $8,742 **business class required due to medical need*/$327 (Conakry) max daily per diem
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Katherine Leasure

HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
530-752-7526
530-752-3318 FAX
kaleasure@ucdavis.edu

From:	Kevin Olival, PhD <olival@ecohealthalliance.org>
To:	David J Wolking <djwolking@ucdavis.edu>
CC:	Jon Epstein <epstein@ecohealthalliance.org>;Hongying Li <li@ecohealthalliance.org>;Molly Turner <turner@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>;predict@ucdavis.edu" <predict@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent:	6/29/2017 9:56:50 PM
Subject:	Re: [predict] Fwd: EPT2 Evaluation- Host government counterparts

Hey David,

Jon and I met w Supaporn today here in Colorado and she has some good people familiar with and supportive of PREDICT from the Thai ministries to nominate for this request. She will reply to Sudarat today.

Thanks,
Kevin

On Jun 29, 2017, at 9:40 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi EHA and SI teams,

Please not this message from RDMA to your country teams with a very tight turnaround (this Friday June 30th), this is part of the EPT-2 external evaluation, which is now gaining momentum.

Best,

David

On Thu, Jun 29, 2017 at 8:18 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

---------- Forwarded message ----------
From: **Sudarat Damrongwatanapokin** <sdamrongwatanapokin@usaid.gov>
Date: Wed, Jun 28, 2017 at 11:04 PM
Subject: Fwd: EPT2 Evaluation- Host government counterparts
To: eshiilegdamba@wcs.org, Tom Hughes <tom.hughes@ecohealthalliance.org>, "Valitutto, Marc" <ValittoM@si.edu>, Ohnmar Aung <ohnmara@gmail.com>, Supaporn Wacharapluesadee <spwa@hotmail.com>, Jon Epstein <epstein@ecohealthalliance.org>, soubanh Silithammavong <ssilithammavong@metabiota.com>, dibesh@cmdn.org, zlshi@wh.iov.cn
Cc: "Kevin Olival, PhD" <olival@ecohealthalliance.org>, Daniel Schar <dSchar@usaid.gov>, "Clements, Andrew(ANE/TS)" <AClements@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>

Dear Marc and Ohnmar Aung, ZhengLi, Soubanh,Supaporn, Tom, Enkee, Dibesh, and Supaorn

Emerging Threat Division is now starting an external evaluation of the EPT2 program. This evaluation will identify whether the objectives of the program are on track for completion. The evaluation identifies on how well the EPT2 program has contributed to the knowledge base, implementation and sustainability of efforts to prevent, detect and respond to emerging pandemic threats, and farthered "One Health." It also focuses on the contribution of the EPT2 program in achieving the objectives of Global Health Security Agenda (GHSA.) Projects that make up the EPT2 program include: PREDICT (Prime - University of California-Davis), Preparedness and Response (P&R) (Prime - DAI Global), and One Health Workforce (OHW) (Prime - University of Minnesota), as well as agreements with WHO and FAO."

We are collecting contact info of the appropriate host government counterparts **(name, title, organization, email)** that you have worked with who will be able to comment on the EPT2 program. The evaluation team will be sending a survey questionnaire to them.

Please email us the contact info (name, title, organization, email) of the appropriate host government counterparts by Friday June 30 COB.

The country list that required information of appropriate government counterparts from PREDICT2:

1) Burma:

Name:
Title:
Organization:
Contact info:
E-mail address:

2) China:
Name:
Title:
Organization:
Contact info:
E-mail address:

3) Laos:
Name:
Title:
Organization:
Contact info:
E-mail address:

4) Malaysia
Name:
Title:
Organization:
Contact info:
E-mail address:

5) Mongolia
Name:
Title:
Organization:
Contact info:
E-mail address:

6) Nepal:
Name:

Title:
Organization:
Contact info:
E-mail address:

7)Thailand:
Name:
Title:
Organization:
Contact info:
E-mail address:

Thank you very much and apologize for such a short notice.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax: +662 -2573099

From: Katherine Leasure <kaleasure@ucdavis.edu>
To: 'Andrew Clements' <aclements@usaid.gov>
CC: 'PREDICTMGT' <predictmgt@usaid.gov>;'Predict inbox' <predict@ucdavis.edu>;'Jonna Mazet' <jkmazet@ucdavis.edu>
Sent: 6/30/2017 6:23:30 PM
Subject: RE: PREDICT International Travel Requests

Thanks, Andrew. I have sent an email to EHA and will follow-up when I have received the requested information.

From: Andrew Clements [mailto:aclements@usaid.gov]
Sent: Thursday, June 29, 2017 3:22 AM
To: Katherine Leasure
Cc: PREDICTMGT; Predict inboc; Jonna Mazet
Subject: Re: PREDICT International Travel Requests

#3 appeoved.

I would like additional information on #8 as to how it relates to PREDICT.

All others approved subject to Mission concurrence.

On Thu, Jun 29, 2017 at 12:53 AM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:
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https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/014901d2f061%246a1942a0%243e4bc7e0%24%40ucdavis.edu

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Andrew Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development

Mobile phone: 1-571-345-4233
E-mail: [redacted]

For more information on cSAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2/

UCDUSR00001655

From:	William B. Karesh <karesh@ecohealthalliance.org>
To:	Karen Saylors <ksaylors@metabiota.com>;Jonna Mazet <jkmazet@ucdavis.edu>
CC:	Peter Daszak <daszak@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>;Ava Sullivan <sullivan@ecohealthalliance.org>;Caroline Fric <cfric@metabiota.com>;technology@eidith.org" <technology@eidith.org>;Chris Johnson <ckjohnson@ucdavis.edu>;Tammie O'Rourke <torourke@metabiota.com>;predict@ucdavis.edu" <predict@ucdavis.edu>;Taylor Elnicki <telnicki@metabiota.com>;Alison Andre <andre@ecohealthalliance.org>;Amanda Fuchs <fuchs@ecohealthalliance.org>;Brooke Genovese <bgenovese@ucdavis.edu>
Sent:	7/6/2017 10:44:18 PM
Subject:	Re: EIDITH access for EHA team members

Great. And there seem to be samples from the Zuniga mine site in EIDTH and those may relate to WCS samples. So a discussion on the subject would be realy helpful.

BK

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
460 West 34th Street - 17th Floor
New York, NY 10001 USA

+1.212.380.4463 (direct)
+1.212.380.4465 (fax)
www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On Jul 6, 2017, at 5:55 PM, Karen Saylors <ksaylors@metabiota.com> wrote:

Thanks Jonna.
I'm traveling this week with Peter and Billy, so we will have time to discus data ownership and data sharing/access for transitioning countries, but I do think it would be good to plan some discussion on this to agree on general principles once our travels are done, as there are analysis and EIDITH implications that we would like to prepare for.

Perhaps we could put something on the calendar for early August? Brooke, might you be able to help coordinate a call for sometime between July 31st and August 4th?

Thanks much,
Karen

From: <jonna.mazet@gmail.com> on behalf of Jonna Mazet <jkmazet@ucdavis.edu>
Date: Thursday, June 22, 2017 at 3:19 PM
To: Peter Daszak <daszak@ecohealthalliance.org>, Eddy Rubin <erubin@metabiota.com>, Karen Saylors <ksaylors@metabiota.com>, Billy Karesh <karesh@ecohealthalliance.org>
Cc: Ava Sullivan <sullivan@ecohealthalliance.org>, Caroline Fric <cfric@metabiota.com>, "technology@eidith.org" <technology@eidith.org>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Tammie O'Rourke <torourke@metabiota.com>, "predict@ucdavis.edu" <predict@ucdavis.edu>, Taylor Elnicki <telnicki@metabiota.com>, Alison Andre <andre@ecohealthalliance.org>, Amanda Fuchs <fuchs@ecohealthalliance.org>, Brooke Genovese <bgenovese@ucdavis.edu>
Subject: Re: EIDITH access for EHA team members

Hi,
Should likely set up a call to discuss any issues and/or concerns. If no one has any concerns, we can give access to existing country data (there isn't a ton, I don't think) and govern data sharing and best collegial behavior through EB.
Whatever best serves all concerned, as I'm totally open on process,
Jonna

On Wed, May 31, 2017 at 11:22 AM, Tammie O'Rourke <torourke@metabiota.com> wrote:
Hi Ava,
I kind hello back!
The change of the organizations in these countries is extremely sensitive and therefore the transition of the data and the access should likely be part of the larger transition plan for these countries.
I am including Jonna in the conversation as she likely has more insight on this subject. Jonna, do you agree?
Please let me know if you have any questions.
Tammie

-----Original Message-----
From: Ava Sullivan [mailto:sullivan@ecohealthalliance.org]
Sent: Wednesday, May 31, 2017 7:51 AM
To: Caroline Fric <cfric@metabiota.com>
Cc: technology@eidith.org
Subject: EIDITH access for EHA team members

A kind hello!
I would like to request access for EHA team members into the country data for Cote d'Ivoire, ROC and if applicable, broader access to the behavioral/human data in China and Indonesia. Please let me know if there are more details I can provide, and if you need a list on names who require access.
Many thanks in advance for all of your help, Ava

From: Karen Saylors <ksaylors@metabiota.com>
To: David John Wolking <djwolking@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>;Billy Karesh <karesh@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>;Caroline Fric <cfric@metabiota.com>;technology@eidith.org <technology@eidith.org>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Tammie O'Rourke <torourke@metabiota.com>;predict@ucdavis.edu <predict@ucdavis.edu>;Taylor Elnicki <telnicki@metabiota.com>;Alison Andre <andre@ecohealthalliance.org>;Amanda Fuchs <fuchs@ecohealthalliance.org>;Brooke Genovese <bgenovese@ucdavis.edu>
Sent: 7/7/2017 2:14:07 AM
Subject: Re: [predict] Re: EIDITH access for EHA team members

Sure David, that would be fine.
Thanks,
Karen

From: David J Wolking <djwolking@ucdavis.edu>
Date: Thursday, July 6, 2017 at 3:12 PM
To: Karen Saylors <ksaylors@metabiota.com>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, Eddy Rubin <erubin@metabiota.com>, Billy Karesh <karesh@ecohealthalliance.org>, Ava Sullivan <sullivan@ecohealthalliance.org>, Caroline Fric <cfric@metabiota.com>, "technology@eidith.org" <technology@eidith.org>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Tammie O'Rourke <torourke@metabiota.com>, "predict@ucdavis.edu" <predict@ucdavis.edu>, Taylor Elnicki <telnicki@metabiota.com>, Alison Andre <andre@ecohealthalliance.org>, Amanda Fuchs <fuchs@ecohealthalliance.org>, Brooke Genovese <bgenovese@ucdavis.edu>
Subject: Re: [predict] Re: EIDITH access for EHA team members

Hey Karen,

Do you think we need a separate call or would adding this as an item on the next EB call on July 26th work?

Cheers,

D

On Thu, Jul 6, 2017 at 2:55 PM, Karen Saylors <ksaylors@metabiota.com> wrote:
Thanks Jonna.
I'm traveling this week with Peter and Billy, so we will have time to discus data ownership and data sharing/access for transitioning countries, but I do think it would be good to plan some discussion on this to agree on general principles once our travels are done, as there are analysis and EIDITH implications that we would like to prepare for.

Perhaps we could put something on the calendar for early August? Brooke, might you be able to help coordinate a call for sometime between July 31st and August 4th?

Thanks much,
Karen

From: <jonna.mazet@gmail.com> on behalf of Jonna Mazet <jkmazet@ucdavis.edu>
Date: Thursday, June 22, 2017 at 3:19 PM
To: Peter Daszak <daszak@ecohealthalliance.org>, Eddy Rubin <erubin@metabiota.com>, Karen Saylors <ksaylors@metabiota.com>, Billy Karesh <karesh@ecohealthalliance.org>
Cc: Ava Sullivan <sullivan@ecohealthalliance.org>, Caroline Fric <cfric@metabiota.com>, "technology@eidith.org" <technology@eidith.org>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Tammie O'Rourke <torourke@metabiota.com>, "predict@ucdavis.edu" <predict@ucdavis.edu>, Taylor Elnicki <telnicki@metabiota.com>, Alison Andre <andre@ecohealthalliance.org>, Amanda Fuchs

<fuchs@ecohealthalliance.org>, Brooke Genovese <bgenovese@ucdavis.edu>
Subject: Re: EIDITH access for EHA team members

Hi,
Should likely set up a call to discuss any issues and/or concerns. If no one has any concerns, we can give access to existing country data (there isn't a ton, I don't think) and govern data sharing and best collegial behavior through EB.
Whatever best serves all concerned, as I'm totally open on process.
Jonna

On Wed, May 31, 2017 at 11:22 AM, Tammie O'Rourke <torourke@metabiota.com> wrote:
Hi Ava,
I kind hello back!
The change of the organizations in these countries is extremely sensitive and therefore the transition of the data and the access should likely be part of the larger transition plan for these countries.
I am including Jonna in the conversation as she likely has more insight on this subject. Jonna, do you agree?
Please let me know if you have any questions.
Tammie

-----Original Message-----
From: Ava Sullivan [mailto:sullivan@ecohealthalliance.org]
Sent: Wednesday, May 31, 2017 7:51 AM
To: Caroline Fric <cfric@metabiota.com>
Cc: technology@eidith.org
Subject: EIDITH access for EHA team members

A kind hello!
I would like to request access for EHA team members into the country data for Cote d'Ivoire, ROC and if applicable, broader access to the behavioral/human data in China and Indonesia. Please let me know if there are more details I can provide, and if you need a list on names who require access.
Many thanks in advance for all of your help, Ava

From: Andrew Clements <aclements@usaid.gov>
To: Katherine Leasure <kaleasure@ucdavis.edu>
CC: PREDICTMGT <predictmgt@usaid.gov>;Predict inbox <predict@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 7/7/2017 4:25:04 PM
Subject: Re: PREDICT International Travel Requests

Thanks!

Karesh travel approved.

On Fri, Jul 7, 2017 at 6:13 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Hi Andrew. Below is an updated trip purpose for Dr. Karesh's France ITA (#8); please let me know if you have any further questions. Thanks!

Trip purpose: Dr. Karesh will participate in an World Organisation for Animal Health's (OIE) ad hoc group. Dr. Karesh will participate in setting health and IACUC related standards for wildlife farming for OIE code purposes. The farming of wildlife presents opportunities for the emergence of infectious diseases due to the unusual and unnatural groupings of species unnatural habitats in contact with other species in humans that does not occur in the wild. OIE is interested in developing standards and codes for countries to follow that will reduce the risk of disease emergence in both animals and humans. Since good standards such as used in the US in IACUC process also lend themselves to disease risk reduction OIE provides an opportunity to promote similar standards in countries where best practices are currently not being utilized.

From: Andrew Clements [mailto:aclements@usaid.gov]
Sent: Thursday, June 29, 2017 3:22 AM
To: Katherine Leasure
Cc: PREDICTMGT; Predict inbox; Jonna Mazet
Subject: Re: PREDICT International Travel Requests

#3 approved.

I would like additional information on #8 as to how it relates to PREDICT.

All others approved subject to Mission concurrence.

On Thu, Jun 29, 2017 at 12:53 AM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Please find below international travel requests for your review and approval. Please let me know if you have any questions. Thanks!!

1. Monagin (Guinea): $8,742 **business class required due to medical need*/$327 (Conakry) max daily per diem

2. Kelly (Ghana): $2,000 airfare/$331 (Accra) max daily per diem

3. O'Rourke, O'Rourke (USA): $479 each airfare/$341 (San Francisco), $179 (Davis) max daily per diems

4. Zambrana-Torrelio (Colombia): $590 airfare/$411 (Cartagena de Indias) max daily per diem

5. Anthony (Malaysia): $1400 airfare/$263 (Kuala Lumpur) max daily per diem

6. Chmura (China): $5,200 airfare/$241 (Dali), $377 (Beijing), $407 (Guangzhou), and $402 (Shanghai) max daily per diems

7. Zambrana-Torrelio (China): $2,000 airfare/$377 (Beijing) max daily per diem

8. Karesh (France): $8,000 **business class required due to medical need*/$568 (Paris) max daily per diem

9. Smith (Sierra Leone): $2,500 airfare/$319 (Freetown), $221 (Makeni) max daily per diems

10. Tremeau-Bravard (Senegal, Rwanda): $2,800 airfare/$264 (Dakar), $294 (Kigali) max daily per diems

11. Goldstein (Cambodia): $3,300 airfare/$236 (Phnom Penh) max daily per diem

12. Montecino (Tanzania): $2,200 airfare/$309 (Dar es Salaam), $197 (Morogoro) max daily per diems

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2. UC Davis would like to request travel approval for Dr. Terra Kelly to travel from Flagstaff, Arizona, USA to Accra, Ghana from August 5-12, 2017

Trip purpose: Dr. Terra Kelly will be traveling to Accra to meet with PREDICT implementing partners to discuss implementation of surveillance and diagnostic laboratory activities and scoping and planning for upcoming surveillance activities in Year 4. Dr. Kelly will also be conducting training for PREDICT human disease surveillance partners on questionnaire administration for the risk characterization and all laboratory partners on data entry and management in the EIDITH database for laboratory results reporting.

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extracts.

Trip purpose: In San Francisco, they will meet with PREDICT Senior Management to discuss PREDICT Information Management concerns, progress and issues. In Davis, they will meet with the UCD global team and discuss USAID reporting and data extracts and mapping to prepare for the PREDICT data meeting September 2017.

4. EcoHealth Alliance would like to request travel approval for Mr. Carlos Zambrana-Torrelio to travel from New York, New York, USA to Cartagena de Indias, Colombia from July 23-29, 2017, to attend and present at the International Congress for Conservation Biology.

Trip purpose: As part of continued work under the CBD-WHO Joint Work Programme, Mr. Zambrana-Torrelio will present on the indicators for health that links disease emergence and biodiversity loss and the One Health approaches operationalized by PREDICT-2. In addition, he will discuss on the methods and findings from the Deep Forest project to emphasize synergies in biodiversity and disease monitoring. Presentation title: "Integrating biodiversity in conservation planning for human health and well-being." Mr. Zambrana-Torrelio also was invited to participate in a workshop session on ecosystems and human health organized by the International Union for Conservation Nature.

5. EcoHealth Alliance would like to request travel approval for Simon Anthony to travel from New York, New York, USA to Kuala Lumpur, Malaysia from July 23-30, 2017 for in-country trainings with local partners and PREDICT staff.

Trip purpose: The purpose of this trip is to meet with local sequencing companies to discuss local implementation of new technologies developed at CII (VirCapSeq) (24th July). Dr. Anthony will also conduct a three-day training workshop with PREDICT staff at the National Public Health Lab (NPHL) on PCR, cloning and sequencing, as well as sequence analysis and assay design. Dr. Anthony will also conduct a one-on-one training with Mei Ho Lee in paper writing. Outcome: Enhanced local capacity for viral discovery, sequence analysis and assay design. Planning of PREDICT papers to be led by regional staff (Mei Ho Lee).

6. EcoHealth Alliance would like to request travel approval for Mr. Aleksei Chmura to travel from New York, New York, USA to Dali, Beijing, Guangzhou, and Shanghai China from July 31 to September 5, 2017 for meetings with in-country partners, field work, behavioral surveillance, and site selection work.

Trip purpose: Mr. Aleksei Chmura will meet with PREDICT-2 Field Coordinator Dr. Libiao Zhang at Guangxi Normal University in Guilin, and at our Partner Laboratory based at the Guangdong Entomological Institute in Guangzhou in Guangdong, as well as with Dr. Changwen Ke at the Guangdong CDC in Guangzhou. Dr. Zhu and Mr. Chmura will meet with Dr. Yunzhi Zhang of the Yunnan CDC. Together with Field Coordinator Dr. Guangjian Zhu, Mr. Chmura will coordinate and travel with full field team to sites in Yunnan Province to assist with human behavioral surveillance fieldwork, review field, lab, and data entry protocols, and prepare for 2017-18 PREDICT-2 field sampling. Field sites are prioritized along the wildlife trade pathways as per PREDICT-2 site selection criteria and protocols. Mr. Chmura will communicate with

PREDICT-2 Metabiota partners in China as well as new Chinese Academy of Sciences Laboratory collaborators based in Beijing.

7. EcoHealth Alliance would like to request travel approval for Mr. Carlos Zambrana-Torrelio to travel from New York, New York, USA to Beijing, China from August 19-27, 2017, to attend and present at the International Association for Ecology (INTECOL).

Trip purpose: Mr. Zambrana-Torrelio will attend the International Association for Acology to present the results produced by Modeling and Analytics Working Group of the Global Virome Project. Presentation title: "The Global Virome Project: A network of viral-diversity monitoring."

8. EcoHealth Alliance would like to request travel approval for Dr. William Karesh to travel from New York, New York, USA to Paris, France from August 21-24, 2017 to participate in the World Organization for Animal Health's (OIE) ad hoc group on killing methods for farmed reptiles for their skins and meat.

Trip purpose: Dr. Karesh will participate in the World Organisation for Animal Health's (OIE) ad hoc group on killing methods for farmed reptiles for their skins and meat. Dr. Karesh will participate in setting health and IACUC related standards for wildlife farming for OIE code purposes.

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Trip purpose: Mr. Smith will fly to Freetown, then travel on to Makeni to perform laboratory training. The training will include staff from UNIMAK and PREDICT with invitations to MAFFS and MOH to include staff from the TEKO veterinary lab and National Public Health lab to prepare, handle and test samples using Predict protocols.

10. UC Davis would like to request travel approval for Alexandre Tremeau-Bravard to travel from Sacramento, California, USA to Dakar, Senegal from August 12-25, 2017, then to Kigali, Rwanda from August 25-30, 2017 to perform laboratory trainings.

Trip purpose: Senegal – In Dakar, Mr. Tremeau-Bravard will train lab staff from ISRA and ICAD to prepare, handle and test samples using Predict protocols. Rwanda – In Kigali, he will do a refresher lab training for staff based at NRL and RAB.

11. UC Davis would like to request travel approval for Dr. Tracey Goldstein to travel from Sacramento, California, USA to Phnom Penh, Cambodia from August 3-11, 2017 to attend meetings with government and non-governmental partners, as well provide technical guidance to the field team during planned August sampling activities.

Trip purpose: Dr. Goldstein will meet with government and non-governmental partners regarding coordination of PREDICT-2 activities, and will join the field team to assist with technical guidance for the concurrence sampling of human, livestock and wildlife planned for August in a bat guano farming community in Kampong Cham.

12. UC Davis would like to request travel approval for Diego Montecino to travel to Dar es Salaam and Morogoro, Tanzania from August 5-26, 2017 to support the PREDICT Tanzania team in the initiation of new in-depth methods for bat surveillance at high-risk urban interfaces.

Trip purpose: Mr. Montecino (UC Davis-based project scientist) will support the PREDICT Tanzania team to set up new methods for safely and effectively collecting non-invasive samples from a well-established urban straw-coloured fruit bat (*Eidolon helvum*) colony in Morogoro in order to test them for Coronaviruses and other priority viral threats. He will also introduce methods for counting bats present in a colony and assessing bat behavior and their interactions with people. Mr. Montecino will work hand-by-hand with the PREDICT Tanzania team to transfer the knowledge, skills, and capacity to conduct these activities following his return to the US.

Katherine Leasure

HR/Payroll/Financial Assistant

One Health Institute

University of California, Davis

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530-752-3318 FAX

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predictmgt@usaid.gov
https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/014901d2f061%246a1942a0%243e4bc7e0%24%40ucdavis.edu

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Andrew Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health

U.S. Agency for International Development

Mobile phone: 1-571-345-4233
E-mail: aclements@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

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UCDJSR0001665

From: Katherine Leasure <kaleasure@ucdavis.edu>
To: 'Cassandra Louis Duthil' <clouisduthil@usaid.gov>;'Andrew Clements' <aclements@usaid.gov>
CC: predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 7/12/2017 10:42:50 PM
Subject: [predict] RE: PREDICT International Travel Requests

Thanks to you both for this confirmation! I will notify EHA that travel is approved.

From: Cassandra Louis Duthil [mailto:clouisduthil@usaid.gov]
Sent: Wednesday, July 12, 2017 12:59 PM
To: Andrew Clements
Cc: Katherine Leasure; predict@ucdavis.edu
Subject: Re: PREDICT International Travel Requests

Hello All,

Only AOR approval is required for Colombia.

Best,

Telephone: 202-712-5583 **Cell:** 407-731-3155 clouisduthil@usaid.gov

On Wed, Jul 12, 2017 at 3:55 PM, Andrew Clements <aclements@usaid.gov> wrote:
I'm going to assume no concurrence is needed, so consider the travel fully approved.

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jul 12, 2017, at 7:05 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Good morning,

I just wanted to follow-up on the ITA request for Carlos to Colombia (#4 below). Is mission concurrence required for this destination? His departure date is July 23, so time is running short to book travel arrangements.

Thank you,
Katie

From: Katherine Leasure [mailto:kaleasure@ucdavis.edu]
Sent: Friday, July 07, 2017 9:10 AM
To: 'Cassandra Louis Duthil'
Cc: predict@ucdavis.edu
Subject: RW: PREDICT International Travel Requests

Hi Cassandra,

I have not yet seen a request for concurrence for ITA #4 below (Carlos's travel to Colombia). Is mission concurrence required for this destination? The planned departure date is July 23.

Thank you,
Katie

From: Andrew Clements [mailto:aclements@usaid.gov]
Sent: Thursday, June 29, 2017 3:22 AM
To: Katherine Leasure
Cc: PREDICTMGT; Predict Inbox; Jonna Mazet
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Katherine Leasure
HR/Payroll/Financial Assistant
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https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/014901d2f061%246a1942a0%243e4bc7e0%24%40ucdavis.edu

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Andrew Clements, Ph.D.
Senior Scientific Advisor
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For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/pandemic

From: Eri Togami <etogami@ucdavis.edu>
To: Cara Chrisman <cchrisman@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Brooke Watson <watson@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>;Dennis Carroll <dcarroll@usaid.gov>
Sent: 7/20/2017 11:53:56 PM
Subject: GVP meeting notes July 20

Hi GVP team,

Please see the meeting notes from our GVP call this morning (July 20, 2017).

Agenda

London/Oslo follow up: for details, see Brooke's notes

- Main takeaway – we need in-country advocates to move things forward (ex. Wellcome Trust needs UK advocate)
- Lancet
  - More operational discussion to take place in the future
  - Possibility of *Lancet* paper – move forward but with caution, *Science* is the priority
  - Eddy is currently writing a *Nature* paper and GVP is mentioned – could reference Bellagio document
- Wellcome Trust
  - we were not meeting the right people in the leadership level who can control funds
  - they have put 200 million into CEPI
  - Richard Feachem could be our UK GVP advocate
- Sanger Center
  - They are not a funding agency, but were receptive. Good meeting.
  - Potential collaboration for unbiased deep sequencing
  - Possibility to include GVP in their 5-year plan
  - Need Jeremy to post his ideas and present to board of directors. When Jonna met with Jeremy in Seattle, he presented possibility for GVP as a post-CEPI project. He would be more interested if GVP had philanthropist (Allen or Gates etc.) and CEPI support.
- CEPI in Oslo
  - CEPI is a granting agency, purely focused on vaccine + animal models to test vaccine
  - 700 million dollar project
  - It was catalyzed by Norwegian public health person who convinced the government to cooperate
  - Launched successfully as the timing was right amidst Ebola epidemic
  - CEPI vulnerabilities (they are aware, so we can leverage these points):
    - Time to develop and distribute vaccines
    - Often blind-sighted by an unknown virus (GVP can fill gap)
  - Richard Hatchett will be in Washington DC in early October.
- Other notes: large funding agencies and mid-sized agencies are mutually exclusive (ex. If you have Gates, you will not get mid-sized funders)

Other

- Data management portal to be developed by EIDITH team.
- China Pilot project to be implemented
- Costa Rica – Talked with Dan Janzen last week. Currently in communication. Ambassador can be kept in the loop for future communications.
- Budget
  - Currently drastically underbudgeted, according to implementation team calculation.
  - Since so much is uncertain, we can pitch based on theoretical number, and revise estimate based on operational costs of pilot countries
  - Global hub is being pitched at 5 million

Action items

Eddy – follow up with Richard Feachem
Dennis – Set up meeting with Richard Hachett for October
Dennis - meet with Ambassador from Costa Rica, Brian from Princeton

Dennis – follow up with Lancet Pam Das [move forward but with caution, keep Science in view]
All- Send Eri an email for feedback on PMAC launch, suggestions from Cara and Dennis below:

- Length - It would be great to have an overall 1 day meeting (2 1/2day sessions) - but does not need to consecutive on one day. The first of the two sessions would be a closed meeting with internal GVP people and the second would be the open launch. In order to maximize everyone's ability to participate in other meetings, it would actually be helpful if the two sessions were on separate days.
- Closed/Open - Preferable to have one closed (GVP only) and one open (the launch)
- Speakers - Would like to include those people who have already been involved in or working with us on the GVP, particularly who would already be at PMAC (like a Richard Feachem).
- Participants - For the closed session, it would the Beijing folks, particularly if they would already be at PMAC (as many would be), so the SC and WG people. For the launch, once we have the PMAC attendee list, can invite people and keep it open. Those people we particularly want, we can send additional f/u to. The number for the closed would around Beijing size and for the open would be a room for about 100 ppl.
- Room - Flexible and can figure out as agenda evolves, but could have a different set-up for the two different meetings.

Other facts
The second story of the Eagle bar in Cambridge is always kept open, after stories of a ghost of a child who died from a fire who was unable to open the window.

Enjoy the rest of your week!

Best,
Eri

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Thursday, July 20, 2017 6:00 AM
To: Jonna Mazet ; Eri Togami ; Peter Daszak ; Brooke Watson ; Eddy Rubin ; Nathan Wolfe
Cc: Dennis Carroll
Subject: Today's GVP Meeting - Agenda

Hi Team,

Looking forward to catching up with everyone today! Please see below for the agenda and a few discussion points.

For those who didn't get a chance yet to review, Brooke's notes from London/Oslo are also attached.

Best,
Cara

Agenda

1. London/Oslo Readout & F/U
    1. Follow up actions:
        1. Data Management Team - Establish a prototype portal
        2. Lancet Paper
        3. Reconnect with Richard Feachem
2. GVP Updated Agenda
3. PMAC Launch Planning (see Eri's questions for discussion below)
4. Science Paper Update
5. Additional Outreach Updates/Planning

1. Costa Rica
2. Other

6. AOB

PMAC Launch Planning
Here are some of the questions we can discuss for our PMAC concept note:

- How long should the launch be? Options are half day (morning or afternoon), 1 day or 2 days.
- Should we have a closed meeting or a public meeting? Or both?
- Do we want to invite speakers?
- Who are our target participants? What is our estimated number of participants?
- What type of room set up do we want? Options are classroom, theater, roundtable or boardroom.

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E-mail: cchrisman@usaid.gov

From:	Cara Chrisman <cchrisman@usaid.gov>
To:	Jonna Mazet <jkmazet@ucdavis.edu>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>;Peter Daszak <daszak@ecohealthalliance.org>;Brooke Watson <watson@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>
CC:	Dennis Carroll <dcarroll@usaid.gov>
Sent:	7/21/2017 2:26:10 PM
Subject:	GVP Action Items (as of 7/21)

Hi Team,

Glad we were able to touch base yesterday. In order to move things along, please see below for an updated, compiled list of action items, pulled from Eri's Emazing E-Notes. They are also attached (that document includes all the archived action items by date, as well).

If any of these can be taken off the list as they are completed or no longer relevant, please let me know.

Best,
Cara

Current GVP Action Items (7/21/17)

Travel:

- Peter out Aug 1-20, then Sweden, back in office last week of August
- Dennis – In and out in August, will call in to GVP meetings

Jonna

Jonna – Follow up with Richard Hatchett about Zoe

UCD and EHA team – Finalize budget

Eri

Cara and Eri – Update information on website (2-pager and quad chart)

UCD and EHA team – Finalize budget

Eri- look into existing in country capacities through PREDICT

Dennis

Dennis – Set up meeting with Richard Hachett for October in DC

Dennis – Make plans for China trip & check in with Keiji about HK visit (Sept. 4th week)

Dennis - Meet with Ambassador from Costa Rica

Dennis – Meet with Brian Granfield from Princeton during E. Coast trip (WT advocate) w/ Peter

Dennis – follow up with Lancet Pam Das [move forward but with caution, keep Science in view

Dennis - follow up with Illumina

Dennis - Follow up with Ilaria after Switzerland

Dennis - Set up f/u meeting with Chris Elias

Dennis - Follow up with UNESCO individual

Dennis – Keep Larry in the loop as we move forward and run the "ask" by him when completed

Cara

Cara and Eri – Update information on website (2-pager and quad chart)

Cara - Include ELSI and A/P docs in shared folder

Peter

Peter – Work on Science paper

Peter – Check in with George about China Trip in Sept.

UCD and EHA team – Finalize budget

Peter - send Cara various meeting schedules (cell symposium, vaccine congress etc.)

Peter – share slide on why broad spectrum approach is critical

Peter - Follow up with the Norwegians regarding GVP & CEPI

Pete - Follow up on not for profit (in progress)

Peter – Work with Dennis regarding Brian Granfeld & GVP

Brooke

UCD and EHA team – Finalize budget

Eddy

Eddy – Move forward with prototype EIDITH planning

Eddy – follow up with Richard Feachem

Eddy – Continue f/u with Sanger about GVP and the 5 yr plan

Eddy/Nathan – Follow up regarding Verily and decide about inclusion as a partner on the website

Eddy – align with Peter and reach out to Sir Michael Stratton about GVP (in progress)

Nathan

Nathan - Reach out to Peggy Hamburg regarding GVP and CEPI

Nathan – Update post-call with Richard Wilcox

Nathan - Follow up with Lance Brooks at DTRA

Eddy/Nathan – Follow up regarding Verily and decide about inclusion as a partner on the website

All

All- Send Eri an email for feedback on PMAC launch, suggestions from Cara and Dennis below:

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- Room - Flexible and can figure out as agenda evolves, but could have a different set-up for the two different meetings.

All – look at outreach worksheet and send modifications to Cara

All – start brainstorming who to invite to PMAC meeting and send Eri list of names

All - Continue to follow up with Skoll/Mark/Larry (Jonna completed Mark conversation)

All - Identify other key individuals to engage with the core group (Keiji, Steve, Kathleen, etc.) on particular topics

All - Consider next steps with DARPA

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All – look at outreach worksheet and send modifications to Cara
All – start brainstorming who to invite to PMAC meeting and send Eri list of names
All - Continue to follow up with Skoll/Mark/Larry (Jonna completed Mark conversation)
All - Identify other key individuals to engage with the core group (Keiji, Steve, Kathleen, etc.) on particular topics
All - Consider next steps with DARPA

Archived Action Items

7/20 **Action Items**

Eddy – follow up with Richard Feachem
Dennis – Set up meeting with Richard Hachett for October
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- Room - Flexible and can figure out as agenda evolves, but could have a different set-up for the two different meetings.

7/6 Action Items

Nathan – reach out to Debbie and Dan Jansen.
Peter – Work on Science paper
Eri - cancel GVP meeting next week on calendar
Brooke – create water bowl map and send to Cara
Cara and Eri – Update information on website (2-pager and quad chart)
UCD and EHA team – Finalize budget

6/29 Action items

Peter- WHO Bulletin before tomorrow morning + Science comments
Jonna – send Cara, Eddie, Brooke Dennis Zoe's CV and email
Brooke –calculate new country budget

6/22 Action Items

Peter – review WHO bulletin and share with group
Peter – add London outreach names to spreadsheet
Nathan – reach out to Dan Jansen, Costa Rica
Jonna – send email to Thailand group about SOPs etc. (complete 6/22)
Eri – meet with predict team regarding SOP and country budget calibration

6/15 Action items

- Brooke – update operational timeline and country level cost
- All – look at outreach worksheet and send modifications to Cara
- Peter - send Cara various meeting schedules (cell symposium, vaccine congress etc.)
- Dennis – send WHO bulletin draft to Brooke
- Brooke – send revised WHO bulletin draft to Eri
- Eri – send revised WHO bulletin draft to Peter/Jonna
- Peter – share slide on why broad spectrum approach is critical

- (Peter – enjoy Mamawata on Congo river)

6/8 Action items

- Brooke – recalibrate country list and revise table
- Brooke- create country specific map showing sampling units
- Cara – send global map to Eri
- Eri - reach out to design people at UC Davis
- Eri- look into existing in country capacities through PREDICT

May 25th Action items

- Peter – draft timeline for proceedings of the working group
- Cara and Dennis – develop agenda for next week's conference call to look at document closely
- Dennis - follow up with Illumina
- Dennis – send pitch slide decks to group
- Nathan - will reach out to Dan Jansen (no updates on Costa Rica since last communication)
- Brooke – send new map to Dennis
- All – start brainstorming who to invite to PMAC meeting and send Eri list of names

May 11th Action Items

- Cara - Include ELSI and A/P docs in shared folder
- Cara - Follow up with Katherine Littler x2 (done)
- Peter & Brooke - Finalize waterbird modeling (with team)
- Peter & Brooke - Share updated modeling slides for the pitch deck
- Peter - Follow up with the Norwegians regarding GVP & CEPI
- Peter - Check in about paper, given citation in Kevin's paper
- Dennis - Set up mtg with Admiral Ziemer for the week of the 22nd (Peter to attend) (in progress)
- Dennis - Reach out to Richard Hatchett and set up visit to London
- Dennis - Send follow up Illumina email & cc Eddy
- Dennis - Follow up with Ilaria after Switzerland
- Eddy - Work on a visual for the pitch deck "funnel" (done)
- Nathan - Reach out to Peggy Hamburg regarding GVP and CEPI
- All - Update the pitch deck (in progress)
- All - Read working group concept notes and be prepared to discuss on May 25th call.

Remaining 3/2 - 4/13 Actions

- Peter - finalize and resubmit paper (in progress)
- Peter - Follow up on not for profit (in progress)
- Dennis - Set up 1/u meeting with Chris Elias
- Dennis - Follow up with UNESCO individual
- Dennis – Keep Larry in the loop as we move forward and run the "ask" by him when completed
- Nathan – Update post-call with Richard Wilcox
- Nathan - Follow up with Lance Brooks at DTRA
- Nathan & Peter - Coordinate working with Dan Jansen
- Eddy/Nathan – Follow up regarding Verily and decide about inclusion as a partner on the website
- Eddy – align with Peter and reach out to Sir Michael Stratton about GVP (in progress)
- Cara & Dennis - Set up CR consultation when pitch is completed
- Cara – Start list of who to target (including WT) in May with refined "ask"
- Peter – align with Eddy and reach out to Brian Granfield about GVP
- All - Continue to follow up with Skoll/Mark/Larry (Jonna completed Mark conversation)
- All - Identify other key individuals to engage with the core group (Keiji, Steve, Kathleen, etc.) on particular topics
- All - Consider next steps with DARPA

From: Cara Chrisman <cchrisman@usaid.gov>
To: Eri Togami <etogami@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Dennis Carroll <dcarroll@usaid.gov>
Sent: 7/21/2017 9:02:58 PM
Subject: Re: GVP Action Items (as of 7/21)

Hi Eri,

Fantastic, this all sound great, much appreciated!

I'll get you over the updated text early next week.

Thanks,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
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Bureau for Global Health
U.S. Agency for International Developenent (AID)

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On Fri, Jul 21, 2017 at 4:53 PM, Eri Togami <etogami@ucdavis.edu> wrote:

Hi Cara,

Great, I already talked to our communications expert and here are our next steps:

1. We can do this now and move the two documents to a new "archives" section.

2. We will wait for you to alter the language/numbers to change to the Bellagio format. If you send me the text, we can format the document and upload it to our website.

I hope this works and we look forward to receiving the #2 document.

Best,

Eri

Eri Togami DVM MPH

One health fellow

One Health Institute

University of California, Davis

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Friday, July 21, 2017 1:40 PM

To: Eri Togami <etogami@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>; Dennis Carroll <dcarroll@usaid.gov>
Subject: Re: GVP Action Items (as of 7/21)

Hi Eri,

Great, thank you!

For #1 - My web design experience starts and ends with SquareSpace, so don't want to suggest anything that's too complicated. However, either a sub-tab under Resources or a link toward the bottom of the Resources page itself would work. We would certainly defer to the team as to what would be easiest in order to move those older documents so they are no longer a focus, but are available if people would still like to access them.

For #2 - In this case, we're looking for consistency with what else we're putting out there. While matching the powerpoint would be nice, we generally would be handing out the Bellagio Initiative and perhaps since the Comms team drafted that, it would work for them to also do the 2 pager in a similar format. I think this would likely include keeping the two column format with the various sections, but updating the colors (greens, black, etc.), font (so it's the same as the Initiative), and adding the logo (even if just at the bottom). If they have any creative ideas that can be done with minimal effort, we're definitely open to that.

Happy to discuss either/both and please let me/us know if any of this is particularly onerous (or unclear). Given what a great job they did with the Bellagio Initiative, we don't want to be too prescriptive with the 2 pager, but would be happy to have it coordinate with the Initiative (and no idea how to make it look like the Powerpoint - particularly since a black background is not ideal for printing!).

Thanks again,

Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
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On Fri, Jul 21, 2017 at 4:09 PM, Eri Togami <etogami@ucdavis.edu> wrote:

Hi Cara,

Great, yes I can work on that with our communications team. Just some clarifications for #1 and 2.

1. Will we create a new "Archived" section on the website?
2. What exactly does the format change look like? Colors, font, logo, page layout?

Best,
Eri

Eri Togami DVM MPH

One health fellow

One Health Institute

University of California, Davis

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Friday, July 21, 2017 12:58 PM
To: Eri Togami <etogami@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>; Dennis Carroll <dcarroll@usaid.gov>
Subject: Re: GVP Action Items (as of 7/21)

Hi Eri,

Thanks for following up and glad it was helpful. This is timely as I was just trying to figure out the format earlier today!

Dennis and I discussed and the hope was to do a few things:

1. Move the old documents into an "Archived" section on the website. So, still available, but no longer highlighted.
2. Update the 2 pager so that the format aligns with the other current GVP documents (either the Bellagio initiative or the ppt.).
3. Update the language in the 2 pager & remove older numbers

After our discussion, we have some ideas for #3 that I can work on today and early next week and then share for review and feedback. Would #1 & 2 be things that could be handled on your end?

Thanks,

Cara

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On Fri, Jul 21, 2017 at 12:08 PM, Eri Togami <etogami@ucdavis.edu> wrote:

Hi Cara,

Great idea to compile action items.

For the following item, did you want to wait for the team to agree on a budget, or edit the two documents now so that it does not include specific numbers for the time being?

Cara and Eri – Update information on website (2-pager and quad chart)

Best,

Eri

Eri Togami DVM MPH

One health fellow

One Health Institute

University of California, Davis

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
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Jonna – Follow up with Richard Hatchett about Zoe

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Eri- look into existing in country capacities through PREDICT

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Brooke

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Eddy

Eddy – Move forward with prototype EIDITH planning

Eddy – follow up with Richard Feachem

Eddy – Continue f/u with Sanger about GVP and the 5 yr plan

Eddy/Nathan – Follow up regarding Verily and decide about inclusion as a partner on the website

Eddy – align with Peter and reach out to Sir Michael Stratton about GVP (in progress)

Nathan

Nathan - Reach out to Peggy Hamburg regarding GVP and CEPI

Nathan – Update post-call with Richard Wilcox

Nathan - Follow up with Lance Brooks at DTRA

Eddy/Nathan – Follow up regarding Verily and decide about inclusion as a partner on the website

All

All- Send Eri an email for feedback on PMAC launch, suggestions from Cara and Dennis below:

- Length - It would be great to have an overall 1 day meeting (2 1/2day sessions) - but does not need to consecutive on one day. The first of the two sessions would be a closed meeting with internal GVP people and the second would be the open launch. In order to maximize everyone's ability to participate in other meetings, it would actually be helpful if the two sessions were on separate days.

- Closed/Open - Preferable to have one closed (GVP only) and one open (the launch)

- Speakers - Would like to include those people who have already been involved in or working with us on the GVP, particularly who would already be at PMAC (like a Richard Feachem).

- Participants - For the closed session, it would the Beijing folks, particularly if they would already be at PMAC (as many would be), so the SC and WG people. For the launch, once we have the PMAC attendee list, can invite people and keep it open. Those people we particularly want, we can send additional f/u to. The number for the closed would around Beijing size and for the open would be a room for about 100 ppl.

- Room - Flexible and can figure out as agenda evolves, but could have a different set-up for the two different meetings.

All – look at outreach worksheet and send modifications to Cara

All – start brainstorming who to invite to PMAC meeting and send Eri list of names

All - Continue to follow up with Skoll/Mark/Larry (Jonna completed Mark conversation)

All - Identify other key individuals to engage with the core group (Keiji, Steve, Kathleen, etc.) on particular topics

All - Consider next steps with DARPA

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UCDJ5R0001690

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Molly Turner <turner@ecohealthalliance.org>
CC: Evelyn Luciano <luciano@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>;predict@ucdavis.edu" <predict@ucdavis.edu>;Alice Latinne <latinne@ecohealthalliance.org>
Sent: 7/28/2017 5:44:18 PM
Subject: [predict] RE: Taking over contract from MB for Ejikman

No information on the proper payment accounts (meaning in-country bank accounts?) for LANADA and IPCI. You would have to get that information from Beth. I don't see any problem with Metabiota continuing to pay those partners until your new subawards are setup so there isn't a stoppage of activities, you would just need to work those details out with them. We're doing something similar in Guinea and Sierra Leone. Reviewing the invoices for those partners before Metabiota pays them is a good idea. Please copy predict@ucdavis.edu on correspondence with Metabiota regarding any arrangements for them to continue to pay partners while we work on getting new subawards established.

Thanks,
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Molly Turner [mailto:turner@ecohealthalliance.org]
Sent: Friday, July 28, 2017 8:06 AM
To: Elizabeth Leasure
Cc: Evelyn Luciano; Ava Sullivan; predict@ucdavis.edu; Alice Latinne
Subject: Re: Taking over contract from MB for Ejikman

Hi Liz,

I believe Peter and Jonna discussed this already, but it would be good if Metabiota could continue to disburse funds at least in the case of our collaborators in Ivory Coast (and probably Indonesia and China as well). We're still ascertaining what the understanding is between Metabiota and LANDA and IPCI (I'm writing separately to Beth about this) regarding ongoing financial obligations, but we do know that IPCI has a trip planned before the end of the project year that we may want to go ahead with if we can ensure that everything's in order training- and compliance-wise. We want to make sure that all financial transactions are conducted properly of course; I am happy to review financial reports, and I believe there also remains a question as to the proper payment accounts for both entities, please advise if you have any information on that point.

Please let us know how you'd like to proceed.

Thanks,
Molly

On Tue, Jul 25, 2017 at 4:51 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Hi Molly. The approvals for the new EHA subs in Indonesia, China, RoC, and Cote d'Ivoire will come through approval of the ceiling increase budget that was submitted, which OAA is pushing to have done (approved/processed) before the end of the current fiscal year. Now, how soon before 9/30 I can't say, as it all depends on OAA and how quickly they can review and whether or not they have any questions or require additional information from us before they approve. Too many unknowns to say for sure at this point. My opinion (based on past experience) is that it will come down to the wire, so I wouldn't count on getting approval until the end of September.

I had not planned on UCD setting up any interim subawards given our ability to get multiple subs approved at once through the ceiling increase process, but that could potentially be revisited or discussed if you feel very strongly about

it. Honestly, given that we're almost to August and I'll be travelling from 8/1-8/10 and laser-focused on Y4 budgeting from 8/11-8/31, I'm not sure interim UCD subawards are a good option at this point. Continuing to have Metabiota make certain payments (for salaries of staff, etc.) is an option, but that is also something we should discuss.

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

From: Molly Turner [mailto:turner@ecohealthalliance.org]
Sent: Tuesday, July 25, 2017 7:13 AM
To: Elizabeth Leasure
Cc: Evelyn Luciano; Ava Sullivan
Subject: Re: Taking over contract from MB for Eijkman

Hi Liz,

Just following up.

Thanks,
Molly

On Tue, Jul 18, 2017 at 1:22 PM, Molly Turner <turner@ecohealthalliance.org> wrote:
Hi Liz,

I'd been waiting until after the cooperative-agreement-ceiling-raise madness was over to bring this up with you -- and kind of assumed that the outcome of that activity might determine the answer -- but do you know what the plan is in terms of a formal handover for the cooperative agreements in Indonesia (and RoC, China, and Ivory Coast)? I know we are hoping to secure approval via this activity to do this for Year 4, but is there any chance of it happening before the end of Year 3? And will Davis manage these agreements in the interim?

Thanks,
Molly
---------- Forwarded message ----------
From: **Kevin Olival, PhD** <olival@ecohealthalliance.org>
Date: Tue, Jul 18, 2017 at 1:05 PM
Subject: Taking over contract from MB for Eijkman
To: Evelyn Luciano <luciano@ecohealthalliance.org>, Ava Sullivan <sullivan@ecohealthalliance.org>, Molly Turner <turner@ecohealthalliance.org>, Alice Latinne <latinne@ecohealthalliance.org>

Hi Evelyn and everyone,

I had a good meeting with Dodi and Tina from Eijkman Institute today. One question that is outstanding is when will EHA take over the contract, especially for the next few months before year 4 starts. Do you have an answer to this? When we were at the UC Davis meeting one option was UCD taking this over until the end of year 3, but last month MB continued to pay salaries etc to keep the project running during the transition. It's important that we provide support so that predict trained staff etc aren't lost during the transition, and that we continue to have some funds to organize the human surveillance work that will begin soon (<1 mo) once we get IRB approval.

If you have any thoughts please let me know, I have a high-level meeting with Eijkman tomorrow afternoon Jakarta time.

Cheers,

Kevin

--
Molly Turner
Federal Grants Coordinator

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--
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From: Hongying Li <li@ecohealthalliance.org>
To: Karen Saylors <ksaylors@metabiota.com>
CC: Jon <epstein@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;David McIver <dmciver@metabiota.com>;Aleksei Chmura <chmura@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>;Molly Turner <turner@ecohealthalliance.org>;Emma Lane <lane@ecohealthalliance.org>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 8/1/2017 6:00:06 PM
Subject: [predict] Re: checking in on China

Thank you very much, Karen.

Seems I copied the wrong PREDICT email address, so have corrected it in this email.

Best,
Hongying
On Aug 1, 2017, at 1:49 PM, Karen Saylors <ksaylors@metabiota.com> wrote:

Thank you Hongying for the guidance. We will begin the process of contract closeout and will certainly keep you in copy.

Best wishes,
Karen

From: Hongying Li <li@ecohealthalliance.org>
Date: Tuesday, August 1, 2017 at 9:50 AM
To: Karen Saylors <ksaylors@metabiota.com>
Cc: Jon <epstein@ecohealthalliance.org>, Peter Daszak <daszak@ecohealthalliance.org>, David McIver <dmciver@metabiota.com>, Aleksei Chmura <chmura@ecohealthalliance.org>, "predict@ucd.edu" <predict@ucd.edu>, Evelyn Luciano <luciano@ecohealthalliance.org>, Molly Turner <turner@ecohealthalliance.org>, Emma Lane <lane@ecohealthalliance.org>
Subject: Re: checking in on China

Thank you, Jon!

Dear Karen,

What you propose does make fiscal sense, so please shut down your current contracts with GDCDC and GDIPH. We will recommence work with these partners as soon as we secure permission from USAID and Peter has met with Drs. Ke and He this year.

Please copy me on the emails to these two institutions confirming close-out.

Thank you again for all the help David, Neal, and you have provided during this transition.

Sincerely,
Hongying

On Aug 1, 2017, at 11:06 AM, Jon Epstein <epstein@ecohealthalliance.org> wrote:

Hi Karen,
Thanks for reaching out. I'm looping in Hongying Li, who is our country liaison and main point person for China work. She'll be able to update and provide guidance on plans for these partnerships.

Cheers,
Jon

On Tue, Aug 1, 2017 at 9:32 AM, Karen Saylors <ksaylors@metabiota.com> wrote:

Hi Jon and Peter.
Recognizing that Peter is out for a few weeks, I want to see whether Jon, you may have guidance on how you want to proceed with the China contracts with Guangdong CDC and Guangdong Institute of Public Health? Since we stopped human hospital surveillance several months ago and since lab analyses are finished, it would make the most sense, fiscally speaking, to shut down our contracts with GDCDC and GDIPH, so that we do not continue to pay them monthly for doing nothing. I of course want to verify that you do not intend to restart hospital surveillance in the coming months, as there is no concurrent work going on in these sites, but assuming that is the case, we would prefer to close these out, so that there is a firm stop in our China work, and we can close out those contracts.

Please advise, but in hearing nothing, we may proceed with communications with Directors He and Ke to move this forward.

Best wishes,
Karen

From: Karen Saylors <ksaylors@metabiota.com>
Date: Tuesday, July 18, 2017 at 10:48 AM
To: Peter Daszak <daszak@ecohealthalliance.org>
Cc: David McIver <dmciver@metabiota.com>, "chmura@ecohealthalliance.org" <chmura@ecohealthalliance.org>
Subject: checking in on China

Hi Peter.
I hope you traveled on safely post our Cote d'Ivoire trip last week.
Funny that we didn't get a chance to discuss China when we spent a full week together, but since we didn't, I want to check in with you about next steps for this handover.
In my discussions with Dave McIver, our Regional Coordinator for China, we had a couple of specifically things we want to check in with you on:
It would be good to know when you plan to get in touch with Directors He and Ke, if in fact you do want to keep moving along with them.
Much as we did with LANADA, since there is no ongoing work at the GDCDC lab or the clinical sites, we want to close that contract with GDIPH as soon as possible, so I'd like to get your thoughts on how to proceed.

Perhaps we should plan a call with all of us to discuss the transition once we both get back, as we did for Indonesia? It'd be good to get clear on data sharing as a discussion point, as well.

I know you are out this week, so copying Aleksei (hello Aleksei!) but please let me know if I should get in touch with Jon or others in the meantime.

Best wishes,
Karen

Karen Saylors, Ph.D.
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Director, Scientific Operations, PREDICT-Metabiota
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From:	Cara Chrisman <cchrisman@usaid.gov>
To:	Peter Daszak <daszak@ecohealthalliance.org>
CC:	Brooke Watson <watson@ecohealthalliance.org>;Aleksei Chmura <chmura@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>;Jonna Mazet (jkmazet@ucdavis.edu) <jkmazet@ucdavis.edu>;Dennis Carroll (DCarroll@usaid.gov) <DCarroll@usaid.gov>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>
Sent:	8/1/2017 9:25:37 PM
Subject:	Re: Scheduling discussion of GVP lab platform and cost of VirCapSeq etc.

Hi Peter,

Thanks for your email and the efforts to engage the lab platform group as part of this process.

I am flexible and plan to be on the upcoming calls. Dennis will be on vacation for the next several but plans to call in. He will be in the office for the 8/24 call and we could also look to extend that call if it works for others and if you think it may be needed in order to have this discussion.

In terms of determining the best time for us to speak, the key deadlines for having this sorted out as much as possible/reasonable include the China/HK visits (week of Sept. 4th) and the SF visit (Sept. 14-15), so we should definitely build in enough time for any additional conversations which you think may be helpful to have before then as well.

Best,
Cara

Cara J. Chrisman, PhD
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On Mon, Jul 31, 2017 at 6:35 PM, Peter Daszak <daszak@ecohealthalliance.org> wrote:

Hi everyone,

Brooke looped me into the discussion re. the cost of VirCapSeq vs. expanding from the current PREDICT protocols for the GVP. First of all, I want you all to know I'm also concerned about 1) the costs of VirCapSeq vs. standard PCR as per PREDICT, and 2) the risk of running a new technique and the possibility that this might not pan out rapidly, or give the results we expect and may delay things.

I agree with your comment Jonna that this is something the Core Group should discuss, and then I need to convene a meeting of the Lab Platform WG and talk this through with them, so that we can get a refinement of their recommendations, and agreement on a way forward that is affordable.

Can we put the discussion as a Core Group on hold for a couple of weeks. I'm on vacation in Peru, then over to Sweden to visit my brother. I could do the regular scheduled GVP call on Thursday Aug 17th, or 24th, and maybe that's a good time to go through the costing and rationale for the different lab approaches.

If you're all agreeable with that, I can set up a Lab Platform WG call for some time during the last two weeks of Aug so we can get this discussion back to the folks who proposed VirCapSeq.

There are some compromise options we can push for:

1) Start GVP expansion with PREDICT protocols, mixed in with some random samples going for Next Gen Sequencing – i.e. not to use VirCapSeq as a GVP tool

2) Start as above, but trial out some VirCapSeq at the same time and see how the costs and results pan out. The real issue here would be to push hard for economies of scale and leveraging cost reductions early on.

3) Seek a fully leveraged and cost-reduced access to VirCapSeq so that the GVP uses this platform, as well as the proposed random samples for NGS.

4) Use VirCapSeq as a follow-up for the final sequencing (as suggested in Jonna's email) – the cost will be cPCR costs plus VirCapSeq costs for a subset of samples.

I think we have time to set this all up, with a goal of fixing this issue by early Fall, so we can actually start some work in China and Thailand using the correct testing platform.

Cheers,

Peter

Peter Daszak

President

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From:	Cara Chrisman <cchrisman@usaid.gov>
To:	Jonna Mazet <jkmazet@ucdavis.edu>;Eri Togami <etogami@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Brooke Watson <watson@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>
CC:	Dennis Carroll <dcarroll@usaid.gov>
Sent:	8/2/2017 4:25:06 PM
Subject:	GVP Meeting Agenda - 8/3/17

Hi All,

It sounds like we will not have quite a full house tomorrow, but looking forward to catching up with those who are able to attend. If you will not be able to attend, but have any updates, please let me know! Also, please note that, as per Peter's email, we will push back the discussion of the budget details (around sequencing, etc.) until a future call.

Talk to you then,
Cara

Agenda 8/3

- Science Paper - Any feedback
- GVP Business Plan
- Outreach - Readouts
    - NIH
    - Costa Rica & George Mason
    - Army Research Labs
    - Paul Allen/Vulcan
    - Additional Readouts
- Outreach - Planned
    - Meeting Participation
    - San Francisco area (BioHub, Chan-Zuckerberg Foundation, Richard Feachem, Harvey Feinberg, etc.)
    - China (including Hong Kong)
    - CEPI Meeting (Sept. 13)
    - Additional Planning
- AOB

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From: William B. Karesh <karesh@ecohealthalliance.org>
To: David Wolking <djwolking@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Catherine Machalaba <machalaba@ecohealthalliance.org>;Amanda Andre <amanda.andre@ecohealthalliance.org>;Brooke Genovese <bgenovese@ucdavis.edu>;Elizabeth Leasure <ealeasure@ucdavis.edu>
Sent: 8/3/2017 10:42:02 PM
Subject: Re: need decision - PREDICT Semi-Annual Meeting

Fascinating

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On Aug 3, 2017, at 6:40 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Uh oh, Andrew didn't have the meeting on his calendar (he pulled it after the data meeting cancellation discussion) so has no plans to attend at this time :-(

D

On Thu, Aug 3, 2017 at 2:24 PM, David J Wolking <djwolking@ucdavis.edu> wrote:
Hi Catherine, how about 8:30AM PDT, if that works let me know. I'll be reachable by cell (415) 690-9955.

Best,

David

On Thu, Aug 3, 2017 at 2:11 PM, Catherine Machalaba <machalaba@ecohealthalliance.org> wrote:
Hey David,

Could you connect with Billy on Monday any time from 8am Davis / 11am NYC or later? Please let us know when is best for you.

When you guys connect could you double check which day the advisors plan to attend? We were thinking at one point that it was the reverse (attending on Wednesday), but it may have changed.

Many thanks!

Kind regards,
Catherine

Catherine Machalaba, MPH
Policy Advisor

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Program Officer, IUCN SSC Wildlife Health Specialist Group

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On Aug 3, 2017, at 2:28 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Billy,

Thanks for your thoughts well received. I have an updated draft agenda from a discussion Jonna and I had yesterday (attached) that will likely still evolve before sharing with EB next week. If you have any time free between today and Tuesday could we connect to talk over what you think would be most valuable for the second day with the external panel? I do have your report but am wondering if I'm missing any context from your debriefs or discussions that would help inform topics of interest beyond behavior for the structure that day.

Thanks,

David

On Fri, Jul 28, 2017 at 11:59 AM, William B. Karesh <karesh@ecohealthalliance.org> wrote:
Thanks David.

I don't think we should let any of the old data meeting concept affect the planning for this year since we are really focused on internal efforts.

A couple of quick thoughts now:

1) For USAID and the advisor's also, it would probably be useful to spend 15-20 minutes on some of the collaborations with other EPT-2 partners so that they see that we are coordinating. We can gleen that from the 2 sections you have on Monday when it's just internal, and then summarize and polish it up and maybe have Catherine present to the larger group. Some are easy for the audience to relate to (like sharing samples or protocols with FAO or CDC) and some are a bit less familiar to most folks (multi-lateral policy frameworks and implementation initiatives like the World Bank, WHO, CBD, DRR work). The latter also are delivering some policy level bahavioral interventions which would be good for people to see since that "deliverable"

seems to always fall in the behavioral surveillance bucket.

2) one topic that came up several times from the advisors last year was that the behavioral risk worked "seemed" patchy and they didn't understand how it all fit together. Leilani knows about that and has been focused on ensuring that all of the different components are pulled together in a coherent and unified story. Once again, I think the discussions on Monday will help consolidate and tie up any loose bits to help with a presentation to USAID and the advisors.

BK

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On Jul 28, 2017, at 1:50 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Jonna and Billy,

To get moving on hotel reservations for NYC we need a draft agenda so partners can prioritize who should attend.

I've started a mock-up of one (attached here) based on the Pacifica meeting, but with the external advisory folks joining for Day 2 and USAID on Day 3 instead of the full 2 days as in CA, this will need some careful thought and consideration. Starting with you two for now as Billy has the best handle on what would be of value to the panel (maybe sourced from their report and interests in seeing in the future?) and Jonna, you are dialed into the USAID sensitivities and needs more than the rest of us.

Also Billy, I'm attaching last year's data sharing meeting agenda here too. I'm not sure if we need to revisit any items from last year or if we are simply moving ahead now with our own version, reincarnated as the semi-annual.

Happy to put more work into this but would really appreciate your guidance on structure. My apologies for taking so long to get something out for initial reaction and feedback.

Thanks!

David

On Mon, Jul 3, 2017 at 2:24 PM, William B. Karesh <karesh@ecohealthalliance.org> wrote:
Thanks David.

Sent from my iPhone

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Executive Vice President for Health and Policy

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On Jul 3, 2017, at 4:57 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Billy,

Our UCD team seems fine with Sunday as a travel day so the Monday to Wednesday meeting plan seems like it will work.

David

On Fri, Jun 30, 2017 at 07:56 David J Wolking <djwolking@ucdavis.edu> wrote:
Thanks Billy I'll reach out today and get you a response soon.

D

On Thu, Jun 29, 2017 at 8:30 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Actually, I'm on vacation now, but I'll let David and Liz check in with them and get back to you,
J

On Thu, Jun 29, 2017 at 8:17 PM, William B. Karesh <karesh@ecohealthalliance.org> wrote:
Thanks.

I'm leaning towards all day Monday, Tuesday (advisors) and half day Wednesday or until we finish with USAID. Your Tues-Thursday version works also, but Peter and I need to leave by 11:00 on Thursday cause I arranged another meeting based on the original thinking. But, I think it still could be fine with the team and Andrew and Shana on Thursday. I'm guessing they will be the only USAID people coming.

Can you discuss with your team Friday and let me know.

Thanks!!!

B

Sent from my iPhone

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

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President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

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On Jun 29, 2017, at 7:45 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Brooke just told me that it's Hotel Edison, so got that info.
J

On Thu, Jun 29, 2017 at 4:41 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Hi Billy,
For me, personally, it doesn't really matter, as I'll be coming from Florida. For all of the rest of the travelers from the West Coast, though, a half day to start doesn't make a lot of sense because there aren't any flights that allows a morning departure and arrival for a half day because of the time difference. So a Monday half day start means travel all day Sunday, just to sit and wait for a half day to start the meeting.
Likely better for most travelers would be to travel Monday and have a full day start on Tuesday (just Predicters), full day with advisors Wednesday, then half day with USAID on Thursday (no advisors). Advisors and USAID could overlap for dinner on Wednesday night. Half day on Thursday allows those who want to get going to travel home the same day (works going in that direction). I think USAID suggested that they shouldn't overlap with advisors, and we all decided that we might do better to have a day on our own without any outsiders to get tougher issues addressed in advance. The data part of the meeting isn't really

conducive to just a half day with USAID, though, so we could do a full day with Andrew to get the data part in with a subset of us. I don't know -- you know best, as I wasn't there last year.

I know that isn't the best schedule for those going to Marburg, but I'm guessing that is just 2-3 of us, and they can just miss Thursday. That said, if you don't have the option with the hotel or conference room space, we can go with what you have already arranged.

Like I said, I'm flexible, just trying to think about the more travel-restricted.

What's the name of the hotel you have planned?

Final decision on all of this is yours, as you have been working on the arrangements,
J

PS-- I think the wrong David was accidentally copied on the first couple of messages in this chain.

On Thu, Jun 29, 2017 at 11:36 AM, William B. Karesh <karesh@ecohealthalliance.org> wrote:
We had been planning 2 and a half days, with USAID and Advisors on the last day.

Right now we have meeting room booked starting Monday afternoon through the end of the day Wednesday.

Question 1: We can change to Monday morning if you think we need more time or want to end early on Wednesday.

But, if USAID and Advisors come for the last day (wednesday), it seems like a half day is a bit short for them for discussions, etc.

Thanks,

We need to finalize meeting room, and then we will follow up quickly for Hotel rooms to hold - number of people for each night.

BK

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prevent pandemics.

--
Sent from Gmail Mobile

From: Cara Chrisman <cchrisman@usaid.gov>
To: Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>;Jonna Mazet <jkmazet@ucdavis.edu>;Eri Togami <etogami@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Brooke Watson <watson@ecohealthalliance.org>
CC: Dennis Carroll <dcarroll@usaid.gov>
Sent: 8/10/2017 4:17:01 PM
Subject: 8/10 GVP Call Agenda

Hi All,
Looking forward to speaking with those who will be available later today. Here's the agenda for today's call (we'll see how much of it we get through!):

- Science Paper - Mon. deadline for comments
- GVP Business Plan/Pitch
    - BCG: 8/23 11am-12pm
    - McKinsey: 8/23 2-3pm
    - Dalberg: 8/25 11:30am-12:30pm
- Outreach - Readouts
    - Canada
    - Merieux
    - Additional Readouts
- Outreach - Planned
    - San Francisco Area (BioHub, Chan Zuckerberg, Richard Feachem, Harvey Feinberg, Science Philanthropy Alliance, etc.)
    - China/HK (George, Keiji, Embassy, CAS, HKU, etc.)
    - Additional Planning
- Communications
    - Website
    - 2 pager
- Technical Updates
    - Waterfowl Mapping status
    - Others?
- Working Group Updates
    - ELSI - Co-chair update
    - Others?
- AOB

Talk to you soon!
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (AID)

Desk: (202) 712-1161
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

From:	Molly Turner <turner@ecohealthalliance.org>
To:	Elizabeth Leasure <ealeasure@ucdavis.edu>
CC:	David John Wolking <djwolking@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Predict inbox <predict@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Aleksei Chmura <chmura@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>
Sent:	8/23/2017 6:48:46 PM
Subject:	Re: Year 4 revised budget

Hi Liz,

The budget you sent us to revise was for $1,237,199 ("total USAID"). The revised budget I sent was for $1,237,163.

Molly

On Wed, Aug 23, 2017 at 2:35 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Hi Molly and Aleksei. Can one of you please confirm whether or not the budget you sent actually includes rollover funds? I haven't looked at it in detail (I'm working on that now), but it seems that your overall budget went up by $90K from the 8/15 version submitted, and I had thought we discussed trying to reduce. Please clarify.

Thanks,

Liz

Elizabeth Leasure

One Health Institute

University of California, Davis

530-754-9034 (office)

530-304-1403 (cell)

From: Molly Turner [mailto:turner@ecohealthalliance.org]
Sent: Friday, August 18, 2017 6:14 PM
To: Elizabeth Leasure; David John Wolking
Cc: Jonna Mazet; Predict inbox; Peter Daszak; Aleksei Chmura; Evelyn Luciano; Ava Sullivan
Subject: Year 4 revised budget

Hi Liz and David,

Thanks for all your comments and the quick chat today. Attached please find our revised Year 4 budget based on your feedback and below bullets on what we modified:

- EHA HQ costs were reduced by $193,529 (including salary, fringe, and indirect) by reducing time from Billy and Jon as well as our Modelling and Analytic Team (Kevin, Noam, and Anna's). Peter asked me to

mention that he does not think this is ideal and he hopes this will not be a red flag for USAID, but we have done this specifically to reduce our Global and Administrative costs. He also wanted to assure you that all staff who have been reduced will remain engaged with PREDICT at the same level

- In-country testing budgets for RoC and CIV were increased by $193,529 (amount of HQ reduction) (note that only salary from Billy and Jon previously allocated to Ebola Money was used in CIV)

- Bangladesh hospitals have been reduced to only two and the funds allocated to diagnostic costs in RoC

- Core funds being rolled over from Year 3, totaling $232,194 are obligated to cover our sample testing costs in Bangladesh, China, and Egypt. These assays will be completed in Q1 of Year 4 ($62,071 of Year 3 GVP funds will go towards planned salary & travel in Year 4)

- We project a rollover of $804,193 in EHP funds. In terms of Year 3 costs, $160,000 is earmarked for the 1,850 Liberia samples that have just arrived at Simon's lab (that's $50/sample plus 60% overhead), and the rest will go to cover Year 4 costs

- IRB approval has already been obtained for India and will definitely be secured in Bangladesh before the start of Year 4

- RoC and Ivory Coast IRBs will be amended to transfer from Mutabaruka to CDA before Year 4 begins.

- Our team is developing the entry tool for the Malaysia human surveillance data, and the updated survey will be sent to CKJ next week.

Please let Aleksei and me know (cc to Evelyn and Ava) if there are any questions or if you'd like to talk through any details in the budget.

Best,

Molly

--

Molly Turner

Federal Grants Coordinator

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To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: David John Wolking <djwolking@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Predict inbox <predict@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Aleksei Chmura <chmura@ecohealthalliance.org>;Evelyn Luciano <luciano@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>
Sent: 8/23/2017 9:05:51 PM
Subject: Re: Year 4 revised budget

Hi Liz,

After our email exchange I took another look, and what you're seeing is an increase to the Liberia budget based on discussions with Jim and Simon (cell highlighted in red in the version we sent to you) -- we increased the number of samples that we propose to test in-country next year. Sorry, I overlooked that change when I composed the accompanying email that we sent on Friday.

Ebola funds were also altered because we increased the diagnostic testing budget for CIV using funds re-allocated from global salaries; however, this should not be an overall increase, as I used only the portion of Jon, Billy, and Peter's time previously allocated to Ebola funds.

The overall reduction of $87K in the first revision was largely taking out the line item for a China country liaison ($50K plus overhead and fringe). I did think that we were being asked in this revision to stay within the original budget amount that we were asked to reallocate, so that money went towards increased diagnostic costs.

I am happy to discuss further any time.

Molly

On Wed, Aug 23, 2017 at 3:43 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

The Y4 template that I sent you to revise was for $12,237,199, but we asked you to cut back HQ costs (Global/Admin Management) and make sure country budgets are appropriate for planned Y4 activities. The budget you submitted on 8/15, had somewhat reduced HQ costs and an overall reduction of $87K, but there were some concerns with diagnostic testing budgets in some countries. This most recent version further reduces HQ costs as requested, but the $87K reduction from the 8/15 submission was lost. I thought our direction had been to at least stay within the reduced overall figure from the 8/15 submission ($12,149,975), but it sounds like that was not made clear.

Since we're still waiting on guidance on USAID to move forward with core budgeting, I'm really only addressing Ebola funding at this time. For the Ebola budget specifically, there was a $426K increase from the 8/15 version and a $393K increase from the Ebola amount in the template I sent to you to revise. I'm just trying to understand where the increase came from, hence my question about whether or not there is carryover funded included in any of your numbers. It sounds like there aren't based on your response, so I'll move forward with my review.

Thanks,

Liz

Elizabeth Leasure

One Health Institute

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530-754-9034 (office)

530-304-1403 (cell)

From: Molly Turner [mailto:turner@ecohealthalliance.org]
Sent: Wednesday, August 23, 2017 11:49 AM
To: Elizabeth Leasure
Cc: David John Wolking; Jonna Mazet; Predict inbox; Peter Daszak; Aleksei Chmura; Evelyn Luciano; Ava Sullivan
Subject: Re: Year 4 revised budget

Hi Liz,

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Elizabeth Leasure

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To: Elizabeth Leasure; David John Wolking
Cc: Jonna Mazet; Predict inbox; Peter Daszak; Aleksei Chmura; Evelyn Luciano; Ava Sullivan

Subject: Year 4 revised budget

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Best,

Molly

--

Molly Turner

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From:	Eri Togami <etogami@ucdavis.edu>
To:	daszak@ecohealthalliance.org <daszak@ecohealthalliance.org>;Dennis Carroll <dcarroll@usaid.gov>;Cara Chrisman <cchrisman@usaid.gov>;Brooke Watson <watson@ecohealthalliance.org>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent:	8/24/2017 9:47:08 PM
Subject:	GVP call notes 8/24

Hi everyone,

Here are the call notes from Aug 24.

Agenda

- Meeting Readouts
  - Consulting firms (BCG and Mckinsey)
    - § GVP will choose to work with one of the three firms or not, based on proposals that will be sent next week.
    - § Current priority is to establish a functional hub (NGO) that is financially supported.
    - § Money is set aside for this cost if needed. Dalberg meeting will be tomorrow 8/25.
- Planned outreach
  - San Francisco Area
    - Harvey Fineberg will not be in SF on Sep 15
    - Open philanthropy – Eddy has not heard back
    - Science philanthropy – Dennis sent out note
  - Seattle (Vulcan) – planning trip after SF in Sep
  - Canada/Vancouver – Eddy will visit on Sep 19 to engage scientific community in Canada
  - China/HK
    - week of Sep 4. Embassy meeting confirmed on Tues and other scheduling ongoing. There will be a smaller lunch, meeting, dinner reception etc.
    - Eddy will give a talk at Beijing Genomics Institute Oct 25 and 26. Inform colleagues in China.
  - Norway – Peter will meet with Ministry of Health in October
  - Bush/Skowcroft – Dennis will give GVP talk in Texas October 16 and 17 and will engage them by highlighting the policy opportunity.
- Communications
  - Science Paper Status – Peter has submitted revisions
  - 2 pager – to be finalized
  - As the Virome Turns – work on next issue as a way to bring Work Groups together
- Technical Updates
  - Laboratory testing – on hold and discuss when Jonna is back
- Working Group Updates
  - o ELSI – Cara circulated documents. Send feedback by Sep 1.
    Jonna, Eri and Liz (UCD financial officer) will have a call with Sam Halabi and Gian Luca at the end of Sep regarding ELSI budget.
  - Data management – Eddy is currently developing prototype. Schedule a call before Sep 15 with Tami and Damian.
  - Thailand SOPs – next batch of SOPs to be sent soon. Jonna and Eri are scheduling a call with Thai colleagues regarding SOPs and implementation etc.
- PMAC Launch
  - Eri has drafted concept note, which is being reviewed by Jonna. This will be circulated with the team.
  - New deadline for concept note is Oct 15 (two days after Oct 13!) .
  - Begin to think about inviting key people.

Action items

Eddy – follow up with open philanthropy
Cara – draft updates on As the Virome Turns
Peter – email Keiji to make sure right people will be at China meeting
All – review and comment on ELSI one-page briefs

Eri – finalize two pager and create new page on website
Eddy and Cara – schedule data management call before Sep 15

Best,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Eri Togami <etogami@ucdavis.edu>
To: Cara Chrisman <cchrisman@usaid.gov>;Dennis Carroll <dcarroll@usaid.gov>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Brooke Watson <watson@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 8/28/2017 5:21:49 PM
Subject: PMAC 2018 GVP concept note

Hi everyone,

Please see a draft of our concept note for the PMAC launch. As per our previous discussions, we can propose one closed session and one open session. Jonna and I would appreciate your comments and suggestions by Wednesday 9/6.

Best wishes,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

Concept Note for Side Meeting at PMAC 2018

Meeting title The Global Virome Project: the Beginning of the End of the Pandemic Era

Organizers

Core group of the Global Virome Project: Dennis Carroll [1], Jonna A.K. Mazet [2¶], Peter Daszak [3], Eddy Rubin [4], Nathan Wolfe [4], Cara Chrisman [1], Brooke Watson [1], Eri Togami [2¶]

1. U.S. Agency for International Development
2. One Health Institute, University of California, Davis
3. EcoHealth Alliance
4. Metabiota

¶Corresponding members:

Jonna A.K. Mazet jkmazet@ucdavis.edu
Eri Togami etogami@ucdavis.edu

Duration

We propose two half-day sessions during the following times.

- Half-day session 1, Sunday 28 January 2018, 9.00-12.30 or 14.00-17.30
- Half-day session 2, Monday 29 January 2018, 9.00-12.30 or 14.00-17.30

Background

We live in an era when the threats posed by global pandemics are greater than at any other point in human history. We live in fear of a previously-unknown pathogen suddenly emerging and sweeping through every household, through every community, irrespective of borders, or of its hosts' social and economic standing. This fear alone can cost billions, as we saw in the global panic that followed the SARS and H1N1 influenza virus outbreaks. It is not unfounded, as evidenced by the 35-year HIV/AIDS epidemic that has cost over 35 million lives.

Despite the potential impact of viral threats, the world remains unable to predict when, where, or from what species the next emerging virus will break out. Global trends indicate that over the course of this century, new microbial threats will continue to emerge at an accelerating rate, driven by the world's expanding population, growing interconnectedness, and increasing interactions with animal populations (1). The majority of these threats originate in a seemingly endless pool of viruses carried by our relatives in the Animal Kingdom (2). Modern science has been able to characterize some of these viruses and trace their roots to their mammalian origins – for example, HIV-1 that spilled over from chimpanzees to people and Ebolavirus carried by bats in Africa (3). However, recent estimates put the total number of these animal viruses that could threaten us at more than 1.5 million, spanning 24 viral families (4). Compared to the 260+ viruses currently known from humans (5), this viral "dark matter" represents 99.9% of the potential pandemic threat. It means that, for every known strain of the SARS virus there are likely thousands of unknown "SARS-like" viruses (6) circulating in wildlife that could emerge in the future.

UCDUSR0001719

The Global Virome Project (GVP) was conceived in response to the challenge posed by the repeated and unpredictable emergence of high impact viral epidemics. These outbreaks compromise global health security and the well-being of the people of the world (1). The recently launched Coalition for Epidemic Preparedness Innovations (CEPI) represents a critical step to address known but long-neglected viral threats, such as MERS-CoV, Lassa Fever, and Nipah Virus (7). This vital work addresses long-known but underfunded viral threats; however, a tremendous challenge remains: how do we best prepare for unknown future threats?

The GVP's goal is to characterizing the vast pool of unknown viral threats in wildlife, their natural hosts. Knowing what viruses are available and able to infect humans and their epidemiological circumstances will allow us to prepare for viruses before they jump into people. It will transform our culture from one that responds to outbreaks to one that predicts and prevents future pandemics. It will also better prepare us to prevent accidental or intentional release of laboratory-enhanced virus variants. With broad support for the GVP, the world will be better prepared to deal with the consequences of escalating spillover of deadly viruses, likely in just ten years. The initiative will generate an unprecedented atlas of viral diversity, build global surveillance and laboratory capacity in the most high-risk areas, catalyze technological advances in diagnostics and vaccines, and establish a global framework for triaging and neutralizing novel viral outbreaks before they spread between humans.

The project is now at a critical point of gaining increasing support from new partners and collaborators, starting pilot projects in several countries, and ready for its official global launch. We believe that GVP's concept and goal aligns perfectly with the subtheme for PMAC 2018 - Making the World Safe from the Threats of Emerging Infectious Diseases and would very much appreciate the opportunity to officially launch the initiative in the ideal setting. In short, the GVP is designed to herald in the beginning of the end of the Pandemic Era, and PMAC 2018 will be the optimal stage for launching this next 'big science' project.

Objectives

Our primary objective is to have two half-day side meetings at PMAC in order to bring scientists together and officially launch the Global Virome Project. Our specific objectives are as follows:

- First, in a closed session, assemble members of the Global Virome Project Steering Committee and Working Groups and provide a platform to discuss specific critical points, including but not limited to in-country operations, laboratory testing, data sharing and ethical and legal topics.
- Second, in an open session, officially launch the initiative by introducing the concept, objectives, approach and anticipated outcomes of the Global Virome Project to PMAC attendees.
- Share information with project members and PMAC attendees on pilot projects in first-wave countries that are ready for operation, or are in the final planning stage (Thailand, China, Costa Rica).
- Foster collaboration between GVP members and country officials who are interested in participating in the project in the future.

UCDUSR0001720

Proposed meeting format

- Half-day session 1
  We propose a roundtable conference for the closed session. Presentations will be made by the core working group members on the progress of GVP since its last meeting in Beijing, China in February 2017. Working groups will split up into smaller discussions (in the same single room) to address specific challenges and improve the operational flow of the overall project.

- Half-day session 2
  The open session will consist of presentations and moderated panels. This format will allow for the official launch with presentations by the core members to introduce the progress of GVP, and to have discussions to further identify, discuss and address challenges that GVP will likely face and overcome as the project launches.

Expected output/outcome

Through two half-day meetings, we anticipate the following outcomes.

- Strengthened collaborations between Steering Committee members and Working Group members and an improved operational infrastructure for launch of GVP activities.
- Enhanced interest from countries who are willing to participate in this global initiative, and communication between country officials and GVP members.
- Defined short-term, mid-term and long term goals for GVP to track its development since the last international planning meeting in Beijing in February 2017 and onward.
- An internal report of the proceedings of the closed session meeting for information sharing within the GVP and core PMAC group.
- A report outlining proceedings of the open launch session. This piece has been drafted, and will be published and publicly available in form of a manuscript.
- New media content (photographs, discussions and other news) to be shared with the public through PMAC and GVP outreach activities.

Target and estimated number of participants

- Half-day session 1
  Approximately 40 participants are expected to attend this side meeting. This session will be closed to invited members only. The targeted audience will be members of the Steering Committee and Working Groups of the Global Virome Project who have been instrumental in launching the project, as well as honored PMAC organizers.

- Half-day session 2
  Approximately 100 participants are expected to attend this side meeting. This meeting will be open to PMAC participants. /*Need input from team: some targeted invites & first come-first served for the rest of the slots? */ The targeted audience will be relevant authorities in the international organizations, governments, academia and non-governmental organizations.

UCDUSR0001721

Room set up

- Half-day session 1: Roundtable style
- Half-day session 2: Theater style

References

1. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, et al. Global trends in emerging infectious diseases. Nature. 2008;451:990-3.
2. Prediction and prevention of the next pandemic zoonosis. (2012).
3. Leroy EM, Kumulungui B, Pourrut X, Rouquet P, Hassanin A, Yaba P, et al. Fruit bats as reservoirs of Ebola virus. Nature. 2005;438:575-6.
4. Carroll DD, Peter; Wolfe, Nathan D.; Gao, George F.; Morel, Carlos; Morzaria, Subhash; Tomori, Oyewale; Mazet, Jonna A.K. The Global Virome Project. Science (in review). 2017.
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UCDUSR0001722

From: Eri Togami <etogami@ucdavis.edu>
To: Eddy Rubin <erubin@metabiota.com>;Cara Chrisman <cchrisman@usaid.gov>;Dennis Carroll <dcarroll@usaid.gov>;Nathan Wolfe <nwolfe@metabiota.com>;Brooke Watson <watson@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 9/1/2017 9:31:25 PM
Subject: RE: PMAC 2018 GVP concept note

Hi Eddy,

Thank you very much for your comments on the PMAC concept note.
Best,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Eddy Rubin [mailto:erubin@metabiota.com]
Sent: Tuesday, August 29, 2017 12:00 PM
To: Eri Togami ; Cara Chrisman ; Dennis Carroll ; Nathan Wolfe ; Brooke Watson ; Peter Daszak ; Jonna Mazet
Subject: Re: PMAC 2018 GVP concept note

Good. A few small suggestions.
I do not think that GVP will better prepare us " to prevent accidental or intentional release of laboratory-enhanced virus variants."

From: Eri Togami <etogami@ucdavis.edu>
Sent: Monday, August 28, 2017 10:21 AM
To: Cara Chrisman; Dennis Carroll; Nathan Wolfe; Eddy Rubin; Brooke Watson; Peter Daszak; Jonna Mazet
Subject: PMAC 2018 GVP concept note

Hi everyone,

Please see a draft of our concept note for the PMAC launch. As per our previous discussions, we can propose one closed session and one open session. Jonna and I would appreciate your comments and suggestions by Wednesday 9/6.

Best wishes,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Cara Chrisman <cchrisman@usaid.gov>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: Andrew Clements <aclements@usaid.gov>;David John Wolking <djwolking@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Shana Gillette <sgillette@usaid.gov>;Alisa Pereira <apereira@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>;Ashna Kibria <akibria@usaid.gov>
Sent: 9/7/2017 9:11:27 PM
Subject: Re: Outstanding P-2 Items

Hi Liz,

Thanks for confirming. While they are swamped and understaffed, these have been outstanding for some time. We'll follow up with them again ASAP. If other items should be added, please let us now. In the interim, we'll see what can be done about these.

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (AID)

Desk: (202) 712-1161
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

On Thu, Sep 7, 2017 at 5:07 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Hi Cara. Thanks for following up. None of the items on your list have been resolved.

Elizabeth Leasure

One Health Institute

University of California, Davis

530-754-9034 (office)

530-304-1403 (cell)

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Thursday, September 07, 2017 2:04 PM
To: Elizabeth Leasure
Cc: Andrew Clements; David John Wolking; Jonna Mazet; Shana Gillette; Alisa Pereira; predict@ucdavis.edu; Ashna Kibria
Subject: Outstanding P-2 Items

Hi Liz,

As a follow up to your update for Andrew on the Lao NCLE, I wanted to check in on the other OAA-related items that we had previously discussed.

The management team on this end reached out to OAA to ensure that these would be followed up on and resolved, so I wanted to check in with you to see if any were still outstanding? With the obvious exception of #1, if there are any others which remain, as well as others to add (particularly which are not dependent on the ceiling increase), please let us know so that we can make sure we don't lose track of them.

Here's the old list:

1. Ceiling Increase
2. Kenya - Response on Suspension of Activities questions, as per June 8th request
3. VAT Items - 2-3 pending (China, Viet Nam, and Egypt)
4. Myanmar - Responses to questions regarding the provision, as per April 11th email.

Thanks

Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (AID)

Desk: (202) 712-1161
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

On Thu, Sep 7, 2017 at 4:42 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

The NCLE subaward approval is currently wrapped up in the ceiling increase process. We were planning to obtain approval for the new NCLE subaward through the ceiling increase, so until the ceiling increase budget and narrative with the new NCLE subaward included is approved, we are unable to move forward with establishing a subaward with NCLE. Same story as with the new EHA subwards for leadership transition in CDI and RoC.

Elizabeth Leasure

One Health Institute

University of California, Davis

530-754-9034 (office)

530-304-1403 (cell)

From: Andrew Clements [mailto:aclements@usaid.gov]
Sent: Thursday, September 07, 2017 8:09 AM
To: David John Wolking; Elizabeth Leasure
Cc: Jonna Maret; Cara Christner; Shana Gillette; Alisa Pereira
Subject: Fwd: EPT-2 Meeting in Lao PDR

Hi David and Liz,

What is the status of the Laos/NCLE award? Anything I can do to move it along?

Thanks!

Andrew

Andrew P. Clements, Ph.D.

Senior Scientific Advisor

Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health

U.S. Agency for International Development

Mobile phone: 1-571-345-4253

Email: aclements@usaid.gov

Begin forwarded message:

From: David McIver <dmciver@metabiota.com>
Date: September 7, 2017 at 4:38:11 PM GMT+2
To: Soubanh Silthammavong <sSilithammavong@metabiota.com>, "Sudarat Damrongwatanapokin" <sdamrongwatanapokin@usaid.gov>
Cc: "Clements, Andrew(ANE/TS)" <AClements@usaid.gov>, "Corwin, Andrew Lee" <CorwinAL@state.gov>, Daniel Schar <dSchar@usaid.gov>, Anchalee Jatapai <ajatapai@usaid.gov>, PREDICTMGT <predictmgt@usaid.gov>
Subject: Re: EPT-2 Meeting in Lao PDR

Hello Sudarat,

Unfortunately, I don't think there is much we can do about this from our end. To my understanding, there are many of these agreements that USAID Washington is working on right now, for many different countries. I think we just need to wait until we get some sort of confirmation from the Washington office, which will come to us through UC Davis. Thank you very

much for the offer.

Thanks,

Dave

—

David McIver, PhD

PREDICT Asia Regional Coordinator | Epidemiologist

Metabiota

e: dmciver@metabiota.com

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On Sep 7, 2017, 3:21 AM -0300, Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>, wrote:

Dear Dave and Soubarh,

Since you mentioned that you are "still waiting for final USAID approval for contract agreements with NCLE, you haven't been able to move forward with human sample testing yet".

Is there anything that we can help follow up with Andrew, P2 AOR, and PREDICT Management team in DC to speed up the process?

Best regards,

Sudarat Damrongwatanapokin, D.V.M., Ph.D.

Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax: +662 -2573069

On Thu, Sep 7, 2017 at 4:11 AM, David McIver <dmciver@metabiota.com> wrote:

Hi Andy,

In terms of data sharing and virology surveillance, we have worked on a separate document that outlines rules and regulations surrounding sharing of data, samples, results, and the release of test results. In addition to the PREDICT-standardized data sharing agreements, our Lao PDR PREDICT team also went a step further to create a document that specifically states when, and under which circumstances, data can be shared or viewed, and by whom. This document has been signed by representatives from PREDICT, DLF, DCDC, and FAO. I'll be happy to share copies of all these agreements with you when I'm in Laos, if you like.

While we have already collected some human samples already, testing has not yet begun. Since we're still waiting for final USAID approval for contract agreements with NCLE, we've haven't been able to move forward with testing yet. Right now, we have about 180 human samples frozen in LN2 at NCLE. We're all very eager to get started on testing!

I'm looking forward to catching up with you in October, and I'll be happy to share our updates with you.

Thanks for your help.

Dave

—

David McIver, PhD

PREDICT Asia Regional Coordinator | Epidemiologist

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On Sep 5, 2017, 10:49 PM -0300, Corwin, Andrew L <CorwinAL@state.gov>, wrote:

Thanks David and Sudarat for the clarification. While there is an MoU arrangement between the MoH and MoAF, I thought the focus of the agreement was on information sharing and a one Health approach to outbreak investigations. I have not heard before of an arrangement in which MoAF provides permission on behalf of the MoH in terms of virological surveillance with associated laboratories diagnostics. But there may be indeed just such an agreement.

Have you already begun collecting human specimens and testing at NCLE? I would suggest scheduling a meeting with Dr Reiko who has replaced Dr Dapeng at WHO LAOS, if you have not already communicated with her. I would also be happy to brief her regarding this activity. It should be noted that all the virological work up at NCLE is supported by WHO Laos visa vi laboratory expertise and oversight.

With regards to your Lao travel, I will be available to meet with you the first week of October (except the 6th), and possibly

the early afternoon of the 29th. We are all very excited to learn how this Activity is progressing.

Please address your request for Mission Concurrence to Alex Huerta, the Lao Country Representative.

Best regards,

Andy

From: David McIver <dmciver@metabiota.com
Date: September 5, 2017 at 8:37:59 PM GMT+7
To: Damrongwatanapokin, Sudarat (RDMA/OPH) <sdamrongwatanapokin@usaid.gov>, Corwin, Andrew L <CorwinAL@state.gov
Cc: Anchalee Jatapai <ajatapai@usaid.gov>, Schar, Daniel (RDMA/OPH) <dschar@usaid.gov>, Karen Saylors <ksaylors@metabiota.com>, Clements, Andrew (GH/HIDN) <aclements@usaid.gov>, Kongchay, Vongsaiya (USAID) <KongchayV@state.gov>, Ricardo Echalar <rechalar@usaid.gov>, Bounheuang, Kounnavong <BounheuangK@state.gov>, . <predict@ucdavis.edu>, predict@ucdavis.edu <predict@ucdavis.edu>, Martz, Robin (USAID) <rmartz@usaid.gov>, Soubanh Silitharrenavong <sSilitharrenavong@metabiota.com>, Huerta, Alexandria I <AHuerta@state.gov
Subject: Re: EPT-2 Meeting in Lao PDR

Hi Andy and Sudarat,

Sudarat is correct, in that the MOU was signed between Metabiota and the DLF/MoAF with the intention that they would subcontract to NCLE as the coordinator of the human surveillance portion of the program. To the best of my understanding, no further MOUs are required and human surveillance in the Khong District Hospital is ready to begin as soon as we have final approval from USAID Washington.

We do plan to make a visit to Champasack while I am in Laos, but we are not certain yet of the days - it will likely be the last week of September. I will work on processing a USAID Mission Concurrence Request and send that along to Alex. And of course, we'll be more than happy to be at an EPT meeting and give everyone an update on the PREDICT program.

Thanks very much,
Dave

--
David McIver, PhD
PREDICT Asia Regional Coordinator | Epidemiologist
Metabiota

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c: +1 778-269-2965

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On Sep 5, 2017, 7:15 AM -0300, wrote:

USAID Mission Concurrence Request

USAID EPT-2
PREDICT PROJECT
Year 4 GHSA Workplan Narrative

October 2017-September 2018

Prepared by:
The PREDICT Consortium
http://consortium.predict.global

UCDUSR0001730

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PREDICT-2 GHSA country workplans for 2017-2018 are provided in the Excel workbook.

Overview

The PREDICT-2 team is currently working with the USAID AOR and Office of Acquisitions and Assistance to finalize funding levels for the remainder of the project. These funding levels have major implications on FY18 budgets and corresponding workplans, especially for Asia countries that are currently financed through PREDICT's EPT-2 core mechanism. In addition, budgets for the Ebola Host Project countries (Guinea, Liberia, and Sierra Leone) are awaiting finalization as we determine country specific funding levels within the overall Ebola Host Project ceiling.

As a result, we are only able to provide FY18 budgets for the following GHSA Phase1 Africa countries: Cameroon, Cote d'Ivoire, Ethiopia, Kenya, Senegal, Tanzania, and Uganda. Ebola Host Project (Guinea, Liberia, and Sierra Leone) and Asia region GHSA workplans (Bangladesh, India, Indonesia, and Viet Nam) are subject to change until the budget is finalized. All EHP and Asia country technical plans provided in the GHSA workbook and corresponding country narratives are to be considered drafts; activities presented will be implemented as budget allows.

CAMEROON
Year 4 (October 2017-September 2018)

Implementing Partners: Metabiota Inc. and Mosaic
Country Coordinator: Moctar Mouiche, Mosaic
Global Point of Contact: James Ayukekbong, Metabiota Inc.

Partners

- Ape Action Africa
- Centre Pasteur Cameroon
- Food and Agriculture Organization (FAO)
- Metabiota Cameroon
- Ministry of Defense (MINDEF)/ Military Health Research Center (CRESAR)
- Ministry of Environmental Protection and Sustainable Development
- Ministry of Forestry and Wildlife (MINFOF)
- Ministry of Livestock, Fisheries and Animal Production (MINEPIA)
- Ministry of Public Health (MINSANTE)
- National Program for the Control and Fight Against Emerging and Remerging Zoonoses (NZP)
- National Veterinary Laboratory (LANAVET)
- One Health Workforce (OHW)
- Preparedness Response (P&R)
- Researchers from the University of Douala and the University of Maroua
- South Cameroon Hevea (SUDCAM)*
- US Centers for Disease Control

*Partnership in development

Prevent and Detect Zoonotic Disease

PREDICT strengthens One Health partnerships and conducts zoonotic disease surveillance activities by sampling wildlife and people and conducting behavioral risk investigations at high-risk interfaces for zoonotic disease transmission. This work directly supports the national surveillance system, contributes to the development and implementation of the country GHSA roadmap, and provides opportunities to strengthen the mechanisms for responding to zoonotic diseases, including priority zoonotic diseases such as avian influenza virus, hemorrhagic fevers (Ebola, Marburg, etc.), and emerging viral threats. In addition, PREDICT supports the development of Cameroon's One Health workforce by training and engaging staff from the Ministries of Public Health, Livestock, Forestry and Environment in surveillance and disease detection activities.

UCDUSR0001734

Where we work

PREDICT/Cameroon activities are implemented at three sites (Sangmelima, Meyomesala and Ebolowa) within the South region of Cameroon. The South region is bordered by the countries of Equatorial Guinea, Gabon, and the Republic of Congo. This area of the country is characterized by rivers, which encompass the Dja Reserve and form part of the Congo River basin. There are significant land conversion activities in the region, such as mining, logging, timber exploitation, and offshore drilling. Also, most of the population live in rural settings and are involved in subsistence farming, cattle rearing, hunting, and fishing. All three sites feature a prominent bushmeat value chain, including village areas where animals are hunted and traded, meats are consumed locally, and in some cases where meat is sold to restaurant owners and to traders for market in larger urban centers. PREDICT's zoonotic disease surveillance activities at these sites engage government staff through in-service training and provide opportunities for multisectoral coordination from district to national levels through One Health in action.

Zoonotic Disease Surveillance Sites

- **Sangmelima, South Cameroon** is situated along the Lobo River and is the capital of the Dja and Lobo division of the South region of Cameroon. There is large-scale landscape change with forested areas converted into industrial rubber plantations. This site also includes large-scale animal production farms, as well as movement of hunted animals through the value chain from neighboring villages to urban markets.
  - Sampling targets:
    - Wildlife: hunted animals in markets (rodents, non-human primates, and pangolins); bats and rodents in and around houses in rural areas
    - Syndromic surveillance of people at the Sangmelima District Hospital
    - Behavioral and community surveillance targeting individuals with high levels of occupational exposure to wildlife (hunters, trappers, butchers, market sellers, middle men, transporters)

- **Meyomesala, South Cameroon** is about 200km from Sangmelima within the Dja and Lobo division of the South region of Cameroon. There is significant landscape change due to modification of forest for construction of a hydroelectric dam (Mekin dam on the Dja River) and for an industrial rubber plantation (Hevea Sud). There is also increasing intensity of animal production in this area to supply a large population of rubber plantation workers.
  - Sampling targets:
    - Wildlife: Bats and rodents in and around houses, in villages and areas of landscape disruption
    - Syndromic surveillance of people at the Meyomesala District Hospital

UCDUSR0001735

    - Behavioral and community surveillance targeting individuals with high levels of occupational exposure to wildlife (hunters, trappers, butchers, market sellers, middle men, transporters)

- **Ebolowa, South Cameroon** is the capital of the South region of Cameroon and covers an impressive rural-urban gradient. The bushmeat value chain at this site includes village areas where meats are consumed locally and sold to restaurant owners and to traders for transport and sale in large urban centers. The area includes large-scale animal production with poultry and swine farms, as well as farms with a mix of poultry, ducks, goats, sheep, and swine. There is also landscape change resulting from a hydroelectric dam construction project (Memve'ele).
    - Sampling targets:
        - Wildlife: hunted animals sold in markets (rodents, non-human primates and pangolins)
        - Behavioral and community surveillance targeting individuals with high levels of occupational exposure to wildlife (hunters, trappers, butchers, market sellers, middle men, transporters)

Strengthening Laboratory Systems

PREDICT engages and directly supports the national laboratory system in Cameroon through our primary partner lab at the Military Health Research Centre (CRESAR) in Yaoundé. CRESAR has existing capability to detect both priority zoonotic diseases and emerging viral threats. In addition, PREDICT is available to work closely with FAO and the National Veterinary Laboratory (LANAVET) to enhance disease detection capability in the animal health sector. PREDICT has provided training and technical support to LANAVET staff at CRESAR and will continue to examine opportunities for deployment of expertise and capacity strengthening in other laboratories, such as the Cameroon National Public Health Laboratory.

Animal and Human lab: CRESAR, Yaoundé

Workforce Development and Improving Real-time Surveillance

PREDICT provides training opportunities to strengthen One Health workforce capacity in Cameroon, as central, regional, and local ministry staff participate in zoonotic disease surveillance activities and use these opportunities to obtain in-service training in One Health skills and techniques. PREDICT also contributes technical expertise on zoonotic disease surveillance in weekly Ministry of Health epidemiological surveillance meetings and when requested by the government of Cameroon (and approved by the PREDICT Management Team) and continues to support outbreak response and preparedness. These investments are helping support the operationalization of the One Health approach in central and local

UCDUSR0001736

administrations, providing critical linkages between ministries from the district to national levels. Data sharing and communication processes were established with the government through MINFOF, MINRESI, MINEPIA, MINSANTE, and MINEPDED further improving communications and information flows between animal and human health sectors. These efforts will continue to be expanded to integrate with the National Zoonoses Program and other government partners as appropriate with the goal of strengthening data platforms and improving the ease of dissemination of relevant animal, human, epidemiological, and ecological data.

UCDUSR0001737

COTE D'IVIOIRE
Year 4 (October 2017-September 2018)

Implementing Partners: EcoHealth Alliance (EHA), Institut Pasteur de Côte d'Ivoire (IPCI), Laboratoire d'Appui au Développement Agricole (LANADA)
Country Coordinator: Dr. Julien Kalpy Coulibaly, IPCI
Global Point of Contact: Dr. Peter Daszak, EHA

Partners

- Centre de Recherche en Ecologie (CRE)*
- Centre Suisse de Recherche Scientifique (CSRS)*
- Food and Agricultural Organization (FAO) of the United Nations
- Ivorian Office of Parks and Reserves*
- Ministry of Agriculture and Rural Development
- Ministry of Animal and Fish Resources
- Ministry of Health and Public Hygiene
- Ministry of Health, Environment and Sustainable Development
- Ministry of Water and Forests
- University Félix Houphouet Boigny, Department of Ethnosociology (UFHB)*

*Partnership in development

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts zoonotic disease surveillance for priority zoonotic diseases and other emerging threats. In Cote d'Ivoire, PREDICT puts One Health in action through zoonotic disease surveillance, sampling wildlife and people and conducting behavioral risk investigations at high-risk human-animal transmission interfaces. This work directly supports the national surveillance system, contributes to the development and implementation of the country GHSA roadmap, and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases, such as highly pathogenic avian influenza, viral hemorrhagic fevers (Ebola, Marburg, etc.), and SARS and MERS Coronaviruses. In addition, PREDICT supports the development of Cote d'Ivoire's One Health workforce from the national to district level through field and lab-based training and engagement of staff from the Ministries of Health and Public Hygiene, Agriculture and Rural Development, Animal and Fish Resources, and Environment and Sustainable Development, as well as national research institutes, universities, and non-governmental organizations in surveillance and disease detection activities

UCDUSR0001738

Where we work

Bouaflé (Marahoué National Park) and surrounding areas. Established in 1968, Marahoué National Park occupies an area of approximately 100,000 hectares and straddles the boundary between the Sudan-Guinea savannah and dense rainforest. With a unique geography and abundance of floral and faunal diversity, the area is a popular destination for tourists as well as contributor to local livelihoods through resource extraction, subsistence hunting, and poaching. The area immediately surrounding the park has seen an intensification of agricultural activities and animal husbandry, which have begun to infiltrate the park area, leading to increased human-wildlife interaction.

Zoonotic Disease Surveillance Sites

- **Bouaflé (Marahoué National Park)**: agricultural intensification, land use change, deforestation
  - Sampling targets:
    - Wildlife: rodents in and around dwellings, bats, and non-human primates
    - Surveys (including in-depth behavioral risk investigations) of people living and working in and around the national park
    - Syndromic surveillance of people at the Centre de Sante Urbain de Bono, the referral hospital for the region

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Cote d'Ivoire and is developing an integrated One Health laboratory network by engaging the animal health lab at the Central Laboratory for Animal Diseases, Bingerville (LANADA) and the Institute Pasteur du Côte d'Ivoire (IPCI) lab for human testing. LANADA is the national lab responsible for outbreak testing and animal health surveillance activities and the ICPI lab provides critical outbreak and surveillance support to the Ministry of Health and Public Hygiene and the entire national laboratory system. At both labs, PREDICT strengthens capacity for detection of priority zoonotic diseases (e.g., highly pathogenic avian influenza, VHFs, SARS and MERS CoVs) and emerging threats. PREDICT's One Health laboratory network fosters communication and coordination between animal and human labs and ministries, provides joint training exercises and routine information exchanges among lab managers, technicians, and ministry focal points, communicates data and findings to inform surveillance, and works to transfer knowledge and capacity to other labs in the national system.

UCDUSR0001739

Animal lab: Central Laboratory for Animal Diseases, Bingerville (LANADA)

Human lab: Institut Pasteur du Côte d'Ivoire (IPCI)

Workforce Development and Improving Real-time Surveillance

PREDICT provides training to strengthen One Health workforce capacity in Cote d'Ivoire, including on-the-job training for government veterinarians in One Health skills and safe wildlife capture and sampling during targeted sampling operations, as requested by the Ministry of Water and Forests. PREDICT puts One Health in action by coordinating triangulated surveillance and sampling strategies with FAO and the Government of Cote d'Ivoire. Through implementing partners IPCI and LANADA, PREDICT also strengthens the foundation for the One Health approach, encouraging multi-sectoral efforts to strengthen data platforms and improve communications and linkages across animal and human sectors and increasing in-country capacity for disease surveillance and outbreak response. PREDICT participates in the Government of Cote d'Ivoire GHSA coordination meetings and contributes to the GHSA surveillance technical working group, which has representation from MOH, Ministry of Animal Resources, CDC and their relevant implementing partners, and FAO. When requested by the government (and approved by the PREDICT Management Team) PREDICT also supports outbreak response and preparedness through field investigations, diagnostic testing, and epidemiological support.

UCDUSR0001740

ETHIOPIA
Year 4 (October 2017-September 2018)

Implementing Partners: University of California, Davis & Addis Ababa University (AAU) Aklilu Lemma Institute of Pathobiology
Country Coordinator: Nigatu Kebede, AAU
Global Point of Contact: Dr. Woutrina Smith, UC Davis

Partners

- Centers for Disease Control and Prevention (CDC), Addis Ababa
- Ethiopian Public Health Institute (EPHI), Ministry of Health (MOH)
- Ethiopian Wildlife Conservation Authority (EWCA)
- Food and Agricultural Organization (FAO) of the United Nations
- Ministry of Agriculture and Natural Resources (MoANR)
- Ministry of Livestock Development and Fisheries (MoLDF)
- National Animal Health Diagnostics and Investigation Center (NAHDIC)
- USAID
  - EPT One Health Workforce
  - EPT Preparedness and Response
  - Feed the Future Innovation Lab for Livestock Systems
  - USAID/Ethiopia

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts surveillance for priority zoonotic diseases and other emerging threats. In Ethiopia, PREDICT puts One Health in action by sampling bats and non-human primates and conducting behavioral risk investigations along the animal value chain for camel trade. Through these activities PREDICT improves in-country capacity to detect, prevent, and respond to zoonotic diseases that may be transmitted from wildlife to livestock and humans and strengthens animal and public health system infrastructure and preparedness. PREDICT is initiating human syndromic surveillance at zoonotic disease surveillance sites as budgets and permissions allow.

Where we work

Awash Region: The Awash region is located along the Awash River and Awash National Park in central Ethiopia, where camels, wildlife, and humans reside and interact regularly. In Awash, PREDICT is continuing to conduct zoonotic disease surveillance targeting humans, bats, and non-human primates along the camel animal value chain.

UCDUSR0001741

Bati Region: The Bati region is in the Wollo area of Amhara Regional State in Ethiopia and borders the Mile Serdo Wildlife Reserve. The Bati region contains a camel holding ground that is part of the region's camel and livestock value chain. In Bati, PREDCIT will conduct zoonotic disease surveillance and sample bats, non-human primates, and humans.

Zoonotic Disease Surveillance Sites

- **Awash Region located along the Awash River and Awash National Park in central Ethiopia:** Animal Value Chain
  - Sampling targets:
    - Wildlife: bats and non-human primates in and around pastoralist communities at camel markets, water sources, and grazing points surrounding and within the Awash National Park
    - Syndromic surveillance of patients at the Awash Health Center (Afar) who present with symptoms of acute respiratory illness and/or fever, and with frequent exposure to camels or wildlife

- **Bati Region located in Amhara State of Ethiopia:** Animal Value Chain
  - Sampling targets:
    - Wildlife: bats and non-human primates around intensifying camel production systems and holding grounds at camel and livestock markets
    - Syndromic surveillance of patients at health centers who present with acute respiratory illness and/or fever, and who have frequent exposure to camels and wildlife

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Ethiopia and a developing and integrated One Health laboratory network by engaging animal health labs at the Aklilu Lemma Institute of Pathobiology (ALIPB – University) at Addis Ababa University and the National Animal Health Diagnostics and Investigation Center (NAHDIC), along with the public health lab at the Ethiopia Public Health Institute (EPHI). Through PREDICT, ALIPB has gained capacity to detect priority zoonotic diseases and emerging threats, a critical step as the ALIPB lab is a training center for the animal health sector and provides reference support to the national surveillance system. PREDICT's One Health laboratory network fosters communication and coordination between animal and human labs and ministries; provides routine information exchanges among lab managers, technicians, and ministry focal points; communicates data and findings to

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inform surveillance; and works to transfer knowledge and capacity to other labs, in the national system.

Animal labs: AAU Aklilu Lemma Institute of Pathobiology, with training and transfer of protocols for the National Animal Health Diagnostic and Investigation Center (NAHDIC) for livestock samples

Human labs: AAU Aklilu Lemma Institute of Pathobiology in coordination with the Ethiopian Public Health Institute (EPHI)

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Ethiopia for government staff from national to subnational levels, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease surveillance, PREDICT strengthens Ethiopia's capacity to sample animals and people, investigate behaviors associated with zoonotic disease transmission, detect priority zoonotic diseases and emerging threats, and perform data analyses to understand zoonotic disease risks. In addition, PREDICT works across ministries and sectors helping build a One Health platform in Ethiopia, improving communications and linkages across animal and human sectors as project data and findings on zoonotic diseases and enabling behaviors underlying transmission are shared and discussed. When requested by the government (and approved by the PREDICT Management Team) PREDICT also supports outbreak response and preparedness through field investigations, diagnostic testing, and epidemiological support.

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GUINEA *(Ebola Host Project country)*
Year 4 (October 2017-September 2018)

Implementing Partners: University of California, Davis and Laboratoire de Fièvres Hémorragiques en Guinée (Viral Hemorrhagic Fever Laboratory of Guinea)
Country Coordinator: Dr. Alpha Camara, Laboratoire de Fièvres Hémorragiques en Guinée (Viral Hemorrhagic Fever Laboratory of Guinea)
Global Point of Contact: Dr. Corina Monagin, UC Davis

Partners

- Institute de Recherche en Biologie Appliqué
- Institute National de Santé Publique (INSP)*
- Institute Superior des Sciences et de Medicine Veterinaire de Dalaba
- Laboratoire de Fièvres Hémorragiques en Guinée
- Ministry of Environment, Water and Forests
- Ministry of Health and Public Hygiene
- Ministry of Higher Education and Research
- Ministry of Livestock and Animal Production
- USAID EPT One Health Workforce
- USAID EPT Preparedness and Response
- USAID/Guinea

*Partnership in development

Plans subject to change as the budget is finalized; activities presented will be implemented as budget allows.

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts zoonotic disease surveillance for priority zoonotic diseases and other emerging threats. In Guinea, PREDICT is working with EPT, GHSA and local partners to implement the Ebola Host Project (EHP), an ambitious initiative seeking to discover the animal origins and spillover of Ebola virus (*Ebola zairevirus*) in Guinea, Liberia, and Sierra Leone. EHP is the most detailed investigation of this devastating public health threat of international concern ever attempted. Through EHP, PREDICT provides Guinea's growing One Health workforce on-the-job training opportunities in the full spectrum of activities required for safe surveillance and detection of priority zoonotic disease threats and conducts surveillance and behavioral risk investigations targeting animals and humans at key high-risk interfaces for Ebola virus transmission. As part of the EHP, surveillance activities in the upcoming year are restricted to sampling wildlife to identify species that may act as reservoir or transmission hosts for Ebola virus by working with ministry and EPT-2 partners to sample at prioritized sites with previously high levels of Ebola virus disease and high human-animal contact in varying ecological zones and conducting longitudinal sampling to capture seasonal

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variations at high-risk sites to span key environmental time-periods among target taxa (e.g., dry season, wet season, and breeding season). In concert with sampling activities, PREDICT plans to collect in-depth, standardized, quantitative data using a targeted questionnaire (where feasible) on human activities and behaviors that may enable zoonotic disease transmission and spread among at-risk populations. There are no plans to collect biological samples from humans or domestic animals and livestock in the upcoming year.

Where we work

Between 2013-2016, West Africa experienced the largest Ebola virus epidemic in history, with more than 28,000 cases and 11,000 deaths recorded before the outbreak was finally brought under control. The unprecedented geographic spread of Ebola virus among human populations across multiple countries raised the prospect that the virus could have not only "spilled over" from wildlife but also "spilled back" from people into previously unaffected animal populations—wildlife, companion animals, and livestock—resulting in a broader geographic distribution of the virus. **The Forest Region,** the primary focus of PREDICT's Ebola Host Project activities in Guinea, is considered the epicenter for Ebola virus emergence in the recent outbreak. The Guinean Forest Region, a lowland forest stretching across West Africa and through Guinea, is a biodiversity hotspot containing an estimated quarter of all of Africa's mammalian fauna. Human encroachment into forested areas has reduced this once vast system to a patchwork forest-agriculture mosaic, putting pressure on wildlife habitat and increasing opportunities for contact and zoonotic disease spillover from wildlife to people, as evidenced by the recent spillover of Ebola virus in December 2013. PREDICT has evaluated various prefectures within the Forest Region and identified specific sites where human-wildlife contact with potential reservoirs and hosts of Ebola is at highest risk. In selecting sites, PREDICT also considered areas with a high number of cases of Ebola during the epidemic (both deaths and survivors).

Zoonotic Disease Surveillance Sites

**Specific sites and activities subject to change based on resource availability*

- **Kissidougou Prefecture**: **Missira (urban), Sangardo**: Animal production, crop production, and market and value chain
  - Sampling targets:
    - Wildlife: sampling of bats and rodents in and around human dwellings and agricultural fields; pristine forest areas; markets and road-side stands selling live and butchered wildlife

- **Guéckédou Prefecture**: **Houndonin (urban), Meliandou (rural), Kassadou**: Animal production, crop production, market and value chain

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- Sampling targets:
  - Wildlife: sampling of bats and rodents in and around human dwellings and agricultural fields; pristine forest areas; markets and road-side stands selling live and butchered wildlife

- **Macenta Prefecture: Patrice (urban), Djomankoidou (rural), Oremai:** Animal production, crop production, market and value chain
  - Sampling targets:
    - Wildlife: sampling of bats and rodents in and around human dwellings and agricultural fields; pristine forest areas; markets and road-side stands selling live and butchered wildlife

- **N'Zérékoré Prefecture: Nyen (urban), Koropara (rural), Soulata:** Animal production, crop production, extractive industry, market and value chain
  - Sampling targets:
    - Wildlife: bats, rodents, and non-human primates in and around human dwellings and agricultural fields; pristine forest areas; markets and road-side stands selling live and butchered wildlife

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Guinea by engaging the Laboratoire de Fièvres Hémorragiques en Guinée (VHF) as the main laboratory partner for collaboration and capacity strengthening in Guinea. At the lab, PREDICT strengthens capacity for detection of Ebola and other hemorrhagic fevers, which are nationally recognized priority zoonotic diseases. Through this lab, PREDICT also works in collaboration ministry partners and the National Veterinary Lab to explore opportunities for training and the transfer of zoonotic disease detection knowledge, skills, and technologies, helping to foster linkages between sectors to strengthen Guinea's One Health laboratory network. To achieve Ebola Host Project objectives, an ambitious scope of work with extremely high volume of samples has been employed. Tests are conducted at both VHF (as capacity is developed) and the University of California Davis.

Animal labs: Laboratoire de Fièvres Hémorragiques en Guinée, with training and to include members of the National Veterinary Laboratory; University of California, Davis

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Guinea for government staff from national to subnational levels, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills

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required for safe and effective zoonotic disease surveillance, PREDICT strengthens Guinea's capacity to sample animals, investigate behaviors associated with zoonotic disease transmission, detect Ebola and emerging threats, and perform data analyses to understand zoonotic disease risks. National governmental focal points and local government are involved in field surveillance activities, and we will continue to engage them to ensure the operationalization of the One Health approach. In addition, PREDICT participates in monthly USAID GHSA and Ministerial One Health Platform meetings and works with partners and across ministries and sectors helping to build and operationalize the newly formed national One Health Platform, and to improve communications and linkages across animal and human sectors by sharing data and findings on zoonotic diseases. Finally, PREDICT will continue to participate in MoH epidemiological surveillance meetings (district and national level).

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KENYA
Year 4 (October 2017-September 2018)

Implementing Partners: Smithsonian Institution (SI), Institute of Primate Research (IPR)
Global Point of Contact: Drs. Dawn Zimmerman and Suzan Murray, SI
Country Coordinator: Dr. Joseph Kamau, IPR

Partners

- Central Veterinary Investigatory Laboratory (CVIL) at the Directorate of Veterinary Services (DVS)
- Community Health Africa Trust (CHAT)
  - Mpala Clinic
  - Ol Jogi Clinic
- Cottage Hospital, Nanyuki
- Emergency Operation Center (EOC), Ministry of Health *(Currently Suspended)*
- Food and Agricultural Organization-Kenya (FAO-KE)
- International Centre of Insect Physiology and Ecology (ICIPE)
- International Livestock Research Institute (ILRI)
- Kenya Medical Research Institute (KEMRI)
- Kenya Wildlife Service (KWS)
- Ministry of Agriculture, Livestock and Fisheries
- Mpala Research Center (MRC)
- One Health Central and East Africa (OHCEA)
- University of Nairobi
  - One Health Centre, University of Nairobi
  - Veterinary College, University of Nairobi
- USAID EPT One Health Workforce
- USAID EPT Preparedness and Response
- USAID/Kenya
- Zoonotic Disease Unit (ZDU)

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts surveillance for priority zoonotic diseases and other emerging threats. In Kenya, PREDICT puts One Health in action by integrating animal and human health sectors from the national to district level through the collection and testing of samples from wild animals, livestock, and humans at high-risk interfaces for zoonotic disease transmission. PREDICT focuses surveillance activities on the priority zoonotic diseases influenza and hemorrhagic fevers (e.g., Ebola, Marburg, etc.) and emerging threats, such as Middle East Respiratory Syndrome (MERS) Coronavirus. PREDICT supports the development of Kenya's One Health

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workforce from the national to district level through field and lab-based training and engagement of national staff, university and NGO partners, and students in surveillance and disease detection activities.

Where we work

Laikipia: Laikipia County is located along the Great Rift Valley and is rich in wildlife and livestock. It borders Samburu County to the north, Baringo to the west, Nyeri to the south, and Meru/Mount Kenya to the east. Ecotourism is a major activity in the county due to wildlife populations that are mainly found within livestock ranches. In addition to ranches, livestock are also kept by the pastoralist community and there is crop production to the south of the county. There is high overlap of wildlife with livestock and humans making this area an important interface for zoonotic disease surveillance.

Zoonotic Disease Surveillance Sites

- **Laikipia County, targeting Laikipia North, specifically Mpala, Loisaba and Suiyan conservancies.** Animal Production, Market and Value Chain, Human Dwellings and Natural Areas
  - Sampling targets:
    - Wildlife: Non-human primates (NHPs), rodents, and bats that interact with camels and livestock in the organized ranches and/or grazing lands, as well as with humans in and around dwellings and natural areas (within and around wildlife research center). The type and number of specimens collected and tested for each taxa will be determined based on budget and presence at interface
    - Community surveillance of people working within camel abattoirs/trade (herders, camel handlers, drivers, middle men, men/women milking or selling milk), in nearby communities, and within wildlife research center

Strengthening Laboratory Systems

PREDICT supports the development of an integrated One Health laboratory network by engaging the Institute of Primate Research (IPR) and the Kenya Medical Research Institute (KEMRI), both national research institutes in zoonotic disease surveillance and detection and active members in developing One Health activities and platforms in-country. IPR is the implementing partner for PREDICT/Kenya, and the lab is testing animal samples for priority zoonotic diseases and other emerging threats. As part of efforts to interlink animal and human laboratory systems, IPR lab staff have trained KEMRI lab technicians in preparation for initiation of human testing at KEMRI facilities. Additionally, PREDICT, in coordination with FAO, is strengthening animal laboratories for improved disease detection through workshops targeting laboratory technicians

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and staff from government and non-government organizations, including Kenya Wildlife service (KWS), Kenya Agricultural and Livestock Research Organization (KALRO), Directorate of Veterinary Service (CVIL-DVS), and several universities. Workshops provide training in laboratory safety, biosafety, and disease surveillance, including molecular techniques for advanced disease detection that are applicable to priority diseases such as Rift Valley Fever and rabies. Through the IPR lab, PREDICT is also providing a two-week intensive training to CVIL-DVS that will further enable this lab to test for priority zoonotic diseases and emerging threats.

Animal Labs: Institute of Primate Research (IPR) laboratory, with plans to transfer protocols and subset of samples for testing at Central Veterinary Investigatory Laboratory under the Directorate of Veterinary Services (CVIL-DVS)

Human Lab: Kenya Medical Research Institute (KEMRI) laboratory

Workforce Development and Improving Real-time Surveillance

PREDICT provides training opportunities to strengthen the One Health workforce in Kenya, as government staff from district to national levels are engaged in implementation of zoonotic disease surveillance and detection activities. PREDICT works closely with the USAID Preparedness and Response (P&R), One Health Central and East Africa (OHCEA), and the School of Veterinary Medicine and College of Health Sciences at the University Nairobi to strengthen One Health capacity in the country through short-term training, internships, and educational programs on One Health. Project data and findings on zoonotic diseases and enabling behaviors underlying transmission are shared and communicated through established channels across animal and human health sectors, strengthening data platforms and improving the ease of dissemination of animal, human, epidemiological, and ecological data. PREDICT participates in national initiatives to strengthen operationalization of One Health in-country, including the Joint External Evaluation, development of the national framework on zoonotic surveillance with FAO and DVS, and zoonotic disease-specific planning initiatives, such as MERS-COV surveillance and control. In addition, PREDICT partners with the Ministry of Agriculture, Livestock and Fisheries; Ministry of Environment and Natural resources (Kenya Wildlife Service), and the University of Nairobi to strengthen preparedness and response in the country and provides outbreak preparedness and response assistance (upon invitation and with approval from PREDICT Management Team) through provision of training materials and protocols, field investigation support, diagnostic testing, and epidemiological expertise, as evidenced during the avian influenza outbreak in neighboring Uganda in early 2017.

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LIBERIA *(Ebola Host Project country)*
Year 4 (October 2017-September 2018)

Implementing Partners: EcoHealth Alliance (EHA), The Society for Conservation of Nature of Liberia (SCNL)
Country Coordinator: Dr. Jim Desmond, EcoHealth Alliance
Global Point of Contact: Dr. Jon Epstein, EcoHealth Alliance

Partners

- Food and Agriculture Organization (FAO) Liberia, Monrovia
- Forestry Development Authority (FDA), Monrovia
- Liberian Institute for Biomedical Research (LIBR), Charlesville
- Ministry of Agriculture (MoA), Monrovia
- Ministry of Health (MoH), Monrovia
- National Public Health Institute of Liberia (NPHIL), Monrovia
- National Reference Laboratory (NRL), Charlesville
- USAID EPT One Health Workforce
- USAID EPT Preparedness & Response
- USAID/Liberia

Plans subject to change as the budget is finalized; activities presented will be implemented as budget allows.

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts zoonotic disease surveillance for priority zoonotic diseases and other emerging threats. In Liberia, PREDICT is working with EPT, GHSA and local partners to implement the Ebola Host Project (EHP), an ambitious initiative seeking to discover the animal origins and spillover of Ebola virus (*Ebola zairevirus*) in Liberia, Guinea, and Sierra Leone. EHP is the most detailed investigation of this devastating public health threat of international concern ever attempted. Through EHP, PREDICT provides Liberia's growing One Health workforce on-the-job training opportunities in the full spectrum of activities required for safe surveillance and detection of priority zoonotic disease threats, and conducts surveillance targeting animals and humans at key high-risk interfaces for Ebola virus transmission. As part of the EHP, surveillance activities in the upcoming year are restricted to wildlife sample collection; there are no plans to collect biological samples from humans or livestock. In concert with sampling activities, PREDICT plans to collect in-depth, standardized, quantitative data using a targeted questionnaire (where feasible), on human activities and behaviors that may enable zoonotic disease transmission and spread among at-risk populations.

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Where we work

Between 2013-2016, West Africa experienced the largest Ebola virus epidemic in history, with more than 28,000 cases and 11,000 deaths recorded before the outbreak was finally brought under control. The unprecedented geographic spread of Ebola virus among human populations across multiple countries raised the prospect that the virus could have not only "spilled over" from wildlife but also "spilled back" from people into previously unaffected animal populations—wildlife, companion animals and livestock—resulting in a broader geographic distribution of the virus. In Liberia over 10,000 total cases or Ebola were reported during the outbreak and after declaring the country free of transmission in May 2015, two additional clusters of cases emerged before the country was declared free of transmission for a third time in January 2016. PREDICT targets five counties in Liberia to maximize the probability for identifying potential Ebola virus host species.

Lofa County, Foya, and Zorzor Districts. Both Foya and Zorzor districts are mixed habitats of natural forest surrounded by 'slash and burn' agricultural areas. Foya District was an area with a high incidence of human Ebola cases.

Montserrado County. Montserrado Country houses Monrovia, Liberia's capital and where there are several large, seasonal, urban bat colonies and people are highly exposed to excreta. Montserrado also contains areas subjected to recent deforestation near human dwellings and agricultural sites, and active bushmeat hunting which creates additional high-risk interfaces.

Nimba County. Nimba country houses Yekepa on the border with Guinea within the Arcelor Mittal mining concession. In Nimba PREDICT is targeting extractive industry interfaces and sampling animals in and around adits and forested areas in old exploratory mine shafts.

Grand Cape Mount. Grand Cape Mount has several areas with pristine forest in the Gola National Forest and other areas with mixed forest/agricultural landscapes. PREDICT has identified multiple sampling sites within this county that are expected to have high wildlife biodiversity and human-wildlife interfaces at agricultural and peridomestic sites.

Bong County. Bong Country houses Suakoko, Panta, and Kpai Districts and if resources allow, provides PREDICT with the opportunity to target areas with increasing land use change and the market and value chain.

Zoonotic Disease Surveillance Sites

**Specific sites and activities subject to change based on resource availability*

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- **Lofa County: Foya & Voinjama districts (Wenegizi Forest)**: Land use change, market and value chain
  - Sampling targets:
    - Wildlife: non-human primates, bats, and rodents in areas with recent deforestation near human dwellings and agricultural sites and the bushmeat value chain from hunting to sale to consumption, as a potential transmission pathway for Ebola virus

- **Montserrado County: Central Monrovia & St. Paul's River Districts**: Land use change, market and value chain
  - Sampling targets:
    - Wildlife: non-human primates, bats, and rodents in areas with recent deforestation near human dwellings and agricultural sites and the bushmeat value chain from hunting to sale to consumption, as a potential transmission pathway for Ebola virus

- **Nimba County: Yekepa in Yarmein District**: Extractive industry, land use change, market and value chain
  - Sampling targets:
    - Wildlife: non-human primates, bats, and rodents in areas with recent deforestation near human dwellings and agricultural sites and the bushmeat value chain from hunting to sale to consumption, as a potential transmission pathway for Ebola virus
    - Extractive industry: sampling of bat colonies dispersed by large iron ore mining concession (operated by Arcelor Mittal)

- **Grand Cape: Mount Tewor, Gola Konneh & Gowular Districts:** Land use change, market and value chain
  - Sampling targets:
    - Wildlife: non-human primates, bats, and rodents in areas with recent deforestation near human dwellings and agricultural sites and the bushmeat value chain from hunting to sale to consumption, as a potential transmission pathway for Ebola virus

Additional targeted sites (as resources allow)

- **Bong: Suakoko, Panta & Kpai Districts:** Land use change, market and value chain
  - Sampling targets:
    - Wildlife: non-human primates, bats, and rodents in areas with recent deforestation near human dwellings and agricultural sites and the bushmeat value chain from hunting to sale to consumption, as a potential transmission pathway for Ebola virus

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- **Grand Bassa County (Buchanan District):** Land use change, market and value chain
  - Sampling targets:
    - Wildlife: non-human primates, bats, and rodents in areas with recent deforestation near human dwellings and agricultural sites and the bushmeat value chain from hunting to sale to consumption, as a potential transmission pathway for Ebola virus

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Liberia by engaging the National Public Health Institute of Liberia (NPHIL) for wildlife testing and through outreach to the Central Veterinary Diagnostic Laboratory and incorporation of Ministry of Agriculture staff for biosafety, biosecurity, and training in zoonotic disease detection. PREDICT strengthens capacity for detection of Ebola, a nationally recognized priority zoonotic disease, and other filoviruses (e.g., Marburg and other emerging threats). At NPHIL, PREDICT builds capacity by identifying equipment needs, assisting with necessary procurement, and training staff with experience from the Ebola outbreak on advanced disease detection techniques, which will include testing animal samples. PREDICT also works in collaboration with EPT-2, GHSA, and ministry partners to explore opportunities to transfer zoonotic disease detection knowledge, technologies, and in-service training opportunities to other laboratories in the national system, helping to foster linkages between sectors to strengthen Liberia's One Health laboratory network. To achieve Ebola Host Project objectives, an ambitious scope of work with extremely high volume of samples has been employed. Tests are conducted at both NPHIL (as capacity is developed) and the Columbia University Center for Infection and Immunity.

Animal lab: National Public Health Institute, Liberia (NPHIL) and Columbia University Center for Infection and Immunity

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Liberia for government staff from national to subnational levels, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease surveillance, PREDICT strengthens Liberia's capacity to sample animals, investigate behaviors associated with zoonotic disease transmission, detect Ebola and emerging threats, and perform data analyses to understand zoonotic disease risks. In addition, PREDICT works across ministries and sectors, helping to build and operationalize the national One Health platform. With Ministry of

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Agriculture (MoA), Ministry of Health (MoH), Forestry Development Authority (FDA), the National Public Health Institute of Liberia (NHPIL), the Liberian Institute for Biomedical Research (LIBR), National Reference Laboratory (NRL), and EPT-2 FAO and P&R partners, PREDICT is improving communications and linkages across animal and human sectors by sharing data and findings on zoonotic diseases and the enabling behaviors underlying transmission. Finally, PREDICT will continue to participate in monthly USAID GHSA and Ministerial One Health Platform meetings.

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SENEGAL
Year 4 (October 2017-September 2018)

Implementing Partners: University of California, Davis; Ecole Inter États Sciences et de Médecine Vétérinaires (Inter State School of Veterinary Science and Medicine of Dakar; EISMV) de Dakar; Université Cheikh Anta Diop de Dakar (Cheikh Anta Diop University; UCAD); Institut Sénégalais de Recherches Agricoles (Senegalese Institute of Agricultural Research; ISRA)
Country Coordinator: Dr. Ismaila Kane, EISVM
Global Point of Contact: Dr. Corina Monagin, UC Davis

Partners

- Cabinet du Premier Ministre, Sénégal (Prime Minister's Cabinet, Senegal), Dakar
- Defense Threat Reduction Agency/Cooperative Biological Engagement Program (DTRA/CBEP)*
- Direction des Parks Nationaux (DPN)
- Institut Pasteur de Dakar (IPD), Dakar*
- ISRA/Laboratoire National d'Elevage et de Recherches Vétérinaires (National Livestock and Veterinary Research Laboratory; LNERV), Dakar
- Ministère de l'Agriculture et de l'Equipment Rural (Ministry of Agriculture and Rural Equipment ; MAER), Dakar
- Ministère de l'Elevage et des Productions animales (Ministry of Livestock and Animal Production; MEPA), Dakar
- Ministère de l'Environnement et du Développement Durable (Ministry of the Environment and Sustainable Development; MEDD), Dakar
- Ministère de la Santé et de l'Action Sociale (Ministry of Health and Social Action; MSAS), Dakar
- Organisation des Nations Unies pour l'Alimentation et l'Agriculture (the Food and Agriculture Organization of the United Nations; FAO), Dakar
- Organisation mondiale de la Santé Sénégal (World Health Organisation Senegal), Dakar
- REDISSE (World Bank), Dakar*
- UCAD / Hôspital Aristide le Dantec (Dantec University Hospital), Dakar
- US CDC, Dakar*
- USAID EPT One Health Workforce

*Partnership in development

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts zoonotic disease surveillance for priority zoonotic diseases and other emerging threats. In Senegal, PREDICT puts One Health in action through zoonotic disease surveillance sampling wildlife and people and conducting behavioral risk

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investigations at high-risk human-animal transmission interfaces. This work directly supports the national surveillance system, contributes to the development and implementation of the country GHSA roadmap, and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases, such as avian influenza and hemorrhagic fevers (Rift Valley, Ebola, Marburg, etc.). In addition, PREDICT supports the development of Senegal's One Health workforce from the national to district level through field and lab-based training and engagement of staff from the Ministries of Health, Agriculture, Livestock, and Environment, national research institutes, universities, and non-governmental organizations in surveillance and disease detection activities.

Where we work

Bandia, Sindia region: The Bandia area is a biodiverse private reserve Senegal and a major tourist attraction, receiving many national and international visitors that are exposed to non-human primates, rodents, and bats through informal contact at locations such as outdoor restaurants. In collaboration with government, GHSA, and EPT-2 partners, PREDICT is investigating risks for zoonotic disease transmission at several sites in the area due to the high potential for viral spillover at this important animal-human interface. Targeted sites include: **the Sindia district** (human surveillance activities), home to a frequented clinic of residents who live near the Bandia reserve and are regularly exposed to wildlife in their daily lives; and the **Bandia Bambara, Kofgoune, and Keniammbour villages** (rodent and bat surveillance activities), which are home to Bandia Reserve workers who live near the Bandia reserve and are regularly exposed to wildlife in their daily lives.

Zoonotic Disease Surveillance Sites

- **Sindia Health Center:** Land Conversion, Animal Value Chain, and Intensification of Animal Production Systems
  - Sampling targets:
    - Syndromic surveillance of patients at health posts/centers
    - Community surveillance of people with frequent exposure to wildlife.
    - Wildlife: rodents, and bats in and around the clinic and human dwellings

- **Bandia Reserve:** Land Conversion, Animal Value Chain, and Intensification of Animal Production Systems
  - Sampling targets:
    - Wildlife: rodents, bats, and non-human primates in and around protected areas with tourists and human dwellings
    - Community surveillance of people working in the reserve with frequent exposure to wildlife

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- **Bandia Bambara:** Land Conversion, Animal Value Chain, and Intensification of Animal Production Systems
  - Sampling targets:
    - Wildlife: rodents, bats, and non-human primates in and around protected areas with tourists and human dwellings
    - Community surveillance of people with frequent exposure to wildlife

- **Kofgouye:** Land Conversion, Animal Value Chain, and Intensification of Animal Production Systems
  - Sampling targets:
    - Wildlife: rodents, bats, and non-human primates in and around protected areas with tourists and human dwellings
    - Community surveillance of people with frequent exposure to wildlife

- **Keniammbour:** Land Conversion, Animal Value Chain, and Intensification of Animal Production Systems
  - Sampling targets:
    - Wildlife: rodents, bats, and non-human primates in and around protected areas with tourists and human dwellings
    - Community surveillance of people with frequent exposure to wildlife

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Senegal and is developing an integrated One Health laboratory network by engaging the animal health lab at the Institut Sénégalais de Recherches Agricoles (ISRA), along with the human lab at the Université Cheikh Anta Diop de Dakar (UCAD). The ISRA Laboratoire National d'Elevage et de Recherches Vétérinaires (LNERV) is the national lab responsible for outbreak testing and animal health surveillance activities. The UCAD lab is the one selected by the MoH for PREDICT work and is the training center the human health sector. In addition, it provides critical reference support to the national surveillance system. At these labs, PREDICT strengthens capacity for detection of priority zoonotic diseases (e.g., zoonotic influenza viruses and VHFs - Ebola, Marburg, and Influenza) and other emerging threats and priority pathogens. PREDICT's One Health laboratory network fosters communication and coordination between animal and human labs and ministries; provides joint training exercises and routine information exchanges among lab managers, technicians, and ministry focal points; communicates data and findings to inform surveillance; and works to transfer knowledge and capacity to other labs in the national system.

Animal lab(s): Institut Sénégalais de Recherches Agricoles (Senegalese Institute of Agricultural Research ISRA)/Laboratoire National d'Elevage et de

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Recherches Vétérinaires (National Livestock and Veterinary Research Laboratory; LNERV), Dakar

Human lab: Université Cheikh Anta Diop de Dakar (Cheikh Anta Diop University; UCAD) / Hôpital Aristide le Dantec (Dantec University Hospital)

Workforce Development and Improving Real-time Surveillance

PREDICT provides training to strengthen One Health workforce capacity in Senegal, as central, regional, and local ministry staff participate in zoonotic disease surveillance activities. PREDICT engages the Ministry of Agriculture, the DPN, the GHSA Task Force, as well as the newly established COUS (Health Emergency Operation Center) at the Ministry of Health in efforts to strengthen national capacity for zoonotic disease surveillance, especially for the animal health sector by training DPN staff in One Health skills and safe wildlife capture and sampling during targeted surveillance operations. PREDICT also works with COUS and other GHSA partners to strengthen data platforms and improve communications and linkages across animal and human sectors, as project data and findings on zoonotic diseases and enabling behaviors underlying transmission are shared and discussed. PREDICT will continue to serve as a resource for the development and operationalization of Senegal's One Health Strategic Plan with local university, government, and research organization personnel. When requested by the government (and approved by the PREDICT Management Team) PREDICT also supports outbreak response and preparedness through field investigations, diagnostic testing, and epidemiological support.

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SIERRA LEONE *(Ebola Host Project country)*
Year 4 (October 2017-September 2018)

Implementing Partners: UC Davis, University of Makeni
Country Coordinator: Dr. Alah Gbakima, UC Davis
Global Point of Contact: Dr. Brian Bird, UC Davis

Partners

- Central Animal-Veterinary Laboratory, (TEKO) Makeni, Bombali District
- Central Public Health Laboratory (CPHRL), Freetown*
- Ministry of Agriculture Forestry and Food Security (MAFFS)
- Ministry of Health and Sanitation (MOHS)
- Tacugama Chimpanzee Sanctuary, Freetown*
- University of Makeni (UNIMAK)
- USAID EPT One Health Workforce
- USAID EPT Preparedness and Response
- USAID/Sierra Leone

*Partnership in development

Plans subject to change as the budget is finalized; activities presented will be implemented as budget allows.

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts zoonotic disease surveillance for priority zoonotic diseases and other emerging threats. In Sierra Leone, PREDICT is working with EPT, GHSA, and local partners to implement the Ebola Host Project (EHP), an ambitious initiative seeking to discover the animal origins and spillover of Ebola virus (*Ebola zairevirus*) in Sierra Leone, Guinea, and Liberia, as well as other priority zoonotic pathogens. EHP is the most detailed investigation of this devastating public health threat of international concern ever attempted. Through EHP, PREDICT provides Sierra Leone's growing One Health workforce on-the-job training opportunities in the full spectrum of activities required for safe surveillance and detection of priority zoonotic disease threats and conducts surveillance and behavioral risk investigations targeting animals and humans at key high-risk interfaces for Ebola virus transmission. As part of the EHP, surveillance activities in the upcoming year are restricted to wildlife sample collection; there are no plans to collect biological samples from humans or livestock. In concert with sampling activities, PREDICT plans to collect in-depth, standardized, quantitative data using a targeted questionnaire (where feasible), on human activities and behaviors that may enable zoonotic disease transmission and spread among at-risk populations. In addition, PREDICT is working with strategic GHSA partners to develop a zoonotic disease risk communication and outreach strategy focused on interventions for reducing the potential for viral transmission between bats and

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people.

Where we work

Between 2013-2016, West Africa experienced the largest Ebola virus epidemic in history, with more than 28,000 cases and 11,000 deaths recorded before the outbreak was finally brought under control. The unprecedented geographic spread of Ebola virus among human populations across multiple countries raised the prospect that the virus could have not only "spilled over" from wildlife but also "spilled back" from people into previously unaffected animal populations—wildlife, companion animals, and livestock—resulting in a broader geographic distribution of the virus. Sierra Leone, a small but ecologically diverse country with the highest recorded number of cases during the outbreak, has numerous settlements in urban and rural areas that are co-habited with bats and other wildlife, a rich animal-human interface with high potential for Ebola (and other zoonotic disease) transmission. PREDICT's EHP locations were selected to increase the opportunity to discover both the potential wildlife reservoir host of the virus (e.g., bats and rodents), along with other animals that may have been exposed to the virus through contact with infected people, contaminated materials, or fomites resulting in further spill-over of Ebola into previously unrecognized animal species. PREDICT collects samples from wildlife in a variety of sites, ranging from urban, semi-urban, and rural environments to deep primary forest sites in six districts of the country.

Zoonotic Disease Surveillance Sites

**Specific sites and activities subject to change based on resource availability*

- **Bombali District, Northern Province**: Animal production systems and market value chain
  - Sampling targets:
    - Wildlife: bats and rodents in and around human settlements, in areas of landscape disruption, and near agricultural sites, and hunted in the bushmeat market value chain

- **Western Areas, Freetown Area**: Animal production systems and market value chain, land conversion for commercialization
  - Sampling targets:
    - Wildlife: sampling of bats and rodents in and around peri-domestic livestock intensification operations in coordination with local private sector and government partners; sampling of animals in contact with domestic livestock animals or animal products destined for human consumption

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- **Kambia District, Northern Province:** Animal production systems and market value chain, land conversion for commercialization
  - Sampling targets:
    - Wildlife: sampling of bats and rodents in and around human settlements, in areas of landscape disruption, and near agricultural sites and hunted in the bushmeat market value chain.

- **Koinadugu District, Northern Province:** Animal production systems and market value chain, land conversion for commercialization
  - Sampling targets:
    - Wildlife: bats and rodents in and around human settlements, in areas of landscape disruption, and near agricultural sites, and hunted in the bushmeat market value chain

- **Kono District, Eastern Province**: Animal production systems and market value chain, land conversion for commercialization
  - Sampling targets:
    - Wildlife: bats and rodents in and around human settlements, in areas of landscape disruption, and near agricultural sites, and hunted in the bushmeat market value chain

- **Pujehun District, Southern Province:** Animal production systems and market value chain, land conversion for commercialization, wildlife management and ecotourism
  - Sampling targets:
    - Wildlife: bats and rodents in deep pristine forest habitats; peridomestic animals in and around human settlements and areas of landscape disruption; hunted animals in villages for pet trade, and hunted in the bushmeat market value chain

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Sierra Leone by engaging the University of Makeni Infectious Disease Research Laboratory. At the lab, PREDICT strengthens capacity for detection of filoviruses (e.g., Ebola, Marburg, and other emerging threats), a viral family that causes viral hemorrhagic fever, which is a nationally recognized priority zoonotic disease. Through this lab, PREDICT also works in collaboration ministry partners from the MOHS and MAFFS to provide training for technical ministry staff and to explore opportunities to transfer zoonotic disease detection knowledge, technologies, and in-service training opportunities to other laboratories in the national system, such as the MAFFS Central Animal Laboratory TEKO and the MOHS Central Public Health Research Laboratory, helping to foster linkages between sectors to strengthen Sierra Leone's One Health laboratory network. To achieve Ebola Host Project objectives, an ambitious scope of work with extremely high volume of

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samples has been employed. Tests are conducted at both University of Makeni (as capacity is developed) and the University of California Davis.

Animal lab(s): University of Makeni Infectious Disease Research Laboratory and the University of California, Davis

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Sierra Leone for government staff from national to subnational levels, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease surveillance, PREDICT strengthens Sierra Leone's capacity to sample animals; investigate behaviors associated with zoonotic disease transmission; detect Ebola, priority zoonotic diseases, and other emerging threats; and perform data analyses to understand zoonotic disease risks. In addition, PREDICT works across ministries and sectors helping to build and operationalize the national One Health platform and improve communications and linkages across animal and human sectors by sharing data and findings on zoonotic diseases and the enabling behaviors underlying transmission. District-level staff are involved in field surveillance activities and will be engaged to ensure the operationalization of the One Health approach. PREDICT facilitates meetings of District-level One Health Platforms in Bombali, Western Area, and Kono and Koinadugu districts, and will continue to support these platforms, while also planning to assist in initial platform meetings in Kambia and Pujehun districts in coordination with other government and EPT partners. Dissemination of One-Health messaging and risk avoidance communications will be an integral part of these and other community engagement activities during the upcoming year. Finally, PREDICT will continue to participate in MoH epidemiological surveillance meetings (district and national level).

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TANZANIA
Year 4 (October 2017-September 2018)

Implementing Partners: UC Davis, Sokoine University of Agriculture (SUA), Ifakara Health Institute (IHI)
Principal Investigator: Rudovick Kazwala, SUA
Country Coordinator: Zikankuba Sijali, SUA
Human Surveillance Coordinator: Grace Mwangoka, IHI
Global Point of Contact: David Wolking, UC Davis

Partners

- Central Veterinary Laboratory (CVL) and Regional and District Veterinary Offices
- FAO Tanzania, Dar es Salaam, Tanzania
- Kibondo District Council, Kibondo, Tanzania
- Kigoma Municipal, Kigoma, Tanzania
- Kyerwa District Council, Kyerwa, Tanzania
- Makerere University Walter Reed Project (MUWRP), Kampala, Uganda
- Ministry of Agriculture, Livestock and Fisheries (MALF), Tanzania
- Ministry of Health, Community development, Gender, Elderly and Children (MoHCDGEC), Tanzania
- Ministry of Natural Resources and Tourism (MNRT), Tanzania
- National Coordinating Unit One Health Steering Committee (OHSC) and Technical Working Groups (TWGs) in Research and Development and Surveillance, Tanzania
- National Institute of Medical Research (NIMR), Dar es Salaam, Tanzania
- One Health Central and Eastern Africa (OHCEA), Tanzania
- Tanzania National Parks (TANAPA), Tanzania
- *Tanzania National Health Laboratory (TNHL), Dar es Salaam, Tanzania
- Tanzania Veterinary Laboratory Agency (TVLA), Dar es Salaam, Tanzania
- Tanzania Wildlife Research Institute (TAWIRI), Tanzania
- USAID EPT One Health Workforce (OHW)
- USAID EPT Preparedness and Response (P&R)
- USAID/Tanzania
- US CDC, Dar es Salaam, Tanzania

*Partnership in development

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts zoonotic disease surveillance for priority zoonotic diseases and other emerging threats. In Tanzania, PREDICT puts One Health in action by engaging animal and human health sectors from the national to district level in the collecting and testing of samples from wild animals and humans and in conducting behavioral risk

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investigations at high-risk interfaces for zoonotic disease transmission, identified by ministry partners as gaps in the national surveillance system. This work contributes to the development and implementation of the country GHSA roadmap and One Health Strategic Plan and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases, such as zoonotic influenza virus and Rift Valley Fever and other hemorrhagic fevers (Ebola, Marburg, etc.). In addition, PREDICT supports the development of Tanzania's One Health workforce from the national to district level through field and lab-based training and engagement of national staff, university and NGO partners, and students in surveillance and disease detection activities.

Where we work

Kibondo, Kigoma, Kigoma rural, and Uvinza Districts, Northwest Tanzania bordering Burundi, Moyowosi game reserve (wetland), and Gombe national park. Agriculture, livestock keeping (in free ranging practice), ecotourism, and fishing are commonly practiced in the area and non-human primates from Moyowosi game reserve and rodents frequently intrude into farms and cause crop destruction. Grazing livestock is also a common practice in the game reserve. Seasonal migratory fruits bats (*Eidolon helvum*) believed to originate from rain forests in the Democratic Republic of Congo have been observed roosting on the mango trees in the densely populated Kigoma town and frequently fly around at Ujiji municipal searching for fruit at night. There have been reported cases of dog bites and illegal hunting in villages surrounding the game reserve. Illegal hunting is believed to be exacerbated by presence of refugees fleeing violence in neighboring Burundi and DR Congo in Kibondo district. Moreover, Tanzania Ministry of Health communicated that this area reports more cases of fever of unknown origin than other areas of the country. PREDICT is targeting the villages in close proximity to the game reserve, park, and city municipal areas with high wildlife- livestock-human interaction. We are evaluating risk of zoonotic disease transmission through animal and human surveillance activities and behavioral risk investigations.

Kyerwa District, northern area of the Lake Zone bordering Uganda. This site is characterized by frequent transboundary movement of people and animals and is inhabited by agriculturalists and livestock keepers. *Rousettus aegypticus* fruit bats, a known reservoir for Marburg virus, are being sampled at a cave in Murongo village. Dogs in the area reportedly feed on this fruit bat species at night, and cases of dog bites and rabies are rampant. Rodents frequently raid farms and damage crops causing agricultural loses. Insectivorous bats have also been observed at numerous sites including schools, health centers, and homes, thereby exposing people to bat feces and urine. PREDICT is targeting the villages and bat roosting sites with high wildlife- livestock-human interaction and is evaluating risk of zoonotic disease transmission through animal and human surveillance activities and behavioral risk investigations.

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Zoonotic Disease Surveillance Sites

- **Kibondo, Kigoma, Kigoma rural, and Uvinza Districts**: Animal production, crop production, market and value chain, hunting
  - Sampling targets:
    - Wildlife: rodents, bats, and non-human primates in and around human dwellings and agricultural fields, and in and around protected areas where refugees and other community members dwell or pursue livelihood activities
    - People living and working in and around game reserves in Kibondo, an area in Kigoma with an increasing influx of refugees from neighboring Burundi and DR Congo where a pilot World Food Programme cash transfer project may be encouraging increased interaction between refugee and local populations and use of forested lands for livelihood and food security
    - Behavioral risk investigations of pastoralist and hunting communities surrounding game reserves to characterize zoonotic disease transmission risk
    - Syndromic surveillance of people with frequent exposure to wildlife presenting at the Ujiji Health Centre, which serves a densely populated urban area and surrounding rural communities in coordination with government partners

- **Kyerwa District**: Animal production, crop production, extractive industry
  - Sampling targets:
    - Wildlife: bats and rodents in forested areas and caves degraded by population growth, settlements, and movement of people and transboundary areas in coordination with government partners
    - Syndromic surveillance of people with frequent exposure to wildlife presenting at the Murongo Health Centre in coordination with government partners
    - Behavioral risk investigations to characterize zoonotic disease transmission risk

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Tanzania and is developing an integrated One Health laboratory network by engaging the animal health lab at the Sokoine University of Agriculture lab in Morogoro and the human health lab at the Ifakara Health Institute in Bagamoyo. SUA's lab, based at the College of Veterinary Medicine, is the primary training ground for technicians and professionals feeding the government laboratory network and provides critical referral services to the national animal health surveillance

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system. The IHI lab maintains strong linkages to the National Institute for Medical Research and the public health laboratory network and is integrated with the national surveillance system. At both labs, PREDICT strengthens capacity for detection of priority zoonotic diseases (e.g. zoonotic influenza viruses and VHFs – Ebola, Marburg, and Rift Valley Fever) and other viral threats and fosters coordination between human and animal sectors through joint training exercises and routine information exchanges, communication of data and findings to inform surveillance, and transfer of knowledge and capacity to other labs in the national system.

Animal lab(s): The Sokoine University of Agriculture (SUA) PREDICT lab with training and transfer of protocols to the Tanzania Veterinary Laboratory Agency (TVLA) lab in coordination with FAO

Human lab(s): Ifakara Health Institute (IHI), with training and transfer of protocols to the National Public Health Laboratory (NPHL) as appropriate

Workforce Development and Improving Real-time Surveillance

PREDICT provides training to strengthen One Health workforce capacity in Tanzania, as central, regional, and district ministry staff are engaged in zoonotic disease surveillance activities. PREDICT coordinates with ministry partners, especially the One Health Coordination Unit within the Livestock Ministry and the Ministry of Health, to strengthen national capacity for zoonotic disease surveillance, and directly bolsters capabilities of the animal health sector by training district veterinary officers in One Health skills and safe wildlife capture and sampling during targeted surveillance operations. PREDICT also works with EPT-2 and GHSA partners to strengthen data platforms and improve communications and linkages across animal and human sectors, as project data and findings on zoonotic diseases and enabling behaviors underlying transmission are shared and discussed. PREDICT will continue to serve as a resource for the development and operationalization of Tanzania's One Health Strategic Plan with government, university, and non-governmental organization partners. When requested by the government (and approved by the PREDICT Management Team) PREDICT also supports outbreak response and preparedness through field investigations, diagnostic testing, and epidemiological support.

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UGANDA
Year 4 (October 2017-September 2018)

Implementing Partners: University of California, Davis, Gorilla Doctors/ Mountain Gorilla Veterinary Project (MGVP), Inc.
Country Coordinator: Benard Jasper Ssebide, MGVP, Inc.
Global Points of Contact: Kirsten Gilardi and Michael Cranfield, UC Davis

Partners

- Bwindi Community Hospital, Buhoma, Kanungu
- Food and Agriculture Organization (FAO) of the United Nations, Uganda, Kampala
- Kagando Hospital, Kasese*
- Makerere University – Uganda Virus Research Institute Center of Excellence for Infection and Immunity (MUII)
- Makerere University Walter Reed Project (MUWRP), Kampala
- Makerere University, College of Veterinary Medicine Animal Resources and Biosecurity (COVAB), Kampala
- Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), Kampala
- Ministry of Health, Kampala
- Mutolere Catholic Hospital, Kisoro*
- National Animal Disease Diagnostics and Epidemiology Center (NADDEC), Entebbe
- National One Health Platform/One Health Technical Working Group
- Uganda National Task Force on Epidemic Preparedness and Response, Kampala
- Uganda Viral Research Institute (UVRI), Entebbe
- Uganda Wildlife Authority, Kampala
- Uganda Wildlife Veterinary Network*
- USAID EPT One Health Workforce
- USAID EPT Preparedness and Response
- USAID Mission Uganda, Kampala

*Partnership in development

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts surveillance for priority zoonotic diseases and other emerging threats. In Uganda, PREDICT puts One Health in action through zoonotic disease surveillance, sampling wildlife and people, and conducting behavioral risk investigations at high-risk human-animal transmission interfaces. This work directly supports the national surveillance system, contributes to the development and implementation of the country GHSA roadmap, and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases, such as zoonotic influenza and

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hemorrhagic fevers (Ebola, RVF, and Marburg). In addition, PREDICT supports the development of Uganda's One Health workforce from the national to district level through field and lab-based training and engagement of national staff, university and NGO partners, and students in surveillance and disease detection activities.

Where we work

Bwindi/Mgahinga Conservation Area (BMCA). Bwindi Impenetrable and Mgahinga Gorilla National Parks are biodiversity hotspots, with thousands of visitors coming from around the world to view habituated primates (mountain gorillas). This region is among the most densely populated in all of continental Africa, with human communities dependent on subsistence agriculture and commercial crop production (e.g. tea), utilizing land that directly abuts park boundaries. Bwindi was relatively recently annexed as a protected area by the government of Uganda, resulting in the migration of hunting-based communities out of the forest and into towns and villages at the park boundaries. As well, this site is on the international border with the Democratic Republic of Congo, with significant movement of Congolese into the region. Wildlife, including non-human primates, exit protected areas frequently to raid crops and enter human dwellings and public buildings (e.g., Bwindi Community Hospital where PREDICT is conducting syndromic surveillance activities). As well, bat populations in the greater BMCA are known carriers of Marburg virus, a priority zoonotic disease.

Queen Elizabeth Conservation Area (QECA). The QECA is a 1,978 km² UNESCO Man and Biosphere Reserve encompassing several national parks and wildlife reserves in the districts of Kasese, Rubirizi, Rukingiri, Kanungu, and Kamwenge in western Uganda. Fishing and salt extraction are primary sources of income for more than 20,000 people living in 11 settlements within the QECA, while the dense populations living just outside the QECA engage in cattle ranching and crop production. QECA is known for its diverse wildlife including many species of non-human primate. In addition to its popularity as a savannah wildlife tourism destination, bat cave tourism in the Maramagambo forest and chimpanzee tracking in the Kyambura Gorge and Kalinzu Forest are increasing. As well, the Uganda Wildlife Authority is developing a BSL 2+ laboratory in Queen Elizabeth National Park, which will bring in additional opportunities for research in diseases transmission dynamics at this human-wildlife interface.

Zoonotic Disease Surveillance Sites

- **Bwindi/Mgahinga Conservation Area in Kabale, Kisoro and Kanungu Districts**: Land conversion for commercialization
  - Sampling targets:

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    - Wildlife: bats and rodents in and around human settlements and areas of land conversion or disruption; human-habituated primates inside and outside park in contact with people and livestock
    - Syndromic surveillance of patients (including park workers) presenting to Bwindi Community Hospital and Ruhija, Byumba and Rubuguri Health Centers who report contact with wildlife
    - Behavioral risk investigations with people living adjacent to the park (human questionnaires only without biological sampling)

- **Queen Elizabeth Conservation Area:** Land conversion for commercialization, animal value chain
    - Sampling targets:
        - Wildlife: Non-human primates bats and rodents in and around human settlements and areas of land conversion or disruption; primates inside and outside park in contact with people and livestock
        - Syndromic surveillance of patients (including park workers) presenting to Kagando Hospital and associated community health centers who report contact with wildlife

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Uganda by engaging the Uganda Virus Research Institute (UVRI), a critical node for outbreak response and surveillance support, for both animal and human testing. Laboratory staff at UVRI are highly experienced in techniques required for zoonotic disease detection and are in communication with our global One Health laboratory network for technical assistance as needed. Through PREDICT capacity building, the Makerere University Walter Reed Project laboratory also maintains capacity to detect priority zoonotic diseases and emerging threats and train the animal health sector. In addition, PREDICT maintains a safe and secured biobank facility at the Makerere University College of Veterinary Animal Resources and Biosecurity (COVAB). In collaboration with EPT and government partners, PREDICT fosters communication and coordination between animal and human labs and ministries; provides joint training exercises and routine information exchanges among lab managers, technicians, and ministry focal points; communicates data and findings to inform surveillance; and works to transfer knowledge and disease detection capacity to other labs in the national system (e.g., the National Animal Disease Diagnostics and Epidemiology Center, Entebbe).

Animal labs: Uganda Virus Research Institute (UVRI), with potential training and transfer of protocols (in collaboration with EPT partners and FAO) to MAAIF's National Animal Disease Diagnostics and Epidemiology Center (NADDEC)

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Human lab: Uganda Virus Research Institute (UVRI)

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Uganda for national One Health focal points, government staff from national to subnational levels, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease surveillance, PREDICT strengthens Uganda's capacity to sample animals and people, investigate behaviors associated with zoonotic disease transmission, detect priority zoonotic diseases and emerging threats, and perform data analyses to understand zoonotic disease risks. In addition, PREDICT works across ministries and sectors helping to build and operationalize the national One Health platform and improve communications and linkages across animal and human sectors by sharing data and findings on zoonotic diseases and the enabling behaviors underlying transmission. PREDICT supports the National Task Force (when approved by PREDICT management team) for outbreak preparedness and response.

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BANGLADESH
Year 4 (October 2017-September 2018)

Implementing Partners: EcoHealth Alliance (EHA)
Country Coordinator: Ariful Islam, EcoHealth Alliance
Global Point of Contact: Jon Epstein, EcoHealth Alliance

Partners

- Bangladesh Forest Department (BFD)
- Chittagong Veterinary and Animal Science University (CVASU)
- Department of Livestock Services (DLS)
- Dhaka Medical College Hospital *
- Dinajpur Medical College Hospital *
- Faridpur Medical College Hospital *
- FAO-ECTAD
- Institute of Epidemiology, Disease Control and Research (IEDCR)
- International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b)

*Partnership in development

Plans subject to change as the budget is finalized; activities presented will be implemented as budget allows.

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts surveillance for priority zoonotic diseases and other emerging threats. In Bangladesh, PREDICT puts One Health in action through zoonotic disease surveillance, sampling of wildlife and people, and conducting behavioral risk investigations at high-risk human-animal transmission interfaces. This work directly supports the national surveillance system, contributes to the development and implementation of the country GHSA roadmap, and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases, such as highly pathogenic avian influenza, Nipah virus, and other emerging threats. In addition, PREDICT supports the development of Bangladesh's One Health workforce from the national to district levels through field and lab-based training and engagement of national staff, university and NGO partners, and students in surveillance and disease detection activities. In addition to One Health surveillance activities at targeted sites, PREDICT collects non-invasive rhesus macaque samples as part of a longitudinal investigation aimed at understanding how anthropogenic and domestic animal pressure on macaque populations affects likelihood of aggressive contact with people, along with individual animal viral load, viral shedding rates, and subsequent zoonotic disease transmission risks.

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Where we work

Madaripur is one of the locations in Bangladesh where macaques are protected. In recent years, the Government of Bangladesh (GoB) ceased feeding the macaques. People and livestock living in this area have regular and frequent contact with macaques here due, in part, to competition for food. The human-macaque contact at this site is often aggressive in nature. PREDICT behavioral risk investigations indicate that contact with macaques occurs frequently, making this an important site to investigate zoonotic disease transmission risks between wildlife, livestock, and people. PREDICT continues to conduct surveillance of urban wildlife and people along with in-depth behavioral risk investigations to characterize disease transmission risk at this important interface.

Dhaka. PREDICT zoonotic disease surveillance sites in the Dhaka districts were selected to understand how anthropogenic and domestic animal pressure on macaque populations affects likelihood of aggressive contact with people, viral load and viral shedding rates of individual animals, and subsequent zoonotic disease transmission risk to people. The urban site in Old Dhaka is a semi-private fenced-in factory lot where macaques are fed by staff, supporting a large troop of macaques in a populous area.

Danipur District is located at the border with India, where people move livestock across national boundaries. PREDICT sampling locations in this area were selected based on known livestock movement from India into Bangladesh. We are collaborating with FAO to identify specific market locations for concurrent sampling of wildlife and livestock around markets. Collectively, the team plans to also evaluate the feasibility of tracking livestock at cross-border markets.

Faridpur District in south-central Bangladesh is home to intensifying agriculture, livestock production, and homestead forests that include vast numbers of date palm, the sap of which is harvested and consumed and has been associated with multiple zoonotic disease outbreaks of Nipah virus. PREDICT is targeting bats and other wildlife in Faridpur for surveillance while exploring collaborations with the Government of Bangladesh and US CDC for syndromic surveillance of patients at the Faridpur Medical College Hospital.

Zoonotic Disease Surveillance Sites

- **Madaripur District**: Land Conversion Gradient (urban-rural gradient)
  - Sampling targets:
    - Wildlife: Rhesus macaques, bats, and rodents. Zoonotic disease surveillance at this site is a continuation of a "longitudinal" study;

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sampling will be conducted along the gradient at six sites within this region (including sites in Dhaka below)
- Community surveillance targeting people living in close contact with macaques and at local clinics/pharmacies
- Behavioral risk investigations of people with routine or occupational exposure to wildlife to characterize risk factors for disease transmission

- **Dhaka District**: Land Conversion Gradient & Intensification of Animal Production Systems
  - Sampling targets:
    - Wildlife: Rhesus macaques, bats, and rodents at urban sites along the urban to rural gradient as part of continuing longitudinal zoonotic disease surveillance of macaque and other urban wildlife populations
    - Livestock: Camels at the only known camel farm and seasonal camel market system in Bangladesh with sampling during the religious festival season annually in August and September
    - Behavioral risk investigations of people living in close contact with macaques, along with farm, market workers, and camel handlers
    - Syndromic surveillance at Dhaka Medical College Hospital, the catchment hospital for the region (includes patients from the Madaripur sites)

  - **Dinajpur District**: Livestock Trade (Animal Value Chain)Sampling targets:
    - Wildlife: Bats and rodents in and around livestock markets
    - Livestock: Cattle, goats, pigs, and buffalo (sampling by FAO)
    - Community surveillance of people working with/in livestock trading, including the traders, drivers, middle men, and others assisting with handling
    - If feasible, syndromic surveillance may be established at the District Hospital(s) at Dinajpur

- **Faridpur District**: Land-use Gradient (rural to urban; wildlife-human contact)
  - Sampling targets:
    - Wildlife: Bats and rodents in close contact with people involved in date palm sap harvest and consumption
    - If feasible, syndromic surveillance at the Faridpur Medical College Hospital (regional hospital that also serves Madaripur) of meningo-encephalitis patients in collaboration with GoB, ICDRRB, and US CDC; communication and coordination with ICDDRB and CDC to ensure synergy and not duplication of efforts in progress

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Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system in Bangladesh by engaging the International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b) and Institute of Epidemiology, Disease Control and Research (IEDCR, Ministry of Health and Family Welfare) labs for animal and human sample testing, respectively. Both the ICDDRB and IEDCR labs are critical nodes for outbreak response and surveillance support. In collaboration with FAO, PREDICT's icddr,b lab also works with GoB partners (Central Disease Investigation Laboratory of Department of Livestock Services and Bangladesh Livestock Research Institute Laboratory) to strengthen capacity for disease detection in the national animal health system. Laboratory staff at both icddr,b and IEDCR are highly experienced in techniques required for zoonotic disease detection, and are in communication with our global One Health laboratory network for technical assistance as needed. Together with EPT and government partners, PREDICT fosters communication and coordination between animal and human labs and ministries; provides joint training exercises and routine information exchanges among lab managers, technicians, and ministry focal points; communicates data and findings to inform surveillance; and works to transfer knowledge and disease detection capacity to other labs in the national system.

Animal lab(s): icddr,b (virology laboratory), Central Disease Investigation Laboratory (CDIL) of Department of Livestock Services (DLS), and Bangladesh Livestock Research Institute Laboratory (BLRI)

Human lab(s): IEDCR (virology laboratory)

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Bangladesh for government staff from national to subnational levels, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease surveillance, PREDICT strengthens Bangladesh's capacity to sample animals and people, investigate behaviors associated with zoonotic disease transmission, detect priority zoonotic diseases and emerging threats, and perform data analyses to understand zoonotic disease risks. Staff from the Bangladesh Forest Department are involved in field surveillance activities and will continue to be engaged to ensure the successful operationalization of the One Health approach. PREDICT works across ministries and sectors, helping to build and operationalize the national One Health platform through the One Health Secretariat, improve communications and linkages across animal and human sectors by sharing data and findings on zoonotic diseases and the enabling behaviors underlying transmission, and support the Government of Bangladesh

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(when approved by PREDICT management team) for outbreak preparedness and response.

This year, as part of global efforts to validate One Health approaches through the development of an evidence base and case studies that inform policies for risk reduction, a One Health Economics Fellow based at IEDCR will examine economic impacts of past and prospective emerging infectious disease events in Bangladesh by assessing effects on different sectors and examining resource flows. This project seeks to determine how to optimally allocate resources to address pandemic threats, whether devising strategies to mitigate the underlying causes or providing the necessary knowledge for individuals, businesses, and society as a whole, to minimize economic damages in the event of a pandemic.

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INDIA
Year 4 (October 2017-September 2018)

Implementing Partners: EcoHealth Alliance (EHA), Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPIMS)
Country Coordinator: Dr. Rajesh Bhatia, EHA
Global Point of Contact: Jon Epstein, EcoHealth Alliance

Partners

- Food and Agricultural Organization of the United Nations
- Forest and Wildlife Department, Government of Uttar Pradesh (UP), Lucknow
- *Indian Veterinary Research Institute, Izatnagar, UP
- Ministry of Environment, Forest and Climate Change, Government of India, New Delhi
- *National Institute of High Security Animal Diseases, Bhopal, Madhya Pradesh
- *National Institute of Virology, Pune, Maharashtra
- *Society for Advancement of Villagers Education & Rural Assistance, Kushinagar, UP
- UP Pt. Deen Dayal Upadhyaya Pashu Chikitsa Vigyan Vishwavidyalaya Evam Go-Anusandham Sansthan, Mathura, UP
- USAID EPT One Health Workforce
- USAID/India
- Wildlife Institute of India, Dehradun, Uttarakhand

*Partnership in development

Plans subject to change as the budget is finalized; activities presented will be implemented as budget allows.

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts surveillance for priority zoonotic diseases and other emerging threats. In India, PREDICT puts One Health in action through zoonotic disease surveillance by sampling wildlife and people and conducting behavioral risk investigations at high-risk human-animal transmission interfaces. This work directly supports the national surveillance system and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases. In addition, PREDICT supports the development of India's One Health workforce through field and lab-based training and engagement of national staff, university and NGO partners, and students in surveillance and disease detection activities.

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Where we work

Maharajganj District is located in the state of Uttar Pradesh in northern India and shares its northern border with Nepal, an area with frequent transboundary livestock movement. In Maharajganj, PREDICT zoonotic disease surveillance focuses on two sites with impoverished frontier villages where people, wildlife, and domestic animals live in close association, presenting opportunities for zoonotic disease transmission and spread. Nichlaul and Bhabnauli are rural, mostly agrarian areas within a matrix of highly disturbed forest fragments that harbor key taxonomic groups for viral spillover and spread, including macaques, bats, and rodents, which commonly live in and around villages.

Zoonotic Disease Surveillance Sites

- **Nichlaul**
  - Sampling targets:
    - Wildlife: Rodents, rhesus macaques, and bats in frequent contact with both macaques and people
    - Livestock: sampling limited to village-based domestic animals, if warranted, during community surveillance activities
    - Community surveillance of people working within livestock trade (traders, drivers, middle men, and others assisting with handling)
    - Syndromic surveillance of patients living in close contact with wildlife and presenting at local clinics close to sampling sites
    - Syndromic surveillance of patients presenting with severe acute respiratory disease (SARI), encephalitis of unknown origin and hemorrhagic fevers, and admitted to the Community Health Centre and the district hospital

- **Bhabnauli**
  - Sampling targets:
    - Wildlife: Rodents, rhesus macaques, and bats in frequent contact with both macaques and people
    - Livestock: sampling limited to village-based domestic animals, if warranted, during community surveillance activities
    - Community surveillance of people working within livestock trade (traders, drivers, middle men, and others assisting with handling)
    - Syndromic surveillance of patients living in close contact with wildlife and presenting at local clinics close to sampling sites
    - Syndromic surveillance of patients presenting with severe acute respiratory disease (SARI), encephalitis of unknown origin and hemorrhagic fevers, and admitted to the Community Health Centre and the district hospital

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Strengthening Laboratory Systems

PREDICT supports the national laboratory system in India by engaging the Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPIMS) for both animal and human testing. Laboratory staff at SGPIMS are highly experienced in techniques required for zoonotic disease detection and are in communication with our global One Health laboratory network for technical assistance as needed. PREDICT is currently formalizing linkages with national reference labs including the diagnostic labs at National Institute of Virology (NIV) and Indian Veterinary Research Institute (IVRI) to provide further characterization of project samples. In collaboration with EPT and government partners, PREDICT also fosters communication and coordination between animal and human labs and ministries; provides joint training exercises and routine information exchanges among lab managers, technicians, and ministry focal points; communicates data and findings to inform surveillance; and works to transfer knowledge and disease detection capacity to other labs in the national system.

Animal and human lab: Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPIMS)

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in India for professional staff from human health, livestock health, and wildlife agencies at federal and state levels, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease surveillance, PREDICT strengthens India's capacity to sample animals and people, investigate behaviors associated with zoonotic disease transmission, detect priority zoonotic diseases and emerging threats, and perform data analyses to understand zoonotic disease risks. In addition, PREDICT works across ministries and sectors, helping to build and operationalize the national One Health platform, improve communications and linkages across animal and human sectors by sharing data and findings on zoonotic diseases and the enabling behaviors underlying transmission, and support the Government of India across federal and state levels (when approved by PREDICT management team) for outbreak preparedness and response.

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INDONESIA
Year 4 (October 2017-September 2018)

Implementing Partners: EcoHealth Alliance (EHA) with the Primate Research Center of the Institut Pertanian Bogor (PRC-IPB) and Eijkman Institute for Molecular Biology (EIMB)
Country Coordinator: Dr. Joko Pamungkas, PRC-IPB
Global Point of Contact: Dr. Kevin Olival, EHA

Partners

- Animal Disease Investigation Center at Maros, South Sulawesi Province, at Denpasar, Bali Province, and at Banjarbaru, South Kalimantan Province
- FAO ECTAD Indonesia
- Gorontalo State University, Gorontalo
- Kawangkoan Primary Health Clinic (Puskesmas Kawangkoan), Minahasa District, North Sulawesi
- Local offices of Livestock and Animal Health Services at Southeast Sulawesi Province (both provincial and district levels)
- Local offices of Livestock and Animal Health Services at West Sulawesi Province (both provincial and district levels)
- Minahasa District Health Office (Dinas Kesehatan Kabupaten Minahasa)
- Ministry of Agriculture
- Ministry of Environment and Forestry
- Ministry of Health, National Institute of Health Research and Development
- Noongan Hospital (Rumah Sakit Umum Daerah Noongan), Minahasa District, North Sulawesi
- Provincial Health Office in North Sulawesi and Gorontalo Provinces (Dinas Kesehatan Provinsi Sulawesi Utara dan Gorontalo)
- Sam Ratulangi University, Manado, North Sulawesi
- USAID EPT-2 One Health Workforce
- USAID EPT-2 Preparedness and Response
- USAID-Indonesia

Plans subject to change as the budget is finalized; activities presented will be implemented as budget allows.

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts surveillance for priority zoonotic diseases and other emerging threats. In Indonesia, PREDICT puts One Health in action through zoonotic disease surveillance by sampling wildlife and people and conducting behavioral risk investigations at high-risk human-animal transmission interfaces. This work directly supports the national surveillance system and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases. In addition, PREDICT supports the

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development of Indonesia's One Health workforce from the national to district levels through field and lab-based training and engagement of national staff, university and NGO partners, and students in surveillance and disease detection activities.

Where we work

Indonesia is a vast and ecologically diverse country and a global biodiversity hotspot. PREDICT activities are centered at several sites on **the Island of Sulawesi**, the fourth largest island in Indonesia. While considered only one of many high-risk areas in Indonesia, Sulawesi is an important site for the wildlife trade and is undergoing rapid land conversion and exploitation of its local fauna. PREDICT surveillance sites in North Sulawesi and Gorontalo provinces were targeted to capture high-risk animal-human interfaces along the wildlife value chain pathway of zoonotic disease emergence, as bats, rodents, non-human primates, and other species are extensively traded for food across this region. These sites capture different stages of the wildlife value chain, from wild source populations of animals, to hunters and middle men, to urban wildlife markets. At these sites, PREDICT conducts concurrent zoonotic disease surveillance of wildlife, domestic animals (in collaboration with FAO-ECTAD partners) and people along with behavioral risk investigations in communities, such as the North Sulawesi markets where live and butchered wildlife are sold for human consumption and from rural and other sites where wildlife hunting and trading from source populations is occurring. Concurrent sampling of domestic animals by FAO-ECTAD overlaps with PREDICT surveillance in Gorontalo, North Sulawesi, and West Sulawesi, though not in the same geographic areas. Finally, PREDICT plans to conduct syndromic surveillance of patients with acute febrile and respiratory illness in local hospitals and clinics within a catchment area that overlaps with animal surveillance activities.

Zoonotic Disease Surveillance Sites

- **North Sulawesi and Gorontalo provinces**: wildlife trade
  - Sampling targets:
    - Wildlife: wild animals captured for trade and human consumption, primarily bats and rodents with opportunistic sampling of macaques in markets when available
    - FAO-led sampling of domestic animals with PREDICT-assisted testing at regional Disease Investigation Center (Maros, Denpasar, and Banjarbaru)
    - Syndromic surveillance of patients with acute febrile and respiratory illness at Noongan Hospital (Rumah Sakit Umum Daerah Noongan) and the Kawangkoan Primary Health Care Center (Puskesmas Kawangkoan)

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    - Behavioral risk investigations with healthy individuals that have occupational exposure from working with wildlife and livestock
    - Community surveillance of people at high-risk interfaces

- **West Sulawesi, Majene**: wildlife trade
    - Sampling targets:
        - Wildlife: wild animals, primarily bats captured for trade and human consumption and rodents in and around dwellings, fields, or other areas with likely contact with people
        - Behavioral risk investigations with individuals involved in wildlife trade
        - FAO-led sampling of domestic animals with PREDICT-assisted testing at regional Disease Investigation Center (Maros, Denpasar, and Banjarbaru)

- **Southeast Sulawesi, South Konawe**: wildlife trade
    - Sampling targets:
        - Wildlife: wild animals, primarily bats captured for trade and human consumption and rodents in and around dwellings, fields, or other areas with likely contact with people
        - Behavioral risk investigations with individuals involved in wildlife trade

Strengthening Laboratory Systems

PREDICT supports the development of the national laboratory system and One Health laboratory network in Indonesia by engaging the Primate Research Center at Institut Pertanian Bogor as the primary laboratory for wildlife sample testing and the Eijkman Institute for Molecular Biology for human testing. Both labs provide critical support to the national surveillance and outbreak response system, and laboratory staff are highly experienced in techniques required for zoonotic disease detection, including detection of emerging viral threats, and maintain capability to conduct additional tests for other viral panels and serological assays upon request and as budget allows. Through this network, and in collaboration with FAO, PREDICT provides training in biosafety and zoonotic disease detection to local laboratory staff and strengthens the laboratory capacity of the Ministry of Agriculture's Animal Disease Investigation Center (DIC), especially at Maros, Denpasar, and Banjarbaru, where PREDICT techniques are actively engaged in livestock and domestic animal surveillance. PREDICT, in collaboration with EPT and government partners, also fosters communication and coordination between animal and human labs and ministries; provides joint training exercises and routine information exchanges among lab managers, technicians, and ministry focal points from national to subnational levels; communicates data and findings to

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inform surveillance; and works to transfer knowledge and disease detection capacity to other labs in the national system (e.g., the DICs).

Animal lab(s): Primate Research Center at Institut Pertanian Bogor, Bogor with support (in collaboration with FAO) to the Ministry of Agriculture's Animal Disease Investigation Centers (DICs)

Human lab (s): Eijkman Institute for Molecular Biology (EIMB), Jakarta

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Indonesia for government staff from national to subnational levels, including individuals from the Ministry of Environment and Forestry, Ministry of Health, and Ministry of Agriculture, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease surveillance, PREDICT strengthens Indonesia's capacity to sample animals and people, investigate behaviors associated with zoonotic disease transmission, detect priority zoonotic diseases and emerging threats, and perform data analyses to understand zoonotic disease risks. This year, PREDICT plans to conduct a workshop on safe wildlife sampling for veterinarians and/or veterinary paramedics who work in the Ministry of Environment and Forestry. The workshop will be organized in coordination with USAID-Indonesia's PRESTASI program and will include a hands-on training for the collection of specimens from bats and rodents in the field. Additional on-site trainings on biosafety and biosecurity, zoonotic disease detection, and bioinformatics analysis are planned with government and medical faculty and staff from laboratories in the region, and a collaborative workshop in disease risk mapping is being planned with FAO partners to support Kemenko PMK's developing risk analytic and mapping capabilities.

PREDICT works across ministries and sectors, helping to build and operationalize the national One Health platform, and improves communications and linkages across animal and human sectors through data sharing and communications on zoonotic diseases and the enabling behaviors underlying transmission. When approval by the Government of Indonesia authorities is obtained, PREDICT findings are disseminated to all other relevant partners. PREDICT also works closely with EPT's P&R and the Coordination Ministry for Human Development and Cultural Affairs (Kemenko PMK) to support activities with local government agencies in North Sulawesi. In addition, PREDICT supports the Government of Indonesia as requested (when approved by PREDICT management team) in outbreak preparedness and response.

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VIET NAM
Year 4 (October 2017-September 2018)

Implementing Partners: Wildlife Conservation Society (WCS)
Country Coordinator: Nguyen Thi Thanh Nga, WCS; Nguyen Van Long, WCS
Global Point of Contact: Amanda Fine, WCS

Partners

- Cat Ba Langur Conservation Program, Cat Ba National Park
- Department of Animal Health (DAH), Ministry of Agriculture and Rural Development (MARD)
- Hanoi School of Public Health (HSPH)
- National Institute of Hygiene and Epidemiology (NIHE), Ministry of Health (MoH)
- Oxford University Clinical Research Unit (OUCRU)
- Pasteur Institute Ho Chi Minh City (PI-HCMC)
- Regional Animal Health Office No. 6 (RAHO6) and Regional Animal Health Office No. 7 (RAHO7), DAH
- Save Vietnam's Wildlife (SVW) and Endangered Primate Rescue Center (EPRC), Turtle Conservation Center (TCC), Cuc Phuong National Park
- The Carnivore and Pangolin Conservation Program, Cuc Phuong National Park
- Viet Nam National University of Agriculture (VNUA), Ministry of Agriculture and Rural Development (MARD)

Plans subject to change as the budget is finalized; activities presented will be implemented as budget allows.

Prevent and Detect Zoonotic Disease

PREDICT builds the workforce, strengthens systems, and conducts surveillance for priority zoonotic diseases and other emerging threats. In Viet Nam, PREDICT puts One Health in action through zoonotic disease surveillance by sampling wildlife and people and conducting behavioral risk investigations at high-risk human-animal transmission interfaces. This work directly supports the national surveillance system, contributes to the development and implementation of the country GHSA roadmap, and provides opportunities to strengthen mechanisms for responding to priority zoonotic diseases. In addition, PREDICT supports the development of Viet Nam's One Health workforce from the national to district levels through field and lab-based training and engagement of national staff, university and NGO partners, and students in surveillance and disease detection activities. This year, PREDICT is continuing to evaluate opportunities for expansion of in-depth targeted and longitudinal zoonotic disease surveillance in animal and human populations.

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Where we work

Dong Nai Province, South Viet Nam near Ho Chi Minh City: A high number of wildlife farms are located in Dong Nai Province. The wildlife farms are stocked with wild animals sourced from captive and wild populations. Government agencies, including the Provincial Forest Protection Department and Sub-Department of Animal Health, support PREDICT's surveillance activities in the wildlife farms and adjacent domestic animal farms. Zoonotic disease surveillance and testing is beyond the mandate of these agencies, and PREDICT has prioritized wildlife farms and nearby livestock for surveillance activities due to the close and frequent human-wildlife contact.

Bac Giang/Lang Son Province, in Northern Viet Nam: Bac Giang/Lang Son is a large cave that provides roosting habitat to migratory bats. The guano produced by the bats is collected by individuals to use as plant fertilizer. Inside the cave, the bat guano harvesters and cave owners are exposed to overhead droppings and regularly walk through piles of feces with bare feet. PREDICT is investigating zoonotic disease spillover risk at this natural site and at constructed bat guano farms where bat guano is collected and harvested by hand (Dong Thap Province). Through in-depth behavioral risk investigations, PREDICT has characterized the guano collection process and identified the roles of individuals within the value chain. Subsequently, we confirmed guano collection, as well as adjacent domestic animal holdings, as priorities for human, bat, and domestic animal surveillance activities.

Ha Noi Metropolitan Area: Ha Noi, population 7.7 million people, is located on an important wildlife trafficking route in Southeast Asia and is an urban site for the field rat market trade (Animal Value Chain) with numerous people engaging in these activities. Domestic animals also move through the same markets and restaurants. PREDICT has confirmed Ha Noi as a priority for human, domestic animal, and wildlife surveillance activities and is planning to conduct surveillance on trafficked animals, as well as rodents, which have been listed as high-risk taxa for zoonotic pathogens.

Quang Ninh Province (LISN site): Quang Ninh is an international border crossing between Viet Nam and China for wildlife trafficking and other cross-border trade (Animal Value Chain) activities for wild and domestic animals. This is one of two sites where PREDICT is closely coordinating with the LISN project for joint surveillance activities.

Dong Thap Province (LISN site): Dong Thap shares a border with Cambodia and is a province with established bat guano production/use (Intensification of Animal Production Systems) and field rat trade activities (Animal Value Chain). In this region, bat guano production involves use of man-made bat roost structures, which can sit in close proximity to intensive livestock production operations. This

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is the second of two sites where PREDICT is closely coordinating with the LISN project for joint surveillance activities.

Opportunistic confiscation locations in the wildlife trade (multiple provinces): The illegal wildlife trade or wildlife trafficking (Animal Value Chain) is an important interface zoonotic disease surveillance. PREDICT has established relationships with partners with knowledge of confiscation events, which may involve a variety of wild animal taxa at destination, source, or transit sites throughout the country. Therefore, as opportunities are available and feasible, our teams conduct surveillance activities on confiscated wildlife and with humans exposed to wildlife in the trade.

Zoonotic Disease Surveillance Sites

- **Dong Nai Province, South Viet Nam near Ho Chi Minh City:** Wildlife farms (Animal Value Chain/Intensification of Animal Production Systems)
  - Sampling targets:
    - Farmed wildlife: rodents, carnivores, ungulates, non-human primates, birds, etc. present on wildlife farms and moving through the trade in urban and peri-urban sites. Focus on rodents and non-human primates and additional taxa as funds allow
    - Livestock: swine and poultry in close proximity to wildlife farms; sampling and testing by FAO
    - Community surveillance of people with occupational risk working on or near wildlife farms (caretakers, animal handlers)
    - Syndromic surveillance of patients presenting in local health clinics and hospitals with febrile illnesses in Dong Nai Province

- **Bac Giang/Lang Son Province, in Northern Viet Nam:** Bat guano production/use (Intensification of Animal Production Systems)
  - Sampling targets (as budget allows):
    - Wildlife: insectivorous bats using limestone karst caves near villages with livestock production facilities
    - Livestock: poultry and pigs on farms in close proximity to bat guano collection caves; sampling and testing by FAO. Additional livestock species in close proximity to bat guano collection caves as funds allow.
    - Community surveillance of people in close contact with bats and engaged in bat guano production
    - Syndromic surveillance of patients presenting in local health clinics and hospitals with febrile illnesses

- **Ha Noi Metropolitan Area:** Wildlife trafficking and field rat market trade (Animal Value Chain)
  - Sampling targets (as budget allows):

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  - Traded wildlife: Wildlife present in restaurants and sold live in markets with a focus on rodents. Sampling/testing of carnivores, ungulates, pangolins, non-human primates, and birds as funds allow
  - Livestock: domestic species traded with wildlife through the same markets/restaurants and trade routes; sampling and testing by FAO
  - Community surveillance of people in close contact or with frequent exposure to wildlife
  - Syndromic surveillance of patients presenting in local health clinics and hospitals with febrile illnesses

- **Quang Ninh Province, International border crossings between Viet Nam and China (LISN site - PREDICT as technical laboratory partner only):** Wildlife trafficking & cross-border trade (Animal Value Chain)
  - Sampling targets:
    - Wildlife: PREDICT will provide outbreak response support if requested by the Government of Viet Nam
    - Livestock: swine and poultry in close proximity or sharing trade routes with wildlife; all sampling and testing by FAO
    - Syndromic surveillance of patients presenting in local health clinics and hospitals with severe acute respiratory illness (SARI); all sample collection and testing by WHO
    - Community surveillance of people in close contact or with frequent exposure to wildlife by LISN/PREDICT as funds allow

- **Dong Thap Province, sharing border with Cambodia (LISN site – PREDICT as technical laboratory partner and leading bat and rodent surveillance):** Bat guano production/use (Intensification of Animal Production Systems) and field rat market trade (Animal Value Chain)
  - Sampling targets:
    - Wildlife: insectivorous bats using artificial roost structures (bat guano farms) erected in villages near intensive livestock production facilities and markets; and field rats in trade or for sale in live markets/restaurants
    - Livestock: swine and poultry in close proximity to artificial roost structures and local markets and restaurants where live rats are sold; all sampling and testing by FAO
    - Syndromic surveillance of patients presenting in local health clinics and hospitals with febrile illnesses and SARI; all sample collection and testing by WHO
    - Community surveillance of people in close contact with bats and rats, such as engaging in bat guano production and in rodent hunting, trade, and sale by LISN/PREDICT as funds allow

- **Potential provinces with opportunistic confiscation locations:** Wildlife trafficking (Animal Value Chain)
  - Sampling targets (as budget allows):

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- Wildlife: confiscated/rescued wildlife moving through the wildlife trade. Focus on pangolins (target 300+ individuals) and additional sampling of rodents, carnivores, ungulates, non-human primates, birds, etc. moving through the trade (markets, restaurants, wildlife farms, and in transit) in urban and peri-urban sites as well as national border crossings as funds allow.

Strengthening Laboratory Systems

PREDICT directly supports the national laboratory system and development of an integrated One Health disease detection network in Viet Nam by engaging two animal health labs, RAHO6 (national diagnostic lab) and the Viet Nam National University of Agriculture (VNUA) lab, and two public health labs, the National Institute of Hygiene and Epidemiology (NIHE) and National Influenza Center of the Pasteur Institute of Ho Chi Minh City (PI HCMH). Through PREDICT, both RAHO6 and VNUA labs have capacity to detect priority zoonotic diseases and other emerging threats. In addition, PREDICT plans to strengthen disease detection capacity at another Department of Animal Health Lab, RAHO7, located in Dong Thap Province in the Mekong Delta region of southern Viet Nam, where PREDICT is conducting surveillance activities. For human sample testing, the NIHE lab is also capable of detecting priority zoonotic diseases, and PREDICT is working with the PI HCMH to facilitate testing of human samples collected in Dong Thap province through the LISN initiative. In collaboration with EPT and government partners, PREDICT's lab network fosters communication and coordination between animal and human labs and ministries; provides joint training exercises and routine information exchanges among lab managers, technicians, and ministry focal points; communicates data and findings to inform surveillance; and works to transfer knowledge and disease detection capacity to other labs in the national system.

Animal labs: Livestock and wildlife: Regional Animal Health Office No. 6 & 7 (RAHO6, RAHO7) - Department of Animal Health; Viet Nam National University of Agriculture (VNUA)

Human labs: National Institute of Hygiene and Epidemiology (NIHE) and Pasteur Institute Ho Chi Minh City (PI HCMC)

Workforce Development and Improving Real-time Surveillance

PREDICT provides critical hands-on and on-the-job training to strengthen One Health workforce capacity in Viet Nam for government staff from national to subnational levels, university staff and students, research institutes, and local communities. By providing opportunities to put One Health in action across the full spectrum of skills required for safe and effective zoonotic disease

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surveillance, PREDICT strengthens Viet Nam's capacity to sample animals and people, investigate behaviors associated with zoonotic disease transmission, detect priority zoonotic diseases and emerging threats, and perform data analyses to understand zoonotic disease risks. Through our work, PREDICT also promotes training and education with all stakeholders regarding the potential role of wildlife trade and consumption as a driver of zoonotic disease emergence. In addition, PREDICT works across ministries and sectors, helping to build and operationalize the national One Health platform, and improves communications and linkages across animal and human sectors by sharing data and findings on zoonotic diseases and the enabling behaviors underlying transmission. PREDICT also supports the Government of Viet Nam (when approved by PREDICT management team) for outbreak preparedness and response for potential zoonotic disease in wildlife and for human outbreaks in which wildlife involvement is suspected.

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From:	Cara Chrisman <cchrisman@usaid.gov>
To:	Jonna Mazet <jkmazet@ucdavis.edu>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>;Peter Daszak <daszak@ecohealthalliance.org>;Brooke Watson <watson@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>
CC:	Dennis Carroll <dcarroll@usaid.gov>
Sent:	9/20/2017 8:23:56 PM
Subject:	9/21 GVP Call Agenda

Hi All,

Looking forward to speaking with many of you tomorrow at 10am/1pm to catch up regarding the GVP. I believe Eri will not be available, but looking forward to speaking with those people who will be able to join.

Please see below for the call agenda.

Best,
Cara

- Outreach - Readouts & Next Steps
  - China
  - Hong Kong
  - BioHub
  - Vulcan
  - Vancouver
- Consultants
  - Next steps (see BCG proposal attached)
- NGO
  - Next steps
- If time:
  - Additional planned outreach (GISAID, Ottawa, etc.)
  - WHO Bulletin feedback and next steps
  - PMAC Launch

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
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BCG

USAID

Global Virome Project
Potential Options for BCG Support

August 31, 2017

THE BOSTON CONSULTING GROUP

Our understanding of GVP and desired support

Recognizing the risk of new viral diseases spilling over from animals to humans, GVP is aiming to map ~85% of the global viriome in three phases over 10 years

USAID's PREDICT project is proof of concept that a larger scale effort could be feasible

The intended structure for GVP is a not-for-profit NGO, with a central hub that consolidates data and coordinates efforts among a federation of national projects and other contributors

GVP will comprise "one part science, and one part social engineering"

- Program will require "big science" approach to gathering and analyzing data from disparate sources
- Also requires change in mind set among global stakeholders to make data-driven investment in potential vs. current threats

Operating model must reflect complexity of coordination across multiple stakeholders, will need to adapt over time as stakeholder interests are expected to evolve as data is gathered

A number of stakeholders have been engaged across sectors

- Scientific community has shown intellectual enthusiasm and shared positive feedback
- Potential public and private sector funders have expressed interest in concept, but have not committed to invest

GVP hopes to launch in January 2018 at the Prince Mahidol Awards Conference; ideally this would include announcement of an anchor funder, but a softer launch may be acceptable

GVP's most pressing needs for support lie in three areas

- Building an investment case that includes an articulation of incremental value delivered over time
- Defining an organizational structure and governance model for the hub
- Creating a resource mobilization plan, and particularly identifying anchor funder(s) for the hub

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An experienced senior team will lead this engagement



Trish and Wendy will lead the team, supported by Andrew, Shalini and Josh. We will also engage Gabrielle Fitzgerald of Penarama who is a BCG subcontractor and resource mobilization expert

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Our proposed support model includes three modules



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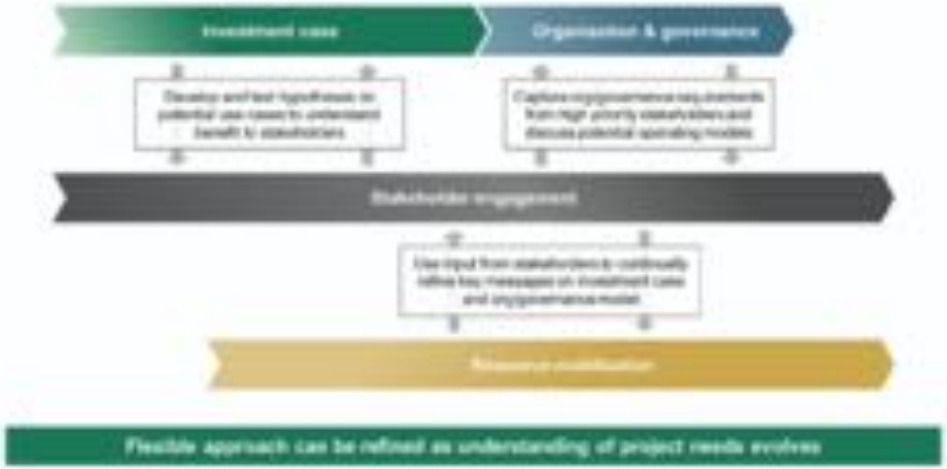
Stakeholder engagement will run throughout the project to ensure buy-in from likely funders and key contributors



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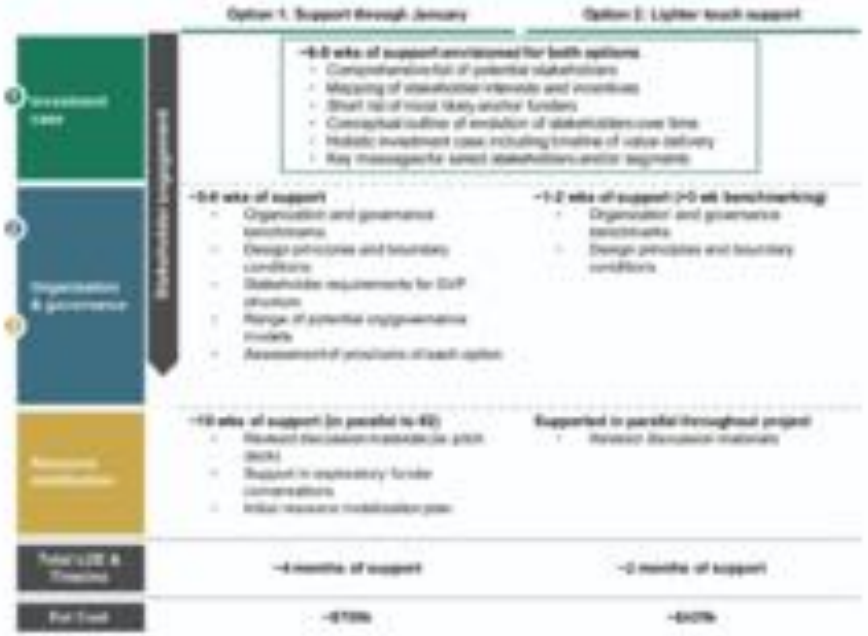
Support would ideally run through planned announcement; scaled back option focuses on investment case



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Workstream details: Investment case

Investment case

Approach

- Interview key QVP participants to understand how incremental value can be delivered over time
- Identify wide range of potential stakeholders across public and private sector
- Create framework to segment stakeholders within each sector
- Develop hypotheses on potential use cases for QVP data for each stakeholder segment
- Conduct stakeholder interviews to test
  - Interest and appetite to play a role in QVP
  - Hypotheses on use cases and expected benefits
  - Concerns and barriers to participation
- Develop short list of most likely anchor funders
- Synthesize interview findings in map of stakeholder interests and incentives
- Outline potential evolution of stakeholder constellation over time
- Document holistic investment case that tells compelling story of value creation over time

Deliverables

- **Craft customized messaging of value to stakeholders** and/or segments
- Articulation of interests and incentives by stakeholder or stakeholder segment
- Short list of most likely anchor funders
- Conceptual outline of potential evolution of stakeholders over time
- Holistic investment case including timeline of value delivery
- Key messages for select stakeholders and/or segments

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Backup: Sample output for stakeholder mapping

A wide range of stakeholders should be explored and grouped into logical segments



Initial segmentation then informs further analysis

Prioritization of segments and individual stakeholders

Engagement with priority stakeholders to identify interests and incentives

Identification of short list of likely near-term funders

Outline of potential longer-term evolution of stakeholder involvement

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Workstream details: Organization and governance



Note: Activities and deliverables in italicized text included only in full support option

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Backup: Sample output of organization benchmarking

Benchmark profiles created for analogous organizations…



…and findings synthesized as implications/guidance



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Workstream details: Resource mobilization

Resource mobilization

Approach

- Partner with external resource mobilization/advocacy expert Gabrielle Fitzgerald to align near term resource mobilization strategy with needs of high priority stakeholders
- Revise pitch deck into tailored set of discussion materials to reflect holistic investment case, intended organization and governance structure, and key messages for likely funders
- Support exploratory conversations with short list of potential anchor funders to discuss desired role in organization, willingness/ability to invest, and remaining issues to be addressed
- Outline high level plan for additional resource mobilization beyond anchor funding, including
  - Near term fundraising goals for short-listed funders
  - Typologies of stakeholders to engage as funding needs grow/evolve
  - Plays to engage additional funders
  - Targeted messages to align with specific stakeholder interests/concerns

Deliverables

- Revised discussion materials for conversations with potential anchor funders
- Support for exploratory conversations with potential funders
- High level resource mobilization plan

Note: Activities and deliverables in dashed text included only in full support option

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BCG is uniquely suited to support this work

Select examples of BCG Global Health experience

Forming new entities and providing support on key design decisions	– Supported establishment of Coalition for Epidemic Preparedness Initiative (CEPI) – Led implementation planning to support launch of MedicInnovate Malaria Venture – Developed operating model for new global humanitarian fund (hosted by UNICEF)
Identifying key benefits and articulating a compelling investment case	– Defined human, social, and financial impact of potential malaria vaccine for the Malaria Vaccine Initiative – Assessed ROI of preparedness initiatives in three countries for WHP
Designing organization structure and optimizing governance models	– Led 18-month transformation of the Global Fund's operating and governance model in response to 2011 crisis – Identified governance best practices for implementation at Yunus Social Business
Engaging stakeholders to understand concerns and align incentives	– Defined partner roles and responsibilities for Roll Back Malaria Partnership – Engaged range of stakeholders to re-align incentives and improve WHO's regulatory structure for vector control
Developing strategies for advocacy and resource mobilization	– Created resource mobilization strategy and estimated funding requirements for Global Malaria Action Plan (GMAP) – Designed integrated multi-disease advocacy strategy for global foundation

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Detailed view: Select examples of BCG experience



- Supported CEPI in defining its investment strategy to deploy resources for vaccine development against initial set of target diseases (Lassa, Nipah, MERS, Ebola)
- Designed a revised governance structure including public and private participation
- Supporting FIND - CEPI partnership, "CEPI-Dx" to develop a joint strategy for diagnostics

- Redefined Global Fund's business model to better utilize strategic investments, and simplified business processes to improve efficiency of funding and monitoring activities
- Designed a new risk framework to customize grant making and other management processes based on risk levels

- Led business and financial planning effort, including development of operational and governance models and detailed project pipeline
- Evaluated portfolio funding strategy and analyzed alternative, innovative funding opportunities (e.g., co-investment and social venture capital)

- Diagnosed and mapped roles and responsibilities of partnership as a whole, and of the board, secretariat, partners, etc.
- Benchmarked other global health partnerships and shared key design principles

- Provided direct support to UN Mission during Ebola outbreak in 2014/5
- Included strategy, planning, program management and stakeholder alignment during initial set up and early deployment of the mission

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Thank you

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From: Cara Chrisman <cchrisman@usaid.gov>
To: Eri Togami <etogami@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Dennis Carroll <dcarroll@usaid.gov>
Sent: 9/25/2017 6:06:34 PM
Subject: Re: PMAC 2018 GVP concept note

Hi Eri,

Thanks for checking. I think it would be okay to continue with the same corresponding authors. Might actually be better with me possibly out when they respond and Dennis on the review committee!

Best,
Cara

Sent from my iPhone

On Sep 25, 2017, at 2:04 PM, Eri Togami <etogami@ucdavis.edu> wrote:

Hi Cara,

That sounds great, thank you. Would it be better to change the corresponding members to you and Dennis?

I hope you are well,
Eri

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Thursday, September 21, 2017 3:00 PM
To: Eri Togami <etogami@ucdavis.edu>; Jonna Mazet <jkmazet@ucdavis.edu>; Dennis Carroll <dcarroll@usaid.gov>
Subject: Re: PMAC 2018 GVP concept note

Hi Eri,

For when you're back - Dennis just updated that the deadline for these was extended to Oct. 15th. Additionally, since our understanding is that a sponsor is supposed to submit, he would be happy to send it in. We can also ask Sudarat to submit on our behalf.

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (AID)

Desk: (202) 712-1161
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

On Fri, Sep 1, 2017 at 5:31 PM, Eri Togami <etogami@ucdavis.edu> wrote:
Hi Eddy,

Thank you very much for your comments on the PMAC concept note.
Best,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Eddy Rubin [mailto:erubin@metabiota.com]
Sent: Tuesday, August 29, 2017 12:00 PM
To: Eri Togami <etogami@ucdavis.edu>; Cara Chrisman <cchrisman@usaid.gov>; Dennis Carroll <dcarroll@usaid.gov>; Nathan Wolfe <nwolfe@metabiota.com>; Brooke Watson <watson@ecohealthalliance.org>; Peter Daszak <daszak@ecohealthalliance.org>; Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: PMAC 2018 GVP concept note

Good. A few small suggestions.

I do not think that GVP will better prepare us " to prevent accidental or intentional release of laboratoey-enhanced virus variants."

From: Eri Togami <etogami@ucdavis.edu>
Sent: Monday, August 28, 2017 10:21 AM
To: Cara Chrisman; Dennis Carroll; Nathan Wolfe; Eddy Rubin; Brooke Watson; Peter Daszak; Jonna Mazet
Subject: PMAC 2018 GVP concept note

Hi everyone,

Please see a draft of our concept note for the PMAC launch. As per our previous discussions, we can propose one closed session and one open session. Jonna and I would appreciate your comments and suggestions by Wednesday 9/6.

Best wishes,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Andrew Clements <aclements@usaid.gov>
To: William B. Karesh <karesh@ecohealthalliance.org>
CC: Peter Daszak <daszak@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;David Wolking <djwolking@ucdavis.edu>;PREDICTMGT <predictmgt@usaid.gov>
Sent: 10/13/2017 3:31:15 PM
Subject: Re: Modeling for plague spread from Maciagascar?

Thanks! Will this be published or publicly-shared somewhere?

BTW: WHO has identified the following countries at risk for international spread:

Comoros, Reunion and Mayotte, Mauritius, Mozambique, Tanzania, Seychelles, and South Africa.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Oct 13, 2017, at 5:03 PM, William B. Karesh <karesh@ecohealthalliance.org> wrote:

Yes.

The highest traffic destinations departing from TNR airport in Madagascar are
(1) Reunion, France,
(2) Sir S. Ramgoolam International (near Mahébourg), Mauritius,
(3) Paris, France, and
(4) Nairobi, Kenya,
(5) Tolanoro, Madagascar.

25% of outgoing traffic from Tana has in-country destinations, landing in other cities Madagascar.

Of the 75% international direct flight traffic, France, Mauritius, and Kenya have the highest incoming traffic from this region.

Because this is a direct flight only analysis, the U.S. is not represented in the results, however, a quick analysis of outgoing direct flights from France, Mauritius, and Kenya show that Dubai, UAE (DXB), Amsterdam, Netherlands (AMS), New York, U.S. (JFK), Istanbul, Turkey (IST), and London, U.K. (LHR) are all highly connected to these regions, indicating these destinations are likely also connected to Madagascar through multi-leg flights.

BK

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

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President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On Oct 13, 2017, at 5:36 AM, Andrew Clements <AClements@usaid.gov> wrote:

Hi Peter and Billy,

Has EHA done any modeling around where plague is most likely to spread based on travel and trade routes? Not necessarily asking you to, but curious to hear the results if you already have.

Thanks!

Andrew

--

Andrew Clements, Ph.D
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4255
E-mail: aclements@usaid.gov

For more information on USAID's *Emerging Pandemic Threats program*, see http://www.usaid.gov/ept2

From: Katherine Leasure <kaleasure@ucdavis.edu>
To: 'PREDICTMGT' <predictmgt@usaid.gov>
CC: predict@ucdavis.edu <predict@ucdavis.edu>;'Jonna Mazet' <jkmazet@ucdavis.edu>
Sent: 10/17/2017 5:38:14 PM
Subject: ITA for E. Rubin - Beijing October 24

Hi Andrew. My apologies for the late submission of this request. Eddy Rubin is travelling to China to speak at the International Conference on Genomics. Through Dennis Carroll, he has been invited by the embassy in Beijing to stop there for a night and meet with various government partners to discuss GVP. He would only need PREDICT to fund one night in a hotel and transport to and from the airport; Eddy's flight is being covered by the conference.

1. Rubin (China): $815 *covered by conference/$377 (Beijing) max daily per diem

Travel Request –

1. Metabiota would like to request travel approval for Dr. Eddy Rubin, Chief Scientific Officer, to travel from San Francisco, California, USA to Beijing, China from Oct. 24-25, 2017 to visit the US Embassy to discuss the Global Virome Project. Dr. Rubin will then travel to Shenzhen, China to attend the 12th International Conference on Genomics.

Trip purpose: Dr. Rubin will visit the US Embassy to discuss the Global Virome Project, meeting with State, HHS, CDC, NSF, NIH, FDA, USDA, FCS, as well as USAID. The meeting will also be attended by various representatives from the United Kingdom, Switzerland, Norway, Germany and Australia.

Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
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530-752-3318 FAX
kaleasure@ucdavis.edu

From: David J Wolking <djwolking@ucdavis.edu>
To: Clements, Andrew (GH/HIDN) <AClements@usaid.gov>;Alisa Pereira Emerging Threats Division <apereira@usaid.gov>
CC: Prof. Jonna Mazet <jkmazet@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 11/13/2017 8:27:02 PM
Subject: PREDICT-2 Q4Y3 Quarterly Financial Report

Hi Andrew,

Just an update that we are working hard on this country by category financial report. This report will include the Ebola funding report, the CORE funding report, and the combined report that includes both CORE and Ebola Funds.

This is my first attempt pulling these figures together and we want to provide accurate information, so I'll do my best to deliver the report as soon as possible.

Best,

David

From: Brooke Watson <watson@ecohealthalliance.org>
To: Dennis Carroll <dcarroll@usaid.gov>
CC: Eri Togami <etogami@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>
Sent: 11/15/2017 9:27:08 PM
Subject: Re: Request for GVP materials for BCG team before Nov.21 meeting

Ah! Yes. The submitted *Science* paper (with supplementary materials) is attached.

Thanks,

Brooke

On Wed, Nov 15, 2017 at 5:23 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:
Thanks Brooke. Do you also have the cleaned up Science paper. Also, Eri, is there a draft MOU with BioHub we can share (noting its a draft)? thanks

On Wed, Nov 15, 2017 at 3:13 PM, Brooke Watson <watson@ecohealthalliance.org> wrote:
Hi Dennis,

Thanks for sending this list. I've attached a spreadsheet with 3 tabs for bullet points 1-3: Outreach-to-date, Upcoming Funding Conversations, and Interested Countries. (also available in our shared Google Drive.) I've updated Cara's old tracking document with the information I have, but there are many missing fields, and likely some additional outreach we've done that wasn't in any of my notes. **Eri, if you notice any outreach that I've missed, could you please update the spreadsheet?**

I was traveling during last week's call, so i imagine you discussed bullets 4-6 (and that Jonna and Eri have access to at least #4 and #6.)

We can discuss tomorrow on the weekly call.

Thanks!

Best,

Brooke

On Mon, Nov 13, 2017 at 3:04 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:
Eri and Brooke, as a follow up to the discussion I had with BCG - they have asked for the materials below. Can you pull these together? Some of these can be topics in our next phone call. Let me know if there are ones you dont have

thanks

d

Hello Dennis,

I hope your week has started off well.

I wanted to follow up here to confirm that you will be able to share the below materials, ideally by week's

end, so that BCG and our team can get up to speed on everything before next week's meeting.

Please let us know if there's anyway that we can help you here.

Thanks,
Jen

Materials Needed before Nov.21 from GVP technical team of Dennis, EcoHealth Alliance, UC-Davis and/or Metabiota

- Table of investors/funders approached with feedback and current status of those discussions (Arie to provide?)
- Calendar of upcoming meetings with potential GVP investors
- List of countries interested in GVP and how they are interested in engaging
- Draft paper on the PREDICT project
- Published paper on MERS virus and its many variants
- Draft MOU in discussion with the Chan Zuckerberg Biohub

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

--

Dr. Dennis Carroll
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The Global Virome Project

Authors: Dennis Carroll[1], Peter Daszak[2*], Nathan D. Wolfe[3], George F. Gao[4,5], Carlos Morel[6], Subhash Morzaria[7], Ariel Pablos-Méndez[8], Oyewale Tomori[9], Jonna A.K. Mazet[10]

Affiliations:

[1]Emerging Threats Division, Bureau for Global Health, U.S. Agency for International Development, Washington, District of Columbia, U.S.A.

[2]EcoHealth Alliance, 460 West 34th Street – 17th Floor, New York, New York, U.S.A.

[3]Metabiota, 425 California Street – 2nd Floor, San Francisco, California, USA.

[4]CAS Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, 1 Beichen West Road, Chaoyang District, Beijing 100101, People's Republic of China.

[5]Chinese Center for Disease Control and Prevention (China CDC), 155 Changbai Road, Changping District, Beijing 102206, People's Republic of China

[6]National Institute of Science and Technology for Innovation in Neglected Diseases (INCT-IDN), Centre for Technological Development in Health (CDTS), Oswaldo Cruz Foundation (Fiocruz), Av. Brasil 4365, Rio de Janeiro, RJ 21040-900, Brazil.

[7]Animal Health Service, Food and Agriculture Organization, United Nations, Viale delle Terme di Caracalla, 00153 Rome, Italy.

[i]Bureau for Global Health, U.S. Agency for International Development, Washington, District of Columbia, U.S.A.

[ii]The World Academy of Sciences & Nigerian Academy of Sciences, Academy House, 8A Ransome Kuti Road, University of Lagos, Lagos, Nigeria.

[iii]One Health Institute, School of Veterinary Medicine, University of California, Davis, California, USA.

*Correspondence to: daszak@ecohealthalliance.org

Abstract: The frequency of pandemics is increasing, driven by demographic and environmental change, globalized trade and travel. Viruses of animal origin in particular have caused significant recent outbreaks (e.g. SARS, pandemic influenza, MERS, Ebola and Zika), yet we estimate that only around 1% of potential viral threats have been identified and fewer have had vaccines or countermeasures developed. We estimate that a pool of a few hundred thousand currently unknown viruses with potential to infect people exist in wildlife populations. Here, we discuss the scientific and economic rationale, and the governance and technical framework of a global initiative to identify and characterize the majority of these viral threats from animal reservoirs. We argue that this is achievable over the next ten years and would cost substantially less than many recent outbreaks. We discuss how this global virome project could improve pandemic preparedness, reduce response times and costs, and may hasten our capacity to proactively deal with pandemics.

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One Sentence Summary: We present the scientific, economic, and public health rationale, governance and technical framework for the Global Virome Project, which aims to pre-empt emerging pandemic threats by identifying, in animal reservoirs, the majority of unknown viruses likely to infect humans.

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Main Text:

Recent outbreaks of novel and deadly viruses, including Nipah, influenzas, SARS, MERS, Ebola and Zika virus, have highlighted our global vulnerability to emerging diseases. Their potential devastation is highlighted by the Influenza Pandemic of 1918-19, during which approximately 50 million people died (5% of the human population) and the HIV-AIDS pandemic which has caused 39 million deaths. Even in the absence of significant mortality, the SARS epidemic in 2003, which killed less than 800 people, cost the economies of Asia at least $16 billion (adjusting for inflation) (*1*). Estimates of the global economic cost of an influenza pandemic range from $374 billion for a mild pandemic to $7.3 trillion for a severe pandemic (*2*).

Policies to address pandemic threats include adaptive measures that reduce disease impacts after emergence, and mitigation measures that reduce the underlying drivers of emergence and risk of initial spillover. Our adaptive toolkit – based largely on vaccines and therapeutics – is often ineffective against novel threats because biomedical countermeasure development is often outpaced by the speed of viral emergence and spread. Our ability to mitigate disease emergence is undermined by our poor understanding of the diversity and ecology of viral threats, and drivers of their emergence. Following each outbreak, the public health community bemoans a lack of prescience, but after decades of reacting to each event with only a tangential focus on mitigation, we remain only marginally better protected against the next epidemic.

Knowing the Enemy

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Nearly all recent pandemics have a viral etiology with animal origins (*2*). Driven by intrinsic factors that enhance their capacity for interspecies transmission, viral zoonoses are prime candidates for causing the next great pandemic (*3, 4*). However, if these viruses are our enemy, we do yet not know our enemy very well. Around 385 viruses from 23 viral families are known to infect humans (*5*) (Figure 1). The shape of the discovery curve since the identification of the first human virus (yellow fever virus in 1901) suggests many more will emerge in the future (*6*). We estimate, from analysis of recent viral discovery data (*7*), that approximately 1.6 million yet-to-be-discovered viral species exist in mammal and bird hosts – the most important reservoirs for viral zoonoses (Supplementary Online Material; SOM). By analyzing all known viral-host relationships (*5, 8*), the history of viral zoonoses (*9*), and patterns of their recent emergence (*2*), we can reasonably expect that between 650,000 and 840,000 of these unknown viruses have zoonotic potential (SOM). We have no readily available technological countermeasures to these as-yet-undiscovered viruses should they emerge and threaten public health. Furthermore, the rate at which animal viruses are spilling over into people is accelerating, mirroring the explosive expansion of our global footprint and travel networks (*1, 2*), leading to a nonlinear rise in pandemic risk and an exponential growth in their economic impacts (*1*). Thus, a program that identifies the bulk of this viral threat may provide timely data for public health interventions, which will become increasingly important in the future, as pandemic risk increases.

Cost, governance and technical framework of the Global Virome Project

Since 2009, USAID has conducted a comprehensive large scale pilot project, spanning more than 35 countries over 8 years at a cost around $170 million, to evaluate the feasibility of pre-

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emptively mitigating pandemic threats. The Emerging Pandemic Threats/Predict project (USAID EPT/PREDICT) has demonstrated that, using existing technologies, it is possible to discover numerous new viruses from high-risk wildlife reservoir hosts, and characterize the ecological and socio-economic drivers that underpin their risk of emerging (*10*). Working with local partners and governments, wildlife and domestic animals and at-risk human populations in geographic hotspots of disease emergence (*2*) are sampled, and viral discovery conducted. A strategy to triage those viruses considered most at-risk of spillover has been developed (*11*), and characterization is conducted on these to further identify potential zoonoses prior to, or in the early stages of, spillover. Metadata from wildlife-livestock-human interfaces and human behavioral patterns in communities are concurrently analyzed so that risk mitigation strategies to reduce spillover can be developed (SOM). To date, EPT/PREDICT has discovered more than 1,000 viruses from viral families that contain zoonoses (data.predict.global). These include viruses involved in recent outbreaks (*12*), and others of ongoing public health concern (*13*). However, to discover the bulk of the remaining 1.6 million unknown viruses in animal reservoirs and characterize the majority of 650-840,000 viruses of highest zoonotic potential requires a challenging scale of operations.

The first challenge to feasibility is cost. To estimate this, we analyzed data on field sampling and laboratory expenditures for viral discovery from (*7*), and estimates of unknown viral diversity in mammalian hosts (SOM). We estimate that discovery of all viral threats and characterization of their risk for spillover, using currently available technologies and protocols, would be extremely costly at over $7 billion (SOM). However, because of the asymptotic nature of discovery curves,

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these costs reduce exponentially in relation to the percent of the global virome discovered (*7*), SOM). For example, we estimate that 85% (i.e. the substantial majority) of the viral diversity from our target zoonotic reservoirs could be discovered, characterized and viral ecology assessed for approximately $1.69 billion (23% of the global costs), annualized at $169 million per year over 10 years (Supplementary Figure 1). There will be fixed costs that mean further reduction in coverage may not produce as significant a return-on-investment, for example we estimate that to cover 70% of the viral diversity from mammals and water birds would cost around $1.2 billion, or $120 million per year over 10 years. Logically, for any discovery effort that identifies a significant proportion of the virome, those viruses remaining undiscovered will, by the nature of sampling bias, represent rarer viral species with reduced opportunity for spillover, and reduced public health risk. Their discovery would require exponentially greater sampling effort and significant funds that could be better spent on countermeasures for the more likely threats (SOM).

Launching a project of this scale requires international cooperation to overcome complex governance, technical and logistical challenges. To begin this process, key international stakeholders from Asia, Africa, the Americas and Europe met at the Rockefeller Foundation Bellagio Center and declared their unanimous support for a Global Virome Project (GVP) Initiative (http://www.globalviromeproject.org/about/). They designed a framework for the governance, management, technical operation and scope of the GVP, and formed a steering committee that includes international stakeholders from industry, academia, intergovernmental agencies, the private sector, and NGOs. They convened working groups in

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three thematic areas: Governance, Science/Technology, and Operations, each of these co-led by scientists who represent geographic and disciplinary diversity. These working groups are tackling diverse challenges: developing finance streams; establishing a transparent, equitable implementation strategy; addressing data and sample sharing challenges; developing laboratory platforms; determining the targeting of host taxa and the choosing of sampling sites; forming collaborative field and laboratory networks; developing risk characterization frameworks for viruses discovered; designing a strategy to assess and mitigate risk behaviors that promote viral emergence; and planning in-country capacity building for sustainable threat mitigation. Funding has been identified to begin work in the first two countries, China and Thailand, and a project launch has been set for early 2018.

The GVP's outputs are intended to serve the global public good, and working groups are developing a transparent and equitable strategy to share data, viral samples and their likely products, including benefits derived from future development of medical countermeasures. These build on the Convention on Biological Diversity Nagoya Protocol and The Pandemic Influenza Products Framework, negotiated by the World Health Organization (WHO). The international collaborative nature and global ownership of the project should help leverage funding from a wider range of sources, including private sector philanthropic donors that are increasingly funding 'big science'. The diversity of tasks within the GVP means that it won't necessarily divert significant funds from current public health programs. For example, discrete work streams have begun on targeted sampling of wildlife, on bioinformatics, and on behavioral risk analysis, and funding streams are being developed for each. Governments and

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corporations with specific remits and geographic responsibilities have been approached to finance subprojects relevant to their sectors (e.g. capacity development, surveillance of specific taxa, geographically-focused activities, medical countermeasure development, training, surveillance, technological platforms). In addition, leaders in China and a number of countries have begun the process of developing national virome projects as part of the GVP.

Technological challenges include safe field sampling in remote locations and cost-effective laboratory platforms that can be standardized in low-income settings. To achieve these goals, existing national, regional and international networks will be enhanced and expanded within standardized sampling and testing frameworks. Existing networks of field biologists from environment ministries, academic institutions, and conservation NGOs have been approached to assist in targeting surveillance. National science and technology agencies, regional One Health platforms, transboundary disease surveillance networks, Institut Pasteur laboratories, WHO, FAO and OIE collaborating and reference centers, and viral discovery laboratories, including USAID EPT/PREDICT are involved in working groups to plan surveillance and capacity building. Laboratory platforms developed by USAID EPT/PREDICT have proven capacity to identify novel viruses and are relatively inexpensive and reliable, being based on PCR using degenerate primers that target a range of viral families of known zoonotic potential. Scaling up to a full global virome project provides an opportunity to incorporate advanced platforms including Next Generation Sequencing and other unbiased approaches to assess for evolutionarily-distinct viral clades (*14*). Assessing the likelihood of novel viruses to infect people or become pandemic remains a significant challenge. The EPT/PREDICT project (*11*) and others

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(*3*, *4*, *8*) have developed zoonotic risk characterization frameworks based on viral and host traits and the ecological and demographic characteristics of the sampling site. These approaches will be used in the GVP to identify a predicted high-risk subsample of novel viruses for further characterization to assess their zoonotic capacity. *In vitro* receptor binding site analyses coupled with *in vivo* models have proven useful in this capacity for some viral families (e.g. coronaviruses (*13*)). While this is not yet feasible for all potentially zoonotic viral clades, applying these techniques to a significantly larger viral dataset as the GVP progresses may increase our capacity to predict zoonotic potential.

The cost of a decade-long GVP represents a significant investment and, even if a large number of potential zoonoses are discovered, only a minority of these is likely to have the potential to cause largescale outbreaks and mortality in people (*2*-*4*, *9*). However, given the high cost of single epidemic events, this approach may still provide substantial return-on-investment. The cost of the GVP is dwarfed by estimates of the likely costs of an influenza pandemic ($570 billion (*15*)) or of the SARS epidemic ($10-30 billion; (*1*)), and is put into perspective by the $5.4 billion Ebola virus response by the U.S. Government, and the around $3.5 billion projected costs of Ebola recovery plans for West Africa in 2015-17 (*16*). The GVP should not be considered an alternative to current pandemic surveillance, prevention or control strategies, but rather a way to improve our efficiency in the face of increasing rates of novel zoonotic viral spillover (*1*, *2*). If we were to invest funds only in surveillance for known pathogens (our current business-as-usual strategy), our calculations suggest we would only be protecting ourselves from less than 0.1% of the pool of viruses that could conceivably infect people, even using the lower bounds of

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our uncertainty of viral estimates (i.e. 263 viruses known from humans out of 351,735 unknown potential zoonoses, SOM). More directly, recent economic analysis of the increasing rate of disease emergence, and their exponentially rising economic damages, suggests that large scale global strategies for pre-emptively dealing with the pandemic threat are urgently needed, and would provide a 10:1 return on investment, using prior World Bank analyses (*1*). To increase return-on-investment from the GVP, we propose further strategic targeting approaches to more rapidly produce public health benefits (SOM): First, by optimizing sampling to target species and regions that are most likely to harbor the highest proportion of 'missing zoonoses' (*8*), or to target species otherwise more likely to become involved in spillover events due to ecological or sociological factors; Secondly, by initially sampling in emerging disease hotspot regions that are most likely to be produce disease outbreaks of significance (*2*), or most likely to lead to spillover of emerging viruses from wildlife (*17*); Thirdly, by using syndromic surveillance in people to help identify regions for wildlife sampling that are proximal to sites where repeated outbreaks of severe influenza-like-illnesses and other unusual fevers-of-unknown origin, encephalitides, livestock abortion storms and other potential emerging disease events have been reported; Fourthly, by initially streamlining viral testing to target RNA viruses, which caused 94% of the zoonoses documented from 1990 to 2010 (*3*); and finally, economies of scale and technological innovation may further reduce costs as the GVP ramps up. These will include use of laboratories that can facilitate regional sample processing, development of centralized bioinformatics platforms, and improved logistics for sample collection and transport. We also expect the cost of testing and sequencing to reduce as technology is enhanced, much as the development of Next Generation Sequencing reduced sequencing costs by up to 4 orders of

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magnitude in less than a decade. By this strategic targeting approach, and by routinely analyzing viral discovery curves to monitor progress, validate global viral estimates and halt sampling when discovery targets are reached (SOM), it may be possible to reduce the cost of the GVP substantially while covering an even higher proportion of global zoonotic risk.

The accelerated pace of viral discovery under the GVP could help transform the virological, phylogenetic and modeling approaches currently used in pandemic preparedness into a data-rich science, enabling a disruptive approach to developing risk analysis, interventions, and countermeasures to future threats. For example, having the sequence data for thousands, rather than a few, viruses from a single family could extend vaccine, therapeutic or drug efficacy to a wider range of targets and ultimately assist in the development of broad spectrum vaccines and other countermeasures. Proof-of-concept comes from USAID EPT/PREDICT fieldwork that discovered a large number of novel SARS-like coronaviruses in bats (*13*) . These were identified as potentially high risk for zoonotic emergence, and further characterization showed that some could bind to human cells using the same receptor as SARS, and that one produced SARS-like disease in humanized mice. However, a monoclonal therapeutic and a vaccine candidate effective against SARS-CoV was ineffective against this new coronavirus (SOM). Thus, identification of novel viruses may be useful to programs like the Coalition for Epidemic Preparedness Innovations (CEPI, cepi.net) in assessing the breadth of action of candidate vaccines and therapeutics, and in helping expand their efficacy. Big data will also enhance phylogenetic analysis of deep viral evolution and revision of viral taxonomy, as has recently been shown for insect viruses (*14*). These data may expand our capacity to assess the

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zoonotic potential of novel viruses and advance our understanding of viral biology, such as what drives competition or cooperation among viruses within hosts, genomic underpinnings of host-virus coevolution, or processes underlying deep evolution of viral families and genera. The GVP will provide metadata on host identity, geography, seasonality, proximity to people, risk behaviors etc. to empirically test and ground truth theoretical models of viral spillover, emergence and spread that are currently based on analysis of published literature (*2-4, 8*). These ecological and human behavioral risk data will refine our mechanistic understanding of spillover and lead to novel mitigation strategies. For example, identification of novel potential zoonoses in hunted, traded, or farmed wildlife species could help enhance biosecurity in markets and farming systems, reducing public health risk and increasing food security. In other cases, data on populations with enhanced exposure to hosts harboring high-risk novel viruses may allow targeted follow-up to examine evidence of spillover (SOM). This may also provide benefits to conservation programs, as well as reducing the risk of spillover of known and unknown viruses. These broad-scale prevention approaches could provide return-on-investment prior to the process of developing vaccines or countermeasures, which would likely require a much longer time.

Finally, if the GVP is managed equitably and capacity built in the regions where diseases tend to emerge (highly biodiverse, rapidly developing countries around the tropics (*2*)), it will improve capacity to detect, diagnose and discover viruses in those regions most critical to preventing future pandemics. At the end of a GVP decade, the most vulnerable countries would have laboratories and trained personnel capable of early detection and characterization of viruses –

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improving disease diagnosis and control for novel and endemic diseases, even for the portion of the virome that remains undiscovered.

The launch of the Human Genome Project in the 1980s catalyzed the development of new technologies that dramatically shortened the time and cost required for its completion, ultimately ushering in the era of personalized genomics and precision medicine. It is estimated that every U.S. federal dollar put into the human genome project resulted in a $178 return on investment (*18*). The GVP will likely accelerate development of pathogen discovery technology, diagnostic tests, and science-based mitigation strategies with potentially higher returns-on-investment, given their more direct relevance to human health, and the accelerating costs of disease emergence. Like the Human Genome Project, this initiative will provide a wealth of publicly accessible data, leading to advances in global health that are currently hard to anticipate, such as the discovery of viruses that cause cancers and chronic physiological, mental health or behavioral disorders. It will also provide us with orders of magnitude more information about future key threats to global health and biosecurity, make us better able to identify populations with the greatest vulnerability to these threats, and allow us to target mitigation and control measures with unparalleled accuracy.

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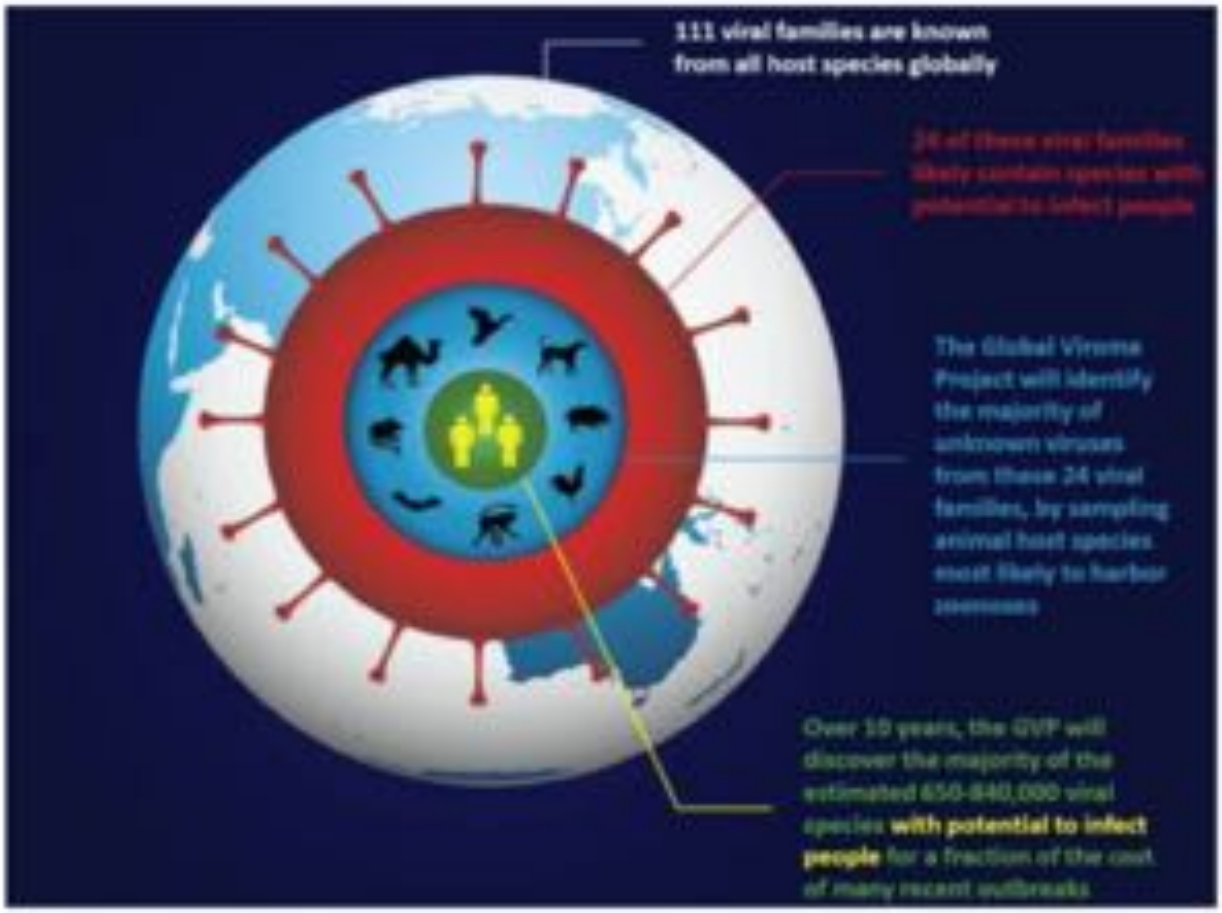

Fig. 1 (version 1). The Global Virome Project is a targeted program of viral discovery to identify the majority of currently-unknown viruses in wildlife with the potential to infect people. Of 111 known viral families, only 24 contain viruses known to infect (or to have substantial risk of infecting) people. We analyzed viral discovery curves in two repeatedly and intensively sampled

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mammalian host species to estimate that there are around 1.6 million unknown viruses of these 24 viral families in mammals and birds (hosts that represent 99% of the risk for viral emergence). Based on ICTV data, we estimate that between 650,000 and 840,000 of these viruses would have the capacity to infect people. Targeting these wildlife host species and 24 viral families, and using field and laboratory expenditures for largescale novel viral detection, we estimate that the cost of a Global Virome Project to identify the substantial majority (70%) of these viruses would be around $1.2 billion. A 10-year Global Virome Project would thus identify the vast majority of currently-unknown viruses of high potential consequence at a cost of around $120 million per year. See Supplementary Online Material for calculations. Artwork by N. Randhawa.

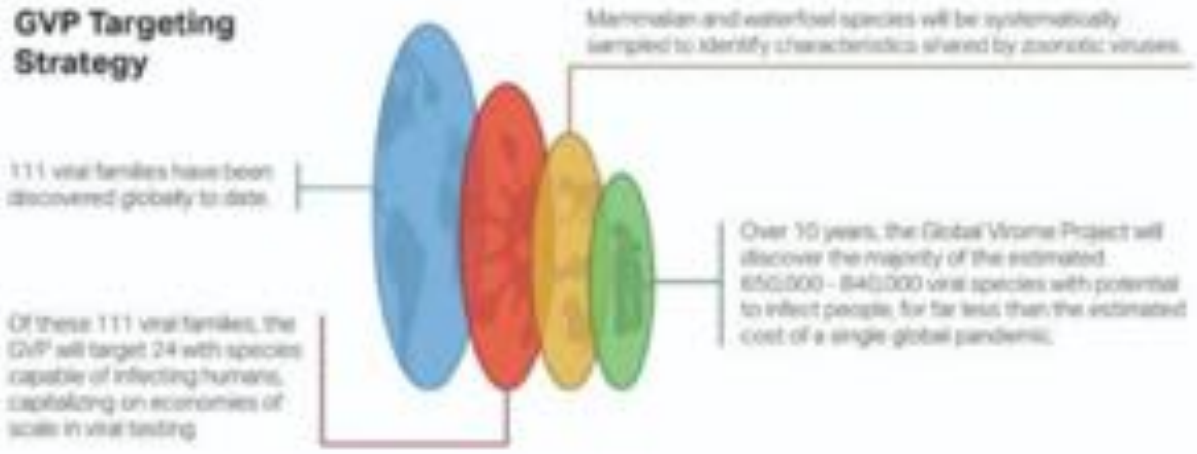

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Fig. 1 (version 2). The Global Virome Project is a targeted program of viral discovery to identify the majority of currently-unknown viruses in wildlife with the potential to infect people. Of 111 known viral families (blue circle, left), only 24 contain viruses known to infect (or to have substantial risk of infecting) people (red circle). We analyzed viral discovery curves in two repeatedly and intensively sampled mammalian host species to estimate that there are around 1.6 million unknown viruses of these 24 viral families in mammals and birds - hosts that represent 99% of the risk for viral emergence (yellow circle). Based on ICTV data, we estimate that between 650,000 and 840,000 of these viruses would have the capacity to infect people (green circle, right). Targeting these wildlife host species and 24 viral families, and using field and laboratory expenditures for largescale novel viral detection, we estimate that the cost of a Global Virome Project to identify the substantial majority (70%) of all potentially zoonotic viruses, would be around $1.2 billion. A 10-year Global Virome Project would thus identify the majority of currently-unknown viruses of high potential consequence at a cost of around $120 million per year. See Supplementary Online Material for calculations. Artwork by J. Goley.

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Supplementary Online Material (SOM):

Estimating viral diversity in wildlife hosts of zoonotic relevance

In the biological context, the phrase 'diversity' includes not only the 'species richness' or number of species (or other taxonomic unit) in a region or of viruses in a host, but also the variability within species, between species and of ecosystems – i.e. it includes the degree of difference among organisms (*1*). However, for the purposes of this paper, we have followed two key previously published papers (*2, 3*) and used the phrase 'viral diversity' to denote the species richness of viruses – i.e. the number of species of viruses in a given host, group of hosts or geographic region.

To estimate the diversity of viruses that threaten to emerge in people we extrapolated from estimates derived from two mammalian wildlife hosts, a bat species and a primate species, representing the only published estimates of unknown viral diversity in vertebrate hosts (*2, 3*). Mammals represent the most important hosts for emerging viral zoonoses, with ~88% (69/78) of emerging viral zoonoses with a confirmed reservoir host in a published database of emerging infectious disease events originating in non-human mammals (*4*), and ~99% in non-human mammals or in birds (69 from mammals, 8 from birds). These include viruses that originate in or have genes that originate in these classes of vertebrates, or are transmitted by them at some stage in their emergence. Estimates of potentially-zoonotic viral diversity for the bat *Pteropus giganteus* are based on repeated sampling of individuals of this species and viral discovery using PCR with degenerate family-level primers targeting 9 viral genera or families, all known to

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contain zoonoses (*2*). Estimates of potentially-zoonotic viral diversity for the rhesus macaque *Macaca mulatta* targeted 21 viral families by PCR, as well as high-throughput sequencing (HTS) (*3*). For each host species, we obtained raw test data from (*2, 3*) and repeated the analysis of unknown viral diversity for each set of viral family-level tests to estimate the expected number of viral species and standard error for all known and expected unknown viruses from each of the 30 viral family test protocols conducted. This gave an average of 11.58 viruses per family (standard error 6.74), indicating that the average viral family has between 4.84 and 18.32 viral species. However, this mean was heavily skewed by the 120 discovered and 200.83 estimated *Picobirnaviruses* in *M. mulatta*. The median number of viral species per viral family was 2.5, indicating that many viral families have only a few viral species in a given host, but rare families can have many more. For the purposes of costing the Global Virome Project, the mean is a more useful and conservative metric, but these central tendencies demonstrate the variability of mammalian viromes and the necessity of monitoring sampling and testing in real time to guide per-species sampling (see below).

All 21 viral families targeted in (*2, 3*) contain known zoonoses, but neither study covered *Bornaviridae* and *Hepeviridae* which also contain zoonoses. The *Arteriviridae* contains a species pathogenic in primates and none that are known from humans, but could reasonably be considered a risk for future zoonotic emergence from either known or unknown viral species. We therefore multiply the per-viral family mean of 11.58 species by 24 (see specific viral families listed below) to estimate total viral diversity of zoonotic potential (277.92, se 116.16-439.68) in each mammalian host species. In addition, influenza viruses derived from mammals

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and birds represent a significant public health threat globally. Therefore, we used the mean viral diversity per viral family in mammal hosts (11.58), and assumed that this may also represent the average per-host species viral diversity for influenza viruses (*Orthomyxoviridae*) in each bird species. Given that there are 5,291 known mammal species (excluding marine mammals which have limited contact with humans relative to terrestrial and volant mammals) (*5*) and 11,862 known bird species (*6*), this would give a total global viral species richness of zoonotic potential of around 1,607,837 (se 672,015 - 2,543,659).

The viral families tested by the GVP include 17 families of RNA viruses known to infect people: *Arenaviridae*, *Bornaviridae*, *Bunyaviridae*, *Coronaviridae*, *Filoviridae*, *Flaviviridae*, *Hepeviridae*, *Orthomyxoviridae*, *Paramyxoviridae*, *Picornaviridae*, *Reoviridae*, *Retroviridae*, *Rhabdoviridae*, *Togaviridae*, *Astroviridae*, *Caliciviridae*, and *Picobirnaviridae*. An additional RNA viral family (*Arteriviridae*) that infects non-human primates will be included, as suggested above. An additional 6 families of DNA viruses also contain known zoonoses (*Herpesviridae*, *Poxviridae*, *Bocaviridae*, *Adenoviridae*, *Papillomaviridae*, *Polyomaviridae*), bringing the total to 24 viral families.

There are a number of assumptions in this approach that need to be considered. Firstly, viruses, and RNA viruses in particular, have remarkable potential for evolution which suggests that estimates of viral species diversity may not remain static over the period of the GVP. However, given that there is a large standard error around these estimates, and given that the GVP calculations are *already* conservative (i.e. err on the side of over-estimation of viral

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diversity by using the mean per-family value), this may not significantly affect the GVP estimates. Furthermore, the work on which these estimates are based used a conservative approach to the definition of viral species which has been followed in these calculations (*2, 3*). It is likely that viral evolution is more constrained in reservoir hosts (the subject of the GVP sampling and testing) than in spillover hosts (the subject of many studies of RNA viral evolution, e.g. [*7*]), which may further reduce the impact of viral evolution on these estimates. Secondly, the estimates of viral diversity are based on two species, the macaque and the giant fruit bat, which may not be representative of all mammalian or avian species in that they are both mammals, both social, the former is widely distributed and the latter lives in dense colonies and is volant. These and other factors (e.g. overlapping host species ranges resulting in viral sharing, long evolutionary distance from related host species resulting in diversification of viral lineages) suggest that our estimates of global viral diversity may be lower or higher than stated. Some of these have been discussed in (*2, 3*), and given the large standard errors presented here for our estimates of viral diversity, seem unlikely to suggest a significant disparity (e.g. by orders of magnitude) between the estimated viral diversity and that which would eventually be discovered. However, to deal with potential disparities, we propose that the test results from the GVP should be analyzed routinely as the project progresses, to monitor and evaluate progress relative to initial estimates and assumptions. Specifically, the same algorithms used in (*2, 3*) could be applied to viral family test results per host species, family, order, and geographical sampling region to ascertain whether the standard error around estimated total viral diversity reduces as the project progresses. A reduction in these standard errors would denote a gain in accuracy of estimates, and if these suggest some viral families are far more (or

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less) speciose than assumed, or some species or taxa have a much greater or lesser viral species richness than assumed, the strategic targeting of the GVP should be altered accordingly to maximize discovery, by expanding, reducing or halting sampling and testing.

Estimating the number of potentially zoonotic viruses

To estimate the number of wild mammal viruses and bird influenzas with the potential to infect people, (i.e. the species richness of unknown viral zoonoses), we used data from (*8, 9*) on the host species range for all known mammalian viruses and the proportion of these viruses that can infect humans. We found that, of 590 known mammalian viruses, 263 (43.7%) infect humans, with 75 exclusively human and 188 zoonotic (31.9% of all known mammalian viruses). Considering that most exclusively human viruses likely originated in animals (*10*), then between 512,900 (214,373 - 811,427) (31.9%) and 702,625 (293,670 - 1,111,579) (43.7%) of known and unknown mammalian viruses have potential to infect humans. We made a conservative assumption that all strains of influenza virus in birds are likely capable of zoonotic transmission, so that our best estimate of the total number of potential zoonoses globally is between 650,262 (351,735 - 948,789) and 839,987 (431,032 - 1,248,941). It is possible that as-yet-undiscovered viruses will include a lower proportion with zoonotic potential than those already known, given our long history of interaction with wildlife on the planet, and our skewed surveillance of hosts known to harbor zoonoses (*8*). However, data show that the rate of disease emergence is increasing after correcting for reporting bias, with zoonotic pathogens originating in wildlife increasing significantly as a proportion of these (*4, 11*). This suggests that any reduced potential for zoonotic emergence in the undiscovered pool may be far less important in driving risk than

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the very large number of pathogens to which we have not yet been significantly exposed to, and the exponentially increasing drivers of high-risk contact with wildlife and disease emergence. Further, the identification of a pathogen as zoonotic also requires that it infects people and is then clinically observed. The discovery of novel pathogens infecting people is hindered by paucity of infectious disease surveillance that includes detailed pathogen discovery, particularly in developing tropical countries where most EIDs have their origin (*12*). Thus it is likely that many of the potentially large pool of viruses in diverse wildlife that aren't peridomestic or involved in global livestock production or trade, have not yet been discovered, even if they have already emerged repeatedly into human populations. This scenario is supported by the origins of HIV-1 (*13*), and has been demonstrated in 'silent' simian foamy virus infections identified in bushmeat hunters in Cameroon (*14*). In addition, a recent detailed analysis of ICTV data and the literature (*8*) suggests that prior surveillance studies have not necessarily focused predominantly on hosts with higher proportions of zoonoses as a product of efforts to identify reservoirs for zoonoses. In fact, the data show that bats have a statistically significant higher proportion of zoonoses than any other mammalian order, even though bats are not a historically well-studied group of mammals (*8*). Indeed, other factors may determine the selection of hosts for surveillance, not least of all convenience. For example, historical surveys of mammals are often based on how easy they are to capture, and therefore tend to have focused more on diurnal terrestrial species (e.g. rodents) than nocturnal volant species (e.g. bats). Finally, the standard error for our estimates of the number of viruses with zoonotic potential is quite large, but still results in a minimum expectation of >350,000 viruses of zoonotic potential. Given the high, and growing, public health impact and economic costs of EID

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outbreaks (*11*), it seems that this lower number would still provide adequate economic and public health rationale for a large project like the GVP.

Targeting the Global Virome Project to maximize discovery of zoonoses

We propose that Global Virome Project (GVP) should be streamlined to discover those viruses with the highest zoonotic potential by targeting host taxa which have historically harbored the majority of zoonoses. Mammalian taxa sampled could reasonably exclude marine mammals, which have a reduced likelihood of contact with people relative to terrestrial and volant mammals, and have not been the primary reservoir from which any prior EIDs have originated (*4*). Target mammal species would be primarily wildlife because 91% of zoonoses reported between 1990 and 2010 involved a wildlife host, with some of those also implicating a domestic animal host for the same virus etiology (*15*). For avian influenza viruses, the GVP could reasonably target only water birds (Anatidae, Laridae, Charadriiformes and others) which harbor a wide diversity of known zoonotic avian influenzas, contain species closely related to widely-domesticated species, are hunted extensively, and have a global species richness of 871 (*6*). Some recent emerging diseases have been caused by viruses transmitted to people from wildlife via domestic animal reservoirs (e.g. Nipah virus and pigs, MERS and camels). The GVP could sample a small number of livestock and poultry species (n=10) in regions that are known emerging disease hotspots (*4*). Because these species are abundant and widely distributed, sampling in 5 regions globally would not be logistically difficult, and would increase the target by an equivalent of 50 species.

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Estimating the cost of a Global Virome Project

To estimate the cost of sampling and discovering unknown viruses, we used cost data derived from the USAID-funded EPT/PREDICT project, which has a goal of conducting zoonotic viral discovery in wildlife to identify potentially zoonotic pathogens (*16, 17*). The USAID EPT/PREDICT project has been operating in over 35 developing countries, in emerging disease hotspots, for 8 years. This project has set up field teams in each country, captured and sampled over 80,000 wildlife and domestic animals, designed and operated diagnostic platforms in-country, and conducted over 400,000 viral discovery tests. The USAID EPT/PREDICT project conducted the work in (*2, 3*). The cost of estimating the virodiversity of *P. gigonteus*, collecting metadata, conducting risk assessment and partial characterization of some of these viruses was $1.2 million. The bulk of these costs were in sample collection, setting up laboratory testing platforms, and conducting sample preparation. Considering that the cost of adding primers to PCR reactions once samples are prepared for analysis, including HTS, is relatively insignificant, we estimate the cost of taking the Global Virome Project to scale is approximately $6.3492 billion (the $1.2 million cost of the *P. gigonteus* work multiplied by the number of extant terrestrial and volant mammals) for 100% of the estimated unknown 1,330,208 mammalian viruses (excluding marine mammals). Because the bulk of these costs comprise the logistics of fieldwork, sample collection and cold chain management, they are therefore driven largely by host species considerations and unaffected significantly by the uncertainty in viral diversity estimates. The GVP would require an additional $1.1052 billion to sample water bird species (n=871) for influenza and limited domestic animal sampling (n=50, as described in the SOM, above). This would bring the total costs of the GVP to $7.454 billion, which, if annualized over a

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decade would cost around $745 million per year to discover virtually 100% of the viral zoonotic threats to our species.

However, considering that the viral discovery curves reported in (*2, 3*) are asymptotic, marginal returns diminish rapidly as the number of samples collected increases. Using the discovery rates and total costs from (*2*), and assuming a linear relationship between samples collected and costs, we examined the relationship between total project costs and the percentage of the undiscovered global virome found. (SOM Figure 1). Based on these calculations, we estimate that 97.4% of targeted viral diversity would be discovered with half of the sampling and testing effort ($3.73 billion), and 85% of targeted viral diversity would be discovered with only 23% of the costs ($1.69 billion). Neither start-up infrastructure costs nor cost savings from economies of scale are included in this model, both of which may reduce the steepness of the curve shown in SOM Figure 1, but this simple model is included to demonstrate the decreasing rate of discovery after an initial sampling phase. This model suggests that a GVP costing $1.69 billion could discover the vast majority (85%) of unknown viral diversity in non-marine mammals and of the zoonotic influenza risk from water birds, with some limited domestic animal sampling. Assuming fixed costs for surveillance, sample handling and testing within target countries, we estimate that to cover 70% of the viral diversity from mammals and water birds would cost around $1.2 billion, or $120 million per year over 10 years. GVP costs would likely not be significantly increased if estimates of viral diversity prove to be low due to, for example, the discovery of a very diverse new viral family, or greater diversity within a known family. The increased number of viruses discovered would not be linearly translated into increased costs of

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the project, because the bulk of the costs are in the collection of field samples rather than sequencing a larger number of PCR products.



SOM Figure 1. *Costs of the GVP vs percentage of the targeted global virome discovered. The targeted global virome includes sampling from all 5,291 terrestrial mammal species and testing for 24 viral families of zoonotic potential, 871 species of water birds tested for influenza viruses, and limited (n=50) sampling of domestic animals and testing for 24 viral families.*

Further strategic targeting to increase return-on-investment

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Further strategies are proposed in the main text for targeting the GVP to increase return-on-investment, and deliver public health value as rapidly as possible. Here we provide additional information and citations to support this approach: **1)** *Optimizing sampling to target host species and regions with the highest number of 'missing zoonoses', or hosts otherwise more likely to be involved in viral spillover.* It is logical that some host species, genera or orders may have a higher risk of harboring zoonoses or of their viral fauna spilling over to people. This may be due to their higher contact with people (e.g. through a propensity to live in human-dominated habitat, involvement in the wildlife trade etc.), due to intrinsic biological factors that lead to them harboring a higher number of viruses, or likely zoonotic viruses, or because they are more abundant or have a wider geographic or ecosystem range and therefore increased potential for direct viral spillover or via domestic animals to humans. Recent analyses suggest that species which have greater contact with humans (*18*), and are more closely related phylogenetically (*19, 20*) are more likely to harbor viruses with the potential to be zoonotic. By analyzing data on all mammalian host-virus relationships in (*9*), and controlling for reporting effort, we have been able to demonstrate that both the total number of viruses that infect a given species, and the proportion likely to be zoonotic are predictable (*8*). The proportion of viral species that are zoonotic in mammal hosts is predicted by phylogenetic relatedness to humans, host taxonomy, and human population within a species range (a proxy for human-wildlife contact). By setting reporting bias in our model to the maximum known for any wild mammal, we can identify geographic regions with the largest estimated number of 'missing viruses' and proportion of 'missing zoonoses' and therefore of highest sampling value. Preferentially targeting these regions and hosts in the early stages of the GVP will likely provide

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a greater yield of novel viruses per unit effort, and a higher proportion of these being potential zoonoses.

2) *Targeting EID hotspots.* Analysis of all infectious diseases reported as emerging in humans since 1960 shows that, when corrected for reporting bias, their geographic origins are correlated with wildlife biodiversity and human population density (*4*). The spatial distribution of these correlated drivers provides a geographic map of EID hotspots which represent the most likely regions for future spillover events. This analysis has been revised significantly, with a new database, new analytical approach, new measures of reporting effort, new validation methods, and specifically targeting zoonotic EIDs (*12*). The results demonstrate that, after accounting for reporting effort, zoonotic EID risk is elevated in forested tropical regions experiencing land-use changes and where wildlife biodiversity (mammal species richness), and human population density, are high. Apart from the correlation with mammal species richness which is already accounted for in the GVP targeting, these results could be used to identify initial GVP sampling sites. Novel viruses identified in wildlife at these sites would have highest relative propensity to emerge, other traits being equal. Thus preferentially targeting these regions for GVP sampling would provide potentially greater benefit to public health as mitigation measures are put in place to reduce the risk of disease emergence. 3) *Syndromic surveillance.* Targeting GVP sampling of wildlife to sites with repeated reports of undiagnosed outbreaks in humans or livestock may increase the probability of identifying causative agents of these outbreaks. For example, there are substantial available data on undiagnosed case clusters and outbreaks of encephalitides and other discrete syndromes with potential infectious etiology from the literature and from internet-based reporting. During the late 1990s, analyses

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of these reports for South Asia suggested that some outbreaks may actually be caused by Nipah virus – at the time not known in the region. This provided the rationale for a survey of fruit bats in Northern India (the reservoirs for Nipah virus elsewhere), which led to the first report of Nipah virus in bats in India (*21*). Syndromic surveillance allowed identification *post hoc*, of the causal agent of outbreaks in South Asia (*22, 23*). Similarly, syndromic surveillance of livestock has been used to identify diseases of significance to livestock production or public health (*24-27*). Data on undiagnosed clusters of potential infectious etiology in livestock could be used to target the planned livestock sampling in the GVP. These approaches may provide more direct benefits from the GVP for public health and food security. **4)** *Initial targeting of RNA viruses.* RNA viruses caused 94% of the zoonoses documented from 1990 to 2010, 28 times higher than the proportion of RNA viruses detected among all vertebrate viruses (*15*). Therefore, to maximize the early detection of likely zoonotic viruses, GVP testing could target RNA viral families, including retroviruses. Alternatively, following testing for all 24 viral families, novel viruses could be triaged initially for further characterization based on their RNA vs. DNA genome. **5)** *Economies of scale.* Economies of scale would potentially reduce the cost of the GVP, providing issues around access to sampling sites, sample movement and intellectual property are negotiated equitably. For example, modeling could be used to identify the maximum return (i.e. number of unique wildlife species adequately sampled) on investment (number of sampling sites and cost) per country. In regions with discrete pockets of biodiversity, algorithms used to identify sites for protected areas could be modified to increase GVP site selection efficiency (*28-30*). At a national scale, the presence of biodiversity hotspots across country boundaries would lead to repetitive sampling over two adjacent countries. A

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regional approach may reduce costs significantly while giving the same species coverage, and would allow for decisions on logistical efficiencies to drive sample site choice. Testing of samples in laboratories that already have a regional (multinational) remit may increase efficiency and reduce costs of laboratory capacity building. Similarly centralized bioinformatics platforms could be used that would not only increase the capacity for analysis of sequence data, but also provide training in bioinformatics for scientists across a region. 6) *Technological innovation.* The decadal timescale of the GVP may allow for technological innovation to significantly reduce testing and bioinformatics costs and increase efficiencies. As an extreme example, the cost of sequencing a human genome fell from $10,000,000 to around $1,000 in 6 years, i.e. 4 orders of magnitude, exceeding the projected increased efficiency under Moore's Law (*31*). Technological advances continue in biased and unbiased viral discovery technology (*32*) and are likely to increase testing efficiency and reduce costs (*33*).

Potential direct benefits of the GVP to reducing risk of zoonotic viral emergence

A 10-year GVP that identifies the bulk of currently-unknown viruses with zoonotic potential from wildlife reservoirs will have substantial potential for preventing and controlling zoonotic viral emergence. However, the development of biomedical countermeasures (therapeutic drugs or vaccines) would require significant financial investment beyond that costed out for the GVP, and significant time following discovery (*34-36*). For example, substantial research on influenza viruses over the past few decades has yielded a wealth of data on virology, immunology, pathology and epidemiology. This has led to strategies to predict the emergence of seasonal flu

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strains and develop vaccines for them in advance of their emergence. However, their efficacy appears to be variable (*37*), and vaccine development to the recently emerging H1N1 pandemic strain lagged its global spread, albeit that speed of production was greatly enhanced (*38, 39*).

Despite the challenges of countermeasure development, there are a number of ways that the GVP could feasibly improve efforts to pre-empt zoonotic viral emergence, diagnose cases and intervene earlier in outbreaks: **1)** having the sequence data for hundreds or thousands, rather than a few, viruses from a single family could enhance our understanding of the efficacy of novel therapeutics, vaccines or other countermeasures to a wider range of targets. For example, following the emergence of SARS-CoV, a large number of diverse related coronaviruses has been discovered from bats, including a group closely related to SARS (the bat SARS-like coronaviruses or SL-CoVs). The spike proteins of a number of recently-discovered SL-CoVs have ability to bind to the human receptor for SARS-CoV and to infect and replicate SARS-like disease in mice when inserted into a mouse-adapted SARS-CoV backbone (*40, 41*). However, a vaccine and monoclonal therapy that reduces SARS-CoV infection in this model failed to protect the host from infection with the SL-CoV chimera, and to neutralize virus respectively (*41*). Thus, expanding our knowledge of the diversity of related SL-CoVs under a GVP program may provide more effective testing protocols for SARS therapeutics and prophylactics; **2)** Sequence data from new relatives of known agents can be used to increase the breadth of coverage of PCR-based diagnostic tests. This may provide more rapid diagnosis of novel viral infections in people or livestock, and reduce the size of outbreaks by allowing more rapid and effective contact tracing, and triaging of cases. **3)** Capacity building under GVP

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would include training of One Health teams in regions most likely to experience novel outbreaks of emerging diseases. In the USAID EPT/PREDICT project, teams of trained wildlife veterinarians and biologists capable of safely sampling wildlife during outbreak conditions have assisted in outbreaks of yellow fever in Africa, Ebola virus disease in West Africa, Nipah virus in Bangladesh and a range of others (*17*). Scaling up of in-country One Health capacity would help more rapidly identify the reservoirs of known or novel viruses causing outbreaks in EID hotspots and identify exclusion measures or other strategies to reduce risk of further spillover – a direct public health benefit; **4)** The identification of viral relatives of known zoonotic pathogens in new regions may enhance capacity to diagnose at-risk populations. For example, the identification of novel and distinct henipaviruses in bats in Africa has led to testing for, and evidence of, their transmission to pigs and humans in the region (*42-45*). This group of viruses can now be included in investigation of future outbreaks of Nipah- or Hendra-like disease in livestock in the region. **5)** The metadata collected by the GVP on viral-host ecology, viral distribution, seasonal dynamics, proximity to dense human populations and travel centers, and to communities with cultural practices that increase risk of spillover can be used to enhance public health. Ecological and human behavioral data collected in the GVP will help refine our mechanistic understanding of spillover, and can be used to develop novel mitigation strategies. For example, the USAID EPT/PREDICT has identified sites in Yunnan Province, China where cave-dwelling bats harbor a high diversity of novel SARS-like coronaviruses, including some capable of infecting human cells and causing illness in humanized mice (*40, 41*). Ecological data collected during site evaluation prior to wildlife sampling, and human behavioral data collected routinely in the USAID EPT/PREDICT project identified populations with significant exposure to bats from these caves.

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Follow-up surveys have now tested a sample of this population and identified serological evidence of human exposure to these bat SARS-like coronaviruses (Daszak, unpubl. data). In more general terms, identification of potential zoonoses in hunted, traded and consumed species may provide a public health rationale for interventions (e.g. public education programs, enhanced biosecurity in farming systems and markets, policy interventions in wildlife trade) to prevent spillover. These mitigation strategies could be used to reduce the risk of spillover of newly discovered viruses, and would also block spillover of yet-to-be identified viruses within the same risk pathway. The GVP metadata will also allow refinement of predictive models of zoonotic disease emergence, and viral host ranges (*4, 8, 12, 16*). For most of these, gaps in globally relevant datasets lower their predictive capacity, something that would be addressed by ground-truthing with much-expanded data on viral-host relationships and geographical distribution.

It would not be feasible to design and target control and intervention programs to all novel viruses identified by the GVP, and it will be difficult to distinguish which viruses have pandemic potential. Knowledge of influenza diversity and evolution has led to seasonal vaccine development based partly on predictive modeling of next year's dominant strain, but this approach is enhanced by a great deal of data on influenza viruses recently and currently circulating in people. To address this issue, the USAID EPT/PREDICT project has developed an approach that characterizes the relative importance of newly-discovered viruses based on viral dependent traits (e.g. proportion of known zoonoses per viral family, phylogenetic relatedness of known zoonoses, host breadth/plasticity,) and viral-independent traits (e.g. host species

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geographic range, abundance and proximity to people; viral prevalence in host; location of host in an EID hotspot). Some of these approaches have been shown to predict zoonotic potential from large databases of virus-host relationships (*8, 15*). In the USAID EPT/PREDICT project, this strategy is used to identify which viruses are most likely to be potentially zoonotic, and to allocate resources for further in-depth characterization (*17*). These methods could be used in a similar fashion for the GVP and, with orders of magnitude more data, could provide far more realistic projections of zoonotic potential.

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From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Dennis Carroll <dcarroll@usaid.gov>
CC: Brooke Watson <watson@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>
Sent: 11/16/2017 5:48:41 AM
Subject: Re: Request for GVP materials for BCG team before Nov.21 meeting

Hi Dennis,
Eri is in Cambodia, so she probably isn't get your emails. I've attached papers to which I think they may be referring, as well as the Predict flyer. I don't have the current version of the MOU language, so we'll have to wait for Eri on that, but I'm not sure what they're after in that, as Billy didn't have much language to add when we first requested.
Hope these are what they were after,
Jonna

On Wed, Nov 15, 2017 at 5:35 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:
Mucho gracious

Dr Dennis Carroll
Director, Emerging Threats Program
U.S. Agency for International Development
Office: (202) 712-5009
Mobile: (301) 646-6235

> On Nov 15, 2017, at 5:28 PM, Brooke Watson <watson@ecohealthalliance.org> wrote:
>
> Ah! Yes. The submitted *Science *paper (with supplementary materials) is
> attached.
>
> Thanks,
>
> Brooke
>
>> On Wed, Nov 15, 2017 at 5:23 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:
>>
>> Thanks Brooke. Do you also have the cleaned up Science paper. Also,
>> Eri, is there a draft MOU with BioHub we can share (noting its a draft)?
>> thanks
>>
>>
>> On Wed, Nov 15, 2017 at 3:13 PM, Brooke Watson <
>> watson@ecohealthalliance.org> wrote:
>>
>>> Hi Dennis,
>>>
>>> Thanks for sending this list. I've attached a spreadsheet with 3 tabs for
>>> bullet points 1-3: Outreach-to-date, Upcoming Funding Conversations, and
>>> Interested Countries. (also available in our shared Google Drive
>>> <https://drive.google.com/a/ecohealthalliance.org/file/d/1y9BvNDqHSYwP-b61Eita1LbcIYKagx1_/view?usp=sharing>.)
>>> I've updated Cara's old tracking document with the information I have, but
>>> there are many missing fields, and likely some additional outreach we've

>>> done that wasn't in any of my notes. *Eri, if you notice any outreach
>>> that I've missed, could you please update the spreadsheet? *
>>>
>>> I was traveling during last week's call, so i imagine you discussed
>>> bullets 4-6 (and that Jonna and Eri have access to at least #4 and #6.)
>>>
>>> We can discuss tomorrow on the weekly call.
>>>
>>> Thanks!
>>>
>>> Best,
>>>
>>> Brooke
>>>
>>>
>>> On Mon, Nov 13, 2017 at 3:04 PM, Dennis Carroll <dcarroll@usaid.gov>
>>> wrote:
>>>
>>>> Eri and Brooke, as a follow up to the discussion I had with BCG - they
>>>> have asked for the materials below. Can you pull these together? Some of
>>>> these can be topics in our next phone call. Let me know if there are ones
>>>> you dont have
>>>>
>>>> thanks
>>>>
>>>> d
>>>>
>>>>
>>>>
>>>>> Hello Dennis,
>>>>>
>>>>> I hope your week has started off well.
>>>>>
>>>>> I wanted to follow up here to confirm that you will be able to share
>>>>> the below materials, ideally by week's end, so that BCG and our team can
>>>>> get up to speed on everything before next week's meeting.
>>>>>
>>>>> Please let us know if there's anyway that we can help you here.
>>>>>
>>>>> Thanks,
>>>>> Jen
>>>>>
>>>>> *Materials Needed before Nov.21 from GVP technical team of Dennis,
>>>>> EcoHealth Alliance, UC-Davis and/or Metabiota*
>>>>>
>>>>> - Table of investors/funders approached with feedback and current
>>>>> status of those discussions (Arie to provide?)
>>>>> - Calendar of upcoming meetings with potential GVP investors
>>>>> - List of countries interested in GVP and how they are interested
>>>>> in engaging
>>>>> - Draft paper on the PREDICT project
>>>>> - Published paper on MERS virus and its many variants
>>>>> - Draft MOU in discussion with the Chan-Zuckerberg Biohub

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>>>>>> --
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>>> pandemics.*
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> <8_23_Carroll et al. Global Virome Project all.pdf>

ANNUAL REVIEWS

Annual Review of Animal Biosciences

Detection of Emerging Zoonotic Pathogens: An Integrated One Health Approach

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Keywords

emerging viruses, zoonoses, diagnostics, community engagement, laboratory networks, polymerase chain reaction, PCR, serology

Abstract

The emergence of novel zoonotic pathogens is one of the greatest challenges to global health security. The advent of increasingly sophisticated diagnostics tools has revolutionized our capacity to detect and respond to these health threats more rapidly than ever before. Yet, no matter how sophisticated these tools become, the initial identification of emerging infectious diseases begins at the local community level. It is here that the initial human or animal case resides, and it is here that early pathogen detection would have maximum benefit. Unfortunately, many areas at highest risk of zoonotic disease emergence lack sufficient infrastructure capacity to support robust laboratory diagnostic systems. Multiple factors are essential for pathogen detection networks, including an understanding of the complex sociological and ecological factors influencing disease transmission risk, community engagement, surveillance along high-risk human–animal interfaces, and a skilled laboratory workforce. Here we discuss factors relevant to the emerging disease paradigm, recent technical advances in diagnostic methods, and strategies for comprehensive and sustainable approaches to rapid zoonotic disease detection.

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THE EMERGING ZOONOSES PATHOGEN CONTEXT

Few threats to human health have the potential to cause more impact than emerging zoonoses. More than half of all known human pathogens have their origins in animals (1–7), and all but one of the 17 US National Institutes of Health Category A pathogens capable of causing severe human illness and mortality are zoonoses (8). However, the entire list of all known pathogens represents what is likely to be only a small fraction of the total potential pathogens that exist in nature (9, 10). It is the threat posed by these unknown, yet-to-emerge pathogens that requires a reinvigorated and sustainable pathogen detection network based on One Health principles to prevent a global widespread pandemic resulting from a zoonotic agent.

A striking example of the need for broad-based and robust detection networks is the recent emergence of a relatively well-known pathogen, Ebola virus (*Zaire ebolavirus*), in 2013 in Guinea, Sierra Leone, and Liberia (11–13). Although Ebola virus disease has been recognized for over 40 years, this devastating outbreak rapidly intensified and was eventually over 60 times larger than any previous Ebola outbreak (14–16). Over nearly three years, more than 11,000 lives were lost, and the virus affected individuals in 7 additional countries, as it stretched local and international pathogen detection and disease control capacities to their utmost limits (17, 18). Despite tremendous advances in diagnostic technology since the virus's discovery in 1976, this outbreak demonstrated that technology alone is not sufficient if resilient and integrated human and animal disease surveillance and laboratory systems are not prepared. A key lesson is that human capital and technical expertise are needed to rapidly identify potential health threats, no matter where they may occur, which requires coexistent and sustainable funding, training programs, and engagement from national and international partners.

Numerous authors (2, 4, 19–21) have defined the modern concept of an emerging or reemerging pathogen. Engering et al. (19) elegantly summarized the pathogen-host-environment interplay in their 2013 work, and their concepts can, at their core, be most simply thought of as an unexpected disease in an unexpected place. It is the concept of time and place that provides the context of emergence. This scenario can vary dramatically, from newly recognized and never before detected threats, such as Lassa fever, Lujo hemorrhagic fever, SARS, and Heartland virus disease (22–25); to macrolevel shifts of known pathogens to new geographic locations, illustrated by migration of West Nile virus to the United States (26, 27) and Ebola virus to West Africa (11); to species jumps into new hosts, including H5N1 avian influenza virus to humans (28) or Nipah virus from bats to pigs to people (29). The concept of place further extends down to the microscopic level, as changes in a pathogen's tropism in tissues and disease pathogenesis result in novel clinical presentations, such as Zika virus neurological sequelae in human newborns (30, 31), or to the molecular scale of genomic mutations resulting in enhanced antimicrobial drug resistance (32). Thus, the drivers of emergence can occur at any level in our broader environment, from massive global-scale events, such as intense climactic weather events resulting in Rift Valley fever virus outbreaks in East Africa (33) to changes in pathogenesis or transmission dynamics that can give rise to a wholly new disease entity, like variant Creutzfeldt-Jakob disease (34). The massive breadth over which emergence can occur defines a primary challenge in detecting newly emerging zoonoses.

Beyond biological factors, the ecology, sociology, and behaviors of humans and animals greatly influence the transmission interface and enable the spillover of a new pathogen from an animal reservoir host into the first human case and can greatly influence further dissemination and transmission through the human population (6, 35–38). Here we seek to explore the complex and dynamic factors leading to zoonotic pathogen emergence, review diagnostic methods to detect these new health foes, and discuss approaches to enhance disease surveillance through local community engagement to ensure rapid identification of new human and animal health threats.

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HUMANS, ANIMALS, AND PATHOGENS: AT THE INTERFACE OF BIOLOGY AND BEHAVIOR

Humans have been interacting with animals and their associated pathogens since the beginning of our species (6, 35, 39). As human society developed, certain animal species were found to be beneficial as sources of food, fiber, and companionship, as well as for use as beasts of burden, and were domesticated and habituated to human contact. Other animals remained wild and were either too elusive to farm, like the African duiker antelope (*Sylvicapra grimmia*), or simply too dangerous for regular close contact and possible domestication by humans, such as the North American brown bear (*Ursus arctos*). In modern times, as a result of explosive human growth and changes in animal and land use patterns, we have dramatically increased our contact with previously wild and otherwise unknown animal species (40–42).

Over time, changes in human population density, mobility, lifestyle, behaviors, and food choices have all influenced the dynamics of zoonotic disease emergence and have served as drivers of pathogen transmission (43–46). As the human population has grown, the influence of increased urbanization, coupled with higher incomes, has also led to greater demands for domesticated and wild animal meat products. This development has greatly expanded both our consumption of animal-source protein and our need for land to grow these animals and their feedstuffs, leading to tremendous modification of previously remote and seldom-visited regions into ever more intense livestock and agricultural production areas (47). This expansion of animal production into areas with greater abundances of wildlife has resulted in numerous examples of zoonotic disease emergence directly related to agricultural practices, including henipaviruses (pigs and horses); Middle East respiratory syndrome-coronavirus (CoV) (camels); Crimean-Congo hemorrhagic fever virus (ostriches); and other tick-borne bunyaviruses, such as severe fever with thrombocytopenia syndrome virus (livestock) (48–51).

However, despite the importance of domesticated and wild animal interactions in zoonotic disease emergence, a key driver of emerging zoonoses remains direct human contact with wildlife, their by-products (e.g., guano), and their meat for consumption (19, 52, 53). The intensification of wild animal meat hunting in the so-called bushmeat trade is driven by human taste preferences and allows for the direct contact of susceptible humans with animal reservoirs of a tremendous diversity of potential pathogens (53–56). In 2005, Wolfe et al. (46) reported that an estimated 4.5 million tons of bushmeat are harvested in the Congo basin alone. Human contact with wild animals during hunting, slaughtering, and consumption has been directly linked to the emergence of several known high-consequence zoonoses, including monkeypox, SARS-CoV, and ebolaviruses, as well as simian retroviruses such as Simian foamy virus and T-lymphotrophic viruses 3 and 4 (57–61).

Understanding and appreciating human behaviors related to wild animal use and the importance of local belief systems and customs regarding the concepts of disease, death, fear, and funeral practices are an often-neglected part of emerging disease surveillance activities (62, 63). The recent West Africa Ebola outbreak exemplifies the need for greater understanding of these human behaviors and how they may further interactions with animal reservoirs and their pathogens. Greater appreciation of these human factors can lead to insights into the magnitude of high-risk behaviors undertaken by community members (64–66). Local traditional health workers are often a societal pillar in many communities and can play a very important role in the recognition and eventual control of emerging pathogens (62, 67). The influence of these traditional healers as key sources of information in local communities can greatly help or hinder efforts to reduce the intensity of disease outbreaks (68). It is essential that they be recruited and encouraged early in the design of any disease surveillance system to become partners in the activities. If properly informed, these individuals can be tremendous facilitators, encouraging ill individuals to seek treatment, influencing

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changes to burial customs if needed, and helping to mitigate the impacts of fear on a population (69, 70).

During the West African outbreak, lack of initial engagement with traditional healers by health professionals, coupled with a pervasive mistrust of outsiders or government workers using non-traditional methods, led to an early reluctance of communities to engage in disease surveillance efforts (71, 72). This misstep likely compounded early efforts to slow the spread of the virus, as reactions to international efforts during the outbreak ranged from reluctance to seek medical help at Ebola treatment centers to, most strikingly, the attacking and killing of international health responders in eastern Guinea (73). To help overcome these tremendous anticipatable challenges in the future, it is imperative to promote early and intensive community-level engagement by medical anthropologists and disease surveillance professionals working in combination with local traditional healers and local village-level governance structures so that these community leaders become a part of any integrated and comprehensive zoonotic disease surveillance system.

THE EMERGING PATHOGEN-DETECTION PATHWAY

The increasingly intense and complex interactions of people, animals, and pathogens across the local and global landscapes all point to an ever-increasing risk of the emergence of a zoonotic pathogen with true pandemic potential that could threaten the survival of millions of animals and people (37, 74, 75). The initial detection of this threat, by necessity, begins at the local level with the observation of sick individuals (persons or animals) by someone familiar with the common diseases of the area. Oftentimes, this initial observation is never reported beyond the local area, as the disease is not recognized as unusual or does not spread, but in some instances the recognition of initial cases or the resulting chain of multiple events may lead to the eventual engagement of regional or national government authorities and possible involvement of international health responders. In many countries, centralized systems have been developed in which epidemiologic and laboratory diagnostic technologies and capacities reside in referral national-level centers distant from many of the high-risk human-animal interfaces at the forefront of disease emergence (76). In these instances, patient or animal clinical information, reports of die-offs or other unusual illnesses, and eventually diagnostic specimens for testing are pulled up from the local level to these referral centers.

Despite successes, this centralized pull pathway can fail at a variety of levels, as the barriers for the flow of information and diagnostic specimens up from the household to the national level can be difficult to overcome. Issues, such as poor transportation or communication networks, lack of trained health workers, limited laboratory systems, poor interagency or ministerial communications between the animal and public health sectors, mistrust of government officials, and sometimes suboptimal national reporting systems, all contribute to delays in the recognition, diagnosis, and eventual control of emerging health threats.

The central challenge then in the rapid detection of emerging zoonoses at a systems level is how best to create robust and resilient surveillance networks capable of detecting the rare and isolated health event at the local level and to link those observations with a highly skilled public health laboratory workforce (77). Is a highly centralized and concentrated network in national- or regional-level reference institutions or government ministries, or instead in a distributed network of local partner-driven surveillance teams with basic laboratory capacity for point-of-care rule-in/out diagnosis, or perhaps even a combination of both most likely to succeed? Key questions that influence the determination as to which of these approaches is most appropriate for a particular country relate to the sustainability of funding, training needs, and sophistication of laboratory techniques needed for pathogen detection. Examples of successes from a combination of

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national- and local-level surveillance networks with support from international organizations have been developed in several countries (78, 79).

Disease surveillance systems that seek to integrate the human and animal health sectors as closely as feasible are likely to be best positioned to rapidly detect emerging zoonotic threats. In these combined surveillance activities, human and animal health workers and field ecology teams would work together with the common scientific and public health goal of detecting novel emerging pathogens from animal reservoirs and the human population as quickly as possible. Combining this integrated approach with efforts to push down as close to the local levels as possible the technical training and laboratory infrastructure needed for zoonotic disease detection may be ideal. Systems that use a locally driven and distributed component may be potentially more expensive and more difficult to manage than exclusively centralized systems, but by being closer and more integrated into the local community, their ability to rapidly detect rare health events for follow-up are likely to be enhanced over completely centralized systems.

Since 2009, the US Agency for International Development (USAID) Emerging Pandemic Threats Program has funded the PREDICT project, providing one such example of this type of integrated program for zoonotic disease detection. Since its conception, the PREDICT program has endeavored to engage with communities and reinforce zoonotic disease surveillance activities by providing in-depth capacity building for human and animal health field and laboratory workers while simultaneously conducting active surveillance and laboratory detection for emerging novel zoonotic viruses in people and animals. The goal of the PREDICT project is to rapidly identify emerging novel viral threats to human and animal health using techniques that are pushed to the local level as far as possible to rapidly detect new and unknown pathogens while building capacity in national systems to characterize and mitigate epidemic risk. The PREDICT team is also active in the global health community, working to assess the potential of these newly discovered viruses to cause large-scale outbreaks or pandemics. At its core, PREDICT seeks to build capacity throughout the world by providing training to scientific staff in over 30 countries, developing networks of institutions, public health and veterinary staff, and technical experts to enable in-country detection of emerging disease threats. PREDICT teams concurrently conduct wildlife, domestic animal, and human surveillance in disease emergence hotspots by safely collecting biological specimens and ecological risk data and conducting behavioral risk assessments from ill human patients at high-risk transmission interfaces (see sidebar titled Note from the Field: The USAID Emerging Pandemic Threats PREDICT Program).

BUILDING EFFECTIVE AND RESILIENT SURVEILLANCE NETWORKS

To be functional, integrated approaches require long-term, sustainable funding and investment in human capital, infrastructure, and laboratory and communications technology to build local or regional surveillance hubs. One impetus that has sped the development of integrated animal and human health surveillance systems for zoonoses is the adoption in 2005 of International Health Regulations (IHR) by 196 World Health Organization (WHO) member countries in the wake of the SARS pandemic in 2001 (80). These regulations, coupled with the increased recognition that disease emergence in one country could easily spread to another through movement of animals or people, has provided an opportunity to more closely link the human and animal disease surveillance sectors. IHR requires the timely notification (<24 h) of outbreaks "of disease with the ability to cause serious public health impact and to spread internationally" and may constitute a "Public Health Emergency of International Concern" (81). The regulations do not stipulate the source of the infection (human or animal) and are meant to be applied as broadly as possible by all member nations.

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NOTE FROM THE FIELD: THE USAID EMERGING PANDEMIC THREATS PREDICT PROGRAM

PREDICT, a project of USAID's Emerging Pandemic Threats Program, was initiated in 2009 to strengthen global capacity for detection and discovery of viruses with pandemic potential that can move between animals and people. Currently, in its second five-year phase, the project is focused on the detection of emerging zoonotic pathogens such as coronaviruses, the family to which SARS and MERS belong; paramyxoviruses, like Nipah virus; influenza viruses; and filoviruses, like the Ebola virus. The PREDICT consortium led by the University of California, Davis, One Health Institute strives to build upon One Health partnerships. These cross-disciplinary collaborations are critical for gaining a fuller understanding of the integral links among human, animal, and environmental health that can provide opportunities for prevention or early detection and control of disease threats. Working across sectors and including a diverse range of stakeholders and expertise help to operationalize efforts that promote public health, effective natural resource management, and development. Toward this overarching goal, the program has worked closely with a wide range of government ministries, scientific and educational institutions, local organizations, and other stakeholders to further One Health initiatives.

Now working with partners in over 30 countries and in over 60 in-country laboratories, PREDICT is continuing to build platforms for viral surveillance and for identifying and monitoring zoonotic pathogens, or those that can be shared between animals and people. Using the One Health approach, the project is investigating the behaviors, practices, and ecological and biological factors driving disease emergence, transmission, and spread. Through these efforts, PREDICT is improving global disease recognition and beginning to develop strategies and policy recommendations to minimize pandemic risk. PREDICT's surveillance for emerging pathogens focuses on areas of the world at the highest risk for zoonotic disease emergence. The goal is to move countries away from a reactive post-outbreak response to a proactive approach in which pathogens of pandemic potential are discovered at their source before large-scale epidemics occur in people.

PREDICT has made significant contributions to strengthening global surveillance and laboratory diagnostic capabilities for new and known viruses. During the first five-year period (2009 to 2014) the project has successfully detected over 800 novel viruses in more than 20 countries. The program's viral detection success lies in the use of broadly reactive consensus (genus/family level) PCR supplemented with high-throughput sequencing (95). These powerful tools produce specific, high-resolution data, allowing for rapid detection of known and new potential pathogens. PREDICT has developed and optimized detection protocols and built capabilities in laboratories serving the countries in which the program is engaged to improve regional capacity to detect pandemic threats (**http://www.predict.global**).

The costs of developing strong disease detection systems that would enable the full enactment of the IHR are relatively modest and attainable (82). The World Bank estimated in 2008 the total costs of implementing a robust One World–One Health work force to be approximately US$852 million in the 49 lowest-income and most at-risk countries (1). This figure, when compared with the estimated costs of the single 2001 SARS pandemic (US$40–50 billion), is cost effective by any measure (83). The comprehensive World Bank approach to building this workforce would leverage outside international aid funding (e.g., World Bank, WHO, UN Food and Agriculture Organization, USAID, or other national governments) to collaborate with and augment existing academic centers, private institutions, and local government partners to ensure that initial start-up costs and training burdens are managed to facilitate rapid training and enhancement of local surveillance and diagnostic capacities (82). Ideally, over time, as technical expertise is established, the role of international aid agencies can be reduced, leaving behind a core staff capable of responding to emerging health threats within each country or region.

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A key first step in this process is the identification of local, national, and regional partners to collaborate and develop structures in concert with these international agencies and to identify talented and motivated individuals. These persons ideally should come from diverse scientific backgrounds and across all sectors, including human, animal, and wildlife health specialists; epidemiologists; laboratory and behavioral scientists; and other junior and senior personnel, to build an experienced and integrated zoonotic disease-detection network of individuals and institutions.

Training needs may vary from country to country and are highly dependent on the preexisting academic and governmental training programs and infrastructure. For example, the PREDICT program (**http://www.predict.global**) has been engaged with multiple countries spanning the spectrum from those with highly advanced tertiary medical care centers and strong internationally focused academic centers to those lacking basic infrastructure and preexisting individuals who can readily conduct disease surveillance or laboratory testing. At a minimum, close peer-to-peer mentoring by experts in the field and hands-on in-person training are necessary to prepare any integrated One Health surveillance team. To sustain these efforts, other key skills, such as scientific writing, design of hypothesis-driven experimental approaches, and grant and proposal preparation, must be included among training activities. By encouraging an academic and entrepreneurial spirit of collaboration and engagement, these teams are more likely to be able to identify sources of funding from the governmental or private sectors to maintain their research efforts well beyond the initial phases of the integrated surveillance project.

INTEGRATED LABORATORY TESTING TO SPAN THE DIAGNOSTIC SPECTRUM

It is important to note the differences in the dynamics of pathogen infection between potential reservoir and nonreservoir hosts (**Figure 1**). In true reservoirs, infection is generally not overtly deleterious to the host in a healthy state and often leads to the establishment of a nonsymptomatic persistent infection with intermittent reactivation of pathogen replication and environmental shedding in response to environmental or hormonal queues, such as those observed for hantaviruses and arenaviruses in rodents or nairoviruses in Egyptian fruit bats (*Rousettus aegyptiacus*) (84–86). This healthy carrier pattern in reservoirs is markedly different from the classical infection paradigm in nonreservoir, susceptible hosts, where infection leads to pathogen replication and either pathogen clearance via activation of immune response or, if immune control is unsuccessful, eventual disease and either a chronic persistent infection, a potential convalescent, a carrier state, or lethality. The initial design of a comprehensive pathogen-discovery program must consider these differences so that the appropriate diagnostic technologies [i.e., molecular nucleic acid amplification techniques (NAAT) versus serological antibody detection–based assays] are used to afford the best opportunity for pathogen/infection detection. To be most effective, laboratory scientists and experts in diagnostic technologies should be involved at the conception and program design stages, as well as be invited to contribute extensively in the implementation of zoonotic pathogen surveillance activities. This integration will help to ensure that relevant specimens are collected, transported, and stored appropriately to allow for the best chance for later identification of etiologic agents and surveillance successes.

Fortunately, the variety and quality of diagnostic technology and specimen collection materials have expanded tremendously over the past 40 years (87). The evolution of diagnostics and the use of these technologies has led to a vast increase in our understanding of the microbial world and the potential zoonotic pathogens capable of impacting human and animal health (**Table 1**). Ideally, the methods employed will be selected or designed both to allow for the detection of emerging

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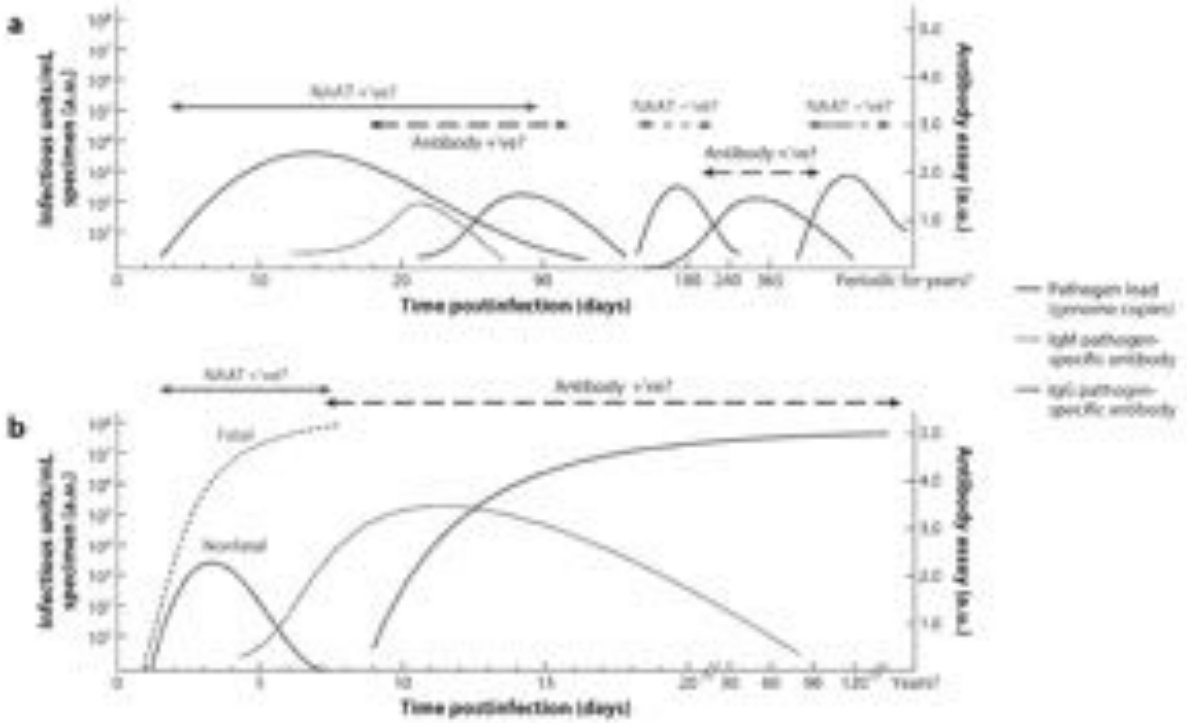

Figure 1

Hypothetical schematic comparing the kinetics of pathogen replication and host immune responses between a potential reservoir and a nonreservoir host that influence detection assay performance and utility. (*a*) Reservoir dynamics: reinfection or persistent infection with intermittent pathogen shedding and detection. (*b*) Nonreservoir dynamics: acute infection, immune response, and pathogen clearance. Comprehensive disease diagnostic systems require both nucleic acid amplification techniques (NAAT) for acute-phase disease detection and serologic techniques to detect convalescent humans or animals, including persistently infected reservoirs. Note that typically classical techniques, such as pathogen culture or isolation, are possible only during the acute-phase (NAAT +ve) time window. Red line indicates pathogen load (genome copies), and blue and purple lines indicate immunoglobulin M (IgM) or IgG pathogen-specific antibody, respectively.

zoonoses during the acute phase of infection, while the patient or animal remains acutely infected with active pathogen replication or shedding, and to monitor for antibody development and persistence after recovery, when the potential pathogen may no longer be present and available to cause disease in the monitored patient or other individuals (**Figure 1**). For many known high-consequence viral pathogens, the acute phase of infection is only a few days long and typically ranges from 2 to 21 days postinfection (88, 89), thus limiting the time that molecular diagnostic techniques targeting the pathogen genomic material, such as polymerase chain reaction (PCR) and its derivatives, may be diagnostically useful.

The advent of highly sensitive and specific molecular techniques that can directly detect a pathogen's genome based on NAAT technologies, such as PCR amplification of RNA (after reverse transcription) and DNA, has revolutionized pathogen discovery. NAATs such as conventional PCR, real-time quantitative PCR, and Sanger whole-genome sequencing have forever changed the diagnostic landscape, especially for viral pathogens (90). However, the exquisite sensitivity and specificity of these techniques limit their use in the detection of widely divergent and unknown novel pathogens, or even variation among strains of known pathogens, owing to genomic sequence

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Table 1 Diagnostic methods and zoonotic pathogens

Method	Technical requirements	Costs	Advantages	Disadvantages	Key examples	Reference
Acute phase of disease						
Electron microscopy	+++++	++++	Visualization of pathogen in situ	High technical expertise required; expensive	Ebola virus, SARS-CoV	16, 24
Pathogen isolation or culture	+++	+++	Sensitive, pathogen available for further assessment, suitable for unknown pathogens	Lab biosafety requirements; choice of cell line/media may limit sensitivity and unknown pathogen detection	Sosuga virus, SARS-CoV, Nipah virus, Ebola virus	16, 24, 101, 106
Histology/ immunohistochemistry	+++++	++++	Assessment of tissue pathology	Requires cross-reactive antisera and high technical expertise	Zika virus (in neonatal CNS tissue)	30
Rapid diagnostic tests or lateral flow assays	+	+	No electricity needed, generally thermostable, low skill required to operate	Limited sensitivity; interpretation of weak results can be difficult; not suitable for unknown pathogen discovery	Influenza; Ebola virus Mabijula commercial examples	107, 108
Antigen capture and IgM ELISA	+++	+++	Adaptable to high-throughput screening, excellent counterpart to molecular testing for known pathogens during outbreak responses	Requires cross-reactive antisera, moderate technical and lab requirements; some humans/ animals have broadly reactive sticky serum yielding false positives	Mabijula commercial/ experimental examples	98, 109
Conventional PCR/RT-PCR and sequencing	++ to +++	++ to ++++	High sensitivity and specificity depending on primer design; can be broadly reactive; PCR amplicons can be sequenced for further confirmation and pathogen characterization	Moderate technical and lab requirements; cold chain requirements for reagents; easily contaminated techniques can result in inaccurate or difficult-to-interpret results	Sin Nombre virus, Nipah virus coronaviruses, Bundibugyo virus, MERS-like CoV	93, 109–112
Quantitative real-time PCR/RT-PCR	+ to +++	+++ to +++++	Highest sensitivity and specificity available for known pathogens; some systems approaching push-button ease of use; reduced potential for lab contamination and false negative/pos results	Not suitable for unknown pathogen discovery; PCR amplicons not suitable for subsequent genome sequencing and confirmation	Detection of Marburg virus in bat reservoir	109

(Continued)

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Table 1 (Continued)

Method	Technical requirements	Costs	Advantages	Disadvantages	Key examples	Reference
Whole genome Sequencing, VirCap (HTS/NGS etc.)	+++++	+++++	Unbiased genomic detection, highly adaptable to unknown pathogen discovery, bioinformatics risk assessment possible; can be used to track pathogen dispersal in a population (reintroduction versus ongoing transmission)	High cost; high technical expertise required especially for bioinformatics analyses; overall reduced sensitivity compared with PCR techniques	Heartland virus, Sosuga virus, Bas-Congo virus, SFTS virus	25, 105, 113–115
Convalescent phase of disease						
IgG ELISA techniques	++	++	Broad detection of past infections based on specific or cross-reactive antibodies; primary tool for prerequisite seroarways	Requires specific antisera and antigens; validation and establishment of positive/negative cutoff OD values required; antibody cross-reactivity can confound results, host species limitations	Multiple commercial/experimental assays	
Phage display antibody detection	+++++	+++++	Potential to detect wide range of antibodies to diverse pathogens and overall exposure history	Currently in experimental proof-of-concept stage; expensive and technically demanding	Experimental	99
Western Blot (antipeptides)	++++	++++	Highly specific; can be targeted to widely conserved protein peptides	Technically demanding; requires moderate laboratory infrastructure	Multiple commercial/experimental examples	

Abbreviations: CNS, central nervous system CoV, coronavirus, ELISA, enzyme-linked immunosorbent assay, IgM, immunoglobulin M.

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variation. In the past 10 years, strategies to overcome this limitation have been developed and successfully employed in pathogen detection, such as unbiased next-generation sequencing (NGS) or high-throughput sequencing (91–94) and refinements to traditional consensus PCR strategies to use highly degenerate primers to detect and amplify genomic material across entire virus families (95–97).

However, despite the ever-increasing sensitivity and throughput capacities of molecular diagnostics, the amount of pathogen genome in a given specimen type will begin to decrease and can rapidly fall below detectable levels as the infected person or animal ceases to actively shed infectious pathogens. In these circumstances, further pathogen monitoring becomes reliant on specific antibodies that are circulated following activation of the immune response during the acute phase of infection. These form an individual's pathogen exposure record (**Figure 1**). Evidence of previous infection in these individuals may be demonstrated by assays designed to detect pathogen-specific antibodies, such as the commonly employed enzyme-linked immunosorbent assay (ELISA). These techniques and other related antibody-detection modalities are essential to determining the overall scope of disease activity in a given location and species distribution and should ideally be part of any comprehensive laboratory plan (**Table 1**).

An exciting area of diagnostics development in the past five years has been the growth of so-called rapid diagnostics tests, or RDTs, for use in resource-poor settings. These lateral-flow assays are typically self-contained devices that, after addition of clinical specimen, use surface tension to flow specimens and reagents across an absorbent membrane precoated to detect the presence of either specific pathogen antibodies or even pathogen antigens present in the clinical specimen. Results generated from the specimen and relevant controls are observed visually or with a detection reader that quantifies the change in color on the device, indicating the presence or absence of the pathogen in question. The primary advantages of these devices are that they are often thermostable, require no electricity, and have minimal training requirements. Sensitivity and specificity of RDTs are typically lower than other, more sophisticated molecular and antibody techniques, such as PCR and ELISA testing, but their extremely low technological and infrastructure requirements make them highly useful in certain circumstances and represent the ultimate thus far in the ability to push diagnostic technology as far down locally as possible. RDTs for malaria detection and Ebola virus infection rule-out during corpse surveillance in the recent 2013–2016 Ebola virus outbreak in West Africa demonstrated this technology's potential to radically alter the diagnostic possibilities available after further refinement and development of this promising technology (98).

At the other extreme of the technology spectrum is the coupling of high-throughput next-generation sequencing and the power of bacteriophage-display technology to generate multivalent antibody-detection assays (99). This approach could allow for simultaneous detection of the entire repertoire of an individual's viral pathogen or viromic exposure history, rather than screening one or a few closely related pathogens using ELISA-based technology. Although still highly experimental, this technological advance may revolutionize pathogen detection in a manner similar to what PCR technology did in the 1980s and 1990s (100).

Despite the revolution and success of modern molecular and antibody detection techniques to identify acute zoonotic pathogen infections, other more classical techniques (i.e., indirect fluorescent antibody assays, virus isolation and bacterial culture, histology, immunohistochemistry, and electron microscopy) remain highly valuable and should not be neglected (**Table 1**). If a novel zoonotic pathogen is discovered by NAAT or serological techniques, follow-up activities, including pathogen characterization and virulence determination, even fulfilling Koch's postulates if possible, and therapeutics and vaccine development require the isolation of the etiologic agent in question, and these classical techniques are critical. However, certain pathogens are difficult to culture under laboratory settings owing to challenges in determining the selection of appropriate

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cell lines and growth conditions. These difficulties are exemplified by the nearly 16-year period between the discovery of hepatitis C virus in 1989 and the first successful in vitro cell culture of the virus in 2005 (101, 102).

Beyond the technical issues, the growth and characterization of zoonotic pathogens require well-equipped laboratories, higher biosafety and biosecurity infrastructure to protect investigators, specialized reagents, and highly trained laboratory staff that may be difficult to sustain in resource-poor settings, but the value of isolation of the etiologic agent in question cannot be overstated. Because of the high technical demands and the importance of biosafety and biosecurity, the use of these types of classical techniques may be best suited in some circumstances in a comprehensive push-pull detection strategy that employs collaboration between local/national laboratories and an international referral laboratory, as is available through the WHO Global Outbreak Alert and Response Network in an integrated system of laboratories (**http://www.who.int/ihr/alert_and_response/outbreak-network/en**). These latter facilities can assist local and national laboratories in the classical work-up, as well as provide further confirmation of putative PCR or serological assays using molecular NAAT assays that were pushed down to regional or locally based laboratories (101).

THE TANZANIA VISHA (VIRUS-SHARING) PROJECT: AN EXAMPLE OF CAPACITY BUILDING THROUGH INTEGRATED FIELD SURVEILLANCE AND PUSH-PULL LABORATORY SYSTEMS FOR NOVEL ZOONOTIC VIRUS DETECTION

In 2007, the University of California, Davis, One Health Institute and the Sokoine University of Agriculture in Morogoro, Tanzania, collaborated on a model One Health project to foster technical capacity building to improve in-country disease detection to promote the health of animals and livestock keepers throughout central Tanzania. Now in its tenth year, this collaboration, referred to as Healthy Animals and Livelihood Improvement (HALI, **http://haliproject.org/**) (104), has strengthened field ecology and laboratory systems; trained staff and students; and conducted wildlife, livestock, and human surveillance and laboratory detection of a variety of zoonotic pathogens, considering environmental influences and ecological drivers on population and pathogen dynamics. Recently, the collaboration was expanded to include the Ifakara Health Institute, another local counterpart specializing in human health activities. Together, these three research partners are conducting broad cross-sectional disease surveillance in wildlife and people in central Tanzania (**Figure 2**). At four sites in the region with high-risk human–wildlife interfaces, patients presenting at local clinics with nonmalarial undifferentiated febrile illnesses are offered participation in a pathogen discovery project. After informed consent is obtained, a detailed case investigation form is completed for each patient, and whole blood, serum, and oral and fecal swabs are collected. Later, a case investigator administers a survey instrument to determine the individual's exposure and interactions with wildlife and livestock to determine what risk factors may be present at the household level. Concurrently, field ecology teams sample wildlife (nonhuman primates and bats) in the catchment areas surrounding the study clinic sites. From these animals, oral and fecal swabs and blood specimens are obtained via nondestructive sampling techniques. Human patient enrollment forms and specimens are referred to the Ifakara Health Institute for consensus reverse transcriptase (RT)-PCR–based assays capable of detecting five priority virus families (coronaviruses, filoviruses, influenza viruses, paramyxoviruses, and flaviviruses). Identical NAAT assays are completed on all animal specimens at Sokoine University of Agriculture. Presumptive positives obtained via these techniques are then forwarded to the University of California, Davis, for further molecular confirmation (repeat RT-PCR, NGS, and other bioinformatics techniques)

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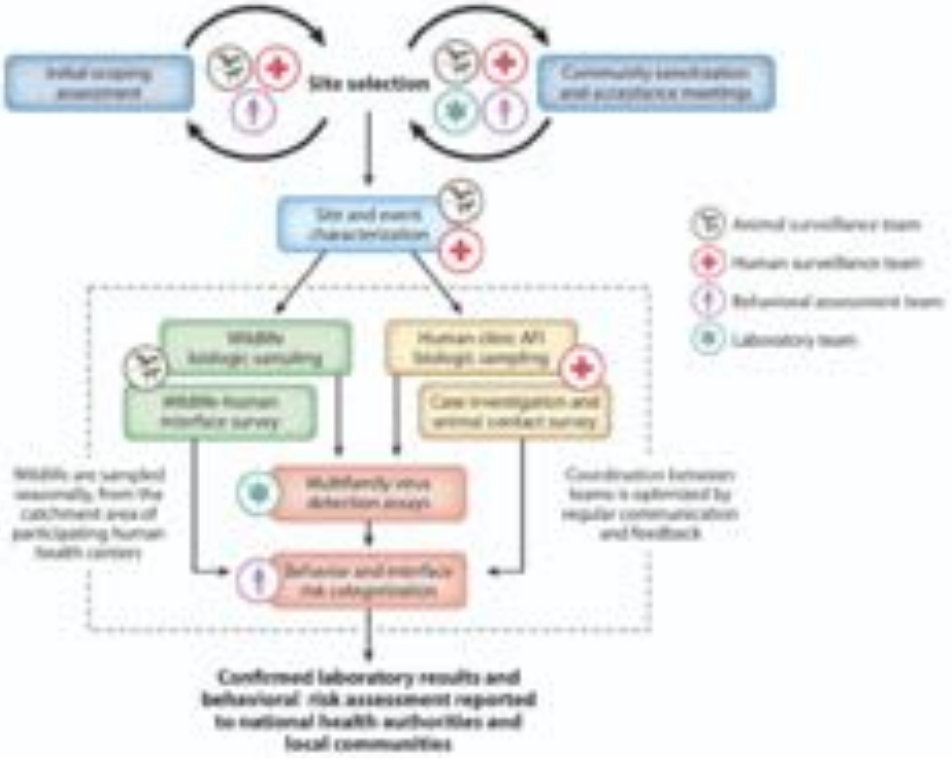

Figure 2

Schematic of the Health for Animals and Livelihood Improvement (HALI) project virus sharing project (VDSHA) implemented in central Tanzania. Active surveillance in both human health clinics for acute febrile illnesses (AFI) and adjacent wildlife populations affords the opportunity to monitor virus spillover and disease emergence at high-risk disease transmission interfaces. This strategy benefited from intellectual developments from the PREDICT Project and its leadership. The authors thank Dr. Leilani Francisco for her assistance with this graphic.

and to provide baseline assessments of the zoonotic and possible pandemic potential of any novel virus detected. Confirmed positives are then pulled to the appropriate international diagnostic reference center specializing in the isolation and characterization of the potential pathogen discovered. Through these combined efforts in active surveillance of animals and humans, novel virus discoveries and the demonstration of contemporaneous virus sharing among these populations are possible. Combining novel virus detection with the risk-behavior data from the patient and household surveys will enable the study team to craft public health messaging to reduce the potential exposure of further individuals to these health threats. Over the course of this US Defense Threat Reduction Agency–funded project, further training and capacity development have been provided for more than 25 individuals ranging from senior investigators to university interns and government field staff in the areas of laboratory diagnostics, field ecology, and human study bioethics and procedures, as well as to clinic staff in the four rural Tanzanian health clinics. It is hoped that the capacities built during this project will provide the basis for continued sustainable growth in Tanzania of a scientific workforce capable of zoonotic disease surveillance to improve the health of animals and the Tanzanian people.

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SUMMARY

Despite tremendous technological advances in the past 25 years, there remain massive challenges to developing robust systems capable of rapidly detecting emerging zoonotic disease threats. Establishing long-term, sustainable, and diagnostic modalities as close to the local level as feasible is a key step to rapidly identifying and alerting public health authorities and avoiding the next global pandemic. Regardless of the technology used and the scientific capacities developed, failure to engage and build trust with local political and thought leaders, traditional health workers, and community groups in disease detection and control will delay diagnosis and response, with potentially disastrous consequences. The rapid expansion of the West Africa Ebola crisis of 2013–2016 is a stark warning that zoonotic threats (novel or known) can emerge and quickly threaten global health security. Avoiding a repeat of this scenario and halting whatever the next global pandemic may be begins at the animal–human interface and with the initial spillover event in local communities. We must be prepared to recognize the signs, identify the threat, and rapidly work together to reduce the spread of infections and health consequences before they harm the health of animals and people throughout the world.

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VIRUS EVOLUTION

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Research article

Global patterns in coronavirus diversity

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Abstract

Since the emergence of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrom Coronavirus (MERS-CoV) it has become increasingly clear that bats are important reservoirs of CoVs. Despite this, only 6% of all CoV sequences in GenBank are from bats. The remaining 94% largely consist of known pathogens of public health or agricultural significance, indicating that current research effort is heavily biased towards describing known diseases rather than the 'pre-emergent' diversity in bats. Our study addresses this critical gap, and focuses on resource poor countries where the risk of zoonotic emergence is believed to be highest. We surveyed the diversity of CoVs in multiple host taxa from twenty countries to explore the factors driving viral diversity at a global scale. We identified sequences representing 100 discrete phylogenetic clusters, ninety-one of which were found in bats, and used ecological and epidemiologic analyses to show that patterns of CoV diversity correlate with those of bat diversity. This cements bats as the major evolutionary reservoirs and ecological drivers of CoV diversity. Co-phylogenetic reconciliation analysis was also used to show that host switching has contributed to CoV evolution, and a preliminary analysis suggests that regional variation exists in the dynamics of this process. Overall our study represents a model for exploring global viral diversity and advances our fundamental understanding of CoV biodiversity and the potential risk factors associated with zoonotic emergence.

Key words: coronavirus; viral ecology; bat; evolution.

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1. Introduction

In 2002/3, SARS-Coronavirus (SARS-CoV) emerged in the Guangdong province of southern China (Drosten et al. 2003; Ksiazek et al. 2003). It quickly spread to twenty-seven countries, infecting 8,098 people with 774 deaths, and was declared the first global pandemic of the 21st century. Bats were identified as the reservoir (Lau et al. 2005; Li et al. 2005) and probable source (Ge et al. 2013) of the outbreak. In 2012, the SARS pandemic was followed by MERS-Coronavirus (MERS-CoV), which emerged in the Middle East (Zaki et al. 2012) with 1,782 confirmed human cases and 640 deaths (as of September 2018). Camels were identified as the likely source of human infections (Reusken et al. 2013; Azhar et al. 2014); however, bats were again found to host closely related (MERS-like) viruses and are therefore assumed to be the original evolutionary source (Woo et al. 2006; Anthony et al. 2012; Corman et al. 2014a,b; Wacharapluesadee et al. 2015; Anthony et al. 2017).

Together, these outbreaks have cemented the coronaviridae as a family of zoonotic concern, and stimulated a surge in viral discovery efforts in bats (reviewed by Drexler et al. (2014)). These efforts appear to show that almost all human CoVs have zoonotic origins or otherwise circulate in animals, including human 229E (bats (Pfefferle et al. 2009); camels (Sabir et al. 2016)), NL63 (bats (Donaldson et al. 2010; Huynh et al. 2012)), and OC43 (cattle (Vijgen et al. 2005)). Even non-human CoVs such as porcine epidemic diarrhea virus (PEDV) may have emerged by host switching from other animals (bats (Tong et al. 2009; Huang et al. 2013)). Overall, it seems that CoV diversity in bats is substantial (Drexler et al. 2014), that these viruses are prone to host switching (Woo et al. 2009), and that they are a current, historic, and future threat to public health.

Despite recent efforts, there are several notable gaps in our understanding of CoV diversity. Foremost, our knowledge of CoVs in resource-limited countries is poor (Drexler et al. 2014). This is particularly problematic given that many of these same areas are predicted to be hotspots of disease emergence (Jones et al. 2008). Second, there has been little effort to understand the evolutionary and ecological drivers of CoV diversity on a global scale, or to evaluate host and regional variation in the factors that contribute to the risk of emergence (e.g. host switching). Indeed, most studies to date have been somewhat limited in their geographic scope and have included only small sample sizes with little epidemiologic or ecological context. In short, there is a critical need for a more global perspective on CoV diversity.

In 2009, the PREDICT project was established, in part, to address this need. Focused on strengthening capacity and identifying viruses in wildlife at high-risk interfaces (PREDICT Consortium 2014), this USAID Emerging Pandemic Threats (EPT) initiative worked with local partners in twenty countries across Latin America, Africa, and Asia over 5 years to better understand the current diversity of CoVs (as well as other viruses) and evaluate the factors that drive this diversity at different scales. Herein, we report a large diversity of CoV sequences (mostly from bats), show that the biogeography of bats has shaped the diversity of CoVs globally, and provide evidence to suggest there could be regional variation in host switching and the risk for zoonotic emergence.

2. Methods

2.1 Animals and samples

Bats (n = 12,333), rodents (n = 3,387), and non-human primates (n = 3,470) were humanely sampled (capture and release) from twenty 'hotspot' countries (Jones et al. 2008), representing central Africa (Cameroon, Gabon, Democratic Republic of Congo, Republic of Congo, Rwanda, Tanzania, Uganda), Latin America (Peru, Bolivia, Brazil, Mexico), and Asia (Bangladesh, Cambodia, China, Indonesia, Laos, Malaysia, Nepal, Thailand, Viet Nam). Samples were also collected from humans (n = 1,124) in seven countries in central Africa and Asia as a pilot to begin to explore the propensity for viral sharing with wildlife. In all twenty countries, wildlife samples were collected from 'high risk' interfaces, where direct or indirect contact with humans might promote zoonotic viral transmission. The selected sampling sites included areas of land-use change (deforestation, conversion to agriculture); sites in and around human dwellings; foci of ecotourism; markets, restaurants and farms along the animal value chain; and areas where occupational exposure was likely (animal sanctuaries, agricultural activities). When possible, individuals were identified to lowest taxonomic order (genus and species) and assigned to an age class (adult, subadult, neonate) by the field teams. All samples from swabs (e.g. oral, urine, rectal), fluids (e.g. saliva), and tissues were collected into (1) Nucleospin® Lysis Buffer (bioMérieux, Inc., Marcy-l'Etoile, France) and (2) viral transport media, and then frozen in the field in liquid nitrogen and transferred to the laboratory for storage at −80 °C. All animal sampling activities were conducted with permissions from local authorities and under the Institutional Animal Care and Use Committee at the University of California, Davis (protocol number: 16048). All human activities were reviewed and approved by the UC Davis Institutional Review Board (IRB), under protocols: 215253 and 432330.

2.2 Viral discovery

RNA was extracted from all samples, and cDNA prepared using superscript III (Invitrogen). Two broadly reactive consensus PCR assays targeting non-overlapping fragments of the *orf1ab* were used to detect both known and novel CoVs (Quan et al. 2010; Watanabe et al. 2010). The first (the 'Watanabe' assay (Watanabe et al. 2010)) amplified a ~434 bp fragment of the RNA-dependent RNA polymerase (RdRp) corresponding to nucleotides (NTs) 15,156–15,589 in the human CoV OC43 genome (NC_005147), while the second (the 'Quan' assay (Quan et al. 2010)) amplified a ~330 bp fragment of a different peptide downstream of the RdRp, corresponding to NTs 18,323–18,654. Amplified products of the expected size were cloned and sequenced (traditional Sanger dideoxy sequencing) according to standard protocols, and sequences edited manually in Geneious Pro (ver 9.1.3, Biomatters, Auckland, NZ). We note that this approach was adopted to facilitate viral discovery in resource-poor settings, which are the target of pandemic preparedness initiatives such as USAID PREDICT, and where techniques such as high throughput sequencing are largely unavailable.

2.3 Phylogenetics

Coronavirus sequences from the Quan and Watanabe datasets were aligned with reference sequences collected from GenBank using MUSCLE (Edgar 2004), followed by manual alignment in Se-Al v2.0a11 (http://tree.bio.ed.ac.uk). The best-fitting model of nucleotide substitution for each dataset was selected by Akaike's Information Criterion (AIC) using jModeltest v2.1.5 (Darriba et al. 2012). For both alignments, the general time reversible model with a gamma distribution of rate heterogeneity was the best fitting model. Maximum likelihood trees were constructed from each alignment using MEGA v6.06 (Tamura et al.

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2011). Histograms of all pairwise sequence identities (%) were plotted, as described previously for hantaviruses (Klein et al. 2009), and used to define cut-offs between viral sequence clusters for analysis (akin to operating taxonomic units).

2.4 Diversity measures

The Earth's surface was divided into grid cells, each 10° latitude by 10° longitude. Thirty-four of these grid cells included areas from which bats were sampled (bats were identified down to the species level in thirty cells), and twenty-seven cells had samples testing positive for CoVs. If the coordinates listed for a particular bat were on the line between grid cells, it was arbitrarily included in the grid cell with higher latitude/longitude. Viral and host species richness for each cell was calculated by determining the total number of unique virus and bat species within each cell. Alpha diversity was calculated using the Shannon index (Jost et al. 2011), which was chosen over the Gini–Simpson index because it does not place disproportionate weight on dominant species. Since we do not know how representative our sampling was, the Shannon index was deemed the best approach. The effective number of viruses and bats in each cell was then correlated using Kendall's tau, since the values were not normally distributed. Sensitivity analyses were performed by shifting the grid cells in 1° increments and recalculating richness and effective species numbers.

Matrices of beta diversity between each combination of grid cells were developed using the Jaccard index (Jost et al. 2011), and Mantel tests were used to determine whether the distance between grids was associated with the dissimilarity in virus and bat species. Geographic distance matrices were calculated by finding the centroid of each grid cell and calculating the geodesic distance between each pair using the *R* package 'geosphere'(Geosphere 2015) and tests were performed using Spearman's rank correlation. All analyses of diversity were conducted in R version 2.3.2.

2.5 Network model

A presence/absence matrix was constructed to show the distribution of viral sequence clusters across all species. Using the Python package NetworkX (Hagberg et al. 2008), a network model was constructed, connecting bat species to all viral clusters that were identified within that species in our data. The network is made up of thirty-one connected components, eighty-two viral clusters, eighty-five bat species, and 150 edges. Networks were plotted using Gephi using the force-directed algorithm ForceAtlas2 (Jacomy et al. 2014). Specifically, we plotted two bipartite graphs, one where hosts are colored by region and one in which they are colored by family.

2.6 Cophylogeny

The Jane (Conow et al. 2010) software tool was used for cophylogenetic reconstructions. This approach applies an *a priori* 'cost scheme' to different evolutionary events in order to test the degree of congruence between two trees (virus and host). These 'events' include cospeciation, duplication, host switching, and failure to diverge (or sorting) (Charleston 1998; Conow et al. 2010), which are used to create a minimal-cost reconstruction of the evolutionary history between the viruses and hosts. Another cophylogeny program, CoRe-PA (Merkle et al. 2010), uses a parameter-adaptive approach to estimate an appropriate cost scheme without any prior value assignment. For our analysis, we used Jane with the default pre-determined cost scheme where cospeciation is the null hypothesis and, therefore, the 'cheapest' event, with the assumption that host switching would theoretically be more costly than genetic drift within a species to which a virus is already adapted. Analysis was repeated with varied cost values in Jane to test for sensitivity to our cost scheme, as well as in CoRe-PA for robustness, and event types and costs from each reconstruction were compared between the two programs. As these changes ultimately did not significantly influence the outcome of the analysis, exact event assignments used in the final analysis were inferred solely from Jane with the default cost scheme.

The analyses were performed using all unique associations between viruses and their respective hosts (limited to bats). Alpha-CoV sequences and beta-CoV sequences were analyzed separately, since each appears to have diversified independently within bats. This gave us a total of four reconstructions (alpha-Quan, alpha-Watanabe, beta-Quan, beta-Watanabe). Only one instance of each virus–host association was included, even if multiple instances of the same association were observed (i.e. our analysis does not account for the frequency of detection). Associations were excluded if the host was not identified to the species level or if the cytochrome B sequence did not exist in GenBank or could not be amplified by PCR. The topology of the virus tree was inferred from the topology of the full tree for consistency, since subsets of sequences often produce different arrangements.

For each reconstruction, the most recent evolutionary event leading to a virus–host association was recorded. Given that sorting is particularly sensitive to missing data (it indicates a loss on the tree when in fact it may simply be an artifact of under-sampling), we have excluded this event from our analysis. We also distinguished between two potential types of host switching, based on an assumption that there could be differences in zoonotic risk between viruses that only move between closely related bats (e.g. those within the same genus) and those that are able to make more substantive jumps into distantly related species (those in other host genera or families). We therefore use 'host switching' to refer specifically to viral lineages that have moved into a host belonging to another genus or family, and 'sharing' to indicate a viral lineage that has moved into a *different* host species of the *same* genus (without speciating). We selected host genus as the cut-off to be consistent with current conventions of taxonomic hierarchy, and verified that the number of species per genus is relatively consistent between regions. We further verified that the mean genetic distance between host species is consistent between regions (i.e. that the taxonomic distance a virus has to navigate when moving between any two species is roughly similar in all three regions).

A binary regression model with logistic link function was used to investigate whether the degree of host switching varied by region. The dependent variable was host switching, and either cospeciation or sharing was the reference group. Region was the independent variable. We used the generalized estimating equations (GEE) (Liang and Zeger 1986) method in order to account for multiple event types within one family and derive a robust estimate of the standard errors. Event data for all four reconstructions were aggregated for the analysis. Where host–virus associations were duplicated, one was removed. If the duplicated event types did not agree (which can occur given the sensitivity of these methods to variation in topology and number of taxa in each tree (Conow et al. 2010)), we randomly selected one of the two possibilities and repeated the randomization 100 times. The GEE estimates from the 100 random iterations were then combined using rules established by

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Rubin (1987). The analysis was repeated to explore variation based on bat family (independent variable). Some families only possessed one type of event, which would introduce quasi-complete separation into the GEE model, so they were excluded from the corresponding models. However, the numbers of bat species within these excluded families were very small (<5) compared to the overall number of bat species for the whole study, so we felt this would not impact any overall trends.

2.7 Viral discovery effort

The relationship between sampling effort and viral discovery was evaluated using a log-link Poisson regression model, fitted with the count of viruses for each species as the dependent variable and the number of animals sampled as the independent variable. This model is universally applied with count data. The coefficient of the sample number variable is the log of the ratio of the expected number of viruses with (n + 1) samples collected to the expected number of viruses with n samples collected, where n can be any arbitrary positive integer. Using this estimated coefficient, we calculated the estimated numbers of viruses (viral sequence clusters) that can be found with respect to the sampling effort (i.e. all possible numbers of collected animals within a species), and they were then used to plot the estimated curve together with its 95% confidence band. We clarify that we use the term 'expected' to indicate the statistical expectation based on the estimate of the regression model. We acknowledge that the model fit is not as good as the model with an additional quadratic term of the independent variable, nonetheless it avoids the problem of over-fitting and realistically reflects the relationship between sampling effort and viral discovery when the number of animals collected is relatively lower.

2.8 Factors associated with CoV positivity

Due to the small numbers of positive individuals obtained for rodents, non-human primates, and humans, only bat data were analysed for factors associated with positivity. A total of 12,333 bats were tested. This included 5,624 males and 5,767 females (932 were not sexed). Among aged bats 7,385 were adults, 1,029 were sub-adults, and 8 were neonates (3,911 were not aged). Binary logistic regression models were used to evaluate significant variables, restricting analyses to species for which ≥50 individuals were tested. Model selection was first performed in R (version 3.2.5) (R Foundation for Statistical Computing, 2008) using the R package 'geoulti' and the step function, and the best model determined by AIC. A robust estimation of standard error was calculated by clustering by individual Animal Identification number to account for non-independence of multiple tests from the same animal using STATA 13.1, SE (College Station, TX, USA). The independent variables included in analyses were Specimen Type (blood, feces/rectal swabs, guano, oral/rectal sample, oral/nasal swabs, tissue, urine/urogenital swabs), Host Taxon (family, sub-family, genus), Host Age (adult, sub-adult, neonate), Season (wet, dry), and Interface (animal use, human activity, land use, pristine area). Season was designated as 'wet' or 'dry' according to month and proximity to the equator for each country. Interfaces were broadly grouped according to the type and intensity of animal contact with people, specifically (1) Land Use (animals sampled in areas with crops, extractive industries, livestock activities), (2) Animal Use (hunting, markets, restaurants, trade, wild animal farms, wildlife management, zoos/sanctuaries, handling by veterinarian/researchers), (3) Human Activities (ecotourism, in and around human dwellings), and (4) Pristine (where animal human contact was not likely). The model fit for each region was evaluated using the Hosmer–Lemeshow goodness-of-fit test and pseudo R^2 values.

2.9 Virus 'Hotspot' Maps

The number of viral sequence clusters (richness) in each subclade was summarized by host family (Supplementary Table S1), and chi square tests used to evaluate whether viral subclade and host family were independent of each other. Bat species richness maps were then created to infer hotspots of CoV diversity. For each viral clade, spatial distribution data on all bat species belonging to associated families was obtained from the International Union for Conservation of Nature (IUCN). Using ArcGIS version 10 (ESRI 2011), bat species were quantified by counting overlapping polygons. The resulting count data were then converted to a raster and plotted. All sampled bats, as well as all identified sequence clusters within the clade in question, were then plotted over the raster data.

3. Results

3.1 Global diversity of CoVs

A total of 19,192 animals and humans were assayed for the presence of CoV by consensus PCR (cPCR) (Table 1). The majority were bats (n = 12,333), representing 282 species from twelve families. Overall, the proportion of CoV positive individuals was 8.6% in bats (n = 1,066/12,333) and 0.2% in non-bats (n = 17/6,859). In other words, over 98% of all positive individuals were bats.

Partial sequences were obtained from two non-overlapping fragments of the orf1ab gene, yielding 654 sequences for the 'Quan' region and 960 for the 'Watanabe' region (see 'Methods'). There was a 27% overlap, where sequences were obtained for both regions from the same sample. The distribution of pairwise sequence identities defined a 90% cut-off between taxa (Fig. 1), and the resulting monophyletic groups (in which all sequences had ≥90% identity) used as our operating taxonomic units. Groups that shared less than 90% identity to a known sequence were labeled sequentially as PREDICT_CoV-1, -2, -3 etc, while groups sharing ≥90% identity to a sequence already in GenBank were considered to be strains of a known virus and assigned the same name as the matching sequence (e.g. Kenya_bat_CoV_KY35 or HKU-9). Sequences that shared >90% identity but were found in different hosts were considered part of the same taxonomic unit. Based on these criteria, 100 discrete viral taxa were identified, ninety-one of which were found in bats (Table 1; Fig. 2). Importantly, we make no claims that these groups correspond to 'species' as full orf1ab replicase sequences would be required for that (Ong et al. 2012). Instead we clarify that we are using these partial fragments to cluster sequences into 'operational taxonomic units' (analogous to OTU clustering in microbiome research). We also stress that our cut-off was determined based on two discrete regions within the orf1ab separated by >1,000 nucleotides, and that these regions correspond to unique peptides post-translational cleavage.

Of note was the detection of subgroup 2a CoV sequences in bats, humans and non-human primates from four different countries. This sub-clade is largely considered the rodent sub-clade (Lau et al. 2015; Wang et al. 2015; Tsoleridis et al. 2016), but here we detected sequences corresponding to the known virus betacoronavirus-1 in *Pteropus medius* from Bangladesh,

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Table 1. Summary of individuals tested and number positive for at least one coronavirus by host taxa

Host taxa tested	No. individuals tested	No. individuals positive	No. distinct viruses detected
Bats	12,333	1,045	85
Non-Human Primates	3,470	4	2
Rodents and Shrews	3,387	11	7
Humans	1,124	2	2
Total	19,192	1,082	100[a]

[a]Note: Numbers do not total as two viruses were detected in two taxa.

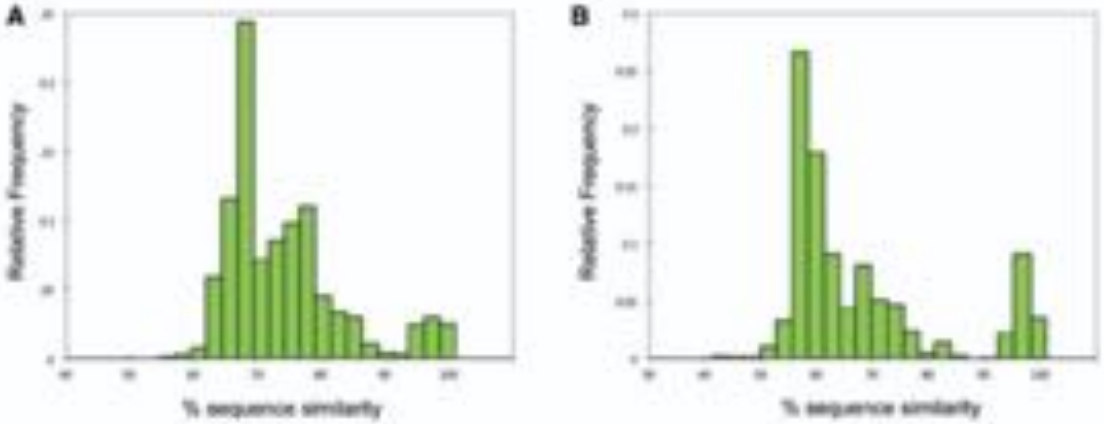

Figure 1. Histogram of the relative frequency of pairwise sequence identities used to define the cutoff between operating taxonomic units for all CoV sequences detected. A bimodal distribution was observed and a cutoff of 90% sequence identity used to separate sequences from both the Watanabe (Panel A) and Quan (Panel B) assays into discrete viral taxa.

Pteropus alecto from Indonesia, and from humans in China, and sequences corresponding to murine coronavirus in non-human primates from Nepal (these sequences were detected by four different laboratories, and no rodent samples were processed at the same time) (Fig. 2). In addition, we report the discovery of several sub-clade 2b and 2c CoV sequence clusters (the SARS and MERS sub-clades, respectively) (Fig. 2), and the detection of human coronavirus 229E-like sequences in hipposideros and rhinolophus bats sampled in ROC, Uganda, Cameroon and Gabon, supporting previous suggestions that 229E has zoonotic origins (Pfefferle et al. 2009; Hu et al. 2011). Finally, we highlight the detection of avian-associated infectious bronchitis virus-like sequences (IBV) in bats and a closely related virus (PREDICT_CoV-49) in non-human primates from Bangladesh, as well as porcine epidemic diarrhea virus (PEDV) in bats (Fig. 2). Again, we confirm that no livestock samples were processed in any of these laboratories that might have acted as a source of contamination.

3.2 Factors driving viral diversity

Viral α-diversity (the 'effective number' of species) was significantly correlated with bat α-diversity (tau = 0.325, $P = 0.022$) (Fig. 1), suggesting that more viruses will be found in regions where bat diversity is higher. This association was maintained when viral richness, rather than effective number of species, was used as the diversity index (tau = 0.421, $P < 0.001$). Viral and bat β-diversity were also significantly correlated (Mantel test, rho = 0.575, $P < 0.001$). In both cases, diversity differentiated almost entirely into three discrete communities by region (Fig. 3). Only Africa and Asia shared any viral sequence clusters (PREDICT_CoV-35 and HKU9; Fig. 4), demonstrating that bats have had a strong biogeographic influence on the global ecology and evolution of CoVs.

Co-phylogenetic reconciliation analysis was used to investigate the evolutionary mechanisms driving the virus-host associations observed, for example host switching, viral sharing, or co-speciation (see 'Methods'). Overall, host switching was the dominant mechanism, followed by co-speciation (Fig. 1). When analyzed by region, host switching (inter-genus transmission) remained dominant in Africa and Asia, but not in Latin America. Despite fewer host-switching events in Latin America, there was a concomitant increase in virus sharing (intra-genus transmission). This suggests that viruses are still switching hosts in Latin America but preferentially move between closely related species, while in Africa and Asia viruses cross between more distantly related species. To assess the sensitivity of our results to our chosen method (i.e. use of a pre-defined cost scheme in the program Jane), we repeated the analysis for the Quan alpha-CoV and beta-CoV reconstructions using CoRePA, a parameter-adaptive approach that estimates an appropriate cost scheme without any prior value assignment. Comparing the results, we noted 91% agreement between Jane and CoRePA in alpha-CoV reconstruction (thirty-four events, of which thirty-one agreed), and 100% agreement in the beta-CoV reconstructions (twenty-six events, all of which agreed). We further note that the cost scheme calculated in CoRePA was 0.7 for host switching and 0.1 for co-speciation—supporting the default cost scheme used in Jane (i.e. that host switching should be considered more 'costly' than co-speciation).

A bipartite network model connecting viral sequence clusters to their hosts supports these results, illustrating that bat CoVs were connected to several host families in Africa and Asia while being largely restricted to a single bat family in Latin

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Table 2. Variables associated with coronavirus positive bat tests in Africa, Asia, and Latin America. Regional datasets for each logistic regression model consisted of bat species where greater than fifty bats were tested. Age datasets were a subset of the regional datasets as age class was not determined for all individuals. Numbers in bold are statically significant for $P < 0.05$.

			Odds ratio	P	95% Confidence Intervals	
Africa						
	Sample type				Lower	Upper
		Feces/rectal swab	**350.98**	**<0.001**	**146.64**	**840.07**
		Oral/nasal swab	**5.05**	**<0.001**	**2.03**	**12.54**
		Oral/rectal swab	**30.98**	**<0.001**	**13.46**	**71.30**
		Blood	1.65	0.540	0.33	8.09
		Tissue	1.00			
	Host family					
		Hipposideridae	1.12	0.559	0.62	2.41
		Pteropodidae	**3.84**	**<0.001**	**2.27**	**6.49**
		Molossidae	1.00			
	Season					
		Dry	**2.42**	**<0.001**	**1.79**	**3.25**
		Wet	1.00			
	Interface					
		Animal use	**1.98**	**0.001**	**1.35**	**2.91**
		Pristine area	**1.39**	**0.026**	**0.37**	**5.29**
		Land use	**1.66**	**0.219**	**0.74**	**3.74**
		Human activity	1.00			
	Age					
		Subadult	**5.91**	**<0.001**	**4.28**	**8.17**
		Adult	1.00			
Asia						
	Sample type					
		Feces/rectal swab	**62.80**	**<0.001**	**35.44**	**255.49**
		Oral/nasal swab	**13.25**	**<0.001**	**3.13**	**56.38**
		Urine/urogenital swab	**46.93**	**<0.001**	**10.85**	**202.80**
		Guano	**22.12**	**<0.001**	**5.68**	**133.56**
		Tissue, Oral/rectal swab	1.00			
	Host family					
		Emballonuridae	0.35	0.26	0.06	2.37
		Miniopteridae	**9.78**	**<0.001**	**5.69**	**16.81**
		Pteropodidae	**2.16**	**<0.001**	**1.29**	**3.62**
		Rhinolophidae	1.08	0.82	0.57	2.03
		Vespertilionidae	**3.67**	**<0.001**	**2.18**	**6.18**
		Hipposideridae	1.00			
	Season					
		Dry	**1.45**	**0.03**	**1.03**	**2.16**
		Wet	1.00			
	Interface					
		Animal use	**3.30**	**0.01**	**1.29**	**8.40**
		Human activity	**3.48**	**0.01**	**1.36**	**8.95**
		Pristine area	1.81	0.35	0.52	6.35
		Land use	1.00			
	Age					
		Subadult	**1.84**	**0.00**	**1.26**	**2.67**
		Adult	1.00			
Latin America						
	Sample type					
		Feces/rectal swab	**15.68**	**0.006**	**5.02**	**48.79**
		Oral/rectal swab	**27.84**	**0.000**	**6.86**	**113.22**
		Oral/nasal swab	1.00			
	Host subfamily					
		Carolliinae	6.95	0.06	0.90	53.76
		Stenodermatinae	5.04	0.12	0.67	37.89
		Glossophaginae	1.00			
	Interface					
		Animal use	**5.25**	**0.01**	**1.48**	**18.65**
		Human activity	2.73	0.12	0.77	9.69
		Land use	4.22	0.10	0.78	22.95
		Pristine area	1.00			
	Season					
		Dry	1.30	0.52	0.58	2.89
		Wet	1.00			
	Age					
		Subadult	1.73	0.15	0.83	3.62
		Adult	1.00			

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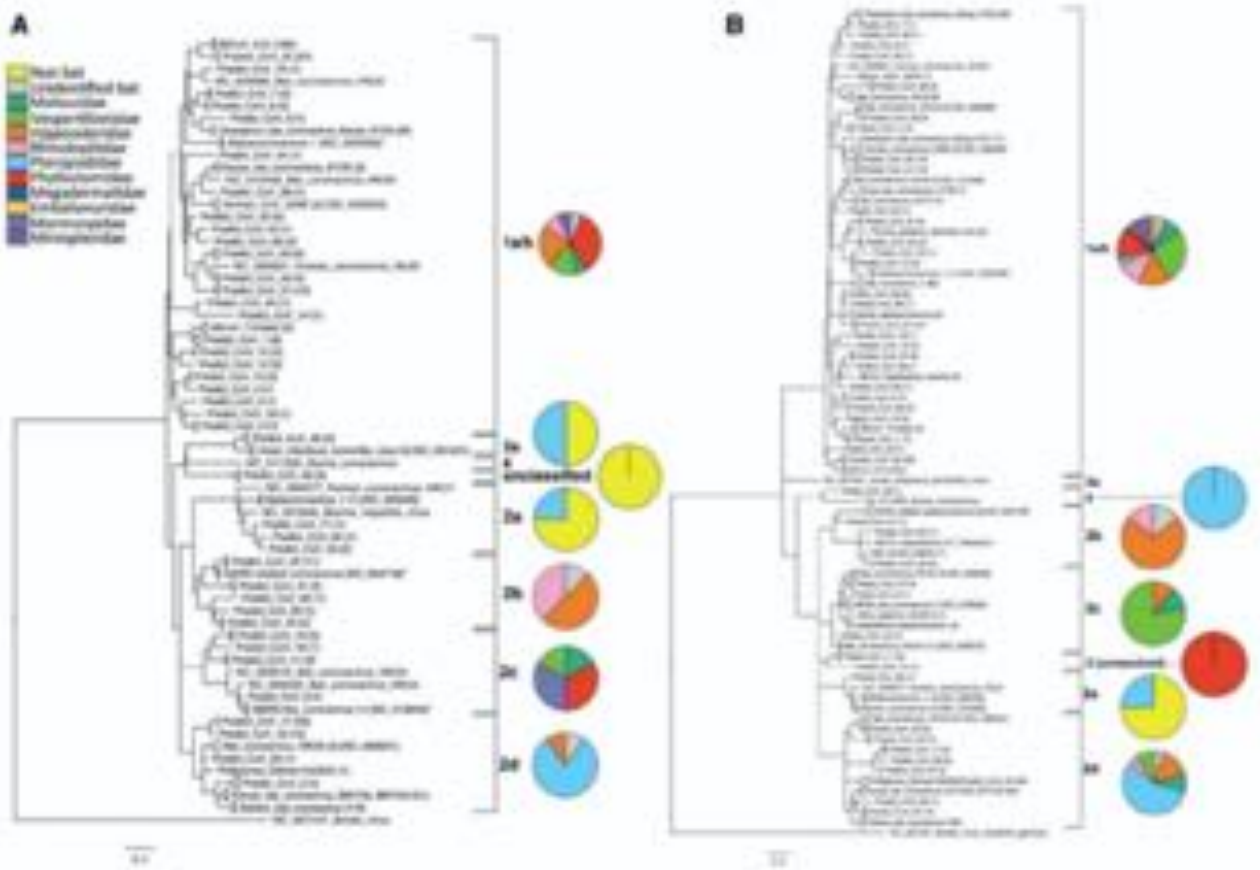

Figure 2. Maximum likelihood phylogenetic reconstructions for all partial CoV RdRp fragments for both the Qsun (Panel A) and Weisnabe (Panel B) assays. Sequences are collapsed into clades, representing our operating taxonomic units (sequences sharing >90% identity) and number of sequences for each taxon is indicated in parentheses. Representative published sequences from GenBank have been included for comparison (GenBank accession number indicated). Both trees were rooted using the related Breda virus (NC_007987) and all nodes have >60% bootstrap support. Pie charts indicate the distribution of viral taxa by host (bat) family, in each virus subclade.

America (Fig. 4, Panel B). Further, host switching was nearly four times more likely than virus sharing in Africa, when compared with Latin America (OR: 3.858; $P = 0.040$). CoVs in Asia were also more likely to host switch than share when compared with Latin America, however the results were not significant (OR: 2.474; $P = 0.143$). No particular bat family was associated with increased host switching, but this may reflect small sample sizes when the data are summarized by family.

3.3 Estimated number of CoVs in bats

A large number of host (bat) species in our study were negative for CoV (n = 197), however none of these species were sampled extensively (Fig. 5). We found that all species with sample sizes >110 individuals were positive for one or more CoVs, suggesting that we would have detected CoVs in some of the negative species in our study if sampling effort were increased. Due to the high number of these negative species and their effect on the average number of virus sequence clusters per species, they were excluded from our estimates. By retaining only those species for which >110 individuals were sampled (there were twenty-seven species that qualified), we estimated the average number of CoVs per species to be 2.47 (std = 1.38), thus accounting for the likely scenario that some species will have more viruses and others less. We then extrapolated the average to all 1,200 bat species to estimate a total potential richness of 3,204 CoVs (range = 1,200–6,000 CoVs), most of which have yet to be described.

3.4 Factors predicting CoV positivity

In order to refine future surveillance efforts to find the undiscovered diversity of CoVs in bats, we evaluated the factors predicting CoV positivity. For each region, the best model included specimen type, bat family (or in the case of Latin America, subfamily), season, and animal–human interface (Table 2). Season was not included in the top model for Latin America, but the model with the season included was within two AIC (delta AIC = 1.06) and therefore considered to have as much support as the top model (Burnham and Anderson 2002). Specimen type was highly associated with CoV positivity, and samples containing feces or fecal swabs were significantly more likely to test positive than other specimen types in all regions. Bat family was important in Asia and Africa. Season was also significant, with samples collected during the dry season more likely to test positive in Africa and Asia than those collected during the wet season (albeit with low odds ratios). Age class appears to be important, as sub-adults were more likely to test positive than adults in Africa and Asia. Sex was not related to CoV positivity in Asia or Latin America while males were slightly more likely to be CoV positive in Africa (OR = 1.3, 1.2–1.9 CI, $P < 0.001$). Broad categories of animal–human interfaces were significantly

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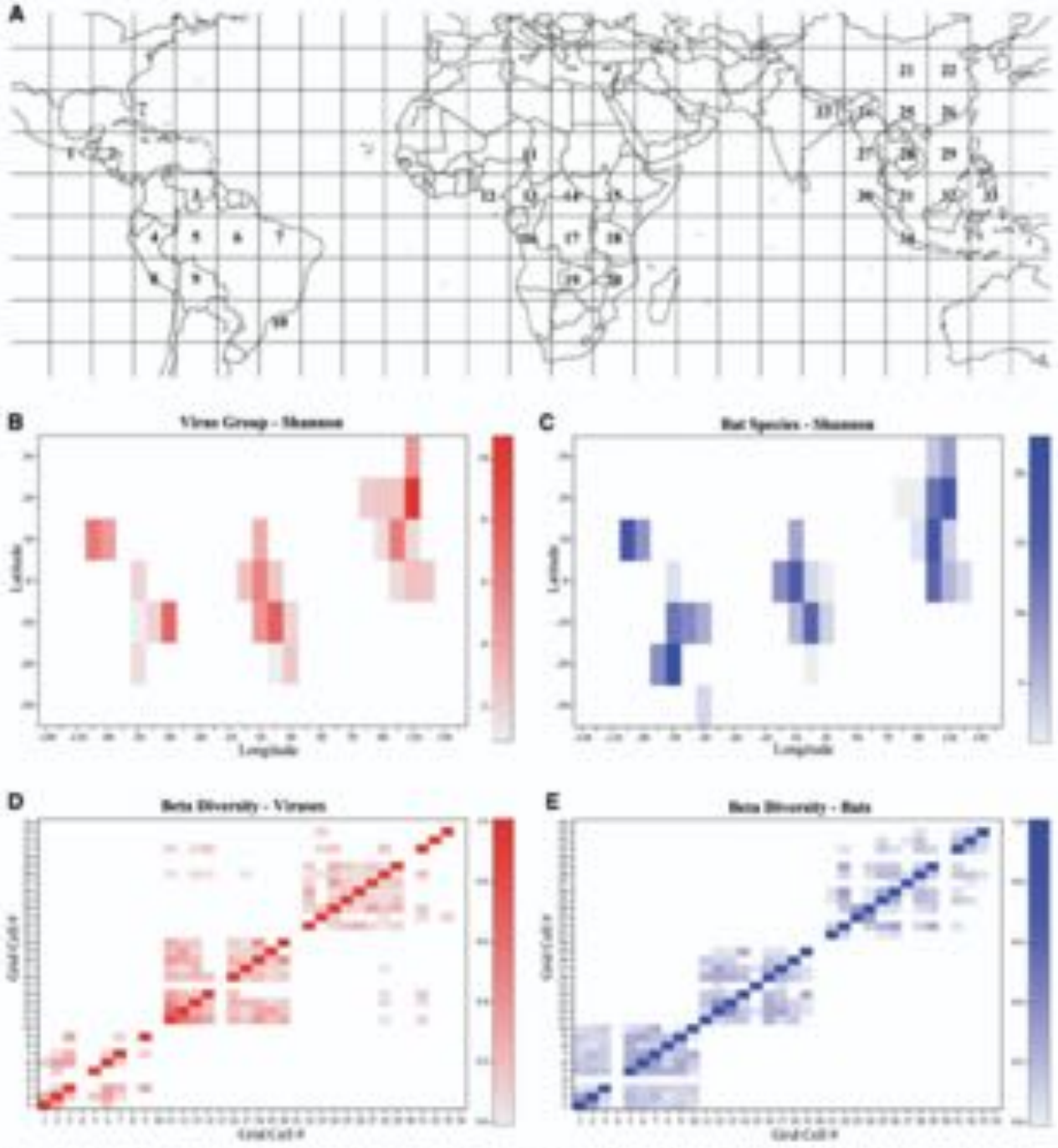

Figure 3. Comparison of viral and bat diversity. The earth's surface was divided into grid cells by latitude and longitude (30 × 30 degree units) for diversity calculations (Panel A). Grid cells where bats were sampled are numbered in each region. Alpha diversity (Shannon H) for virus (Panel B) and host (Panel C) were correlated, indicating that areas of high bat diversity also have high viral diversity. Darker cells indicate higher alpha diversity (i.e. more viral or host taxa) in each grid cell. Beta diversity was also correlated between virus (Panel D) and host (Panel E), and differentiated into three discrete communities by region: Latin America (grid cells 1–10), Africa (grid cells 11–20), and Asia (grid cells 21–34). Shading indicates that either viruses (in red) or hosts (in blue) are shared between two corresponding grid cells, with darker cells indicating higher pairwise similarity.

associated with CoV positivity among bats in all three regions: in Africa and Latin America, bats sampled at the animal use interface category were more likely to be positive, and in Asia, bats sampled at the animal use and human activities interfaces were more likely to be positive than those sampled at other interfaces. The significance of the animal interface in all three regions suggests that practices around animal use may be important for disease transmission.

3.5 Future sampling effort

Based on our study, we were able to estimate the sampling effort that would be required to find all CoVs in bats, based on a

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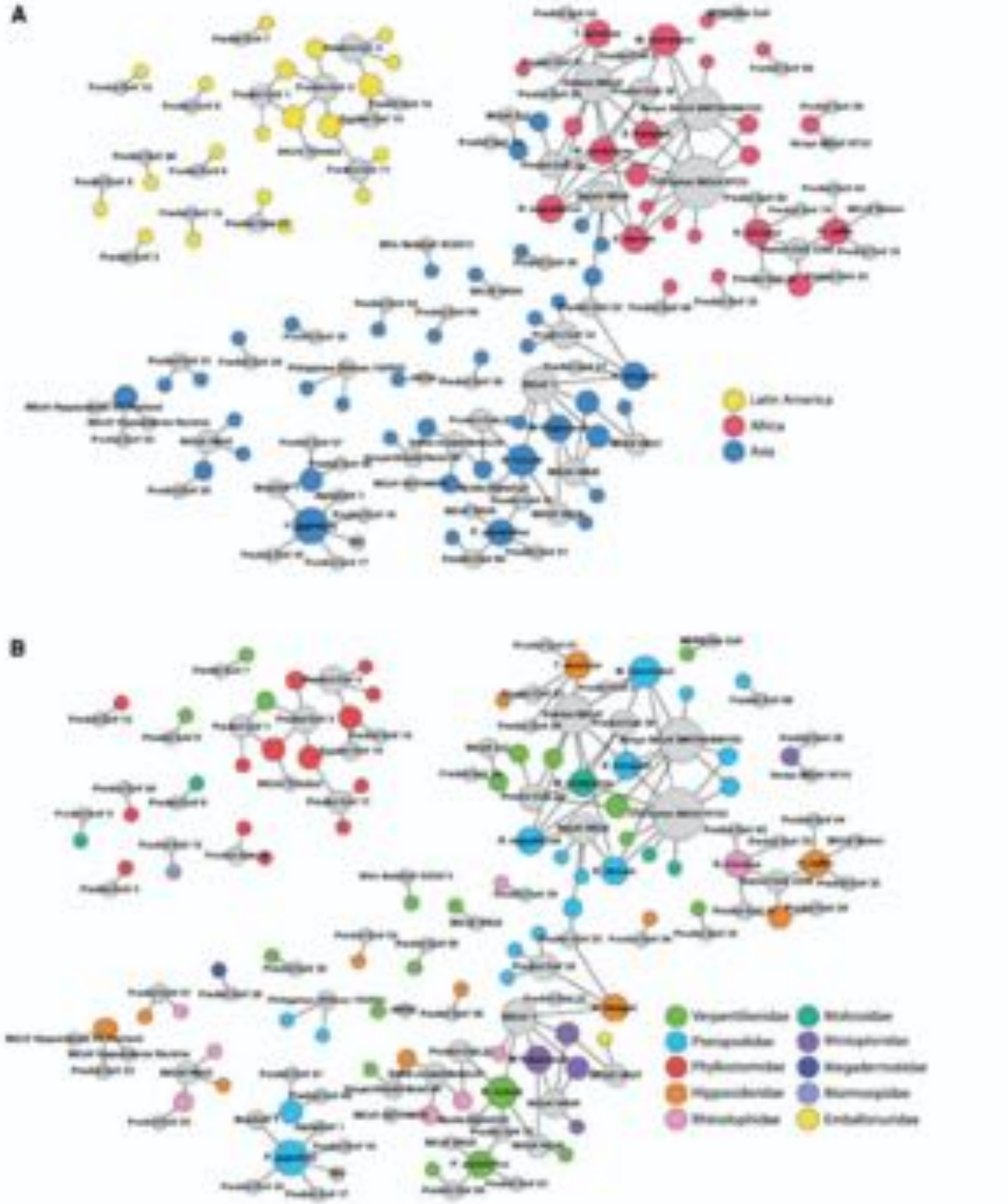

Figure 4. Network model showing the connections of CoVs and their hosts. Viral sequence clusters (colored grey) are connected to host species, either by region (Panel A) or family (Panel B). Viral and host and communities separate almost entirely by region, only Africa and Asia are connected by two shared viruses (RSCH and PREDICT_CoV-35) found in species from both continents. Networks also show that viruses appear to be shared by multiple host families in Africa and Asia, while being more restricted to a single family in Latin America.

Poisson regression model of our data (Fig. 6). With 154 individuals, we estimate that an average of one CoV will be detected (95% CI 136–177). With 597 individuals, we estimate that up to five CoVs will be detected (95% CI 353–458). As we did not observe any species with greater than five viral sequence clusters, we make the assumption that sampling 597 individuals should capture the full diversity of CoVs in each bat species.

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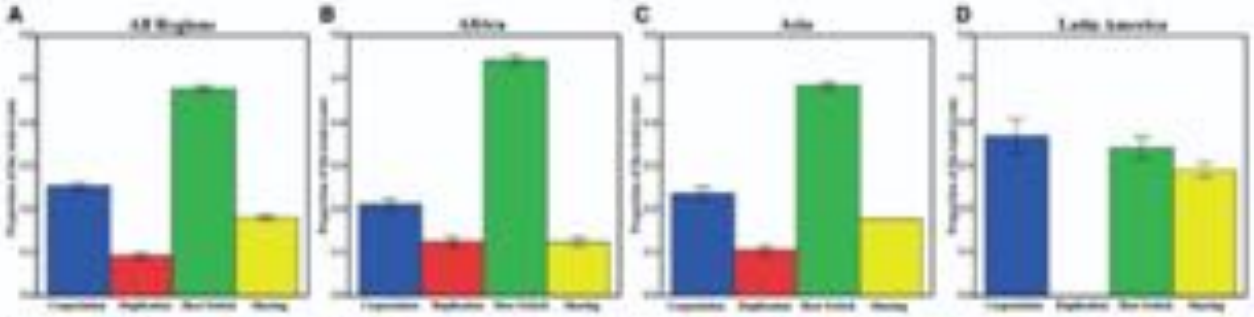

Figure 5. Relative proportion of evolutionary events leading to observed virus-host associations for CoVs in bats. Cophylogenetic reconstructions were used to identify each event (Supplementary Fig. S1: Panels A–D), and significance evaluated by region. Across all regions, host switching was the dominant evolutionary event (Panel A). When separated by region, host switching remained dominant in Africa (Panel B) and Asia (Panel C), but not in Latin America (Panel D).

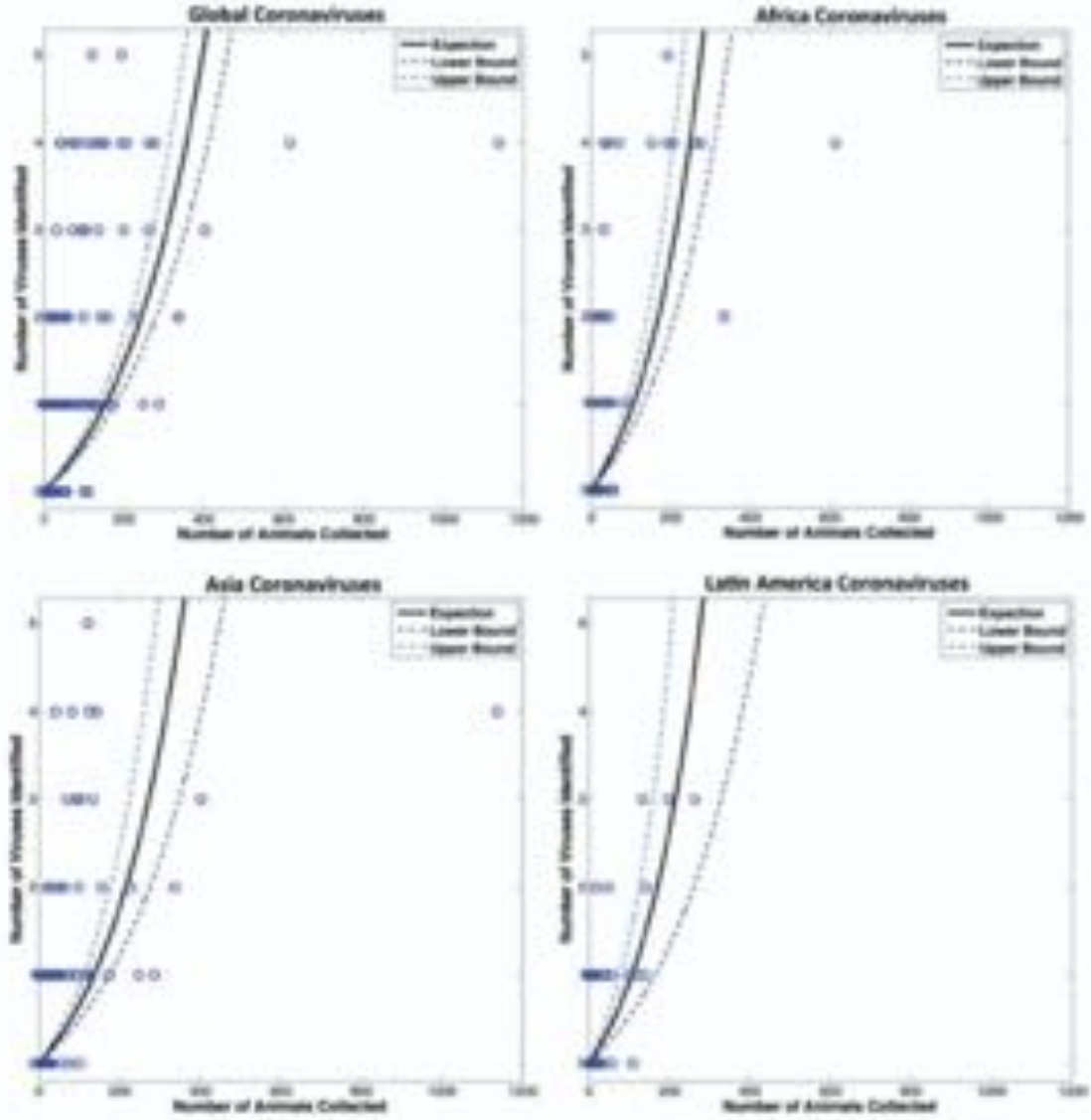

Figure 6. Relationship between sampling effort and viral detection among all bat species sampled. A Poisson regression model was used to estimate the expected number of viruses based on the number of animals sampled, by species (each circle indicates a separate species). The 95% confidence intervals are indicated.

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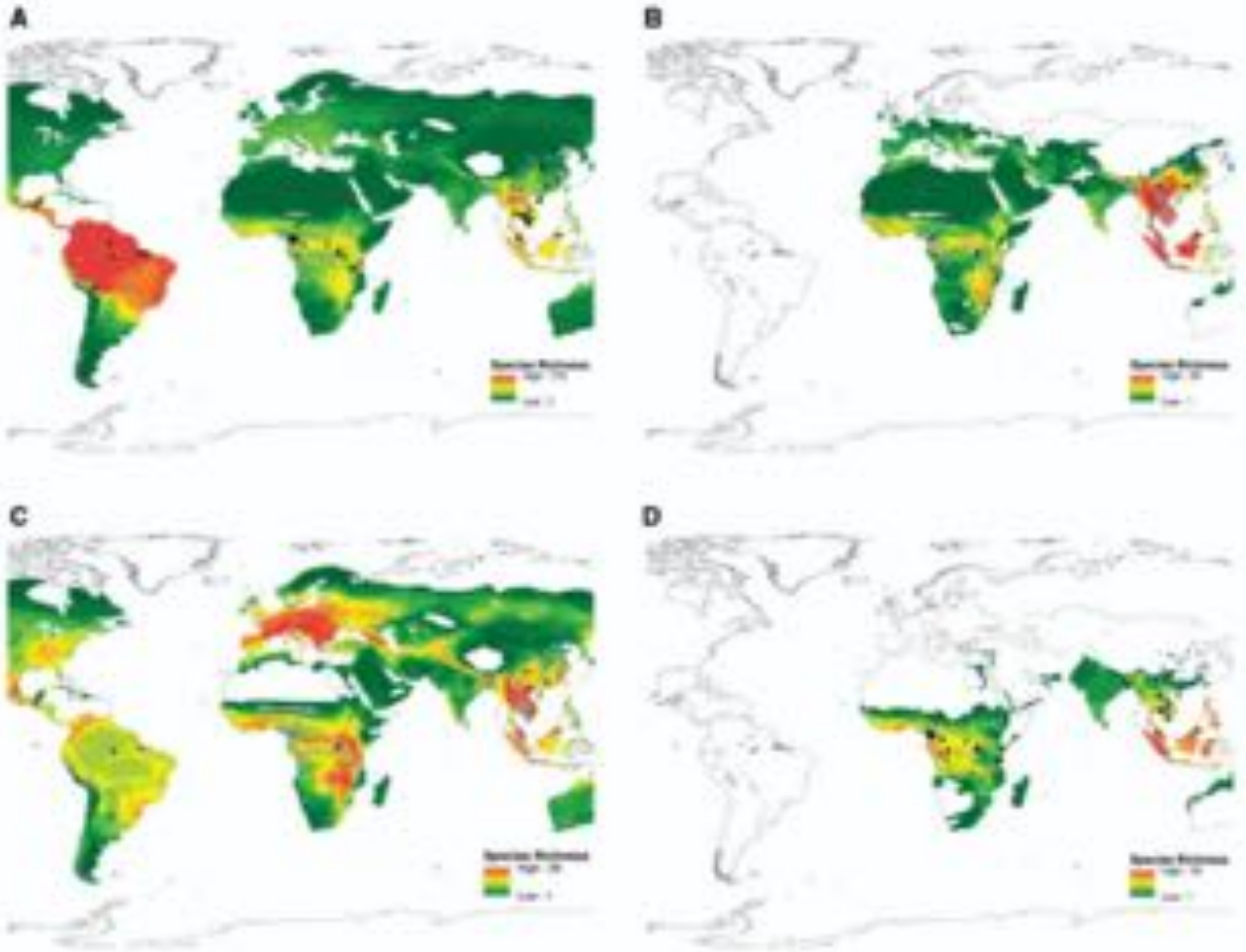

Figure 7. Viral diversity 'hotspot' maps. Panel A shows the potential hotspots for CoVs based on the distribution of bats worldwide. Location of alpha CoV sequences from this study are shown in black and beta CoV sequences in blue, indicating there is no geographical bias based on viral genus (i.e. alpha and beta CoVs are equally likely to be found in all regions). Some viral sub-clades were associated with particular bat families, and the spatial distribution data of all species belonging to these families were plotted to indicate the potential hotspots of viral diversity (richness) for these sub-clades. Panel B indicates the potential distribution of 2b CoVs based on the distributions of rhinolophus and hipposideros bats. Locations of 2b-positive animals identified in this study are indicated in black, and coincide with areas of high species richness (for these families). CoV-positive animals for other sub-clades shown in light blue. Panel C indicates the potential distribution of 2c CoVs based on the distribution of vespertilionid bats. Locations of 2c positive animals identified in this study are indicated in black. This map suggests there are hotspots of 2c diversity in regions not covered in this study (e.g. Europe). Panel D indicates the potential distribution of 1d viruses based on the distribution of pteropid bats. The map suggests these viruses may have a more limited distribution, compared with viruses of other sub-clades. Locations of 1d positive animals identified in this study are shown in black.

3.6 Predicting the distribution of unknown CoVs

Viral sub-clade and host family were not independent of each other (χ^2 by clade – $P < 0.001$, Supplementary Table S1), demonstrating that different clades have significant associations with specific bat families. For example, subgroup 2d CoVs were significantly associated with pteropid bats, and were only identified in regions where pteropid bats exist. Likewise, subgroup 2b CoVs were associated with rhinolophid and hipposiderid bats and 2c with vespertilionid bats. To 'predict' the potential distribution of unknown CoVs, we plotted the known distribution of bats belonging to these families and assume that 'hotspots' of bat diversity infer hotspots of viral diversity for each sub-clade (Fig. 7). We note that the alphaCoV genus has been considered as one group, since they do not resolve well into sub-clades (de Groot et al. 2009), and that no 2a map was generated given that only one bat virus from this clade was identified.

4. Discussion

The emergence of SARS and MERS has driven a need to understand more about the diversity, ecology and evolution of coronaviruses, particularly at so-called 'hotspots' of zoonotic emergence (Jones et al. 2008; Dobson et al. 2014). To this end, we surveyed the diversity of CoVs from twenty countries in Latin America, Africa, and Asia to identify global factors driving viral diversity and to look for regional differences in factors that contribute to the risk of emergence, such as host switching. In total, we identified sequences from 100 discrete phylogenetic clusters, ninety-one of which were found in bats.

Our data suggest that the diversity of bat CoVs has been driven primarily by host ecology. First, viral richness was strongly correlated with bat richness, suggesting that most CoVs will be found in regions where bat diversity is highest. Second, we showed that CoV diversity separates into three

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distinct communities by region, echoing the distribution of bats and suggesting an ecological dependence on their hosts. And third, we identified particular associations between viral subclade and bat family, indicating that CoVs have evolved with (or adapted to) preferred families. Collectively, these data show that the global diversity and distribution of CoVs in bats is non-random and is driven by variation in the biogeography of bats.

Regional variation was also observed in the proportion of host switching events, relative to other evolutionary mechanisms such as co-speciation, duplication, or sharing (see Methods for definitions). Overall, host switching was the dominant mechanism, supporting the general trend observed for CoVs (Vijaykrishna et al. 2007; Woo et al. 2009; Lau et al. 2012) as well as similar findings for other viral families, including paramyxoviruses (Melade et al. 2016), hantaviruses (Ramsden et al. 2009), and arenaviruses (Coulibaly-N'Golo et al. 2011; Irwin et al. 2012). However, when analyzed by region, there were proportionally fewer events in Latin America compared with Africa or Asia. Given that host switching is the first critical step in zoonotic emergence (Li et al. 2005;Pfefferle et al. 2009; Woo et al. 2012; Anhar et al. 2014), we suggest this finding could reflect regional differences in the risk of disease emergence.

It is important to note that we distinguish 'host switching' (inter-genus or family switching) from 'sharing' (intra-genus switching) in our analysis and that while the proportion of host switches was lower in Latin America, the proportion of sharing events was concomitantly higher. This indicates that CoVs in this region still switch hosts, just like they do in Africa and Asia, but that they preferentially move between closely related species. While we do not yet understand the factors driving this difference, if we assume that the risk of spillover to humans reflects the taxonomic distances that CoVs are able to jump (Kreuder Johnson et al. 2015), our results would indicate a higher risk for zoonotic emergence in Africa and Asia [acknowledging that host switching is not the only important factor driving zoonotic emergence (Jones et al. 2008; Keesing et al. 2010; Kuiken et al. 2012)]. While evidence of regional variation in host switching has not been reported previously for viruses (to our knowledge), similar patterns have been observed in haemosporidian parasites (Ellis et al. 2015).

In total, we estimated that there are at least 3,204 CoVs (based on the cluster definition used in this study) in bats. This suggests that although there is still a large number of coronaviruses that remain to be discovered, their detection remains an achievable goal, and we advocate for their discovery given the potential for even greater insights into the global ecology and evolution of these viruses (e.g. further investigation into regional differences in host switching), and the opportunity to elucidate their individual zoonotic potential (Ge et al. 2013; Wang et al. 2014; Yang et al. 2014; Anthony et al. 2017). Building on our study, we suggest that future surveillance efforts should consider the number of samples carefully and include up to 400 individuals (of either sex) per species in order to maximize the chance of detecting all CoVs, and that including less than 154 individuals per species might reduce the chance of finding even one virus and would likely produce a poor return on investment. We also recommend that feces (or rectal swabs) followed by saliva (or oral swabs) should be prioritized if resources are limited and all sample types cannot be processed, and that sampling should be biased towards immature animals and to the dry season.

To predict where this unknown diversity is likely to be, we plotted the known distribution of all bat families associated with each *CoV* sub-clade. The 2b SARS clade was associated with rhinolophid and hipposiderid bats, so we plotted the distribution of all bat species belonging to these families to generate a map of viral diversity (richness). Based on this map, we would expect the greatest diversity of unknown 2b viruses to be found in South East Asia, which is consistent with previous studies describing 2b viruses in bats, but also in isolated pockets throughout Africa. In contrast, the 2c MERS clade was associated with vespertilionid bats, predicting that 2c diversity will be highest in Mexico, Europe, Central and South East Africa, and parts of South East Asia. Again, this is consistent with the distribution of 2c viruses reported here, and previously in the literature [Woo et al. 2007; Reusken et al. 2010; Anthony et al. 2012; Lelli et al. 2013; Corman et al. 2014a,b; Anthony et al. 2017].

Certain limitations should be considered in the interpretation of our data. First, the diversity of CoV sequences detected is almost certainly biased by our sampling effort. A small number of species were sampled abundantly, thus maximizing our chances of finding a CoV (27/282 species had >120 individuals); however, most were under-sampled (230/282 with ≤50 individuals). While this biases the probability of finding a CoV towards the more abundantly sampled species, we stress that it also reflects the uneven distribution of naturally occurring communities (Magurran 2013), and that targeting the very rare species would be prohibitively expensive. It is also unclear if population size has an effect on the number of viruses present in a species—e.g. do larger populations accommodate more viral diversity? Second our analysis only represents the 'last' evolutionary event identified. It does not represent, or account for, the complete evolutionary history of these lineages. Therefore, while a single event has been ascribed to each association (see 'Methods'), it does not preclude other events having an equal or greater impact in the past. We are limited to using this most recent event type in order to assign a single evolutionary event to each unique association. It should also be noted that events are dependent on the relationships observed in the reconstructed trees and could change as more viruses are added or longer sequences are used. Third, we have only generated partial sequences for analysis, which limits our ability to comment on the specific zoonotic potential of each virus or provide a comprehensive analysis of their genetic histories and taxonomy, for example, estimating the frequency or impact of recombination, which can be an important driver of host switching and disease emergence (Anthony et al. 2017). We certainly support full-genome sequencing wherever possible [and have such efforts underway (Anthony et al. 2017)], however difficulties in virus isolation or sequencing directly from swabs (where material and viral load can be low, yielding variable results) can often preclude extending sequences much beyond the short fragments amplified by consensus PCR (Drexler et al. 2014). Equally, logistic and permitting issues in moving biological samples across borders, and the need to first develop in-country capacity to fully sequence these viruses, have all limited our ability to characterize (most of) these viruses further.

Our 'state of the art' is in the unique scope of our study, focusing on a single viral family at a global scale. To achieve this, the USAID PREDICT project first had to establish a strategy for viral discovery in twenty different countries, many of which had no prior capacity to do this work at all. For this reason, we used a simple yet highly implementable approach based on cPCR. Initially, this approach might not appear to be as powerful as high throughput sequencing (HTS) techniques, however, this study has demonstrated the particular and considerable strengths of cPCR as an affordable screening and discovery tool in resource-poor settings, where HTS is still largely unsupported.

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Studying viral diversity on a global scale is just one component of a larger strategy to understand the factors driving viral diversity. Ecological and evolutionary mechanisms can contribute differently across scales, and we therefore advocate complimenting the global perspective with studies that focus on entire viral communities (rather than only one viral family) within single individuals or host species (rather than only on a global scale) (Anthony et al. 2015). We propose that it is critical to understand both the component parts of the 'zoonotic pool' (Morse et al. 2012) and the nature of their interactions at different scales if we are to move towards better predictive models, and ultimately to reducing zoonotic emergence.

Finally, we offer a specific comment regarding the public health threat posed by bats. While it is tempting to conclude that bats harbor a large number of potentially zoonotic CoVs, most of the putative viruses detected in this study are unlikely to pose any threat to humans—either because they lack the biological pre-requisites to infect human cells or because the ecology of their hosts limits the opportunity for spillover. Studies such as this are intended to advance our understanding of the fundamental biology of viruses, not to create alarm or incite the retaliatory culling of bats. Indeed, such actions often have unanticipated consequences, and can even enhance disease transmission, as seen with rabies in vampire bats (Streicker et al. 2012; Blackwood et al. 2013). Bats are important insectivores, pollinators and seed dispersers and we underscore both their vital ecosystem role and the need to consider any public health interventions carefully.

Supplementary data

Supplementary data are available at *Virus Evolution* online.

Conflict of interest: None declared.

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One Health proof of concept: Bringing a transdisciplinary approach to surveillance for zoonotic viruses at the human-wild animal interface

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ABSTRACT

As the world continues to react and respond swiftly and efficiently to emerging infectious diseases, such as Middle Eastern Respiratory Syndrome and the Ebola and Zika viruses, a growing transdisciplinary community has called for a more proactive and holistic approach to prevention and preparedness – One Health. Such an approach presents important opportunities to reduce the impact of disease emergence events and also to mitigate future emergence through improved cross-sectoral coordination. In an attempt to provide proof of concept of the utility of the One Health approach, the US Agency for International Development's PREDICT project consortium designed and implemented a targeted, risk-based surveillance strategy based not on humans as sentinels of disease but on detecting viruses early, at their source, where intervention strategies can be implemented before there is opportunity for spillover and spread in people or food animals. Here, we share One Health approaches used by consortium members to illustrate the potential for successful One Health outcomes that can be achieved through collaborative, transdisciplinary partnerships. PREDICT's collaboration with partners around the world on strengthening local capacity to detect hundreds of viruses in wild animals, coupled with a series of cutting-edge virological and analytical activities, have significantly improved our baseline knowledge on the zoonotic pool of viruses and the risk of exposure to people. Further testament to the success of the project's One Health approach and the work of its team of dedicated One Health professionals are the resulting 90 peer-reviewed, scientific publications in under 5 years that improve our understanding of zoonoses and the factors influencing their emergence. The findings are assisting in global health improvements, including surveillance science, diagnostic technologies, understanding of viral evolution, and ecological-driven identification. Through its One Health leadership and multi-disciplinary partnerships, PREDICT has forged new networks of professionals from the human, animal, and environmental health sectors to promote global health, improving our understanding of viral disease spillover from wildlife and implementing strategies for preventing and controlling emerging disease threats.

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1. Introduction[1]

Throughout history, societies have been plagued by emerging diseases and their rapid or insidious spread. Recent generations have borne the costs of HIV/AIDS, Severe Acute Respiratory Syndrome (SARS), and Middle Eastern Respiratory Syndrome (MERS), tallied in lives and livelihoods lost and profound impacts on broader-scale economies. The most recent emergence and spread of the Zika virus and Ebola virus disease (EVD) in West Africa demonstrate how ill prepared the world remains to respond to and control rapidly changing disease dynamics. The global panic resulting in significant financial and social consequences also illustrates the disappearing boundaries between the countries and continents working to protect their citizens. The majority of emerging infectious diseases (EIDs) are zoonotic, or those diseases caused by pathogens that are shared between people and animals (Jones et al., 2008). These diseases result in tens of thousands of deaths annually, and the economic losses from a single outbreak can amount to tens of billions of dollars (World Bank, 2012). While prevention and early control of outbreaks could be the key to reducing the impact of epidemics and potential pandemics, especially in less developed countries as demonstrated by the recent EVD epidemic in West Africa, the world still remains positioned only to respond, not to prevent.

Despite greater recognition of the importance of zoonotic diseases, little attention has been given to advancing the understanding of the underlying causes for emergence and drivers of spread (Murray and Daszak, 2013). A growing transdisciplinary community, often led by veterinarians and epidemiologists, has responded to this knowledge gap on disease dynamics by advocating for a more holistic or One Health approach that recognizes the need to expand disciplinary expertise in public health. From the beginning of the One Health movement, veterinarians have strongly advocated for an approach that considers all public, animal, and environmental aspects of health as a problem-solving paradigm (Cook et al., 2004). Notwithstanding the philosophical acceptance of the need for such an approach, the animal and environmental foundations of this three-legged stool often receive only cursory attention when major health problems are addressed in policy and practice.

Recent examples of emerging and re-emerging diseases, such as H1N1 pandemic influenza, H5N1 and H7N9 avian influenza, EVD, and Zika virus, serve as a reminder that the health of humans, animals, and ecosystems are interconnected and that early detection and response to emerging pathogens requires a coordinated, interdisciplinary, collaborative, cross-sectoral approach at local, regional, and global levels (Heymann and Dixon, 2013; Karesh et al., 2012; Morse et al., 2012). In addition to the burden on human and animal health, the economic impacts associated with emerging and pandemic pathogens can be catastrophic, including costs associated with decreased commerce, travel, and tourism, as well as those incurred from treatment and control efforts (Karesh et al., 2012; World Bank, 2012). As our world becomes increasingly connected through trade and travel, emerging infectious diseases pose a greater threat to the global community, requiring collaboration between ministries of health and institutions involved in health, trade, agriculture, and the environment (Mazet et al., 2014). The One Health approach presents important opportunities to reduce the impact of emergence events and also to prevent future emergence through improved knowledge and coordination. In this article, we share One Health approaches applied by the US Agency for International Development's PREDICT project consortium to highlight the potential for successful One Health outcomes that can be achieved through developing cross-sectoral networks and establishing strong collaborative, transdisciplinary partnerships.

2. Observation of need at the human-wildlife interface

Arguably, veterinarians and veterinary epidemiologists have been among the most vocal advocates for the One Health approach. Pioneers of the One Health concept understood the value of comparative medicine and recognized the critical role that environmental factors play in the health of people and animals. Over the past decade, this concept was expanded to be much more inclusive of ecosystem health (Cook et al., 2004), due in part to the contributions of veterinarians witnessing firsthand the intimate connection among animal, human, and environmental health (Gibbs and Gibbs, 2013). For example, although veterinarians working in global health recognize the role that wildlife trade and consumption play in human nutrition and livelihoods in many countries around the world, they have expressed concern about the risks these practices pose with regard to spillover of zoonotic pathogens, as well as to conservation (Abulu-Mundeke et al., 2011; Karesh et al., 2005; Karesh and Noble, 2009; Peeters et al., 2002; Smith et al., 2012; Wolfe et al., 2005). Human immunodeficiency viruses (HIV) types 1 and 2 are examples of pandemic infections resulting from cross-species transmission of simian immunodeficiency virus (SIV) from infected nonhuman primates to humans (Sharp et al., 2010). The documented spillover and pandemic potential of simian retroviruses illustrate the public health threat associated with close and frequent contact with wild animals, as occurs with wildlife trade and consumption (Switzer et al., 2012).

However, it should not be ignored that pathogens spill over in both directions, also threatening the health of wild animals. Tuberculosis in nonhuman primates and Asian elephants has long been associated with contact with infected humans (Mikota and Maslow, 2011; Montali et al., 2001). Investigation into a respiratory outbreak in mountain gorillas in Rwanda by PREDICT veterinarians revealed human metapneumovirus infection in affected individuals (Palacios et al., 2011). The source of the virus remains unknown; however, the strain was most recently described in human patients in South Africa and likely was transmitted to the gorillas by humans, illustrating the potential for bi-directional spillover of pathogens (Palacios et al., 2011). The parks where mountain gorillas reside are surrounded by very dense human populations, and research and ecotourism bring thousands of people into direct and indirect contact with the gorillas annually. Veterinarians documented 18 outbreaks of respiratory disease among these gorillas between 1990 and 2010 (Spelman et al., 2013). It is unclear if the increasing frequency and severity of respiratory disease outbreaks among mountain gorillas in the Virunga Massif (Spelman et al., 2013) are related to the growing human population surrounding the parks. Nevertheless, these findings provided further rationale for implementation of stricter visitation rules in some parts of the mountain gorillas' range in order to minimize the risk of disease transmission between visitors and wild human-habituated gorillas.

In Rwanda, an orphaned Grauer's gorilla confiscated from poachers and held in captivity for more than two years developed oral lesions. The consortium detected human herpes simplex virus Type 1 (HSV-1) in this individual (Gilardi et al., 2014), documenting spillover of another virus from humans into gorillas and further illustrating the need for targeted disease surveillance at the human-wildlife interface (Gilardi et al., 2014).

[1] Much of this review is based on material covered more thoroughly in USAID PREDICT: Reducing Pandemic Risk, Promoting Global Health. PREDICT Consortium, One Health Institute, University of California, Davis, December 2014 (www.report.predict.global).

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3. One health on a regional scale: the PREDICT project

The US Agency for International Development (USAID) initiated the Emerging Pandemic Threats (EPT) program in 2009 with the goal of strengthening capacities in developing countries to prevent, detect, and control infectious diseases. In part because of their One Health leadership and research focused at the animal-human-environmental interface, the agency looked to veterinarians and epidemiologists to build a consortium to implement the surveillance and virus discovery component of the EPT program. The resulting PREDICT project focused on building transdisciplinary collaborations to identify potential zoonotic viral threats at high-risk transmission interfaces where pathogens are most likely to spill over. These interfaces occur in many cultural contexts and regions and usually result from necessary daily activities, such as animal-based food production/acquisition and other income-generating activities, like harvesting bat guano for agricultural fertilizer. Through a consortium of global and in-country partners, PREDICT focused on early detection and response to potentially high-consequence animal viruses in regional "hotspots" for EIDs, such as central Africa, South and Southeast Asia, and parts of Latin America. The consortium was able to overcome geographic and disciplinary constraints to public health protection by developing multidisciplinary partnerships and establishing networks and platforms for surveillance, diagnostics, and data sharing across stakeholders.

PREDICT, which was initially implemented in over 20 countries, improved early detection and response to disease threats through five main strategies: 1) building or strengthening zoonotic viral detection capabilities; 2) developing diagnostic laboratory and disease outbreak response capacities; 3) characterizing high-risk animal-human interfaces; 4) optimizing predictive models for disease emergence and spread; and 5) deploying information management and communication tools to advance a more integrated, global approach to sharing data from zoonotic virus surveillance.

3.1. Identifying threats at the human-wildlife interface

PREDICT's surveillance strategy was designed to address the need for a more holistic, proactive approach to pandemic prevention, in which pathogens are discovered before they emerge or spread widely in people (Karesh et al., 2012; Morse et al., 2012). The strategy targeted high-risk disease transmission interfaces or conditions where people have frequent and direct contact with wild animals (Morse et al., 2012). To maximize discovery of zoonotic viruses, PREDICT focused surveillance activities on wildlife taxa for which there is scientific evidence of pathogen spillover to humans based on recent emerging and re-emerging viral zoonoses. The consortium drew on the diverse expertise of professionals across multiple disciplines, including human and veterinary medicine, epidemiology, ecology, economics, and environmental health to identify a range of high-risk interfaces and wildlife taxa to target for the project's surveillance activities.

By linking networks of key stakeholders in a wide range of government ministries, scientific institutions, and local organizations, PREDICT helped integrate surveillance activities across the animal, human, and environmental health sectors with the aim of breaking down traditionally siloed approaches that currently serve as barriers to understanding the complex ecological and social changes that contribute to infectious disease emergence and therefore, the best interventions to prevent pathogen spillover (Mazet et al., 2014). The consortium worked with in-country partners to enhance capacity for wildlife disease surveillance, including field activities led by veterinarians and specialists experienced in the handling and sampling of wild animals to ensure safe and humane non-lethal methods.

To inform on a strategy designed to detect pathogens prior to spillover into people, the consortium examined the animal hosts and modes of transmission involved in previously reported zoonotic virus spillover events. Settings with diverse animal host assemblages and human activities facilitating cross-species disease transmission posed the highest risk for zoonotic virus spillover and were, therefore, important targets for surveillance for viruses of zoonotic potential (Johnson et al., 2015). Investigation into historic EID events revealed variation in major transmission pathways according to drivers of disease emergence (e.g., land-use change). These findings provided insight into how regional predominance of drivers can help with prioritization of pathways to target surveillance activities (Loh et al., 2015). Because pathogens circulating at high-risk interfaces often share modes of transmission (Loh et al., 2015), focusing on transmission pathways for surveillance and implementation of intervention strategies has the potential to prevent spillover from occurring.

To further inform a strategy best targeted for zoonotic virus discovery, PREDICT and its partners examined published virus detection data to compare the discovery potential of syndromic surveillance of diseased animals and active surveillance of apparently healthy animals (Levinson et al., 2013; Olson et al., 2012a). Compared to other mammalian taxa, there were fewer reports of clinical signs with viral infection in bats and rodents, providing further evidence that they serve as important healthy wildlife reservoirs to target for surveillance activities (Levinson et al., 2013). In addition, a mixed surveillance strategy of actively sampling healthy suspected wildlife reservoirs and animals involved in morbidity and mortality events, especially susceptible primates, was found to be the best for maximizing virus detection and discovery (Levinson et al., 2013; Olson et al., 2012a).

3.2. Assessing needs

At the beginning of the project, the consortium worked with partners to assess capacity for zoonotic pathogen surveillance in wildlife. Capabilities in each country were evaluated to identify needs for infrastructure and human capacity strengthening and to provide baseline information for monitoring change in capacity over time. As part of this process, wildlife officials and in-country PREDICT project scientists were surveyed to better understand perspectives regarding opportunities, challenges, and priorities for capacity development (Schwind et al., 2014a). Survey results indicated that enhancing coordination across agencies and sectors and increasing human and diagnostic laboratory capacities presented the most important opportunities for capacity strengthening (Schwind et al., 2014a). This information, as well as input from other in-country partners, was then used to target capacity enhancement priorities for the project.

3.3. Optimizing noninvasive sampling techniques

Priorities identified for capacity strengthening by stakeholders acknowledged the need to overcome logistical challenges of wildlife sampling in remote regions and when hands-on sampling was not ethically justified, feasible, or permitted. For example, many primate species inhabit areas that are logistically difficult to access, challenging for safe application of field anesthesia, or where their capture is not permitted. PREDICT developed a non-invasive sampling technique to obtain saliva samples from primates via a rope soaked in a fruit-based attractant (e.g. jam). The primate was allowed to chew on the rope that was subsequently retrieved for laboratory analysis (Smiley Evans et al., 2015). PREDICT also helped develop a noninvasive method to detect antibodies against Ebola virus in gorilla feces (Reed et al., 2014). In coordination with this effort, the consortium determined optimal sampling strategies for

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detection of fecal samples from great apes in Central Africa (Olson et al., 2012b). In addition to improving early detection of circulating virus, these methods will aid in identifying immunologically naïve populations of wild apes that are vulnerable to EVD and could benefit from prevention measures (Reed et al., 2014).

3.4. Strategies for maximizing discovery of zoonotic viruses and understanding drivers of viral diversity

PREDICT's strategy for virus detection and discovery centered around the need for a cost-efficient approach that can concurrently detect known and novel viruses and be effectively implemented in resource-constrained regions. Because technologies used for viral discovery can be prohibitively expensive and require a high level of expertise, PREDICT virologists compiled a set of relatively simple and inexpensive protocols for the detection of known and novel viruses within viral families that had previously been recognized in animal hosts and known to cause human disease outbreaks, and coupled this cost-effective approach with the selected application of high through-put sequencing (Anthony et al., 2013c; Anthony et al., 2013a; Goldstein et al., 2013). Using this strategy, the team detected hundreds of known and novel viruses. For example, the consortium first isolated and characterized a SARS-like coronavirus from a Chinese horseshoe bat (*Rhinolophus sinicus*; Ge et al., 2013). The virus was found to bind to the human ACE-2 cell receptor, suggesting that direct transmission to humans from bats would be possible. During the 2003 SARS outbreak, it was originally thought that bat viruses infected people through civets serving as intermediate hosts. However, this discovery provided compelling evidence that an intermediate host may not be necessary and that mitigation strategies should focus on decreasing human-bat contact (Ge et al., 2013).

Still, gaps in our knowledge of the viral diversity in wildlife hosts and the mechanisms involved in spillover and spread impeded the consortium's ability to fully implement a science-based surveillance strategy, including setting sample size targets for virus discovery. To investigate the potential pool of zoonotic viruses in target wildlife hosts and the effort required to better understand the diversity of mammalian viruses, the consortium investigated viral diversity in *Pteropus giganteus* fruit bats and the sampling effort needed to evaluate viral richness. PREDICT and its partners repeatedly sampled the bats and used PCR with consensus viral primers for nine viral families to saturate the discovery of new viruses in the species (Anthony et al., 2013b). Using statistical techniques similar to those used for estimating vertebrate diversity, the total viral richness within the nine viral families examined in this host was estimated to be 58 viruses. In addition, it was estimated that there is a minimum of 320,000 mammalian viruses that have yet to be discovered in these nine viral families. Sample size targets calculated from this information indicated that while approximately 7000 samples would need to be analyzed to identify 100% of these new viruses, a much more feasible target of 1300 samples would be needed to identify 80% of the novel viruses (Anthony et al., 2013b).

As a first step toward improving our understanding of how environmental drivers influence viral diversity in wildlife hosts and whether it might be possible to anticipate changes in viral communities, the consortium assessed whether viral communities identified in macaque feces were assembled through predictable or stochastic (unpredictable) processes (Anthony et al., 2013). Viral communities occurred mostly in non-random patterns between sites and within individuals, suggesting that forecasting changes in viral diversity in wildlife hosts in the face of environmental drivers of disease emergence might be possible (Anthony et al., 2013). The ability to predict shifts in viral communities in wildlife reservoir hosts could allow us to evaluate various intervention strategies aimed at mitigating the risk of zoonotic pathogen emergence.

3.5. Assisting governments with zoonotic disease outbreak investigations

Because of the project's commitment to advancing the cutting edge of surveillance science, some in-country governments invited PREDICT team members to serve on national task forces and to provide technical assistance during disease outbreak response and prevention efforts. For example, consortium members helped inform on the science-based foundation for the Government of Rwanda's One Health Steering Committee, which aims to improve cross-sectoral coordination for human and animal disease outbreak response. PREDICT assisted with the Steering Committee's formulation of a One Health policy statement, which serves as an important platform for promoting and operationalizing One Health approaches. During disease outbreak investigations, consortium teams worked with local governments on strategies for and implementation of wildlife disease surveillance. PREDICT also collaborated with ministries on pathogen detection and characterization during outbreaks when traditional diagnostic assays for specific viral pathogens provided inconclusive results.

Results from PREDICT's viral discovery efforts have also been used to direct wildlife surveillance activities during human disease outbreak investigations. For example, PREDICT's discovery of a betacoronavirus (b-CoV) with 96.5% amino acid identity to Middle Eastern Respiratory Syndrome Coronavirus (MERS-CoV) in a bat in Mexico informed on the target species for sampling in Saudi Arabia during MERS outbreak investigations (Anthony et al., 2013c). Sampling led to the discovery of a MERS-CoV sequence in a Saudi Egyptian tomb bat with 100% nucleotide identity to the virus from the MERS human index case (Memish et al., 2013). The consortium also generated evidence-based recommendations for disease surveillance during a series of human Ebola outbreak investigations in Africa, focusing mainly on strategies for animal sampling during resource-constrained response efforts, target species, and which diagnostics should be prioritized to rapidly screen for the presence of virus in animal hosts (Olson et al., 2012a). The consortium also provided technical assistance to governments through pathogen detection and characterization during a number of human-only disease outbreaks. For instance, the team developed and optimized a new, highly sensitive technique to reconstruct the genome of a novel rhabdovirus (Bas-Congo virus, or BASV) associated with three human cases of acute hemorrhagic fever in Democratic Republic of Congo (Grard et al., 2012). Although the rhabdovirus family had never been documented to cause hemorrhagic fever in people, they are now included in the list of viruses evaluated during hemorrhagic fever outbreaks (Grard et al., 2012).

3.6. Improving early recognition of disease events through innovative tools

PREDICT partnered with HealthMap, an established global leader in digital disease event monitoring, to develop a public platform to share sampling data and viral testing results and to contribute to the variety of data sources that HealthMap brings in to increase awareness regarding the state of infectious diseases. Once the project's virus detection results were shared with and approved for public release by in-country governments, the results (including reporting of negative findings) were uploaded into the HealthMap system for open, public access.

In addition to digital media's value for early event detection, there is also potential for its use as an early warning system through

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monitoring drivers of disease emergence (Olson et al., 2015). The consortium developed a scientific framework for a digital disease driver surveillance platform (Olson et al., 2015). The platform has the potential to identify locations and periods of time with elevated infectious disease risk with alerting of public health officials to the need for active surveillance and intervention prior to pathogen spillover events.

PREDICT also worked with in-country partners to explore the value of local media to enhance surveillance and early recognition of disease events (Schwind et al., 2014b). Over a 16-week evaluation period, health reports in local media sources were compared to reports in the global HealthMap system to identify unique health event coverage. Selected media sources were reviewed to ensure they were not already feeding into main aggregation sites, including HealthMap. The local media surveillance was found to fill gaps in digital surveillance coverage of events through valuable localized information on risk and disease events and by supporting diverse languages. This effort demonstrated the utility of local media surveillance as an addition to active digital surveillance networks in regions with less-developed capacity for disease detection and response (Schwind et al., 2014b).

3.7. Addressing re-emerging disease threats of major global importance

Lessons learned during recent disease outbreaks, such as EVD and highly pathogenic avian influenza (Hpai), highlight the need for a new paradigm focused on interruption of pathogen transmission prior to human spillover. However, this new paradigm is only plausible with an improved understanding of the biological and ecological factors driving disease emergence and mitigation strategies aimed at these underlying drivers. Following a series of HPAI outbreaks in the countries where PREDICT was active, the consortium worked in collaboration with partners to improve our understanding of how and where HPAI strains are emerging. Researchers evaluated data on influenza A viruses reported in the public domain in 32 different countries over a 12-year period (2000–2011; Rejmanek et al., 2015). Virus evolution was found to be higher in Asian countries, especially in East Asia, relative to North America, providing further evidence of an increased risk of emergence of novel pathogenic strains in East Asia. In addition, large gaps in reporting of influenza A virus activity were identified in Africa and South America. Reporting effort and health care spending (indicator of economic development) were strong predictors of subtype diversity at the country level, emphasizing the need to increase sampling and reporting efforts in under-sampled regions in order to better understand the underlying drivers of influenza A infections around the world (Rejmanek et al., 2015).

PREDICT also assisted partners during the 2013 influenza A (H7N9) outbreak investigation in China. Morbidity associated with H7N9 infection had not been previously reported in people, and little was known about this subtype in wild bird populations. To inform on the investigation and potential role of wild birds as sources of the human infections, the consortium examined the prevalence and distribution of influenza A (H7N9) virus previously reported in wild bird populations and the sample size needed to detect this strain in wild birds (Olson et al., 2013). The prevalence of H7N9 in wild birds was very low, requiring high sample sizes (>30,000 wild birds) for detection. Given the low prevalence in wild birds, PREDICT and its partners recommended targeted risk-based surveillance as an efficient and cost-effective strategy to monitor wild bird populations as a potential source of continued H7N9 infections in poultry and people (Olson et al., 2013).

3.8. Scaling and sustaining one health initiatives

Despite the substantial progress made in recent years, challenges to implementing and sustaining One Health initiatives remain. Successful One Health approaches require cross-sectoral coordination in which partners look beyond their disciplines to function as a team, despite their diverse organizational mandates, funding sources, and standard operating procedures (Mazet et al., 2014). One Health initiatives often arise from shared threats requiring a multi-agency, cross-sectoral response (Rubin et al., 2014). For example, the H5N1 HPAI outbreak, which brought together a diverse network of partners from the animal and human health sectors, fostered a number of One Health achievements, including a coordinated tripartite surveillance system, which has enabled improved information and data sharing and joint risk assessment (Rubin et al., 2014). However, sustaining effective coordination once the threat has diminished presents a significant challenge. Strong collaborations built during these periods of necessary cooperation, can provide a platform for scaling successful approaches into sustainable One Health programs. The One Health Strategic Plan for Rwanda (https://www.google.com/?gws_rd=ssl#q=one+health+strategic+plan+rwanda) provides another good example of how a clearly defined strategy and a fundamental understanding of the specific roles and mandates of the partners involved can be an effective approach for scaling and sustaining One Health initiatives.

4. Conclusions

The examples above, as well as the seriousness of the risks associated with viral spillover among hosts, has led to the recognition of the utility of a One Health approach in the design and implementation of emerging infectious disease surveillance strategies. PREDICT's One Health consortium has advocated for inclusion of multiple and diverse disciplines to shift the world's currently reactive approach (once a disease is spreading in populations) toward a proactive, predictive approach for emerging infectious disease prevention and timely control. The general lack of specific medicines and vaccines for new and spreading zoonotic viruses puts a premium on developing non-pharmaceutical interventions based on a detailed understanding of when, where, and how zoonotic viruses are moving among wildlife, domestic animals, and people. The PREDICT consortium provides just one example of the potential for success that can be achieved by a collaborative, transdisciplinary team.

Through integrated efforts to promote health, effective natural resource management, and economic development, the PREDICT project and its partners have advanced One Health capacity and infrastructure in over 20 countries considered to be hotspots for zoonotic disease emergence. PREDICT worked cooperatively with a wide range of government ministries, scientific institutions, local organizations, and other stakeholders to further local and global One Health initiatives by enabling a structure for effective collaboration across disciplines and geographic boundaries in countries where PREDICT was active. Utilizing a One Health approach, PREDICT focused its efforts on strengthening surveillance and laboratory capacity to detect known zoonotic pathogens and novel viruses at the wildlife-human interface, monitoring human-wildlife interactions for the potential spillover of viral pathogens posing a health threat, and investigating ecological drivers of pathogen spillover into people with the ultimate aim of improved prevention of zoonotic disease emergence. By emphasizing the links among human, animal, and environmental health, PREDICT enabled and supported integrated efforts to promote public health,

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effective natural resource management, and socio-economic development.

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FROM THE AMERICAN PEOPLE



REDUCING PANDEMIC RISK, PROMOTING GLOBAL HEALTH

PREDICT, a project of USAID's Emerging Pandemic Threats (EPT) program, was initiated in 2009 to strengthen global capacity for detection and discovery of zoonotic viruses with pandemic potential. Those include coronaviruses, the family to which SARS and MERS belong; paramyxoviruses, like Nipah virus; influenza viruses; and filoviruses, like the ebolavirus.

PREDICT has made significant contributions to strengthening global surveillance and laboratory diagnostic capabilities for new and known viruses.

Now working with partners in 31 countries, PREDICT is continuing to build platforms for disease surveillance and for identifying and monitoring pathogens that can be shared between animals and people. Using the One Health approach, the project is investigating the behaviors, practices, and ecological and biological factors driving disease emergence, transmission, and spread. Through these efforts, PREDICT will improve global disease recognition and begin to develop strategies and policy recommendations to minimize pandemic risk.

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SURVEILLANCE

PREDICT's surveillance for emerging pathogens focuses on areas of the world at the highest risk for zoonotic disease emergence. The goal is to move countries away from a reactive post-outbreak response to a proactive approach in which pathogens of pandemic potential are discovered at their source before large-scale epidemics occur in people.

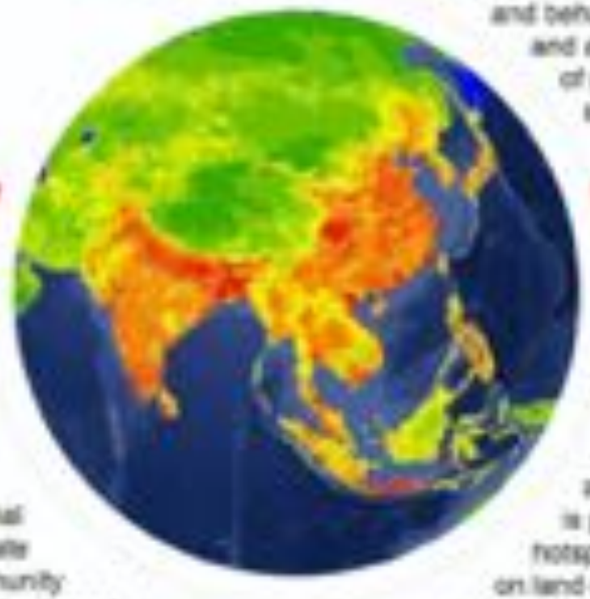
PREDICT's disease surveillance strategy is based on the inextricable link between animals, humans, and the environment. Rather than prescribing an across-the-board surveillance plan, PREDICT works in each focus country to cultivate targeted, measurable, adaptive, and responsive approaches that are integrated across health and environmental sectors.



CAPACITY STRENGTHENING

Preparing for emerging disease threats requires investments in infrastructure, institutions, and human resources across a broad array of health and social systems to operationalize One Health platforms. In collaboration with country governments and EPT partners, PREDICT is committed to developing the infrastructure and core skills and capabilities required by tomorrow's One Health workforce.

Through PREDICT, more than 2,500 people (and counting) have been trained in biosafety, field epidemiology and surveillance, laboratory diagnostics, social sciences and behavioral risk investigations, and modeling and analytics, creating an extensive network of global One Health professionals to support long-term zoonotic disease surveillance.



PATHOGEN DISCOVERY & DIAGNOSTICS

PREDICT's diagnostic success lies in the use of broadly reactive consensus (genus/family level) PCR supplemented with high throughput sequencing. These powerful tools produce specific, high-resolution data allowing for rapid detection of known and new potential pathogens. To date, PREDICT has developed and optimized detection protocols and capacities in laboratories in all of the countries in which we have engaged, ensuring regional capacity to detect pandemic threats.

The PREDICT approach is especially important for the diagnosis of mystery illnesses in medical hospitals and veterinary labs where testing options are often limited. By testing targeted samples based on the circumstances that promote disease transmission and the route of exposure, PREDICT can detect known and novel pathogens in tandem, rather than sequentially.



BEHAVIORAL RISK

PREDICT uses a multidisciplinary approach to identify groups of populations at highest risk of exposure to emerging pathogens, and the 'how' and the 'why' of risk.

Our teams assess community perceptions of animal exposure and disease risk and evaluate widely held assumptions of community practices (e.g., high risks from bushmeat hunting). PREDICT is identifying and monitoring the risk factors for zoonotic diseases with pandemic threat potential.

Our methods will lead to well-rounded understanding of disease spillover and transmission dynamics, essential to the design and evaluation of mitigating interventions, and to informing policy by identifying barriers to change and acceptable alternatives.

MODELING & ANALYTICS

PREDICT will use state-of-the-art modeling and analytic approaches to guide surveillance and help countries develop disease control and prevention strategies. PREDICT is producing next-generation, fine-scale hotspots maps, combining in-country data on land use, socioeconomic, and agricultural changes with surveys of human behavior, market value chains, and livestock production to identify where zoonoses will spillover, where they will amplify, and who is at risk.

By using data direct from PREDICT viral testing and conducting outbreak scenario modeling, PREDICT will provide information on which pathogens are most likely to become pandemic and which control and mitigation strategies can be most effective.

INFORMATION MANAGEMENT

PREDICT works closely with host governments and partners to interpret and share information through systems designed to protect and ensure data quality and accuracy. PREDICT data are managed in a purposefully-designed internal information management system, in which all data undergo a rigorous quality control process. Diagnostic test results are interpreted in light of all available scientific literature by PREDICT virologists.

After interpretation, results are provided to host governments for examination, to inform policy, and for approval for public release through the PREDICT data site powered by HealthMap. This open access platform allows users to visualize PREDICT data along with disease events worldwide (http://data.predict.global).



ONE HEALTH PARTNERSHIPS

PREDICT at its core is built upon One Health partnerships. Cross-disciplinary collaborations are critical for gaining a more full understanding of the integral links between human, animal, and environmental health that can provide opportunities for prevention or early detection and control of disease threats. By working across sectors and including a diverse range of stakeholders and expertise, PREDICT helps operationalize efforts that promote public health, effective natural resource management, and development.

On a country basis and at a global level, PREDICT enables and supports implementation of One Health practices. Toward this goal, PREDICT has worked closely with a wide range of government ministries, scientific institutions, local organizations, and other stakeholders to further One Health initiatives. These have taken the form of inter-ministerial data sharing and interpretation, interdisciplinary capacity building and surveillance, and coordinated outbreak response activities. Building on these best practices, PREDICT is working with Emerging Pandemic Threats program partners to develop an evidence base to demonstrate the value of the One Health approach.



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RESEARCH ARTICLE

Further Evidence for Bats as the Evolutionary Source of Middle East Respiratory Syndrome Coronavirus

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ABSTRACT The evolutionary origins of Middle East respiratory syndrome (MERS) coronavirus (MERS-CoV) are unknown. Current evidence suggests that insectivorous bats are likely to be the original source, as several 2c CoVs have been described from various species in the family *Vespertilionidae*. Here, we describe a MERS-like CoV identified from a *Pipistrellus cf. hesperidus* bat sampled in Uganda (strain PREDICT/PDF-2180), further supporting the hypothesis that bats are the evolutionary source of MERS-CoV. Phylogenetic analysis showed that PREDICT/PDF-2180 is closely related to MERS-CoV across much of its genome, consistent with a common ancestry; however, the spike protein was highly divergent (46% amino acid identity), suggesting that the two viruses may have different receptor binding properties. Indeed, several amino acid substitutions were identified in key binding residues that were predicted to block PREDICT/PDF-2180 from attaching to the MERS-CoV DPP4 receptor. To experimentally test this hypothesis, an infectious MERS-CoV clone expressing the PREDICT/PDF-2180 spike protein was generated. Recombinant viruses derived from the clone were replication competent but unable to spread and establish new infections in Vero cells or primary human airway epithelial cells. Our findings suggest that PREDICT/PDF-2180 is unlikely to pose a zoonotic threat. Recombination in the S1 subunit of the spike gene was identified as the primary mechanism driving variation in the spike phenotype and was likely one of the critical steps in the evolution and emergence of MERS-CoV in humans.

IMPORTANCE Global surveillance efforts for undiscovered viruses are an important component of pandemic prevention initiatives. These surveys can be useful for finding novel viruses and for gaining insights into the ecological and evolutionary factors driving viral diversity; however, finding a viral sequence is not sufficient to determine whether it can infect people (i.e., poses a zoonotic threat). Here, we investigated the specific zoonotic risk of a MERS-like coronavirus (PREDICT/PDF-2180) identified in a bat from Uganda and showed that, despite being closely related to MERS-CoV, it is unlikely to pose a threat to humans. We suggest that this approach constitutes an appropriate strategy for beginning to determine the zoonotic potential of wildlife viruses. By showing that PREDICT/PDF-2180 does not infect cells that

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express the functional receptor for MERS-CoV, we further show that recombination was likely to be the critical step that allowed MERS to emerge in humans.

KEYWORDS bat, MERS coronavirus, spike, Uganda, zoonoses

In 2012, Middle East respiratory syndrome (MERS) emerged in Saudi Arabia. Clusters of fatal pneumonia in adults were determined to be caused by a novel lineage C betacoronavirus (2c CoV), termed MERS-CoV (1). This was the first 2c CoV known to cause disease in humans and at the time of its discovery was most closely related to two known bat coronaviruses (2), raising the possibility that bats were a reservoir and source for the virus. Concurrently, epidemiologists identified an association between MERS infections in patients and their contact with dromedary camels (3, 4). MERS-CoV was subsequently detected in camels at a farm linked to two human cases in Qatar (5) and in camels in Egypt (6), followed by surveys that demonstrated widespread exposure to the virus in the Middle East and in North and East Africa as early as the 1980s (7–10). It is now clear that camels play an important role in the transmission of MERS-CoV to people (11), with seroprevalence highest among those who have had contact with camels (12).

While camels are thought to be important for the transmission of MERS-CoV, bats are widely considered to be the evolutionary source of the virus. Several 2c CoVs have now been described in bats, including HKU4 from *Tylonycteris pachypus* (13), HKU5 from *Pipistrellus abramus* (13), and the recently identified NeoCoV from *Neoromicia capensis* (14). NeoCoV is the closest relative yet discovered (85% identical to MERS) and shares sufficient genetic similarity in the replicase genes to be considered part of the same viral species (15); however, despite being closely related across much of the genome, the S1 subunit of the spike gene is highly divergent as a result of a prior recombination event. Recombination in the spike gene is particularly significant because the derived protein is responsible for host receptor recognition and membrane fusion (16) and thus is central in determining host specificity. The S1 subunit contains the receptor binding domain and therefore has a specific role in defining host tropism (17). Other processes are also important, such as the activation of the spike protein by host proteases (18), but the ability of S1 to bind with a host receptor is a critical step in the emergence pathway—and it can be quickly altered by a single recombination event. The sequence variation in the S1 region of MERS-CoV and NeoCoV could therefore indicate differences in host binding preferences.

Predicting the interactions of virus binding domains with a particular host receptor (for example, the human MERS-CoV receptor DPP4) is possible through the use of structural modeling and the generation of infectious clones. Protein-protein interactions can be modeled using a related homologous complex (19, 20) while reverse genetic strategies can test the permissiveness of human or other primate cells for infectious clones expressing the novel receptor binding domains or complete spike glycoprotein (21–24). Pseudotyped lentivirus systems have also been used, for example, to show that DPP4 is the receptor for HKU4 but not for the closely related HKU5 (25, 26). And while pseudotypes are not always accurate predictors of spike glycoprotein function (23), these findings indicate that multiple cell-entry strategies could exist for 2c viruses and that not all MERS-like CoVs pose an equal risk of zoonotic emergence.

Here, we investigated the receptor binding properties of a new strain of MERS-like CoV found in a bat from Uganda. This virus (PREDICT/PDF-2180) shares the same putative S1 subunit recombination that was observed in NeoCoV, allowing us to also consider whether the spike recombination was critical for the emergence of MERS-CoV in humans.

RESULTS

Sampling and site characterization. A bat (identifier [ID] OTBA03-20130220) was trapped on 20 February 2013 in the Nkuringo area of Kisoro District, in southwestern Uganda (latitude −1.12, longitude 29.68) (Fig. 1). This area is an established settlement

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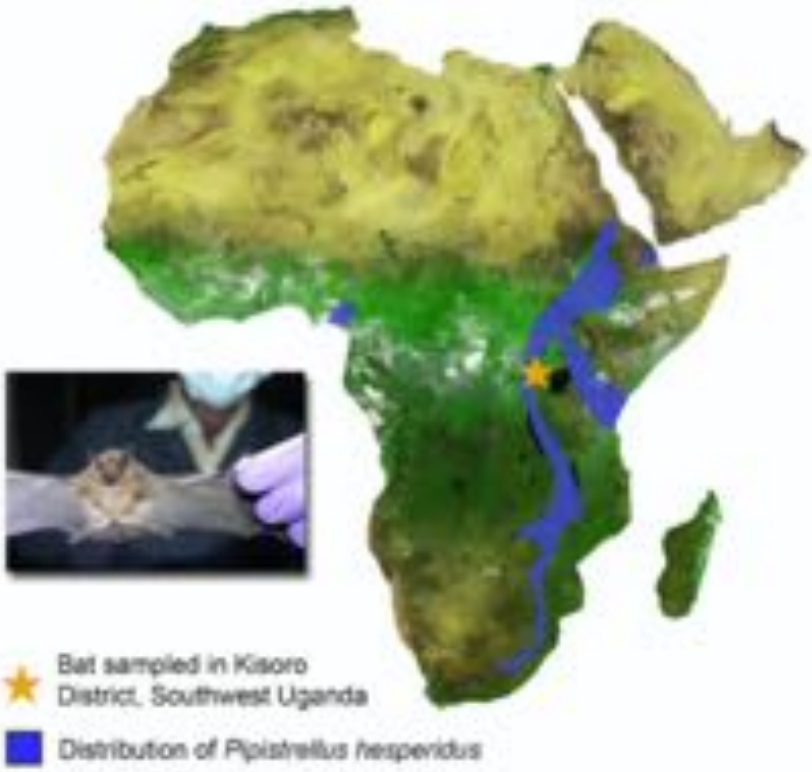

FIG 1 Map showing the distribution of *Pipistrellus hesperidus* (based on International Union for Conservation of Nature [IUCN] data) and the location of the bat sampled for the study.

of villages comprising approximately 13,000 inhabitants adjacent to the southwestern boundary of Bwindi Impenetrable National Park. Communities include subsistence farmers growing small crops, with some members working inside the national park or supporting tourism-related businesses. Livestock, including cattle, pigs, sheep, goats, and poultry, are present in the village and are raised on a small scale primarily for local consumption.

The sampled bat weighed 3.0 g and had a forearm length of 25 mm (Fig. 1). It was identified as *Pipistrellus cf. hesperidus* based on 95% sequence identity in the cytochrome *b* (Cytb) gene. The cytochrome oxidase subunit 1 (CO1) was also sequenced, but no corresponding CO1 sequences for *P. hesperidus* were available in GenBank for comparison. We therefore relied on the Cytb sequence for species identification.

Discovery and sequence characterization. The oral swab, rectal swab, and whole blood of bat OTSA03-20130220 were assayed for the presence of coronavirus by consensus PCR (cPCR). Two separate assays were used, each targeting a different region of the ORF1b RNA-dependent RNA polymerase (RdRp). Bands of the expected size were amplified from the rectal swab (PDF-2180) by both assays and confirmed to represent viral products by traditional Sanger dideoxy sequencing. Both fragments showed >98% amino acid sequence identity to MERS-CoV, prompting further characterization of the virus. The oral swab and blood were negative.

The near-full-length genome (identified as PREDICT/PDF-2180) was assembled from 100-nucleotide (nt) Illumina single-end reads at an average depth of 26×. Only the 5′ and 3′ noncoding regions were left incomplete. The order of all predicted open reading frames (ORFs) was consistent with MERS-CoV and with the recently described NeoCoV (KC869678) identified in a bat from South Africa. Similarly, the hexanucleotide transcription regulatory sequence (AACGAA) was conserved and found in the same position as both MERS and NeoCoV upstream of each predicted ORF.

Across the full genome, the sequence had 86.5% amino acid identity to MERS-CoV and 91% to NeoCoV; however, considerable variation was observed in different genes.

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TABLE 1 Pairwise amino acid sequence identity of subunit 1 of spike protein of 2c CoVs

Accession no. and/or isolate	% identity for subunit 1 (% identity for receptor binding domain)											
	NeoCoV	PDF-2180	ErinCoV/2012/174	ErinCoV/2012/216	BtCoV/133	HKU4	HKU5-1	HKU5-5	SC2013	EMC-2012	Al Hasa1	MRC-HKU205
KC809678, NeoCoV												
Predict/PDF-2180	91.0 (89.1)											
KC545383, ErinCoV/2012/174	54.7 (59.7)	54.3 (60.4)										
KC545386, ErinCoV/2012/216	54.9 (59.7)	54.4 (60.4)	99.9 (100)									
DQ648794, BtCoV/133	45.1 (42.5)	45.5 (42.5)	43.9 (50.0)	44.0 (50.0)								
EF065505, BatCoV HKU4	45.1 (41.8)	45.7 (41.8)	44.3 (50.0)	44.4 (50.0)	91.6 (96.2)							
EF065509, BatCoV HKU5-1	47.8 (46.3)	47.7 (47.0)	45.8 (53.7)	45.9 (53.7)	57.7 (63.4)	58.4 (63.4)						
EF065512, BatCoV HKU5-5	47.4 (45.5)	47.8 (46.3)	44.6 (50.7)	44.7 (50.7)	56.3 (61.8)	56.7 (61.8)	90.1 (93.9)					
KJ473821, SC2013	45.3 (42.5)	46.2 (44.0)	45.8 (55.2)	46.0 (55.2)	59.7 (57.5)	59.7 (56.7)	63.7 (73.9)	64.1 (73.1)				
KC669074, EMC-2012	43.3 (40.3)	44.4 (41.0)	43.9 (47.8)	44.1 (47.8)	61.2 (64.9)	61.1 (63.4)	56.5 (63.4)	56.7 (61.1)	61.4 (61.2)			
KF186567, Al Hasa1	43.5 (40.3)	44.4 (41.0)	43.9 (47.8)	44.1 (47.8)	61.4 (65.6)	61.2 (64.1)	56.5 (63.4)	56.7 (61.1)	61.4 (61.2)	99.9 (99.2)		
KJ477102, MRC-HKU205	43.7 (39.6)	44.4 (40.3)	43.8 (47.0)	43.9 (47.0)	61.1 (64.9)	61.0 (63.4)	56.3 (62.6)	56.4 (60.3)	61.4 (60.4)	99.1 (98.1)	99.2 (99.2)	

Amino acid identity could be as high as 97% to both MERS-CoV and NeoCoV in ORF1b or as low as 45% to MERS-CoV in subunit 1 of the spike protein. For the full spike protein, identity was 94% to NeoCoV and 53% to MERS-CoV. Percent sequence identity of the spike protein (subunits 1 and 2) to other 2c viruses is shown in Tables 1 and 2, respectively. Based on the current criteria for species demarcation established by the International Committee for the Taxonomy of Viruses (>90% amino acid sequence identity in the replicase protein), PREDICT/PDF-2180 shares sufficient genetic identity to MERS-CoV to be considered a member of the *MERS-like Coronavirus* species.

Phylogenetic analysis. Maximum likelihood phylogenetic reconstructions showed that PREDICT/PDF-2180 is most closely related to NeoCoV (Fig. 2). The two viruses were basal or formed sister clades to MERS-CoV in all genes except subunit 1 of the spike. The full-genome alignment was scanned for recombination using seven different algorithms (RDP, GENECONV, Bootscan, MaxChi, Chimaera, 5iScan, and 3seq) implemented in RDP v4.46. A single recombination event was detected within the spike gene by RDP, Bootscan, MaxChi, Chimaera, SiScan, and 3seq (Bonferroni-corrected *P* of $<<0.001$), suggesting that the incongruent phylogenies observed between spike subunit 1 and the rest of the genome are the result of recombination. Attempts to date the divergence of these two viruses to estimate the "minimum" number of years since this recombination were prevented by evidence of strong negative (purifying) selection across the genome (Fig. 2). Given that purifying selection can confound true phylogenetic depth, we felt that attempts to estimate the number of years to common ancestry were inappropriate and would result in artificially "recent" dates.

Zoonotic potential of PREDICT/PDF-2180. The high genetic variability in subunit 1 suggests that human and bat strains of MERS have different receptor binding properties. To investigate this, we modeled the specific affinity of the PREDICT/PDF-2180 spike protein for the human MERS-CoV receptor DPP4 (27). We utilized the crystal structure of the MERS-CoV spike binding domain in complex with DPP4 to create a homology model for the comparable region of the PREDICT/PDF-2180 spike (Fig. 3). Previous work has demonstrated 11 specific amino acid residues in MERS-CoV that

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TABLE 2 Pairwise amino acid sequence identity of subunit 2 of spike protein of 2c CoVs

Accession no. and/or isolate	% identity											
	Al-Hasa1	EMC-2012	NRC HKU205	NeoCoV	PDF-2180	ErinCoV/2012/174	ErinCoV/2013/216	BtCoV/133	HKU4	HKU5-1	HKU5-5	SC2013
KF186567, Al-Hasa1												
KC667074, EMC-2012	99.7											
KJ477102, NRC-HKU205	98.6	98.7										
KC869678, NeoCoV	84.7	84.9	84.4									
Predict/ PDF-2180	85.5	85.7	84.9	97.6								
KC545383, ErinCoV/2012/174	67.8	67.8	67.8	70.2	70.4							
KC545386, ErinCoV/2013/216	68.3	68.3	68.3	70.5	70.7	96.9						
DQ648794, BtCoV/133	72.9	72.9	72.5	73.7	73.3	69.0	68.2					
EF065505, BatCoV HKU4	73.0	73.0	72.7	73.8	73.5	69.0	68.3	98.4				
EF065509, BatCoV HKU5-1	71.2	71.2	70.9	74.3	73.6	66.9	66.6	79.6	79.1			
EF065512, BatCoV HKU5-5	71.7	71.7	71.4	74.5	73.9	66.9	66.6	79.9	79.4	97.9		
KJ473821, SC2013	73.5	73.5	73.2	72.5	71.7	67.6	66.8	81.0	80.5	81.8	82.0	

facilitate binding interactions with the human DPP4 (28). Of these residues, only one is conserved for PREDICT/PDF-2180. To determine whether the binding interactions may be conserved between DPP4 and PREDICT/PDF-2180 regardless of the differences in amino acid residues at these positions, we analyzed the predicted interactions between PREDICT/PDF-2180 and DPP4, compared to MERS-CoV and DPP4. Overall, we found a global reduction in predicted hydrogen bonding interactions in the DPP4-PREDICT/PDF-2180 binding interface compared with DPP4-MERS-CoV (Fig. 3). While the interactions in conserved residue Y499 were maintained, DPP4 interactions with PREDICT/PDF-2180 residues S01, S02, S10, S11, S13, S39, and S42 were disrupted. The interaction between DPP4 Y322 and MERS D510 is abolished in the PREDICT/PDF-2180 prediction, where D510 is replaced by K510. This is a charge change from negative to positive. Interestingly, a change from R511 in MERS to D511 in PREDICT/PDF-2180 facilitates a potential interaction with Y322 to replace the hydrogen bond lost with K510. Regardless, due to the predicted loss of the majority of the DPP4 binding interactions, the model predicts that PREDICT/PDF-2180 will not bind to DPP4.

To confirm these results *in vitro*, a recombinant MERS-CoV cDNA clone was constructed containing the PREDICT/PDF-2180 spike gene in the context of the full-length MERS-CoV backbone. The chimeric virus maintains the entire ectodomain of the PREDICT/PDF-2180 spike with the exception of the first 20 amino acids of the 5′ end, which were taken from wild-type MERS-CoV. Similarly, the transmembrane domains (TMDs) and cytoplasmic tail of the chimeric virus used the wild-type MERS-CoV sequence in order to minimize incompatibility in virion formation. Following transfection into Vero cells, PCR amplification of leader-containing transcripts for all of the expected nested subgenomic (sg) mRNAs (including the sg spike mRNA) confirmed replication of the recombinant virus (Fig. 4). However, subsequent passages by supernatant transfer to uninfected monolayers failed to reproduce the infection, suggesting that the PREDICT/PDF-2180 spike protein is unable to mediate cell entry in Vero cells as seen with wild-type MERS-CoV (Fig. 4).

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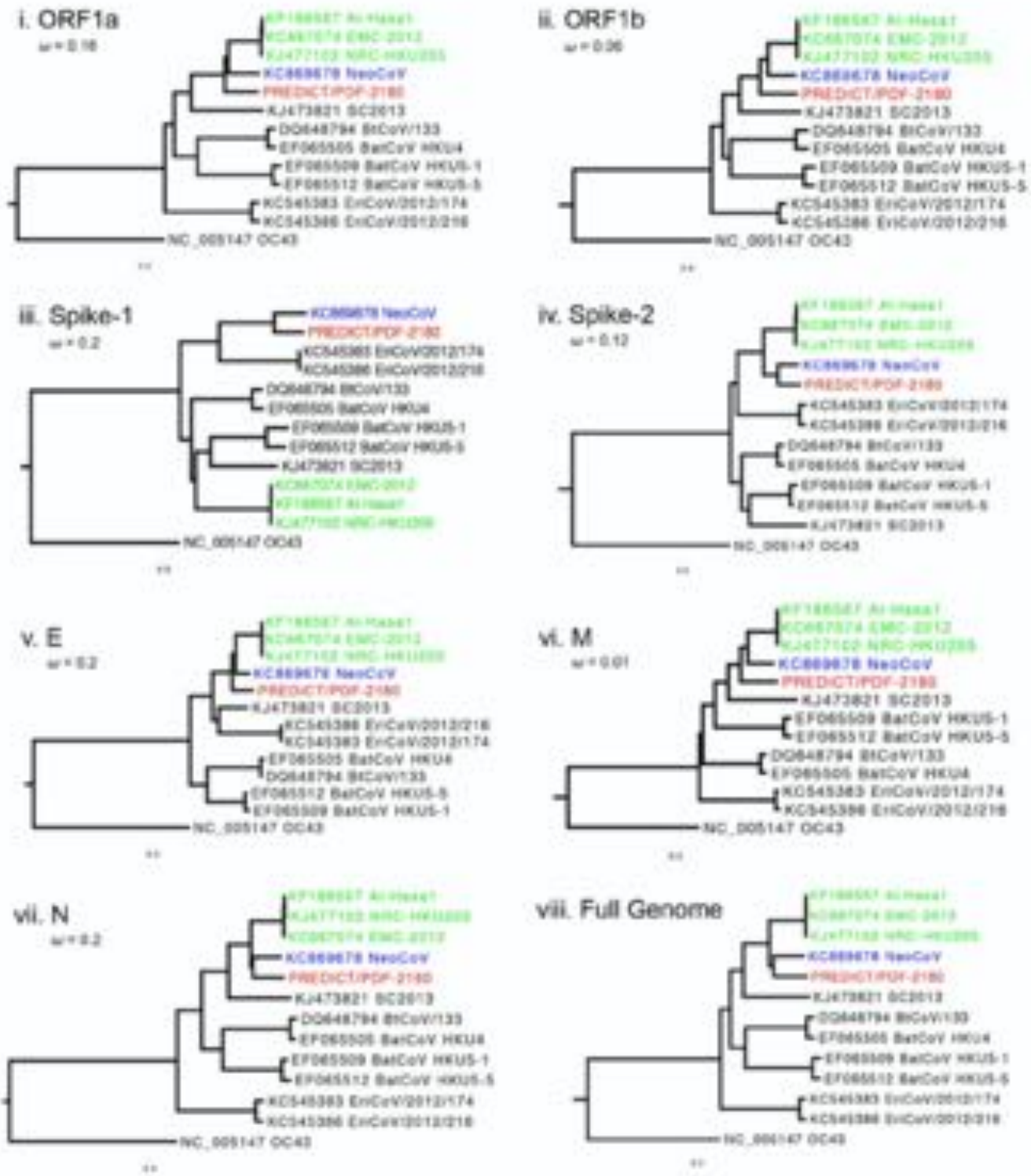

FIG 2 PREDICT/PDF-2180 and NeoCoV are ancestral to MERS-CoV. Maximum likelihood phylogenetic reconstructions of 2c coronaviruses (nucleotide) show that PREDICT/PDF-2180 and NeoCoV are consistently basal to, or form sister clades with, MERS-like CoV (human/camel strains), except in subunit 1 of the spike protein. Human OC43 is the outgroup. All genes were shown to be under purifying selection (ω).

Supernatant from the transfected Vero cells (passage 0 [P0]) was also used to infect primary human airway epithelial (HAE) cells, which were derived from lung donors with no preexisting chronic disease. These well-differentiated primary cells are grown on an air-liquid interface and represent an important model for viral infection of the human

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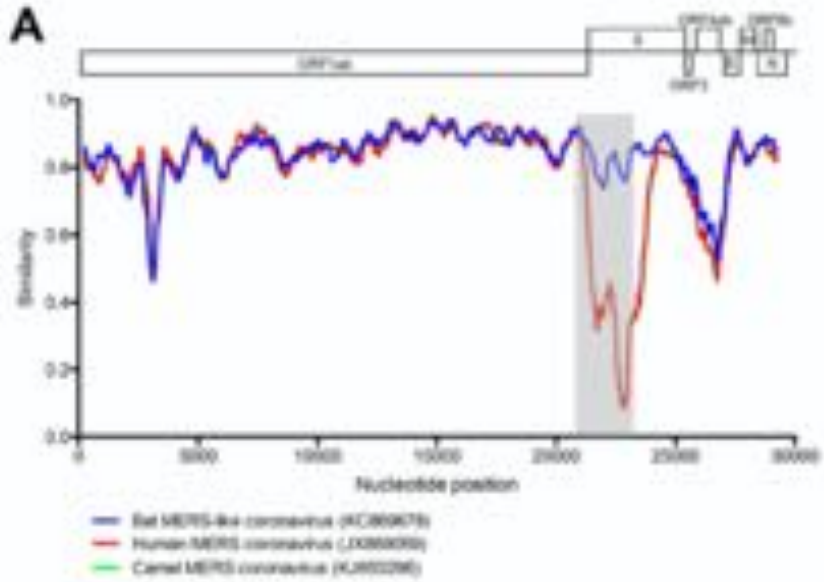

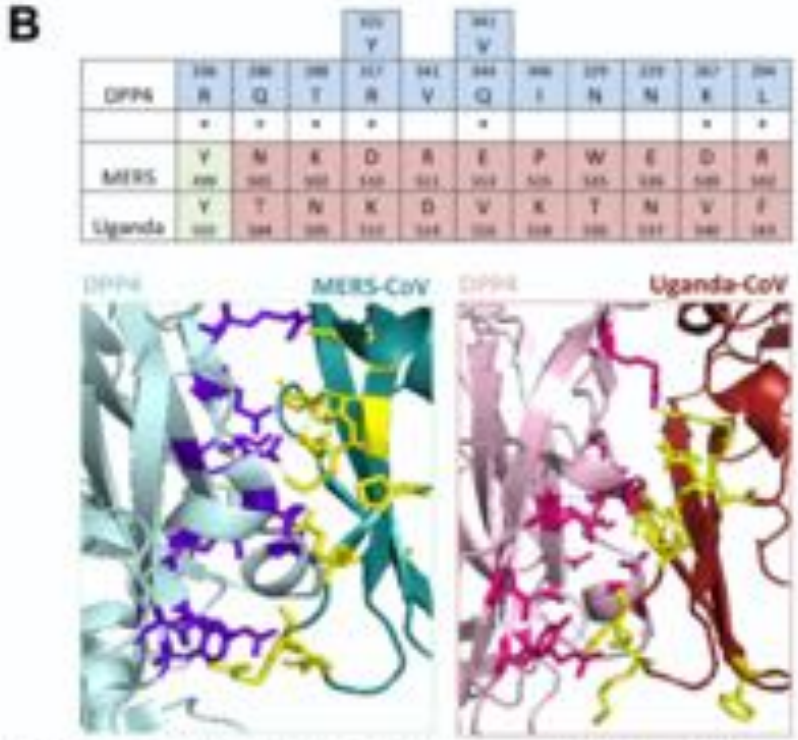

FIG 3 The spike protein of PREDICT/PDF-2180 is highly divergent. (A) A nucleotide identity SimplotT shows that PREDICT/PDF-2180 and NeoCoV are closely related to MERS-CoV across much of the genome but are highly divergent in subunit 1 of the spike protein, suggesting that they may have different receptor binding properties. (B) Variation in key amino acid binding residues (*) and modeling to human DPP4 both suggest that PREDICT/PDF-2180 is unable to bind to DPP4.

lung. Several coronaviruses show improved replication in these polarized primary respiratory cells compared to standard cell lines. Using wild-type MERS-CoV as a control, primary HAE cell cultures were infected with passage 0 from the PREDICT/PDF-2180-MERS chimeric clone and showed no evidence of viral replication (Fig. 5A). Similarly, viral RNA expression analysis indicated no evidence of replication following infection with the PREDICT/PDF-2180 chimeric virus (Fig. 5B). In contrast, wild-type

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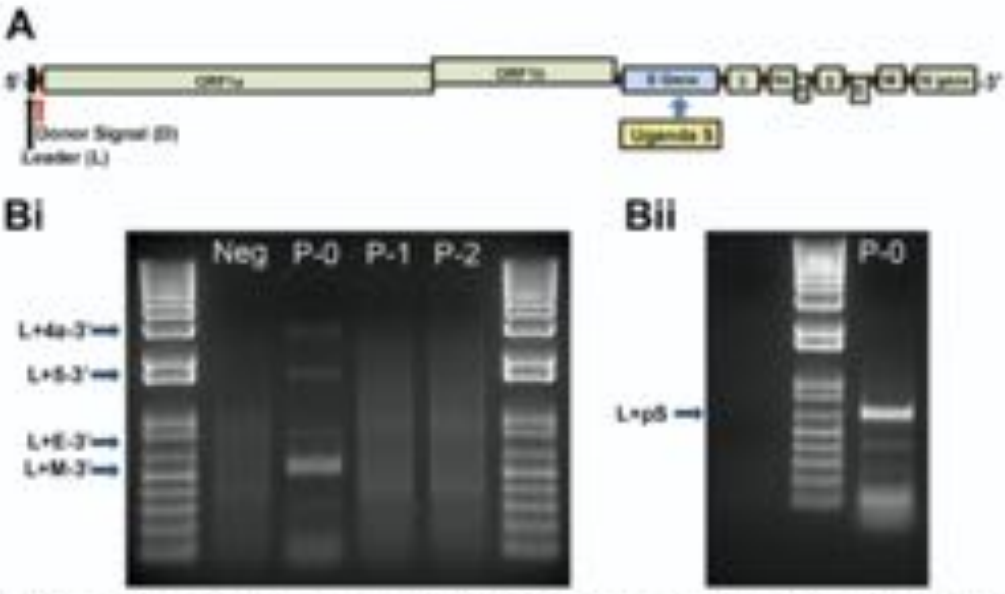

FIG 4 Uganda spike protein does not permit entry into Vero cells. (A) Genome organization of MERS-CoV encoding the Uganda spike glycoprotein. (Bi) Reverse transcription-PCR detection of leader-containing nested subgenomic mRNAs encoding the nucleocapsid transcript, E transcript, and ORF5 and ORF4a transcripts (p0, RNA-transfected cells; p1, passage 1; p2, passage 2). (Bii) Reverse transcription-PCR amplification of leader-containing mRNA 2 containing the Uganda S gene. Note the loss of the leader-containing transcripts in p1 and p2, demonstrating the loss of infectivity associated with insertion of the Uganda S gene. Ladder, 1 kb.

MERS-CoV induces robust replication as measured by plaque assay and viral-leader-containing transcripts. Together, the results indicate that the PREDICT/PDF-2180 spike is not likely to efficiently replicate in the human airway without further adaptation.

DISCUSSION

The discovery of PREDICT/PDF-2180 in Uganda adds to the growing number of group C betacoronaviruses that have now been identified in bats. These include NeoCoV from South Africa (15), Mex_CoV-9 from Mexico (29), BatCoV/KW2E from Thailand (30), P.pipis/VM314 from the Netherlands (31), H.sav/206645-40 from Italy (32), and BetaCoV/SC2013, HKU4, and HKU5, all from China (33). Collectively, these examples demonstrate that the MERS-related CoVs are highly associated with bats and are geographically widespread.

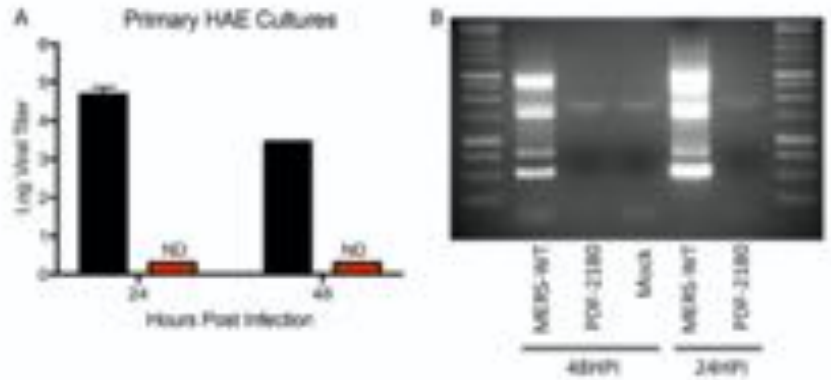

FIG 5 PDF-2180 spike unable to mediate infection of primary human airway cultures. (A) Primary human airway epithelial (HAE) cells grown on an air-liquid interface were infected with wild-type MERS-CoV (black bar) or passage 0 of PDF-2180/MERS chimeric CoV (red bars) and assayed by plaque assay on Vero cells. ND, none detected. (B) Reverse transcription-PCR detection of leader-containing nested subgenomic mRNAs encoding the nucleocapsid transcript, E transcript, and ORF5 and ORF4a transcripts following infection. Ladder, 1 kb. WT, wild type.

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The group 2c viruses appear to have a particular, though not exclusive, association with vespertilionid bats, which form a highly diverse and widely distributed family within the Microchiroptera. NeoCoV, SC2013, HKU4, HKU5, KJ.uav/206645-40, P.pipi/VM314, and PREDICT/PDF-2180 were all found in species belonging to this family. If the full diversity of 2c viruses reflects the number of vespertilionid species described (*n* = 475 species), there is potential for a substantial diversity of MERS-related viruses to be circulating in bats.

Our data suggest that PREDICT/PDF-2180 cannot infect humans and is not likely to pose a threat to human health, at least in its current form. The spike protein of this virus is distinct from the MERS-CoV spike, sharing only 46% amino acid identity, and it appears unable to enter cells that express the functional receptor used by MERS-CoV (DPP4)—or any other receptor expressed by either primate Vero cells or human airway epithelial cells. Importantly, failure to assemble and release viral particles from the initial infection could also explain our results; however, we suggest that receptor incompatibility is more likely given the steps taken to minimize particle disruption (see Materials and Methods). These results suggest that adaptation of the spike would be required to permit PREDICT/PDF-2180 replication in human airways. While we did not examine the specific binding properties of the related virus NeoCoV, the high amino acid sequence identity with PREDICT/PDF-2180 indicates that it shares a similar phenotype and is most likely also refractory for human infections.

Our data suggest that RNA recombination is the mechanism that underlies the observed difference in receptor binding. Recombination can occur at high frequency during mixed coronavirus infection, allowing different viral lineages to exchange specific functional motifs or even entire genes (22, 34, 35). Phylogenetic incongruence was noted in subunit 1 of the spike protein, and breakpoints were observed in this same region by multiple recombination detection algorithms. It is also parsimonious with the high purifying selection observed across the genome of 2c viruses (which argues against receptor adaptation via drift or selection) and with previous reports citing recombination in association with host switching for other coronaviruses (36–38). Given that the recombination is observed in both PREDICT/PDF-2180 and NeoCoV, we support the previous suggestion by Corman et al. (15) that it was the MERS-CoV that acquired a new spike. Given also that the PREDICT/PDF-2180 spike does not use DPP4 and is seemingly not competent for human infection, we further suggest that the recombination event was the critical factor driving the emergence of MERS-CoV.

What is less clear is whether this recombination occurred in bats or an intermediate host. Lineage 2c strains that use DPP4 have been reported in bats (25, 26), and there is also evidence of positive selection in the bat DPP4 that would indicate the existence of a large diversity of (as-yet-unknown) DPP4-competent strains (39). Just as detailed metagenomics studies have revealed the presence of several severe acute respiratory syndrome (SARS)-like bat CoVs that can use the human angiotensin converting enzyme 2 receptor and/or replicate efficiently in human cells (23, 24, 40–42), it seems likely that subsets of diverse MERS-CoV-like bat coronaviruses will also exist which are preprogrammed to efficiently use the human DPP4 receptor. This would support the hypothesis that the recombination occurred in bats; however, the MERS-CoV spike seems to have adapted and acquired a preference for human DPP4 over the bat homologue (26, 43) making it difficult to conclude with certainty that the MERS-CoV spike has bat origins. Increased surveillance will be required to understand the full diversity of spike phenotypes circulating in bats or in intermediate hosts such as camels.

In recent years, global surveillance efforts such as the USAID Emerging Pandemic Threats PREDICT program have advanced our understanding of the viral diversity that exists in wildlife (44). While this knowledge can be useful for proving the existence of novel viruses (29, 30, 45–49), quantifying overall viral diversity (45, 46), and measuring infection prevalence within a population, it does not provide information on their specific zoonotic threat. Given that no single correlate of pathogenicity or virulence has been determined for any viral family (50, 51) and that it is not possible to determine risk through phylogenetic data alone (51), the approach used here is an important tool in

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characterizing the zoonotic potential of viral sequences detected in wildlife. Doing so on a large scale (for example, as part of projects like USAID PREDICT) will also provide critical information on host and geographic variation in key viral traits, like potential host tropism, which are currently missing from most risk-based models forecasting hot spots of disease emergence.

MATERIALS AND METHODS

Sampling. A bat (ID DTB403-201302220) was trapped on 20 February 2013 in the Maramagambo area of Kasoro District in southwestern Uganda. The bat was caught with a mist net (3.9-mm mesh; Avinet, Inc.) according to established protocols and was released unharmed post-sampling. Standard morphometric measurements (weight and forearm length) and photographs were obtained to aid species identification, which was confirmed by DNA barcoding of the cytochrome *b* (Cyt*b*) and cytochrome oxidase subunit 1 (CO1) mitochondrial DNA genes (52). Approximately 200 μl of whole blood was collected into EDTA. Oral and rectal swabs were also collected in duplicate (one into viral transport medium and one dry). Specimens were stored temporarily on gel packs and frozen in liquid nitrogen in the field within 4 h of collection and then transferred to −80°C for storage until testing. Samples were transferred to the Center for Infection and Immunity at Columbia University for viral discovery and characterization.

Coronavirus discovery by consensus PCR. Total nucleic acid (TNA) was extracted using the Roche MagNA Pure 96 platform according to the manufacturer's instructions. TNA was reverse transcribed into cDNA using SuperScript III (Invitrogen) according to the manufacturer's instructions. Two broadly reactive consensus PCR assays targeting partial and nonoverlapping regions of the coronavirus ORF1b (containing the RdRp) were performed (53, 54). Bands of the expected size were excised from 1% agarose, cloned into StrataClone PCR cloning vector, and sequenced to confirm detection.

Sequencing and bioinformatic processing. Total RNA extract was DNase treated (DNase I; Ambion, Life Technologies, Inc.) and reverse transcribed using SuperScript III (Invitrogen, Life Technologies, Inc.) with random hexamer primers. The cDNA was RNase H treated before second-strand synthesis with Klenow fragment (3′ to 5′ exonuclease) (New England Biolabs). The resulting double-stranded cDNA was sheared to 200 bp (average) fragments using a Covaris focused ultrasonicator (E210), according to the manufacturer's standard settings, and used for library construction using the Kapa Hyper library preparation kit (Kapa Biosystems, Roche), again according to the manufacturer's instructions. The final library was quantified using an Agilent Bioanalyzer 2100 and pooled to allocate 20 million reads on the Illumina HiSeq 2500 platform.

The Q30-filtered FastQ files were used to generate quality control reports using PRINSEQ software (v0.20.2) (55) and were further filtered and trimmed. Host background levels were determined by mapping the filtered reads against a bat reference database using Bowtie2 mapper (v2.0.6, http://bowtie-bio.sourceforge.net) (56). The host-subtracted reads were *de novo* assembled using MIRA assembler (v4.0) (57). Contigs and unique singletons were subjected to homology search using MegaBlast against the GenBank nucleotide database. Sequences that showed poor or no homology at the nucleotide level were screened by BLASTX against the viral GenBank protein database. Viral sequences from BLASTX analysis were subjected to another round of BLASTX homology search against the entire GenBank protein database to correct for biased *E* values and taxonomic misassignments. The genome of PREDICT/PDF-2180 was mapped with Bowtie2 against the filtered data set to visualize depth and coverage in Integrated Genomics Viewer.

Genetic and phylogenetic analyses. Sequences were analyzed and edited using Geneious (version 6.0.3). Full genome and individual gene sequences were aligned with ClustalW, and maximum likelihood phylogenetic trees were constructed in PAUP* (500 bootstraps). Models of nucleotide substitution were selected using jModelTest. Nucleotide sequence similarity between MERS-like viruses was assessed using Simplot v3.5.1 (58) with a sliding window size of 500 bp, a step size of 50 nucleotides, and 1,000 bootstrap replicates using gap-stripped alignments and the F84 (maximum likelihood) distance model. The full-genome alignment was scanned for recombination using seven different algorithms (RDP, GENECONV, Bootscan, MaxChi, Chimaera, SiScan, and 3seq) implemented in RDP (v4.46) (59).

Structural modeling. Predicted binding differences between DPP4 and either MERS or Uganda were determined by structural analysis. The crystal structure demonstrating the interactions between DPP4 and MERS spike binding domain has previously been reported (28), and the crystal structure is PDB ID 4KR0. We created a homology model of the region of the Uganda spike protein homologous to the MERS spike binding domain based on the 4KR0 structure in association with DPP4. We first aligned the amino acid sequences for 4KR0 (28) and the Uganda spike using Clustal-Omega (60). We then used MODELLER (61) to create predicted structural coordinates for the Uganda spike based on the coordinates of 4KR0. Because MODELLER requires the two sequences to be the same length, we introduced gaps in the sequences where appropriate to maintain the best sequence identity between the 2 amino acid sequences. Numbering is based on MERS-CoV amino acid residues. We then imported the predicted crystal structure for Uganda and the known DPP4-MERS structure into PyMOL (62) for visualization and comparative analysis. Hydrogen bonding interactions were predicted by selecting the known DPP4 and 4KR0 or the homologous DPP4 and Uganda interaction sites and using the "find polar interactions" function within PyMOL.

Generation of a MERS-CoV recombinant virus. Previously, we reported the isolation of recombinant MERS-CoV that was derived from a cDNA clone (63). To reconstitute a MERS genome expressing the PREDICT/PDF-2180-CoV spike, new E and F plasmids were ordered synthetically (Bio-Basic) to contain the PREDICT/PDF-2180 spike ectodomain; these plasmids were named MERS-Uganda E and F. MERS-D891

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and ORF 2 overlap, so to maintain a functional replicase sequence and signal sequence for spike, the first 20 amino acids of the MERS spike were retained and the PREDICT/PDF-2180 sequence was fused in frame downstream of the MERS-CoV S glycoprotein signal peptidase domain beginning at its 24th amino acid. In short, the sequence of the MERS spike coding for amino acids 21 to 1306 was replaced with the sequence of the PREDICT/PDF-2180 spike coding for amino acids 24 to 1298, so that following processing, an intact spike glycoprotein was expressed during virus infection. The E and F plasmids were sequence verified prior to the assembly of full-length recombinant DNAs.

The MERS A through F inserts (containing the Uganda S gene) were restriction digested, resolved on 0.8% agarose gels, visualized, excised, and purified using a QIAquick gel extraction kit (Qiagen). The MERS A to F inserts were mixed and ligated overnight at 4°C, phenol-chloroform extracted, and precipitated under isopropyl alcohol. Full-length T7 transcripts were generated *in vitro* as described by the manufacturer (Ambion; mMessage mMachine) with certain modifications (63). For MERS-CoV N transcripts, 1 μg of plasmid DNA containing the N gene (amplified using forward primer 5′-ATTTAGGTGACACTATAGATGGCATCCCCTGCTGCACC-3′ and reverse primer 5′-TTTTTTTTTTTTTTTTTTTTTTTTCTAATCAGTGTTAACATCAATCATTGG-3′) was transcribed by SP6 RNA polymerase with a 4:1 ratio of cap analog to GTP. RNA transcripts were added to 800 μl of Vero cell suspension (8.0 × 10^6 cells) in an electroporation cuvette, and four electrical pulses of 400 V at 50 μF were delivered with a Gene Pulser II electroporator (Bio-Rad). The transfected Vero cells were allowed to recover for 10 min at room temperature and then incubated at 37°C for 2 to 4 days in a 75-cm^2 flask. Virus progeny were then passaged several times in Vero cells or primary human airway epithelial cells for 48 h to detect viable viruses. All viruses were maintained under biosafety level 3 (BSL3) conditions with redundant fans, and personnel used powered air-purifying respirators (PAPRs) and Tyvek suits.

To detect leader-containing RNAs, intracellular RNA from wild type and recombinant MERS-CoV-Uganda (rMERS-CoV-Uganda) was reverse transcribed with a primer at the 3′ end of the genome and cDNA was isolated for PCR using a reverse primer located in ORF3 and a forward primer located in the leader RNA sequence at the 5′ end of the genome (5′-CTATCTCACTTCCCCTCGTTCTC-3′). Leader-containing amplicons were sequenced as previously described (64). The cDNA products were separated and visualized in 0.8% agarose gels.

Viruses, cells, and infection. Wild-type and chimeric CoVs were cultured on Vero E6 cells, grown in Dulbecco modified Eagle medium (DMEM) (Gibco, Carlsbad, CA) and 5% fetal clone serum (HyClone, South Logan, UT) along with antibiotic-antimycotic (anti-anti; Gibco, Carlsbad, CA). Growth curves in Vero and primary human airway epithelial cells were performed as previously described (65, 66). Human lungs were procured under University of North Carolina at Chapel Hill Institutional Review Board-approved protocols.

Biosafety and biosecurity. Reported studies were initiated after the NIH and the University of North Carolina Institutional Biosafety Committee approved the experimental protocol (project title, Generating Infectious Clones of Bat SARS-like CoVs; lab safety plan ID, 20167715; schedule G ID, 13982).

Accession number(s). The near-complete genome sequence for PREDICT/PDF-2180 has been deposited in GenBank under accession number KX574227.

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From: Dennis Carroll <dcarroll@usaid.gov>
To: Eri Togami <etogami@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 11/21/2017 1:29:24 PM
Subject: Re: PMAC logistics

Eri, I haven't seen anything. I presume Cara and/or you sent it in. The email should come back to you. It is possible that it came back to Cara if she is the one who submitted. But she hasn't been checking her emails since she went on maternity leave. Do you have visability on the submission?

On Mon, Nov 20, 2017 at 4:11 PM, Eri Togami <etogami@ucdavis.edu> wrote:

Hi Dennis,

I hope you had a great weekend. Jonna and I have a few questions as we start to plan logistics for PMAC.

-Has our side meeting been officially accepted?

-If so, shall we offer an invitation letter similar to Beijing for the Steering Committee and Work Group Leads?

-In order to send the invitation letter, Jonna said that we should be ready to state if funding will be offered for travel. We have the same standard language from Beijing ready to go, but we wanted to be sure that you were okay with us potentially covering the costs for the approximately 36 invitees.

-We will also need an agenda and/or the final PMAC side meeting submission to include with the invite letter. I have the draft before submission but am unsure if changes were made prior to submission.

-We have received funding requests from Keiji, Sam and Gian Luca so far in response to the invites they received from PMAC.

-Should we submit an ITA before sending invitation letters?

Many thanks,
Eri

Eri Togami DVM MPH

Fellow

One Health Institute

School of Veterinary Medicine

University of California, Davis

--
Dr. Dennis Carroll

Director, Emerging Threats Program
Bureau for Global Health
U.S. Agency for International Development

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From: Andrew Clements <aclements@usaid.gov>
To: David J Wolking <djwolking@ucdavis.edu>
CC: Amalhin Shek <ashek@usaid.gov>;Shana Gillette <sgillette@usaid.gov>;Prof. Jonna Mazet <jkmazet@ucdavis.edu>;Alisa Pereira <apereira@usaid.gov>
Sent: 11/22/2017 8:54:56 AM
Subject: Re: PREDICT-2 Q4Y3 Quarterly Financial Report

Hi David,

A follow up on this based on a separate email from Jonna saying that core funds will run out late December/early January.

In the attached table, it shows about 10 million of core remaining at the end of FY17 quarter 3. Using the projected monthly burnrate (1.5 million) from Jonna's email or the quarterly burnrate from your table (3.7 million), the pipeline would appear to be sufficient to go well past the beginning of January. Or am I reading the information incorrectly?

Thanks!

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Nov 22, 2017, at 1:05 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

Andrew,

Please find attached our Q4Y3 country by category financial report. Apologies for the delay.

Please let us know if you have any questions.

David

On Mon, Nov 13, 2017 at 11:54 PM, Andrew Clements <aclements@usaid.gov> wrote:
Thanks, David.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Nov 13, 2017, at 10:27 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Andrew,

Just an update that we are working hard on this country by category financial report. This report will include

the Ebola funding report, the CORE funding report, and the combined report that includes both CORE and Ebola funds.

This is my first attempt pulling these figures together and we want to provide accurate information, so I'll do my best to deliver the report as soon as possible.

Best,

David

From:	Carlos Morel <cmmorel@gmail.com>
To:	Peter Daszak <daszak@ecohealthalliance.org>
CC:	Dennis Carroll (DCarroll@usaid.gov) <DCarroll@usaid.gov>;Nathan Wolfe <nwolfe@metabiota.com>;George F Gao (gaof@im.ac.cn) <gaof@im.ac.cn>;Subhash (FAORAP) Morzaria (Subhash.Morzaria@fao.org) <Subhash.Morzaria@fao.org>;Subhash P Morzaria (subhash.morzaria@gmail.com) <subhash.morzaria@gmail.com>;Ariel Pablos-Mendez <apablos@gmail.com>;Oyewale Tomori <oyewaletomori@gmail.com>;Jonna Mazet <jkmazet@ucdavis.edu>;ap39@cumc.columbia.edu <ap39@cumc.columbia.edu>;Brooke Watson <watson@ecohealthalliance.org>;Cara Chrisman <cchrisman@usaid.gov>;Eri Togami <etogami@ucdavis.edu>
Sent:	12/10/2017 12:55:47 AM
Subject:	Re: Time Sensitive - Science paper on GVP now accepted - Instructions on next steps.

Dear Peter, dear Dennis, dear all,

Congratulations, this is indeed very good news! 18 months since first submission…!

Ready to answer *Science* emails, as soon as they arrive.

best,

Carlos

Em 9 de dez de 2017, à(s) 22:13, Peter Daszak <daszak@ecohealthalliance.org> escreveu:

Dear All,

Letting you all know that the paper we submitted to *Science* on the Global Virome Project has now been accepted. Obviously, this is great news, and comes after two rounds of reviews by the *Science* Board of Reviewing Editors, and two rounds by external reviewers – quite a hassle, but I now think the paper is much better than the original submission (18 months ago!!).

The current version of the paper is attached, in *Science* format, but bear in mind that this will now be edited. First, I'm right now finessing the text by reducing some verbiage and conforming to all of the instructions from the editor. Once that's done it will go back in to our *Science* editor (this weekend) for final edits which they'll send back to me for final approval. This will probably be a very rapid turnaround (24 hours). I'm not sure how long it will then be to publication, but the timing is good for us, with our planned soft-launch of the GVP at the PMAC conference on Jan 31st. Ideally, we could coincide publication with the conference, and I'll ask the editor if that's possible. One thing I'm going to try to avoid is the paper coming out during the December holiday season or the first week of January – papers published then tend to get less publicity and readership.

So we can move this through rapidly, I now need you to check the following items and respond as soon as possible:

1. Please double-check your addresses. We need to use your current academic address. Some of you have two relevant addresses, which is fine. Ariel, it would be fine to use your current address, and have the USAID address as 'formerly'…your decision of course.

2. Please let me know what the best email address is for you, and alternatives so I can get hold of you at short notice re. any issues at the proofs stage (1 day turnaround). Also please send your assistant's email addresses. Please cc Brooke Watson (cc'd above: watson@ecohealthalliance.org) on all emails so I don't miss any.

3. Please get ready for the following email from *Science* – I don't know the timing of this, but if any of you don't respond rapidly, it will delay publication:
Authorship

All authors will be asked to complete an authorship verification and COI form (each author will receive a separate email directing them to our Authorship WWW site). All authors must attest prior to publication that they agree to be so listed, and that they have seen and approved the manuscript, its content, and its submission to Science. Any changes in authorship must be approved in writing by all the original authors.

4. For those of you who are in organizations that have a waiver for open-access, please follow the links below and get a waiver from your employer:
License Waiver
All authors must obtain a waiver from open-access policies of their employer, as at Harvard and MIT.

5. Please get the following information to me by email. The language is from the *Science* instructions to authors.
Funding and Conflict of Interest
You and all co-authors will be asked to disclose all affiliations, funding sources, and financial or management relationships, including those that could be perceived as potential sources of bias. Please declare patents (either applications or awards to the authors or home institutions) related to this work as part of the acknowledgments.

Please let me know by email if you have any comments, questions etc. and please cc Brooke.

I'm really looking forward to finally seeing this in print and to using this paper as a platform for turning the GVP from a vision into a reality!

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4473
www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Andrew Clements <AClements@usaid.gov>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Amalhin Shek <ashek@usaid.gov>;Alisa Pereira <apereira@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 2/1/2018 4:53:50 PM
Subject: PREDICT-2 December 2017 Ebola Financial Report

Hi Andrew. Please find attached the December 2017 Ebola Financial Report for PREDICT. Let me know if you have any questions.

Thanks,
Liz

Elizabeth Leasure
One Health Institute
University of California, Davis
530-754-9034 (office)
530-304-1403 (cell)

PREDICT-2 Expenses - Ebola

December 2017

Cost Category	US Central	Cameroon	Cote d'Ivoire	DRC	Ethiopia	Ghana	Guinea	Kenya	Liberia
Salaries	12,927	37,879	16,502	31,392	26,824	15,330	20,121	21,954	776
Fringe	5,856	14,432	7,224	11,379	9,648	2,960	3,690	7,131	385
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	3,769	8,152	5	2,211	5	524	1,002	1,802	0
Foreign Travel	9	1,202	1,902	3,474	1,202	3,236	14	601	14
Services	0	12,386	9,388	3,698	71	18	0	12,239	46,759
Supplies	7,787	126	126	1,440	126	10,083	15	63	20,854
Other	2	22,169	127	8,010	2,221	2,509	1,699	264	0
Indirects	14,275	44,740	16,414	25,539	18,875	9,780	2,636	12,453	7,324
Total Costs	**$44,626**	**$139,085**	**$53,688**	**$87,144**	**$59,172**	**$44,680**	**$28,176**	**$56,508**	**$76,112**

Cost Category	Senegal	Sierra Leone	Tanzania	Uganda
Salaries	33,024	46,803	35,972	35,236
Fringe	11,698	3,181	11,482	17,517
Equipment	0	0	0	0
Domestic Travel	5	25,970	1,829	2,110
Foreign Travel	2,838	8,014	2,415	5,439
Services	71	0	71	411
Supplies	3,782	3,779	267	2,143
Other	1,063	37,030	9,110	19,658
Indirects	19,970	26,262	22,412	23,664
Total Costs	**$72,453**	**$131,039**	**$83,560**	**$106,179**

$1,002,182 PREDICT-2 Costs (Ebola)

From: Dennis Carroll <dcarroll@usaid.gov>
To: Carlos Morel <cmmorel@gmail.com>
CC: Peter Daszak <daszak@ecohealthalliance.org>;Nathan Wolfe <nwolfe@metabiota.com>;George F Gao (gaof@im.ac.cn) <gaof@im.ac.cn>;Subhash (FAORAP) Morzaria (Subhash.Morzaria@fao.org) <Subhash.Morzaria@fao.org>;Subhash P Morzaria (subhash.morzaria@gmail.com) <subhash.morzaria@gmail.com>;Ariel Pablos-Mendez <apablos@gmail.com>;Oyewale Tomori <oyewaletomori@gmail.com>;Jonna Mazet <jkmazet@ucdavis.edu>;ap39@cumc.columbia.edu <ap39@cumc.columbia.edu>;Brooke Watson <watson@ecohealthalliance.org>;Cara Chrisman <cchrisman@usaid.gov>;Eri Togami <etogami@ucdavis.edu>;Anthony Ramos <ramos@ecohealthalliance.org>
Sent: 2/22/2018 5:51:53 PM
Subject: Re: Instructions from Science re. Press Embargo on our Science Policy Forum on the GVP

Excellent. Thanks Carlos. Question, would you be interested in meeting with US Embassy people while you are in Beijing? The Embassy has been particularly interested in GVP as a possible point for US-China global partnership. Hearing from you and the Brazilian perspective could add additional value. Let me know if you would be interested and I can reach out to Beijing to see if possible during your visit

d

Dr Dennis Carroll
Director, Emerging Threats Program
U.S. Agency for International Development
Office: (202) 712-5009
Mobile: (301) 646-6235

On Feb 22, 2018, at 1:44 PM, Carlos Morel <cmmorel@gmail.com> wrote:

Dear Peter and Dennis,

I am now in Dubai, at the Millennium Dubai hotel, in the next hour I will go to the airport to take the Dubai—>Hongkong flight.

At least two Brazilian newspapers will publish articles or interviews about GVP & the Science paper. Today, from the hotel, I was interviewed by "O Estado de São Paulo" and "O Globo", two of the most relevant newspapers in Brazil. These two journals will publish their articles tomorrow, Friday. As soon as I receive the news when I arrive in China I will share with you.

Now moving to the airport, regards,

Carlos

Em 16 de fev de 2018, à(s) 23:11, Peter Daszak <daszak@ecohealthalliance.org> escreveu:

Dear Co-authors,

I can now confirm that the publication date for our Policy Forum on the GVP will be one week from now – the 23rd February. Apologies for the delay in this, but we were still working on edits with the Editor up until yesterday and it was possible it could have been pushed back a week, but we're now scheduled definitively for the 23rd.

So you are all fully aware of the press guidelines for the paper, I'm forwarding the information from Science regarding the timing of the paper's release, and the embargo that will cover it until its published. I'm not sure

if Science already sent this out to all of you, but I'm forwarding it in any case. I'm supposed to email back to Science to confirm that you're all aware of these guidelines - mainly because Science doesn't want to have their embargo breached by rogue reporters!

That said, it's now time for us to do the following:

1. Contact your institution's press office to let them know about the paper, and the embargo guidelines below. Science will do their own press release that covers our GVP Policy Forum, as part of their weekly reach out to reporters and these are very effective at getting the word out. Because of that, I don't think there's much value in doing a group press release. That said, all of you have key reporters who know you and have written positive pieces on your work. It would be good if every one of us can reach out to one or two high profile reporters to get the word out – but see bullet #2 below that we can't do this until Sunday evening!

2. As per the guidelines below, we are supposed to hold off talking with reporters until **Sunday 8pm US EST (Washington DC time)**, and we need to make sure that all reporters agree to the embargo when we talk to them. So that you have something to share with reporters when you get in touch with them, I've asked Science for the final version of the corrected proofs. If I don't get these by COB today, I'll send you the proofs with corrections embedded, but please bear with me while I hassle Science to send along the corrected ones…

3. Please share your contact details and your availability with all of us from 8pm Sunday (US EPT) so we can all give them to reporters who get in touch. FYI – I'll be available on **my cellphone: +1-845-641-0899** or office +1-212-380-4474 during this time. I've also cc'd Anthony Ramos, who's EcoHealth Alliance's press officer, and will field calls here. He will share all of your contact details with every reporter who gets in touch so we get a good spread of publicity. His cellphone is +1-646-413-3437and office line is +1-212-380-4469

4. Coordination: It would be useful if you could share with us all when you get a reporter contacting you so we can see how much publicity is likely to come out. I also strongly urge you to pass on the contact details of other authors of the paper, so we get a good geographical and disciplinary point of views. Finally, reporters tend to look for other experts to either endorse these ideas, or for alternative viewpoints. Remember we have a Steering Committee of stellar names who I'm sure will be willing and able to answer reporters' questions…

Here's the information from Science, and look forward to seeing this one hit the media…

*******SCIENCE EMBARGO GUIDELINES*******

(1) The paper will be published by *Science* on Friday, **23 February 2018**.

(2) The information will be strictly embargoed--meaning that it cannot be published, broadcast, posted online, routed to list serves, tweeted, announced on Facebook, fed to satellites, shared with anyone other than journalists, or otherwise placed in the public domain--until **2:00 pm U.S. Eastern Time Thursday, 22 February 2018**.

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Please Note: You are strongly encouraged to speak with reporters beginning**Sunday, 18 February 2018, at 8:00 pm U.S. Eastern Time** so long as they agree to hold their stories until the embargo-release time on **Thursday, 22 February 2018, 2:00 pm U.S. Eastern Time**. If your PIO is planning any media outreach in conjunction with a scientific meeting that involves a *Science* paper, they must contact Meagan Phelan at _____ _____ , or the SciPak team at _____ _____ , in advance to coordinate.

(4) If the corresponding author of this paper will not be available to speak with reporters under embargo between **18 February** and **22 February**, please contact our office immediately to develop an alternate plan for communicating this research to the public.

(5) Any news releases must be marked with the embargo time, date, and time zone. For example: "**Embargoed: Not for Release Until 2:00 pm U.S. Eastern Time Thursday, 22 February**." If you convert the time-zone for local reporters, kindly double-check your conversion. We encourage you to work with your institution's public information office now so that they may prepare their embargoed materials. (Your PIO should simply wait until 8:00 pm U.S. Eastern Time on the Sunday evening prior to your publication date before promoting any embargoed content to trusted media contacts.) Please request that your PIOs contact _____ _____ to let us know if they are planning to write a press release or prepare any media outreach activities. The same applies to the press offices at any relevant funders of your research.

(6) Embargoed news releases and related artwork may be posted only to approved, restricted-access sites-- but no sooner than 8:00 pm U.S. Eastern Time on the Sunday evening immediately prior to publication. Do not, under any circumstances, post to open-access sites, or to any searchable address. Your press release may be submitted to EurekAlert! for processing at any time, as long as you note during the submission process that the release is tied to embargoed research in *Science*. Your press release will then be held for formatting and posted live to the embargoed site on the Sunday evening prior to publication. Please consider including the following language in the "Special Notes to Reporters" section of your press release: "More information, including a copy of the paper, can be found online at the *Science* press package webpage at _____ _____. You will need your user ID and password to access this information."

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(11) If you have any questions at all about these guidelines, contact Meagan Phelan, SciPak Executive Director, Office of Public Programs, at +1-202-326-6436._____ _____.

For more information on the *Science* embargo guidelines, contact any member of the*Science* Press Package team at +1-202-326-6440, or scipak@aaas.org

Thank you,

Science Press Package Team, Office of Public Programs
American Association for the Advancement of Science
1900 New York Avenue, NW | Washington, DC 20005
Phone: 202-326-6440 | E-mail: _____ _____
Twitter: _ _____ | _____.

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Cheers,

Peter

Peter Daszak
President

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To: Dennis Carroll <dcarroll@usaid.gov>
CC: Anthony Ramos <ramos@ecohealthalliance.org>;Ariel Pablos-Mendez <apablos@gmail.com>;Brooke Watson <watson@ecohealthalliance.org>;Cara Chrisman <cchrisman@usaid.gov>;Eri Togami <etogami@ucdavis.edu>;George F Gao (gaof@im.ac.cn) <gaof@im.ac.cn>;Jonna Mazet <jkmazet@ucdavis.edu>;Nathan Wolfe <nwolfe@metabiota.com>;Oyewale Tomori <oyewaletomori@gmail.com>;Peter Daszak <daszak@ecohealthalliance.org>;Subhash (FAORAP) Morzaria (Subhash.Morzaria@fao.org) <Subhash.Morzaria@fao.org>;Subhash P Morzaria (subhash.morzaria@gmail.com) <subhash.morzaria@gmail.com>;ap39@cumc.columbia.edu <ap39@cumc.columbia.edu>
Sent: 2/22/2018 6:22:37 PM
Subject: Re: Instructions from Science re. Press Embargo on our Science Policy Forum on the GVP

Hi Dennis,
Yes, I would be interested in meeting people from the US Embassy, but I am not sure whether there will be some time fort hat in my agenda. I am accompanying Prof Nisia Lima, president of Fiocruz, and will have to be with her to meet several Chinese institutions and the Brazilian Ambassador in China, Minister Caramuru. Let me check this in more detail after I meet our Chinese colleagues and our people from the Embassy of Brazil, ok?
The press is liking the GVP, I noticed a lot of interest of the two reporters I talked to.
Best,
Carlos

Em qui, 22 de fev de 2018 às 22:53, Dennis Carroll <dcarroll@usaid.gov> escreveu:
Excellent. Thanks Carlos. Question, would you be interested in meeting with US Embassy people while you are in Beijing? The Embassy has been particularly interested in GVP as a possible point for US-China global partnership. Hearing from you and the Brazilian perspective could add additional value. Let me know if you would be interested and I can reach out to Beijing to see if possible during your visit

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Thank you,

Science Press Package Team, Office of Public Programs
American Association for the Advancement of Science
1900 New York Avenue, NW | Washington, DC 20005
Phone: 202-326-6440 | E-mail: _____ _____.
Twitter: _ _____ | _____.

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You are receiving this email because you are publishing in the 23 February 2018 issue of Science.

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Washington, Dc 20005

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Want to change how you receive these emails?
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Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4473
www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

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--
Carlos M. Morel MD DSc
Director
National Institute of Science and Technology for Innovation in Neglected Diseases (INCT-IDN)
Centre for Technological Development in Health (CDTS)
Oswaldo Cruz Foundation (Fiocruz)
Building "Expansão", 8th floor room 814
Av. Brasil 4036 - Manguinhos
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Brazil

Tel +55-21-3882-9234 Fax +55-21-2290-0494
Email morel@cdts.fiocruz.br or cmmorel@gmail.com
Twitter @cmmorel
http://www.researcherid.com/rid/B-4079-2009

From: Eri Togami <etogami@ucdavis.edu>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 2/28/2018 6:49:35 PM
Subject: BioHub logistics email chain for your record

Hi Jonna,

Here are the email conversations and timeline of events regarding BioHub logistics, for your awareness and record.

[Timeline of events]
Prior to Feb 14: Eri was planning to arrange meeting.
Feb 14: Eri and Jonna meet and plan to defer logistics to Eddy.
Feb 15: Core team verbally agrees on weekly conference call that Eddy will plan the meeting. Eri follows up with an email to core group with personally assigned "Action items" (copied below).
Feb 26: Eri sends personal follow up to Eddy to check status of planning (copied below).
Feb 27: Jonna sends email to Eddy, Eddy responds.

Thanks,
Eri

From: Eri Togami
Sent: Thursday, February 15, 2018 12:06 PM
To: 'Brooke Watson' ; 'Sacchetti, Ben' ; 'Dennis Carroll' ; 'Peter Daszak' ; 'Eddy Rubin' ; 'Nathan Wolfe' ; 'Harris.Samuel@bcg.com' ; Jonna Mazet
Subject: Action items from Feb 15 call

Hi GVP team,

Here are the action items from our call today.

- Dennis
  - share follow up info re: conversation with Suwit and Thai Director of Science and Technology
  - share Peter Bogner call-in info
  - reach out to Cost Rica ambassador Roman
  - reach out to Gian Luca and Sam about organizational structure (including Global Fund registration site)
- Eddy
  - explore GISAID data sharing model to share with group
  - set up meeting on Fri March 16 with BioHub (Eddy, Jonna, Chris Johnson, Eri available to join)
- Peter - Speak with George Gao during next visit
- Jonna – wait for BCG hub budget, wait for Peter's discussion with China re: Taiwan, CHN
- Eri
  - send Peter name and institution of colleagues from Taiwan, CHN
  - send Letter of Intent to Dennis
- BCG team
  - send bottom up hub budget to Jonna, Brooke W, Eri and David Wolking (dwolking@ucdavis.edu, UC Davis) in the next few weeks.

I'm happy to pass the torch back to BCG for call agendas after today.

Thanks,
Eri

>>>>>>>>>>>>>>>>>>Separate chain copied here>>>>>>>>>>>>>>>>>>

Have you checked BioHub's availability on March 16? I have not reached out to the BioHub side, so I wanted to make sure.

Thanks for including me in the email conversation.

Best,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Eddy Rubin [mailto:erubin@metabiota.com]
Sent: Sunday, February 25, 2018 4:51 PM
To: Eri Togami <etogami@ucdavis.edu>
Subject: Re: BioHub visit

sorry not to get back. I think Jim would be the best.
Eddy

On Thu, Feb 15, 2018 at 8:43 AM, Eri Togami <etogami@ucdavis.edu> wrote:
Great Eddy! Would Jim or Cristina be the best point of contact to reach out to?

Thanks,
Eri

From: Eddy Rubin [mailto:erubin@metabiota.com]
Sent: Wednesday, February 14, 2018 10:09 PM
To: Eri Togami <etogami@ucdavis.edu>
Subject: Re: BioHub visit

Hi Eri
Yes I can do the 16th.
Eddy

On Wed, Feb 14, 2018 at 2:48 PM, Eri Togami <etogami@ucdavis.edu> wrote:
Hi Eddy,

Are you available to meet with BioHub sometime on Friday March 16? We are planning to propose an in-person meeting with them now that the MoU is executed. I will reach out to the BioHub team as soon as I hear back from you.

Thanks,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis
>>>>>>>>>>>>>>>>>>Separate chain copied here>>>>>>>>>>>>>>>>>>

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Eddy Rubin [mailto:erubin@metabiota.com]
Sent: Tuesday, February 27, 2018 3:53 PM
To: Eri Togami <etogami@ucdavis.edu>; Jonna Mazet <jkmazet@ucdavis.edu>; Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>; Tammie O'Rourke <torourke@metabiota.com>
Subject: Logistics BioHub visit

Hi
There has been some confusion on reaching out to BioHub. Just want to make sure before I contact Jim Karkanias who runs the BioHub data science team that Eri has not yet already contacted him and that Chris, Jonna and Eri are available (morning ?/afternoon? / both?) March 16th. I think this is the essential group that will participate in the initiation of collaboration face to face and the rest we will arrange to call in. I will keep this group coed in communications with Jim and if he cannot do the 16th I will probe him for other dates.
Eddy
---------- Forwarded message ----------
From: **Eddy Rubin** <erubin@metabiota.com>
Date: Thu, Feb 15, 2018 at 2:09 PM
Subject: Re: BioHub visit
To: Eri Togami <etogami@ucdavis.edu>

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Yes I can do the 16th.

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Thanks,
Eri

Eri Togami DVM MPH
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From:	Andrew Clements <aclements@usaid.gov>
To:	Katherine Leasure <kaleasure@ucdavis.edu>
CC:	PREDICTMGT <predictmgt@usaid.gov> predict@ucdavis.edu <predict@ucdavis.edu>; Jonna Mazet <jkmazet@ucdavis.edu>
Sent:	3/20/2018 7:27:06 AM
Subject:	Re: PREDICT International Travel Requests

Napa and San Francisco travel approved.

All other travel approved subject to mission concurrence.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Mar 20, 2018, at 1:47 AM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Please find below international travel requests for your review and approval. Please let me know if you have any questions. Thanks!

1. O'Rourke, Edison (USA): $579 each airfare/$234 (Napa) max daily per diem
2. Lange (USA): $579 airfare/$350 (San Francisco), $234 (Napa) max daily per diems
3. Chmura (China): $2531 airfare/$402 (Shanghai), $262 (Dali), $377 (Beijing), $415 (Guangzhou) max daily per diems
4. Kelly (Ghana): $2000 airfare/$331 (Accra) max daily per diem
5. Gutierrez-Jimenez (United Kingdom, India): $2,800 airfare/$522 (London), $291 (Other), $400 (New Delhi) max daily per diems

Travel Requests –

1. Metabiota would like to request travel approval for Tammie O'Rourke and Beth Edison to travel from Nanaimo, British Columbia, Canada to Napa, California, USA from April 9 - 12, 2018 to attend the PREDICT 2 semi-annual meeting.

Trip purpose: To meet with PREDICT- 2 consortium members for the Semi-Annual Meeting on April 10 and 11.

2. Metabiota would like to request travel approval for Dr. Christian Lange to travel from Kiev, Ukraine to San Francisco, California, USA from April 7-9, 2018 to meet with Metabiota PREDICT Senior Management on April 8. From San Francisco, California, USA he will travel to Napa, California, USA from April 9-12, 2018 to attend the PREDICT-2 Semi Annual meeting.

Trip purpose: In San Francisco, Dr. Lange will meet with Metabiota PREDICT Senior Management to discuss PREDICT concerns, progress and issues. In Napa, Dr. Lange will meet with the PREDICT-2 consortium at the Semi-Annual meeting on April 10 and 11, 2018. **Dr. Lange will be travelling from Ukraine as he will be traveling there for a different project. After the Semi-Annual meeting, he will travel back to Nanaimo, Canada. Travel costs will be split between the two programs.*

3. EcoHealth Alliance would like to request travel approval for Mr. Alekseii Chmura to travel from New York, New York, USA to Shanghai, Dali, Beijing, and Guangzhou, China from April 16 to May 18, 2018 for meetings with in-country partners, field work, behavioral surveillance, and site selection work.

Trip purpose: Mr. Alekseii Chmura will meet with PREDICT-2 Field Coordinator, Dr. Guangjian Zhu, in Shanghai for PREDICT-2 Y4 wildlife sampling operation discussion, and visit PREDICT sites in Yunnan province (Dali),

meeting with local partner from Yunnan Institute of Endemic Diseases Control and Prevention for community human surveillance. Mr. Chmura will also meet with new lab partner in Beijing at the Institute of Microbiology, Chinese Academy of Sciences for Y4/Y5 laboratory testing planning, and meet with wildlife sampling field team in Guangzhou for Tyvek and other Biosafety refresh training.

4. UC Davis would like to request travel approval for Dr. Terra Kelly to travel from Flagstaff, Arizona, USA to Accra, Ghana from April 21-27, 2018 for meetings and training with in-country partners.

Trip purpose: Dr. Kelly will be traveling to Accra to meet with PREDICT implementing partners. Dr. Kelly will also be conducting training for PREDICT laboratory personnel on data entry and management in the EIDITH database and PCR product/sample shipping.

5. EcoHealth Alliance would like to request travel approval for Dr. Leticia Gutiérrez-Jiménez to travel from New York, New York, USA to New Delhi and Lucknow, India from April 23 to May 31, 2018 to conduct field site exploration, training and field sampling, and meet with the PREDICT-2 India team. **Dr. Gutierrez-Jimenez will stay 1 night in London, United Kingdom and New Delhi, India on both legs of her trip as part of her connecting flights.*

Trip purpose: In New Delhi, Dr. Gutierrez-Jimenez will meet with Country Coordinator, Dr. Rajesh Bhatia. In Lucknow, she will meet with PREDICT-2 India's Field Coordinator, Dr. Debapriyo Chakraborty, and with implementing partners at Sanjay Gandhi Postgraduate Institute of Medical Sciences to coordinate concurrent surveillance activities. In Maharajganj, Uttar Pradesh, Dr. Gutiérrez-Jiménez will conduct wildlife surveillance and disease ecology training. She and PREDICT-2 India Field Coordinator, Debapriyo Chakraborty, will carry out bat, rodent and non-human primate sampling.

Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
530-752-7526
530-752-3318 FAX
kaleasure@ucdavis.edu

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/02a401d3bfc5%240f8ef740%242eace5c0%24%40ucdavis.edu.

From: Dennis Carroll <dcarroll@usaid.gov>
To: Oyewale Tomori <oyewaletomori@gmail.com>
CC: Guy Vernet <guy.vernet@fondation-merieuxusa.org>;Lipkin, Ian W. <wil2001@cumc.columbia.edu>;Capua,Ilaria <icapua@ufl.edu>;Gian Luca Burci <gian-luca.burci@graduateinstitute.ch>;Prasert Auewarakul <prasert.aue@mahidol.ac.th>;FUKUDA, Keiji <kfukuda@hku.hk>;Ariel Pablos <apablos@gmail.com>;George F GAO <gaof@im.ac.cn>;Morzaria, Subhash (FAORAP) <subhash.morzaria@fao.org>;Subhash P Morzaria (subhash.morzaria@gmail.com) <subhash.morzaria@gmail.com>;Carlos M Morel <morel@ccts.fiocruz.br>;Renata Curi Hauegen <rcuri@ccts.fiocruz.br>;David Nunes Nabarro <dnnabarro@gmail.com>;Peter Bogner <peter@gisaid.org>;Brooke Watson <watson@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;Cara Chrisman <cchrisman@usaid.gov>;Eri Togami <etogami@ucdavis.edu>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Jonna Mazet <jkmazet@ucdavis.edu>;Mundaca-Shah, Ceci <CMundaca@nas.edu>;Kathleen VICTOIR <kathleen.victoir@pasteur.fr>;sfh9@georgetown.edu <sfh9@georgetown.edu>;Ong Joanna <joannaong@hku.hk>
Sent: 6/1/2018 1:18:20 PM
Subject: Re: UPDATE: The GVP Steering Committee Meeting June 11

Thank you for your continued support Oyewale. I look forward to your phone-in participation on the 11th.

all my best

d

Dr. Dennis Carroll
Director, Emerging Threats Program
Bureau for Global Health
U.S. Agency for International Development

Office: 571-551-7109
Mobile: 301-646-6235

On Fri, Jun 1, 2018 at 4:54 AM, Oyewale Tomori <oyewaletomori@gmail.com> wrote:
Dear Dennis
Greetings. Thank you for the update. Looking forward to joining the meeting through call in
Regards

Oyewale

Oyewale TOMORI
Tel: +234 803 499 6524

On Thu, May 31, 2018 at 7:39 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:

GLOBAL VIROME PROJECT

May 31, 2018

Dear Colleagues,

Much has been happening on the GVP front since we last met on the edges of the Prince Mahidol Awards Conference in Bangkok. We've published two papers on the GVP, in Science Policy and the WHO Bulletin, and have been getting significant press attention, as illustrated by a recent article in the China Daily. The GVP also got a nice "shout out" at the Smithsonian's Museum of Natural

History's exhibit, "Outbreak," as an example of why the world will be better able to prevent future epidemics.

There has also been significant maturation in our thinking on how GVP can best evolve from its current post-Bellagio "transitional state" to a fully operational global partnership. As those who were in attendance will recall, in Bangkok we introduced representatives of the Boston Consultancy Group (BCG), who had been hired under the auspices of the Governance Thematic Area to assist us in thinking more precisely about the operational "way forward" for the GVP. BCG had played a similar role in the formative stages of CEPI and GAVI. In the course of their consultancy, BCG was able to interview a broad cross-section of the international community to get their thoughts, insights, and suggestions as to what would be essential ingredients for GVP to be a successful enterprise. It is on the basis of this outreach that we are now asking members of the Steering Committee to consider a package of actions covering GVP's organizational structure, staffing, funding, and outreach for your guidance.

On June 11, we are inviting each of you to participate in a half day meeting to review specific recommendations that address GVP's:

- Near and long-term operational vision (*The Go Forward Vision*) with particular focus on actions needed to support the limited launch of field operations (during an "incubation period") that are designed to "test" the systems required to go to full scale operations
- Organizational structure (*Towards a Governance Structure*) required during this two year "incubation period"
- Need to establish itself as a legal entity and find an immediate "home" (*Establish a Legal Home*)
- Budget requirements to support operations over the next two year (*Incubation Period Budget*)
- Outreach plans for the coming year (*Global Outreach: Year One*)

Collectively, the decisions made about the operational way forward, organizational structure, staffing and funding will lay the foundation for making a strong business case for the GVP. We are now at a critical juncture as we move from the "idea" to the "reality" of the GVP. The next year will be a pivotal period as we seek to expand the financial and political investment in the GVP.

The meeting will be held in Washington DC at the National Academy of Medicine (see below for venue location). For those unable to join us in person we have also arranged for a call-in line (see below). To maximize the efficiency of the meeting **we are sending you by FedEx the entire packet of briefing materials** that will be used to guide our discussions. This meeting of the Steering Committee is intended as a "decision-making" forum and as such we will be specifically asking participants to consider a number of actions for "approval," "approval with modification," or "rejection" (a *Decision Sheet* identifying those items is included in the packet).

I am looking forward to what I believe will be an important and productive dialogue. In the interim, if you have any questions, comments or early feedback on the materials, please use this feedback form: https://goo.gl/forms/fssddGcGfbflmP5d2.

As a special treat for those joining us in person, following the meeting we will arrange a visit to the Smithsonian's Museum of Natural History exhibit "Outbreak".

All my best,

Dennis Carroll

The GVP Steering Committee Meeting

Date: June 11, 2018

Time: 09:00 – 1:00

Venue: Room 101 at the National Academies Keck Center, 500 5th Street NW, Washington, DC, 20001
Call in number: US/Canada: (713)353-7024
International: (888) 330-1716
Participant Pin: 9903206

From: Eri Togami <etogami@ucdavis.edu>
To: Kristin Burns <kburns@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Eunah Regina Cho <eecho@ucdavis.edu>
Sent: 6/27/2018 11:45:24 PM
Subject: Re: THANK YOU: The GVP Steering Committee Meeting

Hi Kristin,
Wonderful, thank you for getting the article out there!
Best,
Eri

Sent from my iPhone, please excuse any typos.

From: Kristin Burns
Sent: Thursday, June 28, 2018 1:31:49 AM
To: Eri Togami; Jonna Mazet; Eunah Regina Cho
Subject: Re: THANK YOU: The GVP Steering Committee Meeting

Hi,

I retweeted with another quote from the article by Metabiota's chief scientist:

"We make preparations against hurricanes and earthquakes. We need to do the same with diseases. We need to start to collect data and make predictions about where new outbreaks might occur."

I'll retweet from PREDICT and OHI accounts as well.

kb

--
Kristin Burns
Content Marketing Manager
One Health Institute
UC Davis
530-752-0590
onehealth.institute

From: Eri Togami
Date: Wednesday, June 27, 2018 at 3:53 AM
To: Jonna Mazet , Eunah Regina Cho , Kristin Burns
Subject: Re: THANK YOU: The GVP Steering Committee Meeting

Hi Kristin and Eunah,

Could you please tweet the Guardian article out while people are talking about the Nature paper (by Edward Holmes refuting the GVP approaches)?

I just arrived in Tokyo and will also send some pictures that we could tweet.

Thanks!
Eri

Sent from my iPhone, please excuse any typos.

From: jonna.mazet@gmail.com on behalf of Jonna Mazet

Sent: Monday, June 25, 2018 2:33:10 AM
To: Eunah Regina Cho; Kristin Burns
Cc: Eri Togami
Subject: Fwd: THANK YOU: The GVP Steering Committee Meeting

FYI,
J

---------- Forwarded message ----------
From: **Gian Luca Burci** <gian-luca.burci@graduateinstitute.ch>
Date: Sun, Jun 24, 2018 at 3:12 AM
Subject: Re: THANK YOU: The GVP Steering Committee Meeting
To: Dennis Carroll <dcarroll@usaid.gov>
Cc: Guy Vernet <guy.vernet@fondation-merieuxusa.org>, "Lipkin, Ian W." <wil2001@cumc.columbia.edu>, "Capua,Ilaria" <icapua@ufl.edu>, Prasert Auewarakul <prasert.aue@mahidol.ac.th>, Oyewale Tomori <oyewaletomori@gmail.com>, "FUKUDA, Keiji" <kfukuda@hku.hk>, Ariel Pablos <apablos@gmail.com>, George F GAO <gaof@im.ac.cn>, "Morzaria, Subhash (FAORAP)" <subhash.morzaria@fao.org>, "Subhash P Morzaria (subhash.morzaria@gmail.com)" <subhash.morzaria@gmail.com>, Carlos M Morel <morel@cdts.fiocruz.br>, Renata Curi Hauegen <rcuri@cdts.fiocruz.br>, David Nunes Nabarro <dnnabarro@gmail.com>, Peter Bogner <peter@gisaid.org>, Brooke Watson <watson@ecohealthalliance.org>, Peter Daszak <daszak@ecohealthalliance.org>, Cara Chrisman <cchrisman@usaid.gov>, Eri Togami <etogami@ucdavis.edu>, Nathan Wolfe <nwolfe@metabiota.com>, Eddy Rubin <erubin@metabiota.com>, Jonna Mazet <jkmazet@ucdavis.edu>, "Mundaca-Shah, Ceci" <CMundaca@nas.edu>, Kathleen VICTOIR <kathleen.victoir@pasteur.fr>, Sam Halabi <sfh9@georgetown.edu>

Dear Dennis, dear all,

I just bumped into this article on the GVP in the Guardian. Was it planned and initiated by the GVP leadership or a consequence of the criticism in Nature? In any case, I find it a good promotion!
https://www.theguardian.com/science/2018/jun/24/global-pandemic-prevented-map-animal-virus-ebola-sars-zika

Looking forward to the report on the meeting and to next steps.

Best,

Gian Luca

On Sat, Jun 23, 2018 at 4:28 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:
Dear Colleagues, first off my apologies for the tardiness in thanking all of you who were able to join us for the GVP Steering Committee meeting. A particular thanks to those who called it - your endurance was impressive. The discussions were lively, frank and fruitful. The meeting was a great success. I believe the decisions that were made represent a major step towards making GVP an operational reality. We are finalizing a report-out of the meeting with the detailed summary of actions to be taken. We will have that to you shortly. Again, thank you. *The journey continues!*

dennis

Dr. Dennis Carroll
Director, Emerging Threats Program
Bureau for Global Health

U.S. Agency for International Development

Office: 571-551-7109
Mobile: 301-646-6235

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May 31, 2018

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I am looking forward to what I believe will be an important and productive dialogue. In the interim, if you have any questions, comments or early feedback on the materials, please use this feedback form: https://goo.gl/forms/fssddGcGfbflmP5d2.

As a special treat for those joining us in person, following the meeting we will arrange a visit to the Smithsonian's Museum of Natural History exhibit "Outbreak".

All my best,



Dennis Carroll

The GVP Steering Committee Meeting

Date: June 11, 2018
Time: 09:00 – 1:00

Venue: Room 101 at the National Academies Keck Center, 500 5th Street NW, Washington, DC, 20001

Call in number: US/Canada: (713)353-7024
International: (888) 330-1716
Participant Pin: 9903206

From: Cara Chrisman <cchrisman@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>;Eri Togami <etogami@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Dennis Carroll <dcarroll@usaid.gov>
Sent: 7/5/2018 1:11:45 PM
Subject: Today's GVP Call at 10am/1pm

Hi All,

Hope you had a wonderful 4th of July and had a chance to celebrate! I wanted to check in and re-verify that everyone was still available for today's regularly scheduled call? Please let me/us know if you plan to join at 10 am PDT / 1pm EDT.

For those who can join, here's the proposed agenda:

- Update on Nature response
- Follow up from Steering Committee Meeting
    - Sign up for Selection Committee
    - Summary Report
    - Other items
- Bringing Dean Jamison on board
- Thailand National Mtg on GVP
- China Update
- Japan report out
- Website asks - standardizing response
- Video
- AOB

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7403
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSI-III - Social Solutions International, Inc. prime contractor

From:	Andrew Clements <aclements@usaid.gov>
To:	David J Wolking <djwolking@ucdavis.edu>
CC:	Amalhin Shek <ashek@usaid.gov>;Alisa Pereira Emerging Threats Division <apereira@usaid.gov>;Cara J. Chrisman <cchrisman@usaid.gov>;Cassandra Louis Duthil <clouisduthil@usaid.gov>;Elizabeth Leasure <ealeasure@ucdavis.edu>;Prof. Jonna Mazet <jkmazet@ucdavis.edu>;Eunah Regina Cho <eecho@ucdavis.edu>;Valitutto, Marc <ValituttoM@si.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent:	8/28/2018 6:56:04 AM
Subject:	Re: Save the Date: USAID PREDICT Briefing- Findings & Implications, September 12 in Washington, D.C.

No problem. I'm available Wednesday through Friday of this week.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Aug 27, 2018, at 10:59 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Andrew,

Jonna is on vacation today and admittedly I don't have a great handle on where we stand with our own internal organization and plans for this briefing. I'll consult with her tomorrow and we'll be in touch with either another day/time to connect or thoughts for next steps and plans.

Best,

David

On Sat, Aug 25, 2018 at 12:01 AM Andrew Clements <aclements@usaid.gov> wrote:
Sounds good David. Does Tuesday around 1:00 EDT work?

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Aug 25, 2018, at 12:50 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Amalhin, Andrew, and Alisa,

Just wanted to connect again on invites for this Castle briefing, coming up quick (2.5 weeks)!

We had a good discussion last week on our management team call but I think we should touch base briefly on the overall plan for ensuring the attendees are strategically aligned with the goals for the meeting and so we make the best use of the available space. As Jonna mentioned on the call we have a list of folks we can share invites with (and we plan to create an official invitation with an abstract and speaker bios that can be shared) so maybe we can connect early next week on next steps so we're well coordinated and all on the same page?

Enjoy the weekend,

David

On Tue, Aug 21, 2018 at 8:58 AM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

From: predict-request@ucdavis.edu <predict-request@ucdavis.edu> **On Behalf Of** Anuibin Shek
Sent: Tuesday, August 21, 2018 6:53 AM
To: GHSD Unit Mail List (USAID) <ghdunitmaillistusaid@usaid.gov>; Predict inbox <predict@ucdavis.edu>; E3.FAB Mail List (USAID) <e3.fab@usaid.gov>; Korde, Sonali <skorde@usaid.gov>; Damien Joly <djoly@metabiota.com>; Jonna Mazet <jkmazet@ucdavis.edu>; Andrew Tobiason <atobiason@usaid.gov>; GH List <phocentacsotherbureaus@usaid.gov>; Rodriguez, Michelle A. <rodriguezm@si.edu>; rosenthj@fccd.fic.nih.gov; Woods, Debra <woodsd@si.edu>; Ronald Waldman <ronwaldman@gmail.gwu.edu>; murrayv@si.edu; ASHLEYTL <ashleycl@ucia.gov>; Billy Karesh <karesh@ecohealthalliance.org>; ian.watson@dtra.mil; Palmer, Bill <palmerb@si.edu>; stn2@cdc.gov; Tracey Goldstein <tgoldstein@ucdavis.edu>; lisa.hensley@nih.gov; david.spiro@nih.gov; dchamp@umn.edu; Jahrling@niaid.nih.gov; Peter Daszak <daszak@ecohealthalliance.org>; jose.fernandez@hhs.gov; Ramella, Mark <ramellam@si.edu>; Norton, Benjamin <nortonben@si.edu>; ehiggs@niaid.nih.gov; pbright@usgs.gov; Paul Maharna <pmaharna@usaid.gov>; Megan Fotheringham <mfotheringham@usaid.gov>; wsteiger@usaid.gov; Irene Koek <ikoek@usaid.gov>; David Stanton <dstanton@usaid.gov>; Alma Golden <agolden@usaid.gov>; catchisen@usaid.gov; Carter, Hillary H. EOP/NSC <Hillary_H_Carter@nsc.eop.gov>; Luciana L Borio@nsc.eop.gov; jean.m.richards5.civ@mail.mil; Barton Behravesh, Casey (CDC/OID/NCEZID) <dlx9@cdc.gov>; Health and Climate Change <healthandclimatechange@usaid.gov>
Cc: ValituttoM@si.edu
Subject: [predict] Save the Date: USAID PREDICT Briefing- Findings & Implications, September 12 in Washington, D.C.

Dear Colleagues,

This year marks the 100th anniversary of the 1918 influenza pandemic that killed more than 50 million people worldwide in just one year. Since then, there have been numerous other emerging infectious diseases from animals (particularly wildlife) that have spilled over to humans and caused regional epidemics and global pandemics. Diseases such as Ebola, 2009 H1N1 influenza, HIV/AIDS, MERS-CoV, Nipah, SARS, and Zika have demonstrated ability to cause serious health, economic, and social impacts at the country, regional, or global levels. At present, there is a lack of available medicines and vaccines to address many of these diseases which puts a premium on understanding the dynamics of how and where spillover occurs so that risk mitigation measures can be developed and applied.

Since 2005, USAID has been a global leader in addressing emerging infectious diseases spilling over from animals to humans. The USAID/PREDICT project was started in 2009 to begin filling gaps in the understanding of spillover risk of known threats as well as identifying possible future threats. At the same time, PREDICT has strengthened in-country surveillance and laboratory capacity and assisted in outbreak response in Africa, Asia, and the Middle East. PREDICT's work is closely coordinated the other U.S. Government agencies, donors, and international organizations and supports the Global Health Security Agenda which helps protect countries worldwide, including the U.S., from the impacts of disease epidemics and pandemics.

The PREDICT briefing at the Smithsonian Institute on September 12, 2018 will provide an update on key results to date from this unique project as well as expected results over the last year of PREDICT.

See you there!

Anaflin Stock
Bureau for Global Health, Office of Infectious Diseases, Emerging Threats Division
Phone: 571-551-7102(o) 571-236-0989(c) 1 CP3 8092
Subscribe to our Newsletter!

USAID-HECFAA, VP of Community Engagement

USAID **Contractor**
GHSS/IT - Stocks/Solutions International, Inc.

From: Dennis Carroll <dcarroll@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Eddy Rubin <erubin@metabiota.com>;Nathan Wolfe <nwolfe@metabiota.com>;Eri Togami <etogami@ucdavis.edu>;Cara Chrisman <cchrisman@usaid.gov>
Sent: 8/30/2018 4:03:19 PM
Subject: GVP agenda for todays call

1. Prep for Bangkok
2. Word from China?
3. Data platform
4. Cartoon
5. Disease X
6. France - the home of the Cone Heads
7. Selection Committee update

Dr. Dennis Carroll
Director, Emerging Threats Program
Bureau for Global Health
U.S. Agency for International Development

Office: 571-551-7109
Mobile: 301-646-6235

From: Cara Chrisman <cchrisman@usaid.gov>
To: Kevin Olival PhD <olival@ecohealthalliance.org>
CC: Eri Togami <etogami@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Dennis Carroll <dcarroll@usaid.gov>;Peter Daszak <daszak@ecohealthalliance.org>
Sent: 9/28/2018 9:03:28 PM
Subject: Re: For Review - Thai Mtg Attendance

Hi Kevin,

Thanks for confirming!

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GMSI-III - Social Solutions International, Inc. prime contractor

On Fri, Sep 28, 2018 at 3:02 PM Kevin Olival <olival@ecohealthalliance.org> wrote:
Hi Cara,

Yes, please add Hongying and Alice to the attendance list. They will both be in the region and available to attend the Bangkok GVP meeting. It will be valuable to have them both sit in. Hongying Li is coordinating the China GVP meeting planned for the new year, and it would be great for her to have exposure to the parallel work in Thailand. Similarly, Alice Latiane is our PREDICT Liaison for Thailand and very familiar with our ongoing viral discovery work.

I will be the only other attendee from EcoHealth Alliance.

Thank you,
Kevin

On Sep 28, 2018, at 12:25 PM, Cara Chrisman <cchrisman@usaid.gov> wrote:

Hi All,

Eri, Thanks for confirming on the UC Davis end!

Peter/Kevin - Can you confirm who the EHA attendees will be? If Alice and Hongying will be attending (as well as anyone else I missed below), please let me know and I'll add them to the list.

Thanks,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
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Desk: (571) 551-7403
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSI-III - Social Solutions International, Inc. prime contractor

On Fri, Sep 28, 2018 at 12:02 PM Eri Togami <etogami@ucdavis.edu> wrote:

Hi Cara,

The attendance list for UC Davis are correct.

FYI, Katie has also received ITAs for Alice Latinne and Hongying from EHA.

Best,

Eri

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Friday, September 28, 2018 6:45 AM
To: Peter Daszak <daszak@ecohealthalliance.org>; Kevin Olival PhD <olival@ecohealthalliance.org>; maher@ecohealthalliance.org; Eddy Rubin <erubin@metabiota.com>; David McIver <dmciver@metabiota.com>; Nathan Wolfe <nwolfe@metabiota.com>; Jonna Mazet <jkmazet@ucdavis.edu>; Eri Togami <etogami@ucdavis.edu>; Sam Halabi <sfh9@georgetown.edu>; Gian Luca Burci <gian-luca.burci@graduateinstitute.ch>
Cc: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>; Daniel Schar <dschar@usaid.gov>; Anchalee Jatapai <ajatapai@usaid.gov>; Dennis Carroll <dcarroll@usaid.gov>; Andrew Clements <aclements@usaid.gov>; Lindsay Parish <lparish@usaid.gov>
Subject: For Review - Thai Mtg Attendance

Dear Colleagues,

Just wanted to circle back on this request, below is my personal understanding of the attendees for the Thailand GVP meeting (this is not an indication of who should or should not attend, just how I currently understand the status). This list will be used to create the invitation and participant lists for the meeting.

If you are listed incorrectly below, please let me know ASAP so that we can update the list.

Thanks!
Cara

Attending (from outside Thailand)

- Kevin Olival
- David McIver
- Jonna Mazet
- Eri Togami
- Sam Halabi
- Dennis Carroll
- Cara Chrisman

Not Attending (from outside Thailand)

- Peter Daszak
- Samantha Maher
- Eddy Rubin
- Nathan Wolfe
- Gian Luca Burci
- Andrew Clements
- Lindsay Parish

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
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Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSA-III - Social Solutions International, Inc. prime contractor

On Thu, Sep 27, 2018 at 9:57 AM Cara Chrisman <cchrisman@usaid.gov> wrote:

Hi Team,

I wanted to share two items with you all for your action and/or awareness:

1. **Thailand Agenda:** Attached is the current draft of the Thailand meeting agenda. Once the DMSC meets for the third prep meeting, there will likely be an updated agenda, but this is the current version. The goal is for the final version to be issued in the beginning of October.
2. **Thailand Invitation Letters:** If you need an invitation letter for attendance at the Thailand meeting, please let Sudarat (cc'ed), our USAID team member in Bangkok, know by email ASAP. They expected

the invitations to also be sent out in the beginning of October.

Please let me know if you have any thoughts or questions!

Best,

Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSI-III - Social Solutions International, Inc. prime contractor

From: Eri Togami <etogami@ucdavis.edu>
To: Brooke Genovese <bgenovese@ucdavis.edu>
CC: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 10/3/2018 5:24:28 PM
Subject: FW: Thailand National Virome Project: Mtg Attendance

FYI for Jonna's BKK accommodation?
-E

From: Sudarat Damrongwatanapokin [mailto:sdamrongwatanapokin@usaid.gov]
Sent: Wednesday, October 03, 2018 10:10 AM
To: Cara Chrisman
Cc: Jonna Mazet ; Eri Togami ; Kevin Olival PhD ; Daniel Schar ; Anchalee Jatapai ; Dennis Carroll ; stackett@usaid.gov; mcjones@usaid.gov; Ms Monica Lintanakool
Subject: Re: Thailand National Virome Project: Mtg Attendance

The meeting is at Pullman Hotel, King Power. I suggest that you stay at Conrad or Plaza Athenee Hotel. We can go there quite easily by Sky Train and 5 minutes walk to the hotel.

Thank you for your kind offer. I think most of it will be responsible and handled by DMSC, MOH and NSTDA.

The final prep meeting to finalize the meeting agenda is on Oct 9. But it is all set from our end, I thought. How long for Dennis's talk? It is now 1 h 15 mins. Please let us know if he wants to adjust the time or prefers to fix as it is.

Nov 23 is a Thai Holiday, thus there might be the limitation to use the room at RDMA (no air- condition on the holiday). If not, I will reserve the conference room at the Conrad Hotel for 10 people during 10.00 am - 5.00 pm.

Please stay tuned.

Best regards,
Sudarat

Sent from my mobile.

On Oct 3, 2018, at 7:56 PM, Cara Chrisman <cchrisman@usaid.gov> wrote:

Hi Sudarat,

Thanks for submitting and for letting us know! We had a couple other quick questions related to the meeting:

1. Is there anything that we can help with on this end? It sounds like invitations and logistics are pretty set, but please let us know if there's anything we can do to assist.
2. What is the actual location of the meeting?
3. The presenters were planning to meet the day before in order to align our presentations and do further planning. Dennis recommended that we reach out to you to see if there was someone on the team who could assist in getting a room in which to meet? It would be for around 10 people and from approximately 10am to 5pm. He initially suggested the conference room at the Conrad as he'll be staying there. If that's not possible to reserve, he suggested that perhaps there might be a room at RDMA?

Thanks again,

Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GMSI-III - Social Solutions International, Inc. prime contractor

On Tue, Oct 2, 2018 at 10:41 PM Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
I did submit the list of speakers/participants from USAID HQ and GVP, PREDICT 2 Team with the total of 9 to DMSC yesterday evening.

USAID HQ

1. Dennis Carroll at dcarroll@usaid.gov

2. Cara Chrisman at cchrisman@usaid.gov

GVP, PREDICT Team

1.Jonna Mazet at jkmazet@ucdavis.edu

2. Eri Tegami at etogami@ucdavis.edu

3. Kelvin Olival at olival@ecohealthalliance.org

4. Davis McIver at dmciver@metabiota.com

5. Sam Halabi at sfh9@georgetown.edu

6. Alice Latinne at latinne@ecohealthalliance.org (PREDICT Liaison for Thailand)

7. Hongying Li at li@ecohealthalliance.org (PREDICT Liaison for China and is coordinating the China GVP meeting planned for the coming year)

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov

Tel: +662-257-3243, Fax:+662 -2573099

---------- Forwarded message ----------
From: **Noppavan Janejai** <noppavan.j@dmsc.mail.go.th>
Date: Wed, Oct 3, 2018 at 9:33 AM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Cc: Supaporn Wacharapluesadee <spwa@hotmail.com>

ได้รับแล้ว ขอบคุณค่ะ

Noppavan Janejai
Deputy Director
National Institute of Health, Department of Medical Sciences
88/7 Tiwanon Road, Nonthaburi 11000, Thailand

----- ข้อความที่ส่งเดิม -----
จาก: "Sudarat Damrongwatanapokin" <sdamrongwatanapokin@usaid.gov>
ถึง: "Supaporn Wacharapluesadee" <spwa@hotmail.com>, "Noppavan Janejai" <noppavan.j@dmsc.mail.go.th>
ส่งแล้ว: อังคาร, 2 ตุลาคม, 2018 5:18:33 PM
เรื่อง: Fwd: Thailand National Virome Project: Mtg Attendance

Thank you for your eagle's eyes. I did correct it as the list below.
Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

---------- Forwarded message ----------
From: S Wacharapluesadee <spwa@hotmail.com>
Date: Tue, Oct 2, 2018 at 4:50 PM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>, Noppavan Janejai <noppavan.j@dmsc.mail.go.th>

olival@ecohealthalliance.org

แก้ไข email ของ Dr.Kevin Olival ค่ะ (ตัว g ใน org ตกไปค่ะ)

ขอบคุณค่ะ

Supaporn Wacharapluesadee, PhD

ศูนย์วิทยาศาสตร์สุขภาพโรคอุบัติใหม่ โรงพยาบาลจุฬาลงกรณ์
Thai Red Cross Emerging Infectious Diseases - Health Science Centre
WHO Collaborating Centre for Research and Training on Viral Zoonoses
King Chulalongkorn Memorial Hospital
Faculty of Medicine, Chulalongkorn University
Rama4 road, Patumwan
Bangkok, Thailand 10330
Tel 662-256 4000 ext 3561
Fax 662-652 3122

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Sent: Tuesday, October 2, 2018 4:43 PM
To: Noppavan Janejai
Cc: Daniel Schar; Anchalee Jatapai; Wantanee Kalpravidh; Supaporn Wacharapluesadee; Bandit Nuamsrichay; Prasert Auewarakul; Monta Thammasatta; prasit.pal@mahidol.ac.th; Thanat Chookajorn; Jonna Mazet; etogami@ucdavis.edu
Subject: Re: Thailand National Virome Project: Mtg Attendance

Dear Noppavan,

Please see below the list of speakers/participants from USAID HQ and GVP, PREDICT 2 Team with the total of 9.

USAID HQ

1. Dennis Carroll at dcarroll@usaid.gov

2. Cara Chrisman at cchrisman@usaid.gov

GVP, PREDICT Team

1.Jonna Mazet at jkmazet@ucdavis.edu

2. Eri Togami at etogami@ucdavis.edu

3. Kelvin Olival at olival@ecohealthalliance.org

4. Davis McIver at dmciver@metabiota.com

5. Sam Halabi at sfh9@georgetown.edu

6. Alice Latinne at latinne@ecohealthalliance.org (PREDICT Liaison for Thailand)

7. Hongying Li at li@ecohealthalliance.org (PREDICT Liaison for China and is coordinating the China GVP meeting planned for the coming year)

Please issue the invitation letter via e-mail address provided above.

Thank you very much.

Best regards,
Sudarat Darnrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdarnrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

From: Cara Chrisman <cchrisman@usaid.gov>
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Eri Togami <etogami@ucdavis.edu>;Kevin Olival PhD <olival@ecohealthalliance.org>;Daniel Schar <dSchar@usaid.gov>;Anchalee Jatapai <ajatapai@usaid.gov>;Dennis Carroll <dcarroll@usaid.gov>;Siana Tackett <stackett@usaid.gov>;Jones, Melissa (USAID/Dhaka/PHNE) <mejones@usaid.gov>;mlimtanakool@usaid.gov <mlimtanakool@usaid.gov>
Sent: 10/4/2018 8:01:32 PM
Subject: Re: Thailand National Virome Project: Mtg Attendance

Hi Sudarat,

Thanks for all of this! We are having a communications person review the GVP briefer and then we'll re-share for circulation at the meeting.

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSI-III - Social Solutions International, Inc. prime contractor

On Wed, Oct 3, 2018 at 8:07 PM Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
Dear Cara,

Thank you very much. We will adjust Dennis's session to 45 min as suggested. If you have the new GVP briefer/fact sheet in electronic file, we are happy to print out here to distribute at the launching workshop.

See you soon.
Sudarat

Sent from my mobile.

On Oct 4, 2018, at 4:05 AM, Cara Chrisman <cchrisman@usaid.gov> wrote:

Hi Sudarat,

Appreciate all these updates and the hotel suggestions!

In terms of the questions, I just spoke with Dennis and his talk will be around 20-25 minutes. In order to leave time for questions, we were thinking to block around 45 minutes. Does that work on your end? He's flexible.

We also talked about the 23rd and it sounds like the Conrad would make the most sense (people like air

conditioning!). Thanks for your assistance with the reservations!

Best,
Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
U.S. Agency for International Development (USAID) Contractor
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSI-III - Social Solutions International, Inc. prime contractor

On Wed, Oct 3, 2018 at 1:10 PM Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
The meeting is at Pullman Hotel, King Power. I suggest that you stay at Conrad or Plaza Athenee Hotel. We can go there quite easily by Sky Train and 5 minutes walk to the hotel.

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Please stay tuned.

Best regards,
Sudarat

Sent from my mobile.

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Thanks again,
Cara

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U.S. Agency for International Development (USAID) Contractor
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2100 Crystal Drive, CP3-8091A, Arlington, VA 22202

Desk: (571) 551-7413
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

GHSF-III - Social Solutions International, Inc. prime contractor

On Tue, Oct 2, 2018 at 10:41 PM Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:
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1. Dennis Carroll at dcarroll@usaid.gov

2. Cara Christman at cchristman@usaid.gov

GVP, PREDICT Team

1.Jonna Mazet at jkmazet@ucdavis.edu

2. Dr Togami at ctogami@ucdavis.edu

3. Kelvin Olival at olival@ecohealthalliance.org

4. Davis McIver at dmciver@metabiota.com

5. Sam Halabi at sfh9@georgetown.edu

6. Alice Latinne at latinne@ecohealthalliance.org (PREDICT Liaison for Thailand)

7. Hongying Li at li@ecohealthalliance.org (PREDICT Liaison for China and is coordinating the China GVP meeting planned for the coming year)

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia

Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

---------- Forwarded message ----------
From: **Noppavan Janejai** <noppavan.j@dmsc.mail.go.th>
Date: Wed, Oct 3, 2018 at 9:33 AM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Cc: Supaporn Wacharapluesadee <spwa@hotmail.com>

ได้รับแล้ว ขอบคุณค่ะ

Noppavan Janejai
Deputy Director
National Institute of Health, Department of Medical Sciences
88/7 Tiwanon Road, Nonthaburi 11000, Thailand

----- ข้อความที่ส่งต่อ -----
จาก: "Sudarat Damrongwatanapokin" <sdamrongwatanapokin@usaid.gov>
ถึง: "Supaporn Wacharapluesadee" <spwa@hotmail.com>, "Noppavan Janejai" <noppavan.j@dmsc.mail.go.th>
ส่งแล้ว: อังคาร, 2 ตุลาคม, 2018 5:18:33 PM
เรื่อง: Fwd: Thailand National Virome Project: Mtg Attendance

Thank you for your eagle's eyes. I did correct it as the list below.
Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
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USAID Regional Development Mission Asia
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From: S Wacharapluesadee <spwa@hotmail.com>
Date: Tue, Oct 2, 2018 at 4:50 PM
Subject: Re: Thailand National Virome Project: Mtg Attendance
To: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>, Noppavan Janejai <noppavan.j@dmsc.mail.go.th>

olival@ecohealthalliance.org

แก้ไข email ของ Dr.Kevin Olival ค่ะ (ตัว g ใน org ตกไปค่ะ)

ขุดะ

Supaporn Wacharapluesadee, PhD

ศูนย์วิทยาศาสตร์สุขภาพโรคอุบัติใหม่ โรงพยาบาลจุฬาลงกรณ์
Thai Red Cross Emerging Infectious Diseases - Health Science Centre
WHO Collaborating Centre for Research and Training on Viral Zoonoses
King Chulalongkorn Memorial Hospital
Faculty of Medicine, Chulalongkorn University
Rama4 road, Patumwan
Bangkok, Thailand 10330
Tel 662-256 4000 ext 3561
Fax 662-652 3122

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Sent: Tuesday, October 2, 2018 4:43 PM
To: Noppavan Janejai
Cc: Daniel Schar; Anchalee Jatapai; Wantanee Kalpravidh; Supaporn Wacharapluesadee; Bandit Nuansrichay; Prasert Auewarakul; Monta Thammasatta; prasit.pal@mahidol.ac.th; Thanat Chookajorn; Jonna Mazet; etogami@ucdavis.edu
Subject: Re: Thailand National Virome Project: Mtg Attendance

Dear Noppavan,

Please see below the list of speakers/participants from USAID HQ and GVP, PREDICT 2 Team with the total of 9.

USAID HQ

1. Dennis Carroll at dcarroll@usaid.gov

2. Cara Chrisman at cchrisman@usaid.gov

GVP, PREDICT Team

1.Jonna Mazet at jkmazet@ucdavis.edu

2. Eri Togami at etogami@ucdavis.edu

3. Kelvin Olival at olival@ecohealthalliance.org

4. Davis McIver at dmciver@metabiota.com

5. Sam Halabi at sfh9@georgetown.edu

6. Alice Latinne at latinne@ecohealthalliance.org (PREDICT Liaison for

Thailand)

7. Hongying Li at li@ecohealthalliance.org (PREDICT Liaison for China and is coordinating the China GVP meeting planned for the coming year)

Please issue the invitation letter via e-mail address provided above.

Thank you very much.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 11/8/2018 7:35:10 PM
Subject: Re: WHO declines opportunity to do DRC Ebola serosurveys; PREDICT interested?

Proposal written by me. Not even WHO has seen it. When I asked them, I just listed a few suggested activities. As it became clear they may not be able to do it, I drafted this proposal for Predict. Please feel free to modify based on what has been done or will be done by Predict before Sep 2019.

FYI—I was focusing on the end result of how to make detection of human outbreaks faster and worked backward from there to arrive at activities that could help get there.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Nov 8, 2018, at 7:57 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Got it & we will explore.
Some of the activities listed in this description may be achievable during the course of activities we already have planned. Others would be extra and may or may not be possible or appropriate to conduct, based on us not being WHO.
From where did the proposal originate? Is it a WHO plan or from somebody else who doesn't mind it being conducted by others. I just want to be careful that we're not viewed as swooping in to implement something that another group developed & pitched (IP concern).
I'll reply with our current plan in a separate email with more individuals copied.
Thanks for resending and rescuing from cyberpurgatory,
Jonna

On Thu, Nov 8, 2018 at 9:10 AM Andrew Clements <aclements@usaid.gov> wrote:

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

Begin forwarded message:

From: Andrew Clements <aclements@usaid.gov>
Date: November 7, 2018 at 3:50:56 PM GMT+1
To: Jonna Mazet <jkmazet@ucdavis.edu>
Subject: WHO declines opportunity to do DRC Ebola serosurveys; PREDICT interested?

Hi Jonna,

WHO said it doesn't have the bandwidth at the moment to do the work proposed in the attachment.

If there is (a) additional core funding for PREDICT to do this work in year 5 (or the extension) and (b) it doesn't displace other important PREDICT activities in DRC during year 5, would you be interested? Not sure if the budget is realistic not. You would know better.

I am aware that putting money towards this reduces the remaining ceiling available for the extension period, but I think it deserves high priority. Without this information, I'm not sure how DRC will break out of the cycle of waiting for an outbreak and trying to respond. And in DRC, this might be the best thing we could hand over to the country if it allows them to target their early warning human surveillance and prepare HCWs for possible future cases.

Andrew

P.S. just left Jordan. The mission really likes the Predict activities there.

From: cchrisman@usaid.gov
To: jkmazet@ucdavis.edu <jkmazet@ucdavis.edu>;aclements@usaid.gov <aclements@usaid.gov>;etogami@ucdavis.edu <etogami@ucdavis.edu>;maher@ecohealthalliance.org <maher@ecohealthalliance.org>;erubin@metabiota.com <erubin@metabiota.com>;cchrisman@usaid.gov <cchrisman@usaid.gov>;daszak@ecohealthalliance.org <daszak@ecohealthalliance.org>;dcarroll@usaid.gov <dcarroll@usaid.gov>;nwolfe@metabiota.com <nwolfe@metabiota.com>
Sent: 12/4/2018 8:37:54 PM
Subject: GVP call - Agenda

Hi All,

Looking forward to speaking on Thursday. Since the government is closed tomorrow, we wanted to share the proposed agenda for our call in advance. Happy to add any items, as needed!

Best,
Cara

Agenda
- Board, Scientific Committee and 501c-3 plan B
- Fund raising
- Data platform
- Thailand
- China/S Korea/Japan
- Science Animated
- Upcoming fora updates
- AOB

GVP call

Thu Dec 6, 2018 1pm – 2pm

call in line 1-719-785-9461, passcode 97848# (map)

https://hangouts.google.com/hangouts/_/ecohealthalliance.org/gvp-call

- watson@ecohealthalliance.org
- cchrisman@usaid.gov
- etogami@ucdavis.edu
- jkmazet@ucdavis.edu
- nwolfe@metabiota.com
- erubin@metabiota.com
- dcarroll@usaid.gov
- Peter Daszak

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Beth Edison <bedison@metabiota.com>
CC: predict Sympa List <predict@ucdavis.edu>;Hannah R Chale <hrchale@ucdavis.edu>
Sent: 12/7/2018 5:02:55 PM
Subject: [predict] RE: PREDICT rebudget

Attached is also a spreadsheet that shows what I come up with for your final Y4 carryover figures with the proposed rebudget. See attached for details.

With proposed rebudget:
$603,460 total Ebola carryover
$452,520 total Core carryover (includes GVP)
$1,055,980 total Y4 carryover

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: predict-request@ucdavis.edu **On Behalf Of** Elizabeth Leasure
Sent: Friday, December 7, 2018 9:56 AM
To: Beth Edison
Cc: predict Sympa List ; Hannah R Chale
Subject: [predict] PREDICT rebudget

Hi Beth. Using your September 2018 invoice as a base for the balance figures, I came up with the rebudget scheme below to resolve the Core/Ebola budget imbalance. The net impact of the rebudget is zero and would essentially zero out the balances for all of the six transition countries (China, Indonesia, RoC, CDI, Guinea, Sierra Leone), as well as the Global Ebola budget and all but about 40% of the Global Core budget balance. The GVP, Cameroon, DRC, and Lao PDR budgets remain unchanged. Thoughts? I've attached the spreadsheet I used for your reference. Let me know what you think or if you had something else in mind. Thanks!

TRANSITION COUNTRIES

Country Rebudget (Core) - China, Indonesia, RoC	Global Rebudget (Core)	Country Rebudget (Ebola) - CDI, Guinea, Sierra Leone	Global Rebudget (Ebola)	TOTAL
18,775	(79,068)	148,472	(197,854)	*(10*
6,984	(29,413)	55,232	(73,602)	*(4*
(168,406)	-	(289,016)	-	*(45*
(11,104)	1,632	(8,105)	2,778	*(1*
(32,161)	26,471	86,497	62,028	*14*
(472,321)	(38,378)	(28,326)	(134,119)	*(67*
(8,947)	-	64,968	-	*5*
(48,341)	1,415	35,152	2,409	*(*
(26,256)	59,511	622,836	56,865	*71*
(739,778)	(57,831)	667,708	(281,495)	*(39*
(46,507)	5,649	470,325	(38,071)	*35*
(786,285)	(52,182)	1,158,033	(319,565)	

Total Core	**(838,468)**	**Total Ebola**	**838,468**

Elizabeth Leasure

Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

	A	B	C	D	E	F	G	H	I
1									
2	Transaction Listing								
3									
4	Fiscal Periods:	October, 2014 to October, 2018							
5									
6									
7	Chart	Org Code	Account	Sub Account	Object Consolidation	Doc Type	Origin Code	Doc Num	Tracking #
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10	3	VOHI	V473P2E	PRMBX	SB73	PREQ	1	38641672	97912
11	3	VOHI	V473P2E	PRMBX	SB73	PREQ	1	38923008	97912
12	3	VOHI	V473P2E	PRMBX	SB73	PREQ	1	39304475	97912
13	3	VOHI	V473P2E	PRMBX	SB73	PREQ	1	39304667	97912
14	3	VOHI	V473P2E	PRMBX	SB73	GEC	1	39451669	
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18	3	VOHI	V473P2E	PRMBX	SB73	PREQ	1	39889258	97912
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24	3	VOHI	V473P2E	PRMBX	SB73	AVAE	1	40741390	
25	3	VOHI	V473P2E	PRMBX	SB73	AVAE	1	40740475	
26	3	VOHI	V473P2E	PRMBX	SB73	AVAE	1	40741390	
27	3	VOHI	V473P2E	PRMBX	SB73	PREQ	1	41004305	97912
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162	3	VOHI	V473PR2	PRMBX	SB73	AVAE	1	49606584	
163	3	VOHI	V473PR2	PRMBX	SB73	AVAE	1	49606599	
164	3	VOHI	V473PR2	PRMBX	SB73	PREQ	1	49851397	97912
165	3	VOHI	V473PR2	PRMBX	SB73	PREQ	1	50287619	97912
166	3	VOHI	V473PR2	PRMBX	SB73	PREQ	1	50287619	97912
167	3	VOHI	V473PR2	PRMBX	SB73	PREQ	1	50568868	97912
168	3	VOHI	V473PR2	PRMBX	SB73	POA	1	50697598	97912
169	3	VOHI	V473PR2	PRMBX	SB73	PREQ	1	51021907	97912

	A	B	C	D	E	F	G	H	I
170									
171									
172									
173									
174									

	J	K	L	M	N	O	P
1							
2							
3							
4							
5							
6							
7	Description	Posted Date	Appropriation	Expenditure			
8							
9	METABIOTA INC	11-Dec-15	0	0			
10	METABIOTA INC	22-Dec-15	0	443,638.00			
11	METABIOTA INC	25-Jan-16	0	160,218.00			
12	METABIOTA INC	1-Mar-16	0	293,371.00			
13	METABIOTA INC	1-Mar-16	0	910,249.00			
14	01-38923008 : Correct distribution of ...	14-Mar-16	0	-11,944.00			
15	01-38641672 : Correct distribution of ...	14-Mar-16	0	-4,806.00			
16	METABIOTA INC	6-Apr-16	0	0			
17	METABIOTA INC	6-Apr-16	0	400,453.00			
18	METABIOTA INC	26-Apr-16	0	600,488.00			
19	METABIOTA INC	7-May-16	0	0			
20	METABIOTA INC	2-Jun-16	0	341,744.74			

	J	K	L	M	N	O	P
21	METABIO TA INC	7-Jul-16	0	362,157.18			
22	Allocate YR2 subaward budgets (P2E)	12-Jul-16	-5,397,519.00	0			
23	M8 June 2016 Accrual	13-Jul-16	0	678,523.92			
24	M8 May 2016 Accrual	13-Jul-16	0	362,157.18			
25	AUTO REVERSAL-M8 June 2016 Accrual	20-Jul-16	0	-678,523.92			
26	AUTO REVERSAL-M8 May 2016 Accrual	20-Jul-16	0	-362,157.18			
27	METABIO TA INC	2-Aug-16	0	619,980.07			
28	METABIO TA INC	16-Sep-16	0	581,224.67			
29	METABIO TA INC	23-Sep-16	0	0			
30	METABIO TA INC	3-Oct-16	0	796,848.67			
31	01-41587252 : Correct distributio n of ...	14-Oct-16	0	-38,580.45			
32	METABIO TA INC	15-Nov-16	0	661,307.30			
33	METABIO TA INC	14-Dec-16	0	0			
34	METABIO TA INC	20-Dec-16	0	700,915.15			
35	METABIO TA INC	10-Jan-17	0	0			

	J	K	L	M	N	O	P
36	METABIOTA INC	10-Jan-17	0	737,907.23			
37	METABIOTA INC	9-Feb-17	0	620,979.05			
38	METABIOTA INC	10-Mar-17	0	435,230.81			
39	METABIOTA INC	17-Apr-17	0	641,969.45			
40	METABIOTA INC	10-May-17	0	764,366.96			
41	METABIOTA INC	13-Jun-17	0	557,939.19			
42	METABIOTA INC	5-Jul-17	0	740,912.28			
43	Metabiota - June 2017 accrual	13-Jul-17	0	455,248.30			
44	Metabiota Y2 Y3 allocations	13-Jul-17	-6,772,435.00	0			
45	AUTO REVERSAL-Metabiota - June 2017 accr	20-Jul-17	0	-455,248.30			
46	METABIOTA INC	21-Jul-17	0	0			
47	METABIOTA INC	11-Aug-17	0	463,558.96			
48	METABIOTA INC	14-Sep-17	0	443,680.90			
49	METABIOTA INC	5-Oct-17	0	0			
50	METABIOTA INC	1-Nov-17	0	433,021.66			
51	METABIOTA INC	25-Jan-18	0	0			
52	METABIOTA INC	29-Jan-18	0	468,474.50			
53	METABIOTA INC	30-Jan-18	0	576,270.21			
54	METABIOTA INC	31-Jan-18	0	167,710.79			

	J	K	L	M	N	O	P
55	METABIOTA INC	5-Feb-18	0	0			
56	METABIOTA INC	6-Feb-18	0	269,352.21			
57	METABIOTA INC	6-Feb-18	0	0			
58	Metabiota Y4 allocation	14-Mar-18	-3,798,604.00	0			
59	METABIOTA INC	20-Apr-18	0	241,073.10			
60	METABIOTA INC	20-Apr-18	0	230,740.77			
61	METABIOTA	26-Apr-18	0	-32,000.00			
62	METABIOTA INC	23-May-18	0	196,991.14			
63	METABIOTA INC	20-Jun-18	0	227,512.30			
64	METABIOTA INC	6-Jul-18	0	0			
65	METABIOTA INC	6-Jul-18	0	281,057.76			
66	Metabiota, Inc. accrual FY17/18	11-Jul-18	0	224,983.00			
67	Metabiota, Inc. accrual FY17/18	11-Jul-18	0	281,057.76			
68	AUTO REVERSAL-Metabiota, Inc. accrual FY	20-Jul-18	0	-224,983.00			
69	AUTO REVERSAL-Metabiota, Inc. accrual FY	20-Jul-18	0	-281,057.76			

	J	K	L	M	N	O	P
70	METABIOTA INC	2-Aug-18	0	225,157.67			
71	METABIOTA INC	10-Sep-18	0	0			
72	METABIOTA INC	10-Sep-18	0	210,705.64			
73	METABIOTA INC	27-Sep-18	0	262,960.05			
74	METABIOTA INC	8-Oct-18	0	0			
75	METABIOTA INC	5-Nov-18	0	220,729.09			
76	METABIOTA INC	5-Nov-18	0	0			
77	Pending Rebudget		(838,468)				
78			(16,807,025.86)	16,203,566.05		(603,459.81)	Ebola carryover (with rebudget)
79							
80							
81	Description	Posted Date	Appropriation	Expenditure			
82							
83	METABIOTA INC	4-Mar-15	0	0			
84	METABIOTA INC	16-Mar-15	0	780,338.85			
85	METABIOTA INC	16-Mar-15	0	306,217.45			
86	METABIOTA INC	3-Apr-15	0	382,401.34			
87	METABIOTA INC	28-May-15	0	192,983.94			
88	MB May 2015 accrual	8-Jul-15	0	402,875.73			
89	MB June 2015 accrual	8-Jul-15	0	409,522.84			

	J	K	L	M	N	O	P
90	M8 April 2015 accrual	8-Jul-15	0	223,982.81			
91	AUTO REVERSAL - M8 June 2015 accrual	9-Jul-15	0	-409,522.84			
92	AUTO REVERSAL - M8 May 2015 accrual	9-Jul-15	0	-402,875.73			
93	AUTO REVERSAL - M8 April 2015 accrual	9-Jul-15	0	-223,982.81			
94	Rebudget V473PR2 for fiscal close	10-Jul-15	-4,200,001.00	0			
95	METABIO TA INC	22-Jul-15	0	238,875.65			
96	METABIO TA INC	29-Jul-15	0	438,327.40			
97	METABIO TA INC	18-Aug-15	0	320,777.54			
98	METABIO TA INC	21-Sep-15	0	456,953.00			
99	METABIO TA INC	16-Nov-15	0	543,134.53			
100	METABIO TA INC	11-Dec-15	0	0			
101	METABIO TA INC	17-Dec-15	0	537,845.52			
102	METABIO TA INC	22-Dec-15	0	182,259.02			
103	METABIO TA INC	25-Jan-16	0	230,454.14			
104	METABIO TA INC	1-Mar-16	0	219,661.06			

	J	K	L	M	N	O	P
105	METABIOTA INC	1-Mar-16	0	768,299.17			
106	01-38923008 : Correct distribution of ...	14-Mar-16	0	11,944.00			
107	01-38641672 : Correct distribution of ...	14-Mar-16	0	4,806.00			
108	METABIOTA INC	6-Apr-16	0	246,236.13			
109	METABIOTA INC	6-Apr-16	0	0			
110	METABIOTA INC	26-Apr-16	0	172,789.12			
111	METABIOTA INC	7-May-16	0	0			
112	METABIOTA INC	2-Jun-16	0	228,195.48			
113	METABIOTA INC	7-Jul-16	0	180,975.38			
114	Allocate YR2 subaward budgets (PR2)	12-Jul-16	-3,085,984.00	0			
115	MB June 2016 Accrual	13-Jul-16	0	295,971.48			
116	MB May 2016 Accrual	13-Jul-16	0	180,975.38			
117	AUTO REVERSAL-MB June 2016 Accrual	20-Jul-16	0	-295,971.48			

	J	K	L	M	N	O	P
118	AUTO REVERSAL-MB May 2016 Accrual	20-Jul-16	0	-180,975.38			
119	METABIOTA INC	2-Aug-16	0	286,842.83			
120	METABIOTA INC	12-Sep-16	0	0			
121	METABIOTA INC	16-Sep-16	0	192,373.77			
122	METABIOTA INC	3-Oct-16	0	264,273.63			
123	01-41587252 : Correct distributio n of ...	14-Oct-16	0	38,580.45			
124	METABIOTA INC	15-Nov-16	0	212,511.34			
125	METABIOTA INC	14-Dec-16	0	0			
126	METABIOTA INC	20-Dec-16	0	175,970.32			
127	METABIOTA INC	10-Jan-17	0	214,562.28			
128	METABIOTA INC	10-Jan-17	0	0			
129	METABIOTA INC	27-Jan-17	0	0			
130	METABIOTA INC	9-Feb-17	0	244,184.81			
131	METABIOTA INC	10-Mar-17	0	83,704.19			
132	METABIOTA INC	17-Apr-17	0	194,359.26			
133	METABIOTA INC	10-May-17	0	157,767.81			
134	METABIOTA INC	13-Jun-17	0	138,249.33			
135	METABIOTA INC	5-Jul-17	0	176,330.41			
136	Metabiota - June 2017 accrual	13-Jul-17	0	165,274.30			

	J	K	L	M	N	O	P
137	Metabiota Y2 Y3 allocations	13-Jul-17	-3,150,153.00	0			
138	Metabiota Y2 allocation	13-Jul-17	-99,998.00	0			
139	AUTO REVERSAL - Metabiota - June 2017 accr	20-Jul-17	0	-165,274.30			
140	METABIOTA INC	21-Jul-17	0	0			
141	METABIOTA INC	11-Aug-17	0	170,533.72			
142	METABIOTA INC	14-Sep-17	0	127,503.54			
143	METABIOTA INC	5-Oct-17	0	0			
144	METABIOTA INC	1-Nov-17	0	178,809.42			
145	METABIOTA INC	25-Jan-18	0	0			
146	METABIOTA INC	29-Jan-18	0	259,718.25			
147	METABIOTA INC	30-Jan-18	0	81,630.56			
148	METABIOTA INC	31-Jan-18	0	102,405.92			
149	METABIOTA INC	5-Feb-18	0	0			
150	METABIOTA INC	6-Feb-18	0	0			
151	METABIOTA INC	6-Feb-18	0	51,181.37			
152	Metabiota Y4 allocation	14-Mar-18	-1,514,341.00	0			
153	METABIOTA INC	20-Apr-18	0	125,209.38			
154	METABIOTA INC	20-Apr-18	0	128,397.67			

	J	K	L	M	N	O	P
155	METABIOTA	26-Apr-18	0	-22,457.06			
156	METABIOTA INC	23-May-18	0	74,843.79			
157	METABIOTA INC	20-Jun-18	0	94,757.50			
158	METABIOTA INC	6-Jul-18	0	0			
159	METABIOTA INC	6-Jul-18	0	96,412.08			
160	Metabiota, Inc. accrual FY17/18	11-Jul-18	0	89,895.00			
161	Metabiota, Inc. accrual FY17/18	11-Jul-18	0	96,412.08			
162	AUTO REVERSAL-Metabiota, Inc. accrual FY	20-Jul-18	0	-89,895.00			
163	AUTO REVERSAL-Metabiota, Inc. accrual FY	20-Jul-18	0	-96,412.08			
164	METABIOTA INC	2-Aug-18	0	110,234.96			
165	METABIOTA INC	10-Sep-18	0	0			
166	METABIOTA INC	10-Sep-18	0	87,159.54			
167	METABIOTA INC	27-Sep-18	0	106,021.50			
168	METABIOTA INC	8-Oct-18	0	0			
169	METABIOTA INC	5-Nov-18	0	163,941.81			

	J	K	L	M	N	O	P
170	Pending Rebudget		838,468				
171			(11,212,009.14)	10,759,489.10		(452,520.04)	Core carryover (with rebudget)
172							
173							
174			(28,019,035.00)	26,963,055.15		(1,055,979.85)	Total carryover

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: David J Wolking <djwolking@ucdavis.edu>
CC: Brooke Genovese <bgenovese@ucdavis.edu>
Sent: 1/8/2019 3:24:05 AM
Subject: Re: Annual Report 2018 Review - thoughts for Monday

Notes on Annual Report text continued:

- Global/Lab:
  - Page 53, lab numbers listed as 63 here, but it has been 60 throughout report until this point. Also list 41 labs testing for one or more priority virus which is the first time I've seen 41 used. Forty is used in the Preface, then M&E has different numbers, based on that math.
  - Page 54: top figure fuzzy image; figure legend uses British spelling "travelled" rather than American spelling "traveled"
  - Page 55, first sentence missing "are"
  - Page 58:
    - First bullet, 4th line should be "coronaviruses"
    - Second bullet, second sentence: VSV should be spelled-out, but not a big deal if too much trouble
    - Third bullet: have should be has
    - Fifth bullet: small e
    - Second column: *Nature Microbiology*, also italicize two bat names
- Global/M&A:
  - Page 61, second column, g dropped on first line of new section
  - Page 62, figure legend: source should be sources; first sentence of second column, "it's" should be "they are"; last section heading missing and f (or it's white); last paragraph formatted weird and missing an "Insights" in the last line
  - Page 63, list at bottom of second column may be cut off
- Global/One Health Partnerships:
  - Page 65, second column cut off -- you better check all of the pages for this problem
  - Page 66, fifth line of plain text: comma should be a period
  - Page 67, third line needs a commas around "the Ghana Forestry Commission"; sixth line -- globally.Finally
- Global/M&O: spacing on these pages needs to be addressed throughout
  - Page 69, first column, fourth line from bottom: "titled" should be "entitled"
  - Page 69, second column, Partnerships section: that big sentence is screaming for a comma or two
  - Page 70, first column: Memorandums should be Memoranda
  - Page 70, second column, third line from bottom: governmentapproved

Country Reports:

- Love the Key; in the lab strengthening section, need to say that the color of the circle is indicative of the lab's capacity according to the color key below (took me about 10 dashboards to figure that out, thought they were all at the last stage at first read); in the legend box, little problem with this text (pastes here properly, but reads wrong in layout): # of laboratory tests # of viruses detected; bottom right text in blocks also not reading correctly in my pdf version
- Faces of Predict: you switch formats for master's degrees, sometimes Masters, master, master's, or other -- can you pick one & search & replace? If not, probably not worth the time to go through each one again to fix. On another note for this section in the future -- the quotes are really good and make the section interesting. They are much more memorable and moving than the descriptive paragraphs. If we use these in the final book, I think we should try to stick mostly with quotes.
- Page 84, missing the person's title; location given is Senegal, but it's a Kenya page?
- Rwanda's & Ugarda's training numbers are incredibly low and out of step with all of the other

countries. I think we noticed this last time. Are they correct?
- Page 90, missing a space in text under Lo's picture
- Page 91, listing Columbia instead of UCD under lab footnote
- Page 93, fourth line in Grace's quote "liked" should be "like"
- Page 97, first paragraph Community shouldn't be capitalized; fourth paragraph has a bad line break
- Page 100, I noticed on China that we might be double counting viruses in the summary box. If you total all of China viruses in the bottom right, it does come to 93, but 4 of those should be double counted (unless those viruses were originally detected in countries other than China in P-1). Noticing this issue, I went back to Cambodia and Indonesia to check -- definitely think we're double counting.
- Page 105, problem at paragraph break, probably dropping a line
- Page 107, second paragraph, third line from bottom: comma should be period and start of new sentence
- Page 109, second line "my" should be "his"; last sentence ion that paragraph should be the quote; second paragraph, same "my" problem

Publications and Products

- Section reads really well and seems worth the effort to me. If we didn't already, I do think we can ask the authors to write the paragraphs for future papers, giving them this section for examples of what we want.
- This whole section needs to be checked for words that need to be italicized -- all journal and species names.
- Page 119, 121 & 123, weird to have figure legends at the top of the next column
- Page 121, spacing problem in second column at "Perspectives"
- Page 122, first paragraph "specially" should be "especially" (whole sentence is a bit awkward grammatically); line break problem in that paragraph, too
- Page 126, middle of column, one of the pubs isn't bolded
- Page 131, second column, tense should be past ("participated")

Great job on content! Really compelling. I'm not going to review the Appendices.
Let me know if you have an questions about my comments.
J

On Mon, Jan 7, 2019 at 4:58 PM Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Notes on Annual Report text:

- Preface: Not sure if we're keeping the Preface text, as well as the letter or if the letter replaces this section. I think we're replacing it, but if we're keeping the Preface text in the pdf, the first sentence of the second page (GHSA) is very repetitive in comparison with the text on the first page. Also a typo toward the end of that same paragraph "riskreducing".
- Preface: last bullet on third page (Consortium) needs updating. It's cutting off before finishing, and I don't think "Epidemico" is contractually correct.
- Success Stories: There are blue boxes at the end of the sections in this chapter. I don't love them, as they don't always show up, aren't explained, and differ in format from the other chapters. Unless you feel strongly, lets remove them.
- Success Stories: see attached edits that need to be transferred to the pdf version.
- Success Stories/Mongolia: On the second page, the blue geographical shade is distracting and makes the text hard to read -- suggest removing it. Also, in the third paragraph, birds are referred to as shell ducks, when in the legend on the previous page they are shelducks. I think the single word is more correct.
- Success Stories/Thailand: Second paragraph ends strangely & needs an edit. I also think "Wild Boars" could be removed in a couple of places. At the top of the second page -- missing a space "insects,or parasites". Also, photo legend says clockwise, but the photos are described counterclockwise. Another space missing in last sentence, "sharedata".
- M&E: Love this section! I think for the casual reader, it will be confusing to review the indicator table

at the front because it has no data or annual content. Instead, I think we should flip the order and show the infographics, etc. first, with the indicator table at the end. If you think it will cause confusion in comparison with previous reports, maybe use an asterisk on the cover page or first page of the section to refer to the indicator table on page XX.

- Global/Capacity:
  - Heading(s) different from those in both the Word version emailed to me and the file in Box. In the first new heading "hot spot" should be "hotspot".
  - Legend for figure in upper right of first page is cut off. Last paragraph on first page also cut off.
  - The total number of trainees in this section is over 800 for the single year, which differs from M&E and my letter in the Preface. I know the counts are done differently in these sections. The numbers struck me as odd in the letter though, so I think we should change the "270" in the letter to "800", leaving the rest of the numbers in the letter as they are.
  - The line breaks in this section are really distracting with a lot of broken (hyphenated words) and some spaces at the beginning of lines. I suggest we manage line breaks without breaking words where possible.
  - Last paragraph on second page: change "face to face workshops" to "face-to-face workshops".
  - Third page, second column: no link provided at end of paragraph. That paragraph essentially repeats right below its first presentation.
  - Fourth page: two subheadings for the same section -- pick one.
- Global/Surveillance:
  - Second sentence on Livestock page ends in: "and Viet Nam,."
  - Outbreaks, page 39 -- seems weird without a stronger heading. If it appears above the next page, I think it is fine, but if formatting results in it standing alone without the next page, I think it needs a bigger title, such as that on page 40.
  - Text on page 40 is blurry. Is it just a blown up image? If editable, the "who..." clause in item 4 would read much better if moved forward in the sentence to just after "Bogra district". If editing number 4, I think "half eaten" should be "half-eaten".
  - Same with image on page 41. It should at least be pushed up a bit on the page. Item 7 on that page needs editing, as it reads awkwardly (ESL).
- Global/Behavioral Risk:
  - Page 41: First sentence: "The goal of PREDICT'sbehavioral risk activitiesis tobetter understand behaviors that increase the risksof viral emergence, transmission, spreadand"
  - Page 42 in bulleted list:
    - First bullet, change "were" to "have been" since those numbers cover more than just current year.
    - "Living Safely with Bats" should be *Living Safely with Bats* because it is a book.
  - Page 43: bullets are odd, as first sentence aren't sentences (no verb), but they are followed by a complete sentence in all cases but one. Makes the reading awkward.
  - Page 44: remove periods in the bulleted list (second column).
  - Page 45: bullet formatting problem continues
  - Page 47: formatting problem and italics vs quotes on bulleted list
- Global/Information Management, Page 48: Is this what we've always named this section? I find it very confusing, as EIDITH isn't really improving any networks. Can't we just call it what it is: Information Management? The figure legend on this page has "in-clude" for some reason.

I'm sending this stuff now, as I'm getting worried about losing these notes with a computer glitch or something.
More to come,
J

On Thu, Jan 3, 2019 at 3:57 PM David J Wolking <djwolking@ucdavis.edu> wrote:
Hey Jonna,

Brooke mentioned you're planning to review this AR monster on Monday. I'm assuming you'll just pull the PDF from the Box link (here it is for quick reference - Draft PREDICT 2018 Annual Report).

A few thoughts here to help guide your review, section by section (in case you feel like skimming or skipping some entirely).

Preface: Thought it might be nice to have a letter from the Director to break up the monotony of this preface that has been the same each report (and workplan) since 2016. If OK by you, I can draft something for you to customize and sign. Might be nice to highlight the tone of the year (successful wrap up of field work, maturing capacity for our OH workforce, exciting success stories and publications, etc.) as this is likely the only thing people will read :-)

Success Stories: Tried to have partner balance here but didn't have time to complete the stories from Metabiota (DRC Ebola support and follow-up field investigations) and SI (One Health workshops with OHCEA students). I can still get these done for the next version so if you want to feature them I can work with Eunah to get them wrapped up. The ones featured were the most exciting, hopefully not too over the top.

M&E: Pretty straightforward. Corina is the boss of this one so if any questions on how we arrived at the numbers she's your girl. Tiffany now has the workbook with numbers for integration with EPT-2 partners. We haven't received any feedback at all on this stuff since the External Panel report critiqued the framework and it's utility for assessing impact. Might no longer be a huge USAID priority but still takes a ton of staff time to compile.

Global: Nothing remarkable here, just building on the same framework and style from the previous 2 reports. I'm fine with this section for these biannual reports as long as we can design something more informative and exciting as part of the final report process.

Country: Again, just the dashboards so nothing surprising here. The new additions are the Faces of PREDICT profiles that breakup the dashboard monotony.

Pubs and Products: Same old story here. The pubs section takes a ton of time to develop so we may need to consider a different approach for the final report, or just suck it up and do the final year's summaries to significantly lengthen that product (obvious con - cost of printing). In the Media is an easy section to do and will get a facelift in the final we submit to USAID. Lots of formatting issues moving from Word to InDesign here that caused Bridgette and I trouble.

Appendices: Virus table is pretty straightforward. M&A team appendix also the usual. No concerns from my perspective.

Acknowledgments (not currently featured): These reports are now consuming lots of HQ staff time. I think we should drop in some acknowledgments so staff get credit and recognition for helping compile, design, and edit this monster product. Good for their CVs and resumes and a nice way to thank them for what seems like thankless work. If OK by you, I'll put that together as well and likely add it to a page after the Preface.

Welcome back to the grind :-)

David

From:	Elizabeth Leasure <ealeasure@ucdavis.edu>
To:	Elizabeth Leasure <ealeasure@ucdavis.edu>;Beth Edison <bedison@metabiota.com>
CC:	predict Sympa List <predict@ucdavis.edu>;Hannah R Chale <hrchale@ucdavis.edu>
Sent:	1/9/2019 5:39:34 PM
Subject:	[predict] RE: PREDICT rebudget

Hi Beth. Just checking in on the proposed rebudget for your PREDICT subaward. I've been waiting to add Y5 and GVP BCA funds until we get this worked out in order to do it all in one amendment, but let me know if you need more time, and we will proceed with adding those funds now.

Also, I'm hoping to get to your cost share revision request this week. Sorry for the delay!

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: predict-request@ucdavis.edu **On Behalf Of** Elizabeth Leasure
Sent: Friday, December 7, 2018 10:03 AM
To: Beth Edison
Cc: predict Sympa List ; Hannah R Chale
Subject: [predict] RE: PREDICT rebudget

Attached is also a spreadsheet that shows what I come up with for your final Y4 carryover figures with the proposed rebudget. See attached for details.

With proposed rebudget:
$603,460 total Ebola carryover
$452,520 total Core carryover (includes GVP)
$1,055,980 total Y4 carryover

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: predict-request@ucdavis.edu <predict-request@ucdavis.edu> **On Behalf Of** Elizabeth Leasure
Sent: Friday, December 7, 2018 9:56 AM
To: Beth Edison <bedison@metabiota.com>
Cc: predict Sympa List <predict@ucdavis.edu>; Hannah R Chale <hrchale@UCDAVIS.EDU>
Subject: [predict] PREDICT rebudget

Hi Beth. Using your September 2018 invoice as a base for the balance figures, I came up with the rebudget scheme below to resolve the Core/Ebola budget imbalance. The net impact of the rebudget is zero and would essentially zero out the balances for all of the six transition countries (China, Indonesia, RoC, CDI, Guinea, Sierra Leone), as well as the Global Ebola budget and all but about 40% of the Global Core budget balance. The GVP, Cameroon, DRC, and Lao PDR budgets remain unchanged. Thoughts? I've attached the spreadsheet I used for your reference. Let me know what you think or if you had something else in mind. Thanks!

TRANSITION COUNTRIES

Country Rebudget (Core) - China, Indonesia, RoC	Global Rebudget (Core)	Country Rebudget (Ebola) - CDI, Guinea, Sierra Leone	Global Rebudget (Ebola)	TOTAL
18,775	(79,068)	148,472	(197,854)	***(109,676)***
6,984	(29,413)	55,232	(73,602)	***(40,799)***
(166,406)	-	(289,016)	-	***(455,423)***
(11,104)	1,632	(8,105)	2,778	***(14,800)***
(32,161)	26,471	86,497	62,028	***142,835***
(472,321)	(38,378)	(28,326)	(134,119)	***(673,145)***
(8,947)	-	64,968	-	***56,020***
(48,341)	1,415	35,152	2,409	***(9,365)***
(26,256)	59,511	622,836	56,865	***712,955***
(739,778)	(57,831)	687,708	(281,495)	***(391,396)***
(46,507)	5,649	470,325	(38,071)	***391,396***
(786,285)	(52,182)	1,158,033	(319,565)	

Total Core	**(838,468)**	**Total Ebola**	**838,468**

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Beth Edison <bedison@metabiota.com>
CC: predict Sympa List <predict@ucdavis.edu>;Hannah R Chale <hrchale@ucdavis.edu>
Sent: 1/9/2019 7:08:17 PM
Subject: [predict] RE: PREDICT rebudget

Sounds good. Thanks!

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edison
Sent: Wednesday, January 9, 2019 12:00 PM
To: Elizabeth Leasure
Cc: predict Sympa List ; Hannah R Chale
Subject: Re: PREDICT rebudget

Hi Liz,

Sorry for the delay with this. I've been wanting to review it with one of our key finance people who has just returned from a long leave. I should be able to get a response to you this week. Also, I have revised our budget according to our new approved rates. We should probably try and incorporate that in the amendment as well. I'll do my best to get you everything tomorrow and then I'm happy to meet if you have any questions.

Thanks!
Beth

On Wed, Jan 9, 2019 at 10:39 AM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Hi Beth. Just checking in on the proposed rebudget for your PREDICT subaward. I've been waiting to add Y5 and GVP BCA funds until we get this worked out in order to do it all in one amendment, but let me know if you need more time, and we will proceed with adding those funds now.

Also, I'm hoping to get to your cost share revision request this week. Sorry for the delay!

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: predict-request@ucdavis.edu <predict-request@ucdavis.edu> **On Behalf Of** Elizabeth Leasure
Sent: Friday, December 7, 2018 10:03 AM
To: Beth Edison <bedison@metabiota.com>
Cc: predict Sympa List <predict@ucdavis.edu>; Hannah R Chale <hrchale@UCDAVIS.EDU>
Subject: [predict] RE: PREDICT rebudget

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With proposed rebudget:
$603,460 total Ebola carryover
$452,520 total Core carryover (includes GVP)
$1,055,980 total Y4 carryover

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: predict-request@ucdavis.edu <predict-request@ucdavis.edu> **On Behalf Of** Elizabeth Leasure
Sent: Friday, December 7, 2018 9:56 AM
To: Beth Edison <bedison@metabiota.com>
Cc: predict Sympa List <predict@ucdavis.edu>; Hannah R Chale <hrchale@UCDAVIS.EDU>
Subject: [predict] PREDICT rebudget

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		TRANSITION COUNTRIES		
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6,984	(29,413)	55,232	(73,602)	*(4*
(166,406)	-	(289,016)	-	*(45.*
(11,104)	1,632	(8,105)	2,778	*(1-*
(32,161)	26,471	86,497	62,028	*1*
(472,321)	(38,378)	(28,326)	(134,119)	*(67.*
(8,947)	-	64,968	-	*5*
(48,341)	1,415	35,152	2,409	*(*
(26,256)	59,511	622,836	56,865	*71*
(739,778)	(57,831)	687,708	(281,495)	*(39.*
(46,507)	5,649	470,325	(38,071)	*35*
(786,285)	(52,182)	1,158,033	(319,565)	

Total Core	**(838,468)**	**Total Ebola**	**838,468**

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)

Skype: ealeasure

--
Beth Edison
Program Manager | Metabiota
(250)739-8987

From: Samantha Maher <maher@ecohealthalliance.org>
To: Cara Chrisman <cchrisman@usaid.gov>;Dennis Carroll <dcarroll@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Eri Togami <etogami@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>
Sent: 1/28/2019 3:49:07 PM
Subject: china graphic

Hi All,

A discussed in last week's call, attached is a graphic from our preliminary analysis of sampling sites in China for GVP. It shows the top 1% of land for viral sampling, based on viral diversity (using mammal diversity as a proxy) and accessibility to the site.

I ran the model 4 times using Zonation, two times with accessibility included included and 2 times with just viral diversity. Each of those runs was also performed with two different algorithms, one that prioritized total # of species (core area zonation) and one that prioritized contiguous sampling areas for ease of access (additive benefit function).

The graphic shows areas based on how many times they showed up in the results. Dark red areas were tagged as important in all runs of the model.

Let me know if you have any questions.

Cheers,

Sam

--

Samantha M.L. Maher, MESc
Research Assistant, Conservation and Health

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

1.212.380.4464 (direct)
1.713.818.6867 (mobile)
1.212.380.4465 (fax)
www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: Eri Togami <etogami@ucdavis.edu>
To: Dennis Carroll <dcarroll@usaid.gov>;Samantha Maher <maher@ecohealthalliance.org>
CC: Cara Chrisman <cchrisman@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Peter Daszak <daszak@ecohealthalliance.org>
Sent: 1/28/2019 8:24:35 PM
Subject: Re: china graphic

Thank you Sam, looking forward to discussing further on Thursday.
-Eri

From: Dennis Carroll
Sent: Monday, January 28, 2019 11:31
To: Samantha Maher
Cc: Cara Chrisman; Jonna Mazet; Nathan Wolfe; Eddy Rubin; Eri Togami; Peter Daszak
Subject: Re: china graphic

Thanks Sam. Greatly appreciated. Let discuss during our next GVP call

d

Dr Dennis Carroll
Director
Emerging Threats
Global Health
USAID
301-646-6235

On Jan 28, 2019, at 11:49 AM, Samantha Maher <maher@ecohealthalliance.org> wrote:

Hi All,

A discussed in last week's call, attached is a graphic from our preliminary analysis of sampling sites in China for GVP. It shows the top 1% of land for viral sampling, based on viral diversity (using mammal diversity as a proxy) and accessibility to the site.

I ran the model 4 times using Zonation, two times with accessibility included included and 2 times with just viral diversity. Each of those runs was also performed with two different algorithms, one that prioritized total # of species (core area zonation) and one that prioritized contiguous sampling areas for ease of access (additive benefit function).

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Let me know if you have any questions.

Cheers,

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Samantha M.L. Maher, MESc

Research Assistant, Conservation and Health

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From: cchrisman@usaid.gov
To: jkmazet@ucdavis.edu <jkmazet@ucdavis.edu>;etogami@ucdavis.edu <etogami@ucdavis.edu>;maher@ecohealthalliance.org <maher@ecohealthalliance.org>;erubin@metabiota.com <erubin@metabiota.com>;cchrisman@usaid.gov <cchrisman@usaid.gov>;daszak@ecohealthalliance.org <daszak@ecohealthalliance.org>;dcarroll@usaid.gov <dcarroll@usaid.gov>;nwolfe@metabiota.com <nwolfe@metabiota.com>
Sent: 2/7/2019 4:36:42 PM
Subject: GVP call

Hi All,

My apologies, I just realized that I didn't circulate the agenda for today's call. Please find it below and speak with you all soon!

Best,
Cara

- BoD/501c3
- Thailand
- China
- Database
- Benefit-cost analysis
- Comms (Newsletter & Sci Anim)
- AOB

GVP call

Thu Feb 7, 2019 1pm – 2pm

call in line 1-719-785-9461, passcode 97648# (map)

https://hangouts.google.com/hangouts/_/ecohealthalliance.org/gvp-call

- watson@ecohealthalliance.org
- cchrisman@usaid.gov
- etogami@ucdavis.edu
- jkmazet@ucdavis.edu
- nwolfe@metabiota.com
- erubin@metabiota.com
- dcarroll@usaid.gov
- Peter Daszak

From: Jon Epstein <epstein@ecohealthalliance.org>
To: David J Wolking <djwolking@ucdavis.edu>
CC: Tammie O'Rourke <torourke@metabiota.com>;Eri Togami <etogami@ucdavis.edu>;Valitutto, Marc <ValituttoM@si.edu>;Amanda Fine <afine@wcs.org>;Brian H Bird <bhbird@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Churchill, Carolina <cchurchill@wcs.org>;Corina Grigoresou Monagin <cgmonagin@ucdavis.edu>;Dawn Zimmerman <ZimmermanD@si.edu>;Eddy Rubin <erubin@metabiota.com>;Evelyn Luciano <luciano@ecohealthalliance.org>;Karen Saylors <ksaylors@metabiota.com>;Murray, Suzan <MurrayS@si.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;Woutrina A Smith <wasmith@ucdavis.edu>;Sarah Olson <solson@wcs.org>;Simon Anthony <sja2127@columbia.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;William Karesh <karesh@ecohealthalliance.org>;Elizabeth Leasure <ealeasure@ucdavis.edu>;Kevin Olival <olival@ecohealthalliance.org>;Alison Andre <andre@ecohealthalliance.org>;Amanda Andre <amanda.andre@ecohealthalliance.org>;Megan M Doyle <mmdoyle@ucdavis.edu>;Ava Sullivan <sullivan@ecohealthalliance.org>;Molly Turner <turner@ecohealthalliance.org>;Emma Lane <lane@ecohealthalliance.org>;Brooke Genovese <bgenovese@ucdavis.edu>;predict Sympa List <predict@ucdavis.edu>
Sent: 2/20/2019 8:42:13 PM
Subject: Re: [predict] Re: [Agenda] PREDICT EB Feb 20

Awesome!
It looks great.

-Jon

On Wed, Feb 20, 2019 at 1:57 PM David J Wolking <djwolking@ucdavis.edu> wrote:
Hi there,

Just sharing this cool Smithsonian developed feature on PREDICT, part of their "field in focus" series. It's a nice example of what we could do for our digital final report.

David

On Wed, Feb 20, 2019 at 8:47 AM Tammie O'Rourke <torourke@metabiota.com> wrote:
Good morning all,
Below is today's indicator report.

Indicator

countries with data
countries with tests approved by government
animals sampled
humans sampled
human questionnaires
specimens
tests
animals tested
humans tested
animal specimens tested
human specimens tested
tests approved by government
tests active testing ongoing

sequences interpreted
sequences waiting interpretation
individuals barcoded
average days between event and data submission
average days between event and data submission for data submitted in last 2 weeks
number of events/test batches waiting for country input
number of events waiting for IM review
number of test batches waiting for IM review
number of barcode test batches waiting for IM review

On Tue, Feb 19, 2019 at 2:17 PM Eri Togami <etogami@ucdavis.edu> wrote:

Hi PREDICT EB,

Here are your agenda and call-in details for EB tomorrow.

Best,

Eri

PREDICT Executive Board Meeting

Wednesday, February 20, 2019

9:00-11:00am PST/12:00-2:00pm EST

Zoom link: https://onehealth.zoom.us/j/401896666

Additional Zoom info below agenda

1. **Management Team & Administrative updates**
    - DTRA lab tiering updates & brainstorming path forward
    - Notification to slow down activities due to delays in Y5 obligation
    - Updates on TVPA funding restrictions in DRC, Guinea, China, and RoC
    - Brown bags updates
    - Semi-annual meeting participant list for Group ITA
    - Behavioral risk key personnel
    - Year 6 extension plans

2. **Wildlife communications and messaging**

3. **Bangladesh assumed Nipah outbreak & planned economic work**

4. **GHSA meeting in Hague and EPT-2 10 year brainstorming (Billy)**

5. **Mission communications & country roundup essentials**

6. **Objective Team Updates**

7. **Publication, media, and conference updates**

   - Global Health Security 2019, Sydney (June 18-20, 2019)
   - ASM public event panel "Advancing the fight against epidemics through One Health" (June 21, 2019)
   - OHCEA One Health conference in Uganda (July 24-26), abstract submission deadline Feb 28
   - 6th International Symposium on One Health Research in Mongolia (Sep 18-19, 2019)
   - 19th International Congress on Infectious Diseases (Feb 20-23, 2020)

8. **AOB**

Zoom Call-in info

Zoom link: https://onehealth.zoom.us/j/401896666

Or iPhone one-tap :

US: +16468769923,,401896666# or +16699006833,,401896666#

Or Telephone:

Dial(for higher quality, dial a number based on your current location):

US: +1 646 876 9923 or +1 669 900 6833

Meeting ID: 401 896 666

International numbers available: https://zoom.us/u/depX2cn5i

--
Tammie O'Rourke
Metabiota
Senior Information Management Developer
Emerging Pandemic Threats - PREDICT Program
tel +1-250-618-2460

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

1.212.380.4467 (direct)
1.917.385.5315 (mobile)

web: ecohealthalliance.org

Twitter: @epsteinjon

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Beth Edison <bedison@metabiota.com>
CC: Shaun Tse <stse@metabiota.com>;Hannah R Chale <hrchale@ucdavis.edu>;predict Sympa List <predict@ucdavis.edu>
Sent: 4/2/2019 8:53:25 PM
Subject: [predict] RE: Contract mod

Hi Beth. For the rebudget, none of the Y4 carryover funds are going away, they are just being redistributed from Core to Ebola budget to cover overdrafts for the Ebola countries transitioned to UCD/EHA and clear out available balances for core-funded countries that are no longer in Metabiota's PREDICT portfolio. Essentially, all Y4 carryover fund balances for China, Indonesia, and RoC ($786,285 in total) were removed from your Core budget obligation and added to the Ebola budget for CDI, Guinea, and Sierra Leone, which were $1.158M in overdraft. Because the Y4 carryover for China, Indonesia, and RoC was not enough to cover the full $1.158M overdraft for the transitioned Ebola countries, we had to dip into the Y4 Global Ebola carryover (using all $319K available) plus a small amount of Y4 Global core carryover ($52K in total) in order to fully resolve the CDI/SL/Guinea overdraft with a net zero impact to the overall carryover amount. So, the Y4 Core carryover amount is being reduced but the Ebola carryover amount is going up by a corresponding amount (only as much as is needed in order to resolve the CDI/SL/Guinea overdrafts).

You are correct that carryover amounts are being deducted from Y5 obligations, so those carryover amounts plus any Y5 obligations processed will make up your full Y5 operating budget. With the proposed rebudget, your overall Ebola carryover amount goes up to $631,888 (an increase of $838,468 from -$206,580 [over-drafted] carryover balance when including CDI/Guinea/SL) and your overall Core carryover is reduced to $399,286 (a decrease of $838,468 from $1,237,754 available when including China/Indonesia/RoC). Y5 obligations will then be made using your approved Y5 budget figures less carryover amounts. Once the pending amendment is processed, you will have your full Y5 Ebola operational budget ($631,888 carryover + $1,228,035 = $1,859,923). Core is more complicated given the piecemeal modifications and delays on the USAID side, so we're obligating funds in 25% increments. The $359,201 in core funds being obligated in the pending amendment represents 25% of your Y5 operational budget less carryover ($1,836,091 operational budget - $399,286 Y4 carryover = $1,436,805 obligation needed * 25% = $359,201 partial obligation). The GVP amount obligated in the pending amendment is 25% of the $67K GVP operational budget since we rebudgeted GVP carryover to Lao PDR (thus no carryover to subtract). Once the rest of our funds come in from USAID, we'll obligate the rest of partner core budgets less any Y4 carryover. However, as I noted in my previous email, I don't expect that you will get your full Core budget given the TVPA restriction issue. I'll let you know as soon as I have confirmation on that front.

Yes, your plan for tracking the budget category changes sounds fine. If you get near 10% cumulative transfers, please let me know.

If you still have questions, we can have a chat to clarify.

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edison
Sent: Tuesday, April 2, 2019 12:55 PM
To: Elizabeth Leasure
Cc: Shaun Tse ; Hannah R Chale ; predict Sympa List
Subject: Re: Contract mod

Hi Liz,

Two more hopefully easy questions. The re-budget exercise you did previously shows us without carry over under Global Ebola and with very little carry over for Core. I'm operating with the understanding that we are

using our carry over plus the remaining obligation to create our total budget. Having the carry-over reduced confuses that a bit (it might be better clarifying over the phone?).

Also, how do we deal with the budget category issue? A lot of our Laos carry over is in services but I'll need to use those funds elsewhere. Can I move forward and track category totals for the whole budget and identify any global scale issues that go over the 10%?

If it's easier to chat this out, please give me a call!

Thanks,
beth

On Tue, Apr 2, 2019 at 12:47 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Hi Beth. I need to look more closely at the numbers, but I think there is another obligation in the cards for Lao PDR (other than the one I sent to you for review). I'm just not sure of the exact amount yet. I've sent some preliminary estimates for what we can manage to Jonna and am waiting for feedback. We'll also need to get the go ahead from USAID before we do anything, so stay tuned.

Are we okay to proceed with your rebudget and 25% obligation amendment?

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edison <bedison@metabiota.com>
Sent: Monday, April 1, 2019 10:01 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>; Hannah R Chale <hrchale@UCDAVIS.EDU>; predict Sympa List <predict@ucdavis.edu>
Subject: Re: Contract mod

Hi Liz,

This looks good. One question about Laos. Does this mean our total budget for the year will be our carry-over plus this partial obligation and that we should not expect any more funds to come in for this country? Once I have that confirmed I can send you a runway for how long we should be able to maintain operations there.

Thanks!
Beth

On Wed, Mar 27, 2019 at 3:52 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Hi Beth. Please take a look at the rebudget and coming amendment for PREDICT. Basically, we're rebudgeting from Core to Ebola to zero out all transitioned countries (resolving the overdraft for the Ebola countries in the process) and moving GVP carryover to Lao PDR, the idea being that these are FY17 funds that are not subject to the TVPA restriction, and we'll use FY18 money to fund the full GVP budget. Please take a look and let me know what you think. I'll need to process the rebudget with the amendment to add funds, so Hannah will hold off on processing the amendment until you confirm everything looks okay.

The Y5 funding obligation includes 25% of your full GVP budget for Y5 (excluding BCA funds-which will come separately), the balance of your Y5 Ebola budget (so you will now have your full Ebola budget in hand inclusive of

carryover), and enough Core funds to ensure that you have 25% of your core budget in hand for Y5 (inclusive of carryover). Hopefully that makes sense. Let me know if you have any questions.

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530.304.1403 (cell)
530.754.9034 (office)
Skype: ealeasure

From: Beth Edison <bedison@metabiota.com>
Sent: Thursday, February 28, 2019 10:50 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>
Subject: Contract mod

Hi Liz,

Do you have any thoughts on when we might expect a contract mod that includes the Ebola funds and GVP? I know we'll have to wait a while for core funds.

Thanks!
Beth

--
Beth Edison
Program Manager | Metabiota
(250)739-8987

--
Beth Edison
Program Manager | Metabiota
(250)739-8987

--
Beth Edison
Program Manager | Metabiota
(250)739-8987

From: Beth Edison <bedison@metabiota.com>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: Shaun Tse <stse@metabiota.com>;Hannah R Chale <hrchale@ucdavis.edu> predict Sympa List <predict@ucdavis.edu>
Sent: 4/2/2019 10:18:43 PM
Subject: [predict] Re: Contract mod

Understood. Thanks Liz!

On Tue, Apr 2, 2019 at 3:16 PM Elizabeth Leasure <caleasure@ucdavis.edu> wrote:

You have the flexibility to rebudget as you need to between countries and cost elements (within the 10% of total award amount) as long as you don't use Ebola funds for non-Ebola funded countries. So you can move funds from Global Ebola to Cameroon or DRC (or vice versa) but you can't move funds from Global Ebola to Global Core. Does that sound okay? If so, please confirm, and we'll proceed with the amendment.

Thanks,

Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

530-304-1403 (cell)

530-754-9034 (office)

Skype: ealeasure

From: Beth Edison <bedison@metabiota.com>
Sent: Tuesday, April 2, 2019 2:59 PM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>; Hannah R Chale <hrchale@UCDAVIS.EDU>; predict Sympa List <predict@ucdavis.edu>
Subject: Re: Contract mod

Thanks for the detailed explanation Liz. as long as I can allocate the total Ebola and Core amounts where they are needed (being mindful of ceilings) then this should be fine.

Best,

Beth

On Tue, Apr 2, 2019 at 1:53 PM Elizabeth Leasure <caleasure@ucdavis.edu> wrote:

Hi Beth. For the rebudget, none of the Y4 carryover funds are going away, they are just being redistributed from Core to Ebola budget to cover overdrafts for the Ebola countries transitioned to UCD/EHA and clear out available balances for core-funded countries that are no longer in Metabiota's PREDICT portfolio. Essentially, all Y4 carryover fund balances for China, Indonesia, and RoC ($786,285 in total) were removed from your Core budget obligation and added to the Ebola budget for CDI, Guinea, and Sierra Leone, which were $1.158M in overdraft. Because the Y4 carryover for China, Indonesia, and RoC was not enough to cover the full $1.158M overdraft for the transitioned Ebola countries, we had to clip into the Y4 Global Ebola carryover (using all $319K available) plus a small amount of Y4 Global core carryover ($52K in total) in order to fully resolve the CDI/SL/Guinea overdraft with a net zero impact to the overall carryover amount. So, the Y4 Core carryover amount is being reduced but the Ebola carryover amount is going up by a corresponding amount (only as much as is needed in order to resolve the CDI/SL/Guinea overdrafts).

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Yes, your plan for tracking the budget category changes sounds fine. If you get near 10% cumulative transfers, please let me know.

If you still have questions, we can have a chat to clarify.

Thanks,

Liz

Elizabeth Loanzon

Financial Operations Manager

One Health Institute

530-304-1403 (cell)

530-754-9034 (office)

Skype: ealoanzon

From: Beth Edison <bedison@metabiota.com>

Sent: Tuesday, April 2, 2019 12:55 PM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>; Hannah R Chale <hrchale@UCDAVIS.EDU>; predict Sympa List <predict@ucdavis.edu>
Subject: Re: Contract mod

Hi Liz,

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Thanks,
beth

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Are we okay to proceed with your rebudget and 25% obligation amendment?

Thanks,

Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

530-304-1483 (cell)

530-754-9034 (office)

Skype: ealeasure

From: Beth Edison <bedison@metabiota.com>
Sent: Monday, April 1, 2019 10:01 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>; Hannah R Chale <hrchale@UCDAVIS.EDU>; predict Sympa List <predict@ucdavis.edu>
Subject: Re: Contract mod

Hi Liz,

This looks good. One question about Laos. Does this mean our total budget for the year will be our carry-over plus this partial obligation and that we should not expect any more funds to come in for this country? Once I have that confirmed I can send you a runway for how long we should be able to maintain operations there.

Thanks!

Beth

On Wed, Mar 27, 2019 at 3:52 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Hi Beth. Please take a look at the rebudget and coming amendment for PREDICT. Basically, we're rebudgeting from Core to Ebola to zero out all transitioned countries (resolving the overdraft for the Ebola countries in the process) and moving GVP carryover to Lao PDR, the idea being that these are FY17 funds that are not subject to the TVPA restriction, and we'll use FY18 money to fund the full GVP budget. Please take a look and let me know what you think. I'll need to process the rebudget with the amendment to add funds, so Hannah will hold off on processing the amendment until you confirm everything looks okay.

The Y5 funding obligation includes 25% of your full GVP budget for Y5 (excluding BCA funds-which will come separately), the balance of your Y5 Ebola budget (so you will now have your full Ebola budget in hand inclusive of carryover), and enough Core funds to ensure that you have 25% of your core budget in hand for Y5 (inclusive of carryover). Hopefully that makes sense. Let me know if you have any questions.

Thanks,

Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

530-304-1403 (cell)

530-754-9034 (office)

Skype: ealeasure

From: Beth Edison <bedison@metabiota.com>
Sent: Thursday, February 28, 2019 10:50 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>
Subject: Contract mod

Hi Liz,

Do you have any thoughts on when we might expect a contract mod that includes the Ebola funds and GVP? I know we'll have to wait a while for core funds.

Thanks!

Beth

--

Beth Edison

Program Manager | Metabiota

(250)739-8987

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Program Manager | Metabiota

(250)739-8987

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Beth Edison
Program Manager | Metabiota
(250)739-8987

From: Elizabeth Leasure <ealeasure@ucdavis.edu>
To: Beth Edison <bedison@metabiota.com>
CC: Shaun Tse <stse@metabiota.com>;Hannah R Chale <hrchale@ucdavis.edu> predict Sympa List <predict@ucdavis.edu>
Sent: 4/2/2019 10:29:50 PM
Subject: [predict] RE: Contract mod

Excellent, thank you!

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edison
Sent: Tuesday, April 2, 2019 3:29 PM
To: Elizabeth Leasure
Cc: Shaun Tse ; Hannah R Chale ; predict Sympa List
Subject: Re: Contract mod

Hi Liz,

I'm confirming. Please proceed with the amendment.

Thanks,
Beth

On Tue, Apr 2, 2019 at 3:20 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Are you confirming we're okay to proceed with the amendment or do you need more time?

Elizabeth Leasure
Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edison <bedison@metabiota.com>
Sent: Tuesday, April 2, 2019 3:19 PM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>; Hannah R Chale <hrchale@UCDAVIS.EDU>; predict Sympa List <predict@ucdavis.edu>
Subject: Re: Contract mod

Understood. Thanks Liz!

On Tue, Apr 2, 2019 at 3:16 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
You have the flexibility to rebudget as you need to between countries and cost elements (within the 10% of total award amount) as long as you don't use Ebola funds for non-Ebola funded countries. So you can move funds from Global Ebola to Cameroon or DRC (or vice versa) but you can't move funds from Global Ebola to Global Core. Does that sound okay? If so, please confirm, and we'll proceed with the amendment.

Thanks,
Liz

Elizabeth Leasure

Financial Operations Manager
One Health Institute
530-304-1403 (cell)
530-754-9034 (office)
Skype: ealeasure

From: Beth Edisen <bedisen@metabiota.com>
Sent: Tuesday, April 2, 2019 2:59 PM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Shaun Tse <stse@metabiota.com>; Hannah R Chale <hrchale@UCDAVIS.EDU>; predict Sympa List <predict@ucdavis.edu>
Subject: Re: Contract mod

Thanks for the detailed explanation Liz, as long as I can allocate the total Ebola and Core amounts where they are needed (being mindful of ceilings) then this should be fine.

Best,
Beth

On Tue, Apr 2, 2019 at 1:53 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
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Program Manager | Metabiota
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From:	Andrew Clements <aclements@usaid.gov>
To:	Katherine Leasure <kaleasure@ucdavis.edu>
CC:	PREDICTMGT <predictmgt@usaid.gov> Predict inbox <predict@ucdavis.edu>; Jonna Mazet <Jkmazet@ucdavis.edu>
Sent:	4/11/2019 8:40:07 AM
Subject:	Re: PREDICT International Travel Requests

Approved subject to mission concurrence.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Apr 10, 2019, at 7:55 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Please find below international travel requests for your review and approval. Please let me know if you have any questions. Thanks!

1. Gilardi (Rwanda, Uganda): $1800 airfare/$289 (Kigali), $130 (Ruhengeri), $340 (Kampala), $112 (Other) max daily per diems
2. Valitutto (Myanmar): $1500 airfare/$287 (Yangon) max daily per diem
3. Edison (Cameroon, DRC): $2400 airfare/$262 (Yaounde), $394 (Kinshasa)

Travel Requests -

1. UC Davis would like to request travel approval for Dr. Kirsten Gilardi to travel from Davis, California, USA to Rwanda and Uganda from May 13-25, 2019 to meet with PREDICT staff and partners.

Trip purpose: This trip will enable Dr. Gilardi to meet with PREDICT Country Coordinators from Rwanda, Uganda and eastern Democratic Republic of the Congo at MGVP headquarters in Ruhengeri, Rwanda and Kampala, Uganda, and at MGVP's field stations in Kisoro and Buhoma, Uganda, to conduct field and laboratory site visits with staff and partners and to check on Year 5 work progress in all three countries. Dr. Gilardi will also meet with government partners to check in on One Health capacity strengthening for staff and partners. ***Her tentative travel dates in each country are as follows – Rwanda: May 14-17, May 19-22, May 24; Uganda: May 17-18, May 22-24.***

2. Smithsonian Institution requests approval for Marc Valitutto, wildlife veterinarian and Global Lead for PREDICT Myanmar, to travel from Chengdu, China to Yangon, Myanmar from May 11-18, 2019 to participate in community engagement sessions with community members and leaders, as well as regional ministry officials for health, animals, and the environment. **From Myanmar, he will return to New York, NY.* This is intended to be Dr. Valitutto's final PREDICT-related trip to Myanmar.

Trip purpose: to participate in community engagement where concurrent surveillance activity was conducted. Engagement sessions are to include direct discussions and presentations to the community members who were sampled and more formal presentations to community leaders, and regional ministry officials for health, animals, and the environment. Presentations will include videos prepared, outbreak pop-up exhibit panels, bat book, and demonstrations for protection.

3. Metabiota would like to request travel approval for Beth Edison, PREDICT Program Manager, to travel from Nanaimo, Canada to Yaounde, Cameroon from June 1-5, 2019 and to Kinshasa, DRC from June 5 – 9, 2019 to meet with the PREDICT team and ensure in-country close out activities are properly planned and executed.

Trip purpose: Cameroon – To meet with the PREDICT Cameroon team, provide supervision and ensure plans are in place to close-out PREDICT in-country subawards and activities compliantly. DRC – To To meet with the PREDICT DRC team, provide supervision and ensure plans are in place to close-out PREDICT subawards and activities

compliantly.

--
Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
530-752-7508

--
You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
To post to this group, send email to predictmgt@usaid.gov.
To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/CAD6-xM%2BhdRqBO%2B4wpHZGEsaFBLMR%3DcqyPrRp8fNYQ1q7On1m8A%40mail.gmail.com.

From:	Valitutto, Marc <ValituttoM@si.edu>
To:	David J Wolking <djwolking@ucdavis.edu>
CC:	Prof. Jonna Mazet <jkmazet@ucdavis.edu>;predict@ucdavis.edu" <predict@ucdavis.edu>;Murray, Suzan <MurrayS@si.edu>;Zimmerman, Dawn" <ZimmermanD@si.edu>
Sent:	4/14/2019 2:42:24 AM
Subject:	Re: Urgent: TVPA info needed for China, Laos, Mynamar by Noon on Monday April 15th

Hi David,

This message is in response to the TVPA and its potential impact on the PREDICT Myanmar Project.

Project Status: Final stages of data analysis include a second confirmation of 53 human PCR samples, followed by sample shipment for sequencing and animal species barcoding to an external lab. Final project stages also include project and government staff participation in progress meetings, community engagement sessions, and manuscript preparation.

The Smithsonian maintains a Letter of Agreement (LOA) with the Livestock Breeding and Veterinary Department (LBVD) of the Ministry of Livestock, Agriculture and Irrigation and is also operating under an Ethics Review Committee (ERC) approval with the Department of Medical Research (DMR) of the Ministry of Health and Sports.

Specifically:
1. Should funding be no longer permitted for distribution for the P2 Myanmar Project, we would be unable to conduct a final government stakeholder's engagement meeting and fund participation of our country coordinator to the final international PREDICT meeting. All other programmatic needs may be handled by the Smithsonian.

2. Should we be requested for a "full stop" of programmatic activities in Myanmar, the impact additionally includes discontinuation of the contract for the Country Coordinator's salary to continue manuscript preparation through Sept 30th, as well as elimination of community engagement sessions to occur between 11-18 May 2019. All other project needs can be continued out of country. Formal relationships via the LOA with LBVD and ERC with DMR would not cause significant concern should project discontinuation occur.

Marc

From: David J Wolking
Date: Saturday, April 13, 2019 at 1:53 AM
To: Peter Daszak , Hongying Li , David McIver , Karen Saylors , "Valitutto, Marc" , Suzan Murray , Dawn Zimmerman
Cc: Ava Sullivan , Molly Turner , Beth Edison , "Prof. Jonna Mazet" , "predict@ucdavis.edu"
Subject: Urgent: TVPA info needed for China, Laos, Mynamar by Noon on Monday April 15th

Hi China, Laos, and Myanmar teams,

We received an urgent request for information today from Andrew and the USAID management team regarding the ongoing Trafficking Victims Protection Act (TVPA) and implications for our program and activities. Jonna talked to Andrew today and we need some brief and relatively high-level feedback on the question and two points below:

Where will we be in these TVPA countries if we...

1. ***are not permitted to continue funding government contracts?***
2. ***are no longer able to spend any money in country, full stop?***

For example:

1. P2 will not be able to do x, y, z (pay salaries and fund planned outreach and risk communication

events), and focus would shift to _____ (analysis and final report prep with the global team?). Another example: For Smithsonian/Myanmar, funds were recently made available to cover remaining outreach and risk communication campaigns at Marc's request.

- If #1, SI would need to manage the remaining work directly through their team and accounts. What's the impact?
- If #2, then likely the campaign would be cancelled. What are the implications?

If all in-country work is essentially complete and remaining activities are sequencing, data cleaning, analysis, etc. that's also essential information to share, in the event these TVPA implications are minimal. Jonna asked Andrew to explore if universities and parastatals fall under the the "government" category so we are standing by for feedback. Please keep that in mind when preparing any statements.

We need your responses by noon on Monday, April 15th.

Thanks and please let me know if you have any questions.

David

From:	Karen Saylors <ksaylors@metabiota.com>
To:	David J Wolking <djwolking@ucdavis.edu>
CC:	Ava Sullivan <sullivan@ecohealthalliance.org>;Beth Edison <bedison@metabiota.com>;David McIver <dmciver@metabiota.com>;Dawn Zimmerman <Zimmermand@si.edu>;Evelyn Luciano <luciano@ecohealthalliance.org>;Hongying Li <li@ecohealthalliance.org>;Marc Valitutto <ValituttoM@si.edu>;Molly Turner <turner@ecohealthalliance.org>;Murray, Suzan <MurrayS@si.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Prof. Jonna Mazet <jkmazet@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent:	4/15/2019 7:48:41 PM
Subject:	Re: Urgent: TVPA info needed for China, Laos, Myanmar by Noon on Monday April 15th

That looks good to me David.
Thanks, Karen

On Tue, Apr 16, 2019 at 12:35 David J Wolking <djwolking@ucdavis.edu> wrote:
Hi there,

Thanks for all the contributions. Unfortunately we need to move forward with information for Andrew today as this request came to us last Friday marked "very urgent". I'm planning to share the great information you all provided along with the following preamble on financial impact in one hour. If you have any concerns **please let me know before 1:30PM Pacific Time** before this goes to Andrew and USAID.

Programmatically, any unused funds from our approved country budgets will be reprogrammed for travel and communication by the global team in each country as appropriate. If no activities or spending are allowed in these countries (even if spent in-country by the lead global partner), funding will be reallocated to complete analyses and reports by PREDICT's global consortium. If there are remaining funds from the China, Laos, or Myanmar country budgets, we will use them where we have budget deficits for testing and/or wrap-up in PREDICT's other Core-funded countries.

Feel free to reach me by cell if needed (415-690-9955)..

David

On Fri, Apr 12, 2019 at 10:53 AM David J Wolking <djwolking@ucdavis.edu> wrote:
Hi China, Laos, and Myanmar teams,

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Thanks and please let me know if you have any questions.

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From: David J Wolking <djwolking@ucdavis.edu>
To: Hannah R Chale <hrchale@ucdavis.edu>
CC: Brooke Genovese <bgenovese@ucdavis.edu>;Elizabeth Leasure <ealeasure@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 5/15/2019 9:31:14 PM
Subject: Re: PREDICT EB Call - May 15, 2019 @ 9AM PST

Thanks ya'll!

On Wed, May 15, 2019 at 10:54 AM Hannah R Chale <hrchale@ucdavis.edu> wrote:

NOTES FROM CALL:

-

- **TVPA and Y5 obligation updates**

No guidance that they are making us stop but heightening every day, pretty certain no new money spending, don't spend fast cause more not coming, still trying to save that money for that country, orgs. Not going through government

Peter – is travel going to be blocked to those countries? He needs to go to China

Jonna – Jonna has asked this question, its gone up the chain, still no clear answer, can go but not work with governments, Jonna official questions still waiting answer, can we still work with communities and disseminate results but no official conferences or meetings with governments

Cara – in DRC on Y14 money, and DOD, so not a concern at all per Jonna

Y5 – 3 major road blocks, TVPA is one, but not stopping the whole thing– still don't have money – Jonna told them we need to borrow money. Are we getting all money but spend different or lose funds? One major hold up, USAID internal accounting processes, tracking funds per country and caps, trying to track and sort that out. Despite them saying it has nothing to do with the white house, its white house that wants figures

Peter – align $ with GHSA language?

Jonna not sure if that matters?

- **DTRA redux**

Asking USAID for info on countries, USAID not working with them, instead of asking which labs work, asking which labs need to ship samples, for security or destroyed, put those on high risk, and then made a list of not "high risk" but still need to ship for security – DTRA hasn't answered

Billy – not in RoC or DRC, no countries we added were countries that they won't work with

RoC gov. wants samples back – contingent on power and infrastructure should be fixed soon with Y17 money

- **Armed Forces Health Surveillance Branch briefing**

Data management unit, biosurveilance unit, obsorbing other units in army and joint commands, 11million samples, soldiers before and after deployment, they were interested in what we were doing,

Simon – interesting, good experts in the room, more info and experience sharing exercise, facing similar sirology challenges, what platforms, uncharacteratized challenges, they were interested in our outputs and what are findings are

Jonna – they specifically asked how they can get info on results, Jonna left the door open, will share protocols, open to follow ups, difference is they keep the results they do not belong to the country

- **Open data message and follow-up (DDL) - any questions? –**

Tracey – confusing bc a lot of papers wouldn't need data,

Per Jonna, up to author, upload paper or justify why its not uploaded

John, category of papers associated w/ PREDICT, but not directly related, not a core paper,

Jonna – still need write up justification for why not used / uploaded, if there were some USAID samples and some NIH samples up to USAID to figure that out

-

- **Branding soft transition where easy**

Not fixing business cards or slides or anything already made, only changing things going forward

- **Upcoming DC events**

- **PREDICT ITAs and travel guidance**

Basically no traveling for conferences. It is looking really bad, saying we have not money and going to all these conferences

Peter – can't go to meetings already listed in scope?

Jonna – pulled GHSA – make an argument its valuable for PREDICT, those people are presenting, USAID will come back and make sure directly USAID related

Peter & Jonna – make strong justifications in ITA and address how PREDICT related, but don't expect it to be approved.

Peter trying to go to Glasgow, doing an ITA

Per Jonna, if part GVP go that route, everything PREDICT being scrutinized, think about that with any ITAs and equipment

Semi-annual meeting recap and the road to closeout

Jonna - for the last few months we need a simplistic report card for a country to easily gauge, david, brooke, Bridgette, working on a rubric, points to objectives for red, yellow, green, goal everybody all green by September. Good management tool and Andrew and alysa like it. Once a month update, partner and organizational leads will have this tool. Want objective leads to set standards.

Chris – Alyssa wants products that show behavioral data, risk, chris says don't have this data to the end, Jonna says – Alyssa does want this info to fight for more predict funding, Andrew does not want/care about predict future. Reconcile what we can give to USAID while recognizing results not til end. Can provide behaviorial data since other date won't be ready.

Jonna says they already requested all behavioral data for guinea

Simon – usaid has been consistent since before end of predict one don't wait til end for results, they reiterated this several times throughout project, we should not be telling USAID we won't have results until end. Make sure we are not pushing results into Y6

Chris – I will help think about how to get them some preliminary results

3. **Sample disposition & safety**

Jonna – 100% of labs need help w/ budget, each country needs individual plan, before and post Bali meeting need sample plans, if we will not continue relationship with lab, PII needs to be destroyed – anybody want to volunteer to lead this? radio silence, Jonna says she will reach out and assign

Tracey – each country revisit w/ each partner – June 16 deadline to reply with plan. Corina & Tracey will discuss offline

4. **One Health in Action case studies**

Katherine – june 30 deadline to diseminatate before Bali, if you are point person respond to Katherine, if any country interested reach out TZ, Ivory, Liberia, Nepal, Myanmar, Vietnam, Mongolia,

300-400 words with picture. Metabiota will get in touch with Katherine offline,

Jonna – ideally don't we want one for every country in the final report?

Tracey – said reach out to Lucy, already has something

Chris – Nepal has been working hard

5. **Objective team updates**

Simon – interpretations update – 1,500 sequences, finding new viruses, first viral findings from Ivory, next session beginning July, everyone get your sequence data by June 28th,

Tracey – as soon as intrepation data in Edith, government reports

Jonna, - would be nice if you have a milestone, all countries completed, any milestone, make a one page flyer to send to USAID

Brooke – one page briefing, can use quarterly report template, haven't

Chris surveillance- don't a lot of work, clean up work for categories and symptoms,

Worried teams aren't taking data clean up to the country level as seriously, convey sense of

urgency while we have in-country staff, need them to go through data, going through this on surveillance team meetings.

Behavior team came up with a meteric

Barcoding is proceeding along, species, rodents and bats make sure you have identified 5 species as an interface, project risk,

Tracey – there's been some confusion, all positives barcoded, that species, if species positive additional barcoding of negative species?

Tammy - Report in edith to list out positive animals, good report, how to tell which species have been barcoded or not

Jonna – set what's red, yellow, green for barcoding

IM team – cleaning data going well, cleaning up predict one species names, under review will send out to countries next surveillance call, getting lots of data, test results, sequences and barcoding

Modeling – teams been following up after Vancouver, how to support country level teams, bringing over individuals to work with them extensively, from Thailand, Indonesia, and more. Peter – pathways analysis, met internally for framework on that, can share with group what comes out of it,

Worked with IM team and performed wet/dry analysis, used weather data set, rainfall pattern, auto classify as wet dry, 77% same as country coordinator, good alignment, mostly done, chris suggested come on surveillance call to review findings, this is a good tool for country teams. Can discuss surveillance,

Tracey – that tool is great, but that needs to be done BEFORE it goes in EDITH only final determination and result go in EDITH,

Kevin Yes our teams are still doing that before it goes in EDITH, will get M&A out soon to show results but show still need money

6. **Mission communications & country roundup essentials**

Jonna – data workshop in workshop in june, our Ethiopian colleagues have been denied VISA's, we need you to be super on top of making sure your country people get Bali Visas

Jonna – Andrew asked "provide your best estimate for when you have to lay people off if you don't get money, in country and out of country"

Molly – if Y5 obligations doesn't go through, only one month of core funding – so if 30 days notice would need to notify now

Jonna – how much notice time to layoff –

Molly – one month til out of money – need 2 weeks notice

Jonna – we are already too late for in country, will tell usaid we'll need the money anyway for severance

Metabiota – 2 weeks to give people notice – that's Canada not US –

Jonna – contact beth and get that info

Smithsonian – we have money a month or 2 weeks –

Jonna – if you have money your fine

Wcs – out of money this month, need to notify now

Columbia – not sure how much noticed needed

Davis – Liz says – can make it through June, but layoff notices need to go out in 2 weeks or less max, even with that we are borrowing money that has already been spent

And Andrew want to know what won't get done.

Kevin – Andrew sent email yesterday – outbreak Indonesia, kevin responded had call with Indonesia no one was talking about that, but now country coordinated received request to use predict human assays. Cdc collaboration, not asking to respond to in person, asking for tech assistance, and human assays, says specifically for outbreak

Will ask if they can share results, Jonna – ask to sight us, in paper or meeting, It would be great for results but most likely not

7. **Publication, media, and conference updates**

Jonna – in country ones good to know, but not a big deal bc no ITA, Jonna in Dublin next week UCD for gvp also to EU joint program on ONE Health, Jonna tech advisor, Wout going in country, bat one health hard to justify on predict, usaid will raise eyebrows about going to DTRA meeting, need strong justification,

Kevin is going but DTRA is paying for everyone

Jonna – a couple people leaving Bali and going to Poland

Predict symposium in Malaysia,

Jonna – need really good justification for that, get it on management team call

Jonna got invite for MERck future insight – a prize of pandemic preparednees hero getting 1 million euro, have to pay ourselves, Jonna not going, but thinks USAID would pay to tell Jonna if you were invited

Simon – presenting ebola in July

Sara – public media, natgeo, docu-drama- hotzone –

Brooke – euna & Christine on that

Tracey – urban wildlife conference on our PREDICT, a few from davis, chris going using other funds, Amanda going for wcs other funds also, billy from eha, some country people going presenting on predict, Jonna – those ITAs need to be in now, might not be approved, zoey going

Jonna – any pubs coming out? Other media? Usaid was asked to do a CBS interview, asked to talk about environmental factors on DRC ebola,

- Global Health Security 2019, Sydney (June 18-20, 2019)
- ASM Microbe 2019, San Francisco (June 20-24, 2019)
- Bat One Health Research Network Meeting, Phuket Thailand (July 26-28, 2019)
- DTRA Biological Threat Reduction Program Review meeting Warsaw, Poland (Sep 17-19,

2019)

- ID week 2019, Infectious Disease Society of America, Washington DC (October 2-6, 2019)

- 19th International Congress on Infectious Diseases, Kuala Lumpur (February 20-23, 2020)

Please let me know if you have any questions

Thank you!

Hannah Chale, CRA

Research Administrator

One Health Institute

University of California, Davis

Cell – 530-219-9987

http://www.vetmed.ucdavis.edu/ohi/

From: Brooke Genovese <bgenovese@ucdavis.edu>
Sent: Wednesday, May 15, 2019 10:46 AM
To: Hannah R Chale <hrchale@UCDAVIS.EDU>
Cc: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>; David John Wolking <djwolking@ucdavis.edu>; Jenna Mazet <jkmazet@ucdavis.edu>
Subject: Re: PREDICT EB Call - May 15, 2019 @ 9AM PST

Hi there,

Here are my notes from the EB call this morning.

Best,

Brooke

From: David J Wolking <djwolking@ucdavis.edu>
Date: Tuesday, May 14, 2019 at 3:36 PM
To: Jonna Mazet <jkmazet@ucdavis.edu>, Elizabeth Leasure <ealeasure@UCDAVIS.EDU>, Brooke Genovese <bgenovese@ucdavis.edu>
Subject: Re: PREDICT EB Call - May 15, 2019 @ 9AM PST

Here's your agenda with notes…

PREDICT Executive Board Meeting
Wednesday, May 15, 2019
9:00-11:00am PST/12:00-2:00pm EST
Zoom link: https://onehealth.zoom.us/j/401896666
Additional Zoom info below agenda

Jonna, Peter, Jon, Simon, Billy, Kevin, Molly, Catherine, Tracey, Karen, Hannah, Brooke, Corina, Tammie, Sarah, Dawn

1.
2. **Administrative**
3. **updates**

- TVPA and Y5 obligation updates: discuss any potential implications of tagging budgets to countries

on core; awaiting TVPA guidance, but becoming heightened over at USAID so we're fairly certain we cannot use new money/subs on TVPA countries; trying to save money from those countries for respective global personnel who can integrate country data in broader analysis

1. Peter concerned about travel abilities for US partners (project closeout); USAID doesn't want us meeting with gov. or doing anything to benefit TVPA listed countries

- Y5 obligations: TVPA is not stopping USAID from giving us our money; WH wants to know how much aid is going to countries and what for
-
- DTRA redux- still asking us to write down everything again and send it over; now asking which labs need samples shipped for safety vs destroying samples; JM instead gave them high value targets (often labs they would put on high risk list) plus labs that we don't really think are high value targets but where samples need to be shipped for safety; DTRA has yet to respond
- Armed Forces Health Surveillance Branch briefing -Data Management and Technical Support, Epidemiology and Analysis, Global Emerging Infections Surveillance (GEIS),

- Will be absorbing other units/people who do this type of work; huge serum bank from warfighters post-deployment; very specific molecular questions, but JM doesn't feel there are high value targets for follow up

- Simon: thought it was more of an info sharing opportunity; they were interested in PCR and serology and are clearly having similar roadblocks; very interested in looping into our outputs (i.e. what we're finding)

- JM: we did leave door to collaborate open & offered to share protocols, but their client is Army/Naval generals, not public.

- Open data message and follow-up (DDL) – any questions? – soft message sent out to get ready, after we send official message, will only have 30 days to make data accessible; **if you have questions, ask them now via email to David Wolking and Marcy Uhart**
- Branding soft transition where easy: anything already printed or slide sets that are hard to reformat = don't worry about changing, unless your Mission is very sensitive to it.
- Upcoming: DC events
- PREDICT ITAs and travel guidance - request absolutely necessary travel only as we wrap up, ask
- that conference requests are discussed prior to ITA process: basically, no more traveling for international conferences; no guidance yet on domestic

- Need to make a better argument in ITA language about why it benefits PREDICT (will be concerned about World Bank branding & presenting their info)

2. **Semi-annual meeting recap and the road to closeout:** management tool for us/USAID (Andrew & Alisa); BS/BG/DW put rubric together, ask objective leads 1-3 things they want to see completed in their country and solicit their input to set what is yellow vs red vs green; goal is for everyone to have completely green cards by September

- CKJ: thinks Alisa is looking for product that justifies new funding for us (behavioral data, risk communication); Alisa asking for preliminary data analysis so she can advocate for P3 – ***needs follow up with leadership team for how we want to field her questions;** what can we start pushing to USAID/what pieces motivate them for a new award

3. **Sample disposition & safety** - input on this item from Jonna, below

- 100% of labs need to be explored for budget for maintenance; Follow-up recommendations on what we believe should be priority for samples → finalize country documents at Bali meeting → part of long-term storage agreement on an addendum

- Best practice: destroy name or identifying information

1. No updates on sample disposition/safety from CM and TG; general guidance is for everyone to follow up with their country labs and make sure their sample disposition plan is on track

4. **One Health in Action case studies:** Catherine – **Operationalizing One Health** à TZ, CIV, Liberia, Nepal, Myanmar, Vietnam, Mongolia all tentatively suggested ideas; still open to working with other countries if there is interest

1. Addition of Bangladesh; Tracey suggested Catherine reach out to Lucy for

Cambodia; MB countries are still contemplating (w/ Dave McIver)

2. JM – ideally we want one of these for every country that has a success for the final report

5. **Objective team updates: SA**: Interpretations – still finding new viruses (paramyx). CIV interpretations yield influenza, new findings in Cambodia; next interpretation session will be in July; June 28th deadline to submit sequence data into EIDITH

1. TG: Denise working with Dan to generate gov reports for data release; JM discussed 1 page briefs for Mission/USAID as findings and successes come in (basically repurposed CPU's)

CKJ: Surveillance – worried that data cleaning isn't making enough progress with in-country teams; competence assessment of questionnaire created and barcoding underway
TO: IM and EIDITH – just progress update
KO: Modeling team – following Vancouver, will be bringing over individuals to work with EHA team for an extended visit to learn data analytics; pathways analysis is being revisited (land use change, wildlife trade, etc) and are developing a framework for that; will share when there are developments

1. Evan Eskew working with IM team and surveillance to do analysis of seasonality and align with country coordinator expert opinion

2. Cleaned up automatic pipeline for species ID for barcoding data, post tweaks; pulls data through EIDITH R package and does automatic GenBank query; TG – this tool should be used BEFORE things go into EIDITH

3. Working on getting M&A products out

WS/JM: Capacity – data conference at UC Davis underway in June; FYI that Ethiopian team were denied visas; JM urges everyone to start VISA process for Bali now

§ Bridgette & Catherine in touch and working together to synergize on activities between capacity team and EHA

BK/CM: Partnerships – Marcy and Catherine working on review of national biosecurity action plans; reinforcing P2 messaging

"LATE BREAKER FROM ANDREW": if obligation doesn't come through this month "provide your best estimate of when you need to lay people off if you don't get money, including global people, and what won't get done"
EHA à would need to give them 2 weeks notice (only 1 month of funding)
MB à Tammie will contact Beth, but knows they need to give 2 weeks notice
SI à has money until end of project, should be good
WCS à out of money at the end of the month, would need to be telling people now
CU à not sure, would need to check
UCD à enough to get us to end of May, maybe June

Basically, lay off notices would need to go out in 2 weeks or less. Already borrowing against money that's already commited.

6. **Mission communications & country roundup essentials – KO**, Andrew sent email about ProMed/Indonesia outbreak; Indonesia team received request to use P2 assays on human samples for the outbreak, but we haven't been asked to respond, just provide technical support

7. **Publication, media, and conference updates**

- Global Health Security 2019, Sydney (June 18-20, 2019)
    1. ITA's need to be more specific about the benefit to PREDICT/GVP
- ASM Microbe 2019, San Francisco (June 20-24, 2019) à Chris participating
- Bat One Health Research Network Meeting, Phuket Thailand à hard to justify on PREDICT, but could justify for 1 or 2 people; DTRA offered to pay for people; Kevin will be going
- (July 26-28, 2019)

JM in Dublin (not PREDICT ITA) to give talk on GVP at UC Dublin and be a technical advisor to the European Joint Union

- DTRA Biological Threat Reduction Program Review meeting, Warsaw, Poland (Sep 17-19, 2019)
- ID week 2019, Infectious Disease Society of America, Washington DC (October 2-6, 2019)
- 19th International Congress on Infectious Diseases, Kuala Lumpur (February 20-23, 2020)
    1. Would need a really good justification for why this is good for policy to get this through; **need to get this onto SMT agenda**
- JM got invite to a meeting for MERK in Germany in July – not going and would have to pay your own travel, but prize is pandemic preparedness (1M Euro) "Visionary Pandemic Protector"; USAID would want us to engage with MERK, so if someone is invited please consider
- NatGeo releasing hotzone docudrama at the end of this month (Memorial Day weekend) – Eunah and Krisitin need to be on top of it, gather things to tweet out in response

AOB

8.

Zoom Call-in info

Zoom link: https://onehealth.zoom.us/j/401896666

Or iPhone one-tap :

US: +16468769923,,401896666# or +16699006833,,401896666#

Or Telephone:

Dial(for higher quality, dial a number based on your current location):

US: +1 646 876 9923 or +1 669 900 6833

Meeting ID: 401 896 666

International numbers available: https://zoom.us/u/depX2cn5i

On Tue, May 14, 2019 at 3:35 PM David J Wolking <djwolking@ucdavis.edu> wrote:

Hi there EB,

Below is the agenda and call-in details for the meeting tomorrow.

Talk soon,

David

PREDICT Executive Board Meeting

Wednesday, May 15, 2019

9:00-11:00am PST/12:00-2:00pm EST

Zoom link: https://onehealth.zoom.us/j/401896666

Additional Zoom info below agenda

1. **Administrative updates**
   - TVPA and Y5 obligation updates
   - DTRA redux
   - Armed Forces Health Surveillance Branch briefing
   - Open data message and follow-up (DDL) - any questions?
   - Branding soft transition where easy
   - Upcoming DC events
   - PREDICT ITAs and travel guidance

2. **Semi-annual meeting recap and the road to closeout**

3. **Sample disposition & safety**

4. **One Health in Action case studies**

5. **Objective team updates**

6. **Mission communications & country roundup essentials**

7. **Publication, media, and conference updates**

- Global Health Security 2019, Sydney (June 18-20, 2019)
- ASM Microbe 2019, San Francisco (June 20-24, 2019)
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8. **AOB**

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Meeting ID: 401 896 666

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From: Dennis Carroll <dcarroll@usaid.gov>
To: cchrisman@usaid.gov <cchrisman@usaid.gov>
CC: jkmazet@ucdavis.edu <jkmazet@ucdavis.edu>;etogami@ucdavis.edu <etogami@ucdavis.edu>;maher@ecohealthalliance.org <maher@ecohealthalliance.org>;erubin@metabiota.com <erubin@metabiota.com>;daszak@ecohealthalliance.org <daszak@ecohealthalliance.org>;nwolfe@metabiota.com <nwolfe@metabiota.com>
Sent: 7/11/2019 12:22:14 AM
Subject: GVP agenda for July 11

Hey all, hope you can make it. Suggested agenda items:

1. Status of note to prospective Board members on why radio silence

2. China

3. MacArthur grant submission

4. AOB

short but sweet:)

Dr Dennis Carroll
Director, Emerging Threats
Bureau for Global Health
US Agency for International Development
Mobile: 301-646-6235
Personal email: dcarroll008@gmail.com

On Jun 25, 2019, at 11:32 AM, cchrisman@usaid.gov wrote:

Hi All,

Please note that our next two GVP meetings will be canceled - 6/27 (due to travel) and 7/4 (due to the holiday). We will plan to reconvene after that and, as always, please send any pressing items over email.

Best,
Cara

GVP call

Thu Jun 27, 2019 1pm – 2pm

call in line 1-719-785-9461, passcode 97848# (map)

- watson@ecohealthalliance.org
- nwolfe@metabiota.com
- dcarroll@usaid.gov
- Peter Daszak
- jkmazet@ucdavis.edu
- etogami@ucdavis.edu
- erubin@metabiota.com

- cchrisman@usaid.gov

From:	Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>
To:	Tammie O'Rourke <torourke@metabiota.com>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>
CC:	David John Wolking <djwolking@ucdavis.edu>;Denise Greig <denisejgreig@gmail.com>;Daniel O'Rourke <dorourke@metabiota.com>;predict Sympa List <predict@ucdavis.edu>
Sent:	7/17/2019 10:47:15 PM
Subject:	[predict] Re: IM Draft Work Plan for Wrapup

Hi everyone,

Just for transparency, Tammie and I have been discussing this over the last week and I hope to follow up next week with everyone while I'm in Davis.

Corina

From: Tammie O'Rourke
Date: Wednesday, July 17, 2019 at 3:38 PM
To: Chris Kreuder Johnson , Tracey Goldstein , Corina Grigorescu Monagin
Cc: David J Wolking , Denise Greig , Daniel O'Rourke
Subject: IM Draft Work Plan for Wrapup

Dear team,

Dan & I have been drafting on our work plan for the next few months and would like a bit of input from the team. In previous communications with Jonna, we are forging ahead under the assumption that the year 6 extension is a go and that some countries will be continuing on into the extension.

Our plan for the final meeting in Bali is to provide the exiting countries with USB sticks that will contain the following:

- CSV extract of all data (site characterization, animals, questionnaires, specimens, tests, behavioural & training)
- Risk Characterization Report
- Questionnaire Data Review Report
- final government report
- a link to a read-only folder in dropbox (or box) that will have the above contents

To help prioritize our work in preparation for setting up the USB sticks in time for the meeting we have several questions:

- is there anything else we should be including on the USB sticks?
- For the final government report - what did we decide we would provide? I seem to recall we thought just sending the details without a final summary would suffice but we also talked about highlighting the changes.
- Below are the countries with active tests, do we have a feel for who will be submitting sequences? Is there a deadline for submitting these?

Bangladesh	464
China	12
DR Congo	3
Egypt	6
Ethiopia	24

Ghana	17
India	75
Jordan	509
Lao PDR (FAO)	55
Nepal	400

Rwanda	9
Senegal	3
Tanzania	455
Uganda	1
Vietnam	896

- When will the next interpretations be? We assume there will be enough time to send the government reports and get them approved before the end of August?
- What about the next set of genbank submissions? We are thinking we will not have genbank accession numbers before the meeting, but want to confirm as they take a bit of work to get in.
- is there anything we are missing?

We are also happy to setup a time to discuss, but wanted to give you a heads up on what we were thinking.

Thanks in advance for your input!

Dan & Tammie

--
Tammie O'Rourke
Metabiota
Senior Information Management Developer
Emerging Pandemic Threats - PREDICT Program
tel +1-250-618-2460

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
CC: David John Wolking <djwolking@ucdavis.edu>;predict Sympa List <predict@ucdavis.edu>;Matthew Blake <mblake@ucdavis.edu>
Sent: 7/18/2019 6:46:09 PM
Subject: Re: Updated P2 Expense tracker with projections

Hi Liz,
Bullets in response to your sections:

- Distribution of the current cut seems fair for now -- good job.
- EHA amendments approved; only question is that when you say these make EHA whole, except for the $542K, wouldn't it also be missing the Bangladesh $468K?
- All your budgeting looks great in the last section. I'm not totally clear on whether or not we need all of the $502K for supplies to do the remaining testing. Let's assume we do. If not, we could potentially make some of Columbia cuts whole above &/or have carryover for more lab staff & testing that might need to be continued further into Yr 6. Assuming that will be combined with other Yr 6 budgeted costs in this category when we request the rest of the cut back.
- Do you have the UCB contract encumbered in the FY18 GVP projections?

Okay -- so onto Yr 6 budget.
Thanks,
J

On Thu, Jul 18, 2019 at 3:48 AM Elizabeth Leasure <calleasure@ucdavis.edu> wrote:

Hi Jonna. Sorry to be getting this to you later than requested. As you can imagine, balancing everything has proven to be incredibly complicated (and mind numbing), but I think I've got it figured out . I've updated the expense tracker (attached) to now include the FY18 funds obligated for P2 and GVP; both pots of money have their own tabs for tracking of costs. Going forward, I'll refer to the FY17 or older core funds as "old core" for simplicity. Let me apologize in advance for this long email. Please bear with me. J If you make it to the end of this email and have any questions, just let me know. Thanks!

As part of this process, I took a stab at distributing the Y5 "cut" across partners (see below). The $468K Bangladesh figure reflects the amount currently unobligated to EHA for in-country and EHA on behalf of Bangladesh costs; I subtracted that amount from the $1.11M figure to come up with the portion that is Global/Admin attributed to Bangladesh. I then: 1) added the $643K Global/Admin amount for Bangladesh to the amounts withheld for CDI, Ethiopia, Senegal, Tanzania, and Uganda; 2) subtracted the $120K for Columbia; and 3) divided that number by two *($643,146 + ($112,679*5 = $563,395) = $1,206,541 - $120,746 = $1,085,795/2 = $542,898 each for EHA and UCD)*.

Y5 funding cuts			
CDI	*112,679*		
Cameroon	*112,679*		
Ethiopia	*112,679*		
Senegal	*112,679*		
Tanzania	*112,679*		
Uganda	*112,679*		
	676,074		
		Global	*Country specific*
Bangladesh	1,111,528	643,146	468,382
TOTAL	**1,787,602**		

PROPOSED DISTRIBUTION			
	Modeling/VIRCH	Bangladesh	
Columbia	120,746		
MB	112,679		
UCD	542,898		
EHA	542,898	468,382	
	1,319,221	468,382	1,787,603
EHA Global/Admin			
pending	**790,719**		
obligation	**247,821**	*Available to obligate now*	

With regard to EHA's pending obligation of Y5 funds:

- To date, only 75% of EHA's Global/Admin budget for Y5 has been obligated, leaving the last 25% ($790,719) pending obligation from FY18 Core funds. If we take that $790K figure and subtract the $542K that has not yet been received from USAID, we can obligate $247K right now with the FY18 Core funding we have on hand (Amd 13 below).

- We also have sufficient FY18 core funding to obligate the remaining in-country budgets for Indonesia, Malaysia, Thailand, Egypt, Jordan, and RoC ($604,033 in total; Amd 7 below), as well as the EHA on behalf of budgets for these same countries (Amd 13 below).

- In addition, we have enough old Core funding to obligate the remaining in-country budgets for China ($353K) and India ($51,274) from old Core money (Amd 8 below); some error corrections will be needed to move costs from old Core to FY18 core funds in order to align expenditures with amounts obligated from old Core and FY18 money, but I think this is reasonable given the late obligation of funds. I have already worked out the transfers needed, and I am ready to pull the trigger once you give the go ahead.

- Lastly, if we rebudget EHA's budgets on behalf of India, China, and RoC to Global, we can obligate the last $171,604 from FY18 Core funds (Amd 14 below), which would leave EHA fully-funded for Y5 except for the $542K pending receipt from USAID.

ADVANCE PAYMENT SUB	APPROVED BUDGET	Amd 3	Amd 5	Amd 6	proposed Amd 7	proposed Amd 8
Global						
Administrative Management						
Asia						
Bangladesh	883,709	220,927	220,927	-	-	
China	707,893	176,973	176,973	-	-	353,946
India	102,567	25,647	25,647	-	-	51,274
Indonesia	645,378	161,344	161,344	161,344	161,344	
Malaysia	570,624	142,656	142,656	142,656	142,656	
Thailand	444,824	111,206	111,206	111,206	111,206	
Asia Subtotal						
Middle East						
Egypt	551,242	137,810	137,810	137,810	137,810	
Jordan	164,945	41,236	41,236	41,236	41,236	
Middle East Subtotal						
Africa						
Cote d'Ivoire						
Liberia						
RoC	39,118	9,780	9,780	9,780	9,780	
	4,110,300	1,027,580	1,027,580	604,033	604,033	405,220

COST REIMB SUB	APPROVED BUDGET	Amd 10	Amd 11	Amd 12	proposed Amd 13	proposed REBUDGET
Global	2,772,731	693,183	693,183	693,183	247,821	171,604
Administrative Management	390,146	97,536	97,536	97,536		
Asia						
Bangladesh	106,110	26,527	26,527	26,527		
China	161,984	40,496	40,496			(80,992
India	62,463	15,616	15,616			(31,231
Indonesia	115,219	28,805	28,805	28,805	28,805	
Malaysia	68,185	17,046	17,046	17,046	17,046	
Thailand	94,741	23,685	23,685	23,685	23,685	
Asia Subtotal						
Middle East						
Egypt	91,599	22,900	22,900	22,900	22,899	
Jordan	172,176	43,044	43,044	43,044	43,044	
Middle East Subtotal						
Africa						
Cote d'Ivoire						
Liberia						
RoC	136,513	34,128	34,128	8,876		(59,381
	4,171,867	1,042,967	1,042,967	961,602	383,301	-
TOTAL	**8,282,167**					Total n

The attached spreadsheet accounts for the following:

- All funds obligated by USAID to date ($132,262,397)
- All subaward obligations executed to date, as well as new subs that are planned but not officially processed yet (UCB, BCH)
- The obligation of $1,628,813 to EHA as proposed above.
-

UC Davis projected costs in the attached spreadsheet include:

- Staff at current LOEs through January 15, 2020, with a few exceptions (see below)
    - Note that LOE's for some were reduced to account for time attributed to other projects.

*Hannah 10% on YSM July-March
*Jennie on YSM 20% July-Sept; 50% October-March
*Gemma moved to YSM completely as of July
*Brian 40% on CEPI July-Dec; 50% Jan-March
*David 15% CEPI July-March
*Hannah 60% CEPI July-March

- Eri on GVP through February 2020
- Zoe on GVP from October 2019-September 2020
- Lucy K's contract through December 2019
- James B's contract through September 2019 (he'll move to PREEMPT eff. October)
- Additional $5K for Chocolate Pocket
- $50K in honorarium payments for advisory board (Y5 payments not processed yet)
- All Country meeting costs
- Travel for 15 to attend the All Country meeting in Bali
- Travel for Global leads to countries for closeout
- Minimal domestic travel through September (October onwards covered in Y6 budget)
- Supplies/communications through December (Y6 budget adjusted to account for this)
- Payment of Amazon web services for EIDITH through December (funds included in Y6 budget for Oct 19-Sept 20)
- Payment of all outstanding Genscript orders

With the above costs and obligations accounted for, a balance of $502K ($29K Ebola, $17K old Core, $456K FY18 Core) is available for diagnostics/sequencing/additional characterization direct costs.

Budget Category	<FY17 CORE LOP BUDGET	<FY17 CORE LOP EXPENDITURES	<FY17 CORE BALANCE
Personnel	$4,489,938	$4,489,938	$
Travel			
Domestic	$100,888	$100,888	($
International	$428,929	$428,929	$
Equipment	$17,065	$17,065	($
UCD-Based Diagnostics	**$560,927**	**$543,328**	**$17,59**
Supplies (Electronics, Mail, Communications)	$159,992	$159,992	($
Other Costs (ICAs, Meetings, Honoraria)	$407,520	$407,520	$
Subawards			
EcoHealth Alliance	$29,252,813	$29,068,317	$184,49
Metabiota, Inc.	$11,321,643	$11,028,824	$292,82
Smithsonian Institution	$1,730,392	$1,638,250	$92,14
Wildlife Conservation Society	$2,864,624	$2,864,624	($
Center for Molecular Dynamics	$1,730,070	$1,684,570	$45,50
Mountain Gorilla Veterinary Project	$1,482,272	$1,433,756	$48,51
Sokoine University of Agriculture	$191,624	$191,624	$
Institut Pasteur Cambodge	$1,691,160	$1,643,305	$47,85
University of the Philippines Research Institute for Tropical Medicine			**$(**
Georgetown University			$
Columbia University			$
USAMRIID (serology, pending)	$114,185	$0	$114,18
Ifakara Health Institute subagreement			$
Ghana WD subagreement			$
Ghana VSD subagreement			$
NMIMR subagreement			$
ISRA subagreement			$
UCAD subagreement			$
EISMV subagreement			$
Addis Ababa University subagreement			$
VHF subagreement			$
University of Makeni subagreement			$
UC San Francisco			$
UC Berkeley			$
Johns Hopkins University	$0	$0	$
Boston Children's Hospital	$0	$0	$
Uncommitted	**$0**	**$0**	**$(**
Advanced Pathogen Characterization	**$1,619,582**	**$1,619,581**	**$**
Columbia University	**$951,376**	**$951,376**	**$**
Uncommitted	**$668,006**	**$668,005**	**$(**

Budget Category			
Personnel	*$577,181*	*$577,181*	
Travel			
Domestic	*$18,535*	*$18,535*	
International	*$146,227*	*$146,227*	
Equipment	*$0*	*$0*	
UCD-Based Diagnostics	***$0***	***$0***	
Supplies (Electronics, Mail, Communications)	*$1,163*	*$1,163*	
Other Costs (ICAs, Meetings, Honoraria)	*$100,909*	*$100,909*	
Subawards			
EcoHealth Alliance	*$749,698*	*$749,699*	
Metabiota, Inc.	*$174,959*	*$174,959*	
Smithsonian Institution			
Wildlife Conservation Society			
Center for Molecular Dynamics			
Mountain Gorilla Veterinary Project			
Sokoine University of Agriculture			
Institut Pasteur Cambodge			
University of the Philippines			
Research Institute for Tropical Medicine			
Georgetown University	*$33,313*	*$33,313*	
Columbia University	*$0*	*$0*	
USAMRIID (serology, pending)			
Ifakara Health Institute subagreement			
Ghana WD subagreement			
Ghana VSD subagreement			
NMIMR subagreement			
ISRA subagreement			
UCAD subagreement			
EISMV subagreement			
Addis Ababa University subagreement			
VHF subagreement			
University of Makeni subagreement			
UC San Francisco	*$102,675*	*$28,882*	$73,793
UC Berkeley	*$0*	*$0*	
Johns Hopkins University			
Boston Children's Hospital			
Uncommitted	***$0***	***$0***	

Advanced Pathogen Characterization ***Columbia University*** ***Uncommitted***	**$0**	**$0**	
Outbreak Investigations *Columbia University* *Metabiota, Inc.* *EcoHealth Alliance* *Ghana Wildlife Division* ***Uncommitted***			
Indirect costs (57%)	*$495,339*	*$495,339*	
Total	***$2,400,000***	***$2,326,208***	**$73,792**

UCD Only	*$1,339,355*	*$1,339,355*

UCD only, DIRECT COSTS

Elizabeth Leasure

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From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: predict Sympa List <predict@ucdavis.edu>
Sent: 8/14/2019 8:48:28 PM
Subject: RE: P2 Y5Q3 Expend by Country/Category report for review (due 8/14/19)

Hi Jonna. I believe the Y5Q3 accruals done in mid-June were the figures we used to determine that a stop work notice was needed. A quick comparison of the accrual projections for the quarter against the actuals for the same time period show that we're $772K under what was projected for Core spending, with most of that being UCD, EHA, and WCS. Columbia's numbers are short $45K because they could not generate an invoice for June, so actual costs only cover through May. The UCD projections included all of the outstanding Genscript orders, so I'm not surprised that we came up short from the amount projected given the delays we've experienced with invoicing and order completion. For Ebola, UCD and EHA came in way under the amount projected. For UCD, the lingering Genscript orders are the cause, but I'm not sure why the EHA numbers came in so much lower than projected (other than they're just not very good at projecting costs). Metabiota and SI also came in about $50K under what they had projected for Ebola, but SI invoiced more than what was projected on Core, so overall they're slightly higher than what they projected for the quarter.

July lodgers have now closed, so I'll work on generating an expenditure by country report for June so we can see where we're at with country caps as of August 1. Thanks!

Core

	Core Q3 Accrual Totals	Actual Q3	Difference (actual minus projected)
UC Davis	$ 1,391,842	993,657	(398,185)
EHA	$ 2,365,116	2,215,864	(149,252)
MB	$ 443,100	346,086	(97,014)
WCS	$ 445,176	272,959	(172,217)
SI	$ 73,989	146,640	72,651
MGVP	$ 17,527	20,890	3,363
IPC	$ 56,905	70,946	14,041
CMDN	$ 29,622	29,315	(307)
Columbia	$ 346,597	301,596	(45,001)
	$ -		
	$ 5,169,874	4,397,953	(771,921)

EBOLA

	Ebola Q3 Accrual Totals	Actual Q3	Difference (actual minus projected)
UC Davis	$ 1,707,348	1,076,215	(631,133)
EHA	$ 833,152	496,895	(336,257)
MB	$ 312,967	266,417	(46,550)
WCS	$ -	-	-
SI	$ 96,380	48,419	(47,961)
MGVP	$ 54,576	59,748	5,172
SUA	$ 59,309	64,450	5,141
IHI	$ 75,388	83,043	7,655
AAU	$ 9,009	-	(9,009)
Columbia	$ -	-	-
Ghana	$ 55,742	77,569	21,827
UNIMAK	$ 97,919	87,298	(10,621)
VHI	$ 121,264	110,376	(10,888)
Senegal	$ 65,936	67,189	1,253
	$ 3,488,990	2,437,619	(1,051,371)

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From: Jonna Mazet
Sent: Friday, August 9, 2019 10:42 AM
To: Elizabeth Leasure
Cc: predict Sympa List
Subject: Re: P2 Y5Q3 Expend by Country/Category report for review (due 8/14/19)

Okay -- thanks.
How do the expenditures align with the figures/projections you were using to do the financial updates to USAID that resulted in us issuing the stop work notice? Just curious in case I get any questions on that, but I don't need any accounting done to compare. Since the quarter almost exactly matches the one before, I'm hoping it's pretty on target. Also makes sense that they're the same, since we were still in slow-down mode. Next quarter would then reflect the ramp-up. If we see any problems with that in the first month(s)' accounting. If you don't see the ramp-up reflected, please let me know, so I can call & maybe visit those partners to make sure we are on track to spend down.
In any case, approved to send once you adjust for the EHA changes to come.
Have a nice day,
J

On Thu, Aug 8, 2019 at 5:07 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
Hi Jonna. In the interest of getting you something to look at sooner rather than later, attached is the current draft of the Y5Q3 expenditure report. I have not received EHA's 2nd revision to their June invoice, so numbers will change somewhat once received. I've accounted for the transfer of $83K in Global costs for June from FY17 to FY18 core funds (FY17 and FY18 core Global costs are distributed differently), but the China figure should go down with a corresponding increase somewhere else (likely Global). The overall amount should not change, just the distribution of costs across countries. Overall, we're about $70K less than what we reported for the previous quarter, and the difference by country is included below for your reference. Core spending was up about $262K and Ebola was down $332K, likely due (at least in part) to the moving of

Global costs off of Ebola to FY18 core funds effective in June.

China, Myanmar, and RoC numbers are down, which is appropriate given TVPA restrictions and the revised distribution of Global costs to exclude these countries. A portion of Metabiota's Global costs are being attributed to the FY18 Core money for Lao PDR that we received (they have FY17 carryover for the in-country budget), so the Lao PDR number is down overall but only slightly. The revised distribution of Global FY18 core costs to exclude TVPA countries (and India) also results in more costs being applied to the non-TVPA countries, so numbers for those countries generally show an increase except for Egypt and Nepal. Egypt had huge numbers last quarter (hence the big decrease reflected below), and CMDN's burn rate has slowed since they've mostly spent their Y5 budget at this point. We're adding funds for some additional VF testing, barcoding, sequencing, but that decision was only made in July. The Guinea number decreased dramatically because I corrected the distribution of some VIRCH/Dx costs to attribute them to Sierra Leone instead of Guinea.

US Central	**Bangladesh**	**Cambodia**	**Cameroon**	**China**	**Cote d'Ivoire**	**DRC**
-$164,736	$375,791	$94,514	-$13,296	-$671,290	-$11,511	-$4,863

Gabon	**Ghana**	**Guinea**	**India**	**Indonesia**	**Jordan**	**Kenya**
$0	-$26,265	-$214,609	-$97,274	$102,161	$87,726	$12,227

Malaysia	**Mongolia**	**Myanmar**	**Nepal**	**RoC**	**Rwanda**	**Senegal**
$201,195	$39,065	-$26,566	-$3,435	-$122,199	$86,191	-$22,086

Sudan	**Tanzania**	**Thailand**	**Uganda**	**Vietnam**		
$0	$32,703	$100,998	-$45,961	$266,805		**-$70,545**

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From: Andrew Clements <aclements@usaid.gov>
To: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Jonathan Epstein <epstein@ecohealthalliance.org>;William Karesh <Karesh@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>;Tracey Goldstein <tgoldstein@ucdavis.edu>;Simon Anthony, D.Phil <anthony@ecohealthalliance.org>
CC: PREDICTMGT <predictmgt@usaid.gov>
Sent: 11/4/2019 10:52:15 AM
Subject: Fwd: PLOS NTD: Filovirus-reactive antibodies in humans and bats in Northeast India imply zoonotic spillover

FYI

Andrew Clements, Ph.D.
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For more information on USAID's Emerging Pandemic Threats program, see http://www.usaid.gov/ept2

https://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0007733

PLOS | NEGLECTED TROPICAL DISEASES

RESEARCH ARTICLE

Filovirus-reactive antibodies in humans and bats in Northeast India imply zoonotic spillover

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Check for updates

OPEN ACCESS

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Data Availability Statement: All relevant data are within the manuscript and its Supporting Information files. Next generation sequencing files are available from the Sequence Read Archive at the National Center for Biotechnology Information (Accession Numbers: SAMN12259407, SAMN12259408).

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Abstract

Bats are reservoirs for several zoonotic pathogens, including filoviruses. Recent work highlights the diversity of bat borne filoviruses in Asia. High risk activities at the bat-human interface pose the threat of zoonotic virus transmission. We present evidence for prior exposure of bat harvesters and two resident fruit bat species to filovirus surface glycoproteins by screening sera in a multiplexed serological assay. Antibodies reactive to two antigenically distinct filoviruses were detected in human sera and to three individual filoviruses in bats in remote Northeast India. Sera obtained from *Eonycteris spelaea* bats showed similar patterns of cross-reactivity as human samples, suggesting them as the species responsible for the spillover. In contrast, sera from *Rousettus leschenaultii* bats reacted to two different virus glycoproteins. Our results indicate circulation of several filoviruses in bats and the possibility for filovirus transmission from bats to humans.

Author summary

Focused virus surveillance at human-wildlife interfaces enables proactive detection of potentially epidemic pathogens. Filoviruses, including ebolaviruses and marburgviruses, are pathogens with epidemic potential. They were previously detected in bats and have caused disease outbreaks in humans with a high case fatality rate. Here, we tested sera obtained from bats and humans at a high-risk interface for the presence of filovirus reactive antibodies. Human participants were engaged in annual bat hunts, possibly exposing them to bat-borne viruses. We report the exposure of humans to filoviruses that were likely derived from the two sampled bat species. The bats contain antibodies raised to presumably three distinct filoviruses. Our findings suggest bats in South Asia act as a

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Detection, characterization and mitigation of emerging infectious disease risk' to IHM (HDTRA1-17-1-0026; PI: IHM), a Department of Atomic Energy, Government of India award (2012/21/06/BRNS) to UR, and funding from Biological Defense Research Directorate of the Naval Medical Research Center (HT9404-13-1-0021) to CCB; Component Project: Soluble Trimeric Filovirus Envelope Glycoproteins. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing interests: The authors have declared that no competing interests exist.

reservoir host of a diverse range of filoviruses and filovirus spillover occurs through human exposure to these bats.

Introduction

Filoviruses are causative agents of viral haemorrhagic disease in humans and non-human primates although virus spillover is rare [1]. There are ten distinct filoviruses classified into four genera, *Ebolavirus*: Ebola virus, Bundibugyo virus, Taï forest virus, Sudan virus, Reston virus and Bombali virus; *Marburgvirus*: Marburg virus and Ravn virus; *Cuevavirus*: Lloviu virus and *Dianlovirus*: Měnglà virus [2–4].

Bats are the proposed natural reservoir of filoviruses, involved in enzootic virus maintenance and zoonotic virus transmission to susceptible hosts [4]. The majority of described filoviruses are endemic in the African continent, although filovirus-specific antibodies were detected in bats from Bangladesh [5], the Philippines [6], and Singapore [7]. The genome of a novel filovirus, Měnglà virus, was detected in bats from China [8] and is the second Asiatic filovirus described after Reston virus [9]. Lloviu virus was discovered in Spain in 2011 and detected in Hungary in 2016 [10, 11]. Bats are hunted by humans across Africa and Asia, and at least 167 bat species are consumed [12]. High-risk activities, such as bat hunting and mining in bat-dwelling caves, pose a threat of cross-species filovirus transmission [13].

In the Northeast Indian state of Nagaland, local ethnic groups have conducted bat harvests for at least seven generations as a source of food and traditional medicine. These bat hunters are exposed to saliva, blood, and excreta from the bat species *Rousettus leschenaultii* and *Eonycteris spelaea*. We conducted a serological survey of both hunted bat species and human hunters to study if humans have been exposed to filoviruses potentially originating from bats.

Materials and methods

Ethics statement

All study participants provided written informed consent by signing a form in their native language Nagamese. All human samples and surveys were collected under National Centre of Biological Sciences (NCBS) IEC permit 7/001 and National University of Singapore (NUS) IRB permit N-17-034E. Negative control sera were collected under the NUS IRB permit number H-18-029. All bats were sampled under the NCBS, Tata Institute of Fundamental Research IACUC permit #UR-6/2014, which adheres to provisions of the Prevention of Cruelty to Animals Act (1960) and the Breeding of and Experiments on Animals Rules (1998) and the NUS IACUC permit B16-0159 under the National Advisory Committee for Laboratory Animal Research (NACLAR) guidelines in Singapore.

Sample and data collection

In 2017, 85 individuals participating in an annual bat harvest in Mimi village (Fig 1) were provided a paper-based survey to record their gender, age, occupation and number of times involved in the bat harvest. Blood of consenting volunteers was collected in a serum separation tube (Vacutainer, Becton Dickinson, New Jersey, USA). Bat blood from *E. spelaea* (n = 16) and *R. leschenaultii* (n = 30) was collected by cardiac puncture after being sacrificed by the harvesters.

Blood samples were centrifuged at 1,500 x g for 10 min and sera were stored at 4˚C until transport to NCBS, where they were held at -80˚C. All sera were gamma-irradiated at 20KGy

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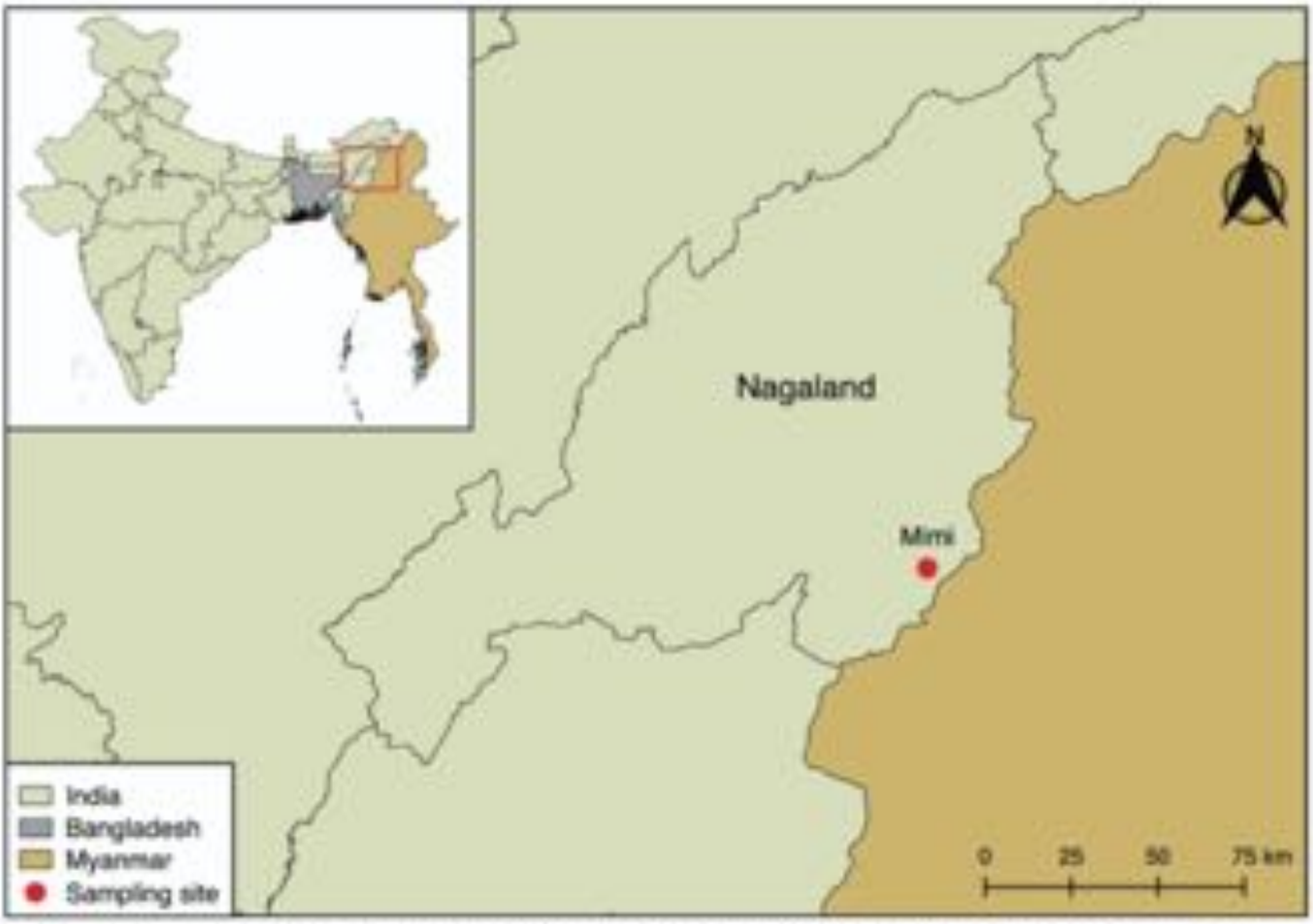

Fig 1. Geographical map of the border region between India and Myanmar. The Indian state of Nagaland and Mimi village are indicated. The map was created using QGIS v2.18.7 software (https://qgis.org/en/site/). The India shapefile was downloaded from the India Remote Sensing and GIS website (http://www.indianremotesensing.com/) and the Bangladesh and Myanmar shapefiles were downloaded from DIVA GIS (http://www.diva-gis.org/gdata). All layers were in the geographic coordinate system WGS 84 and all software and map layers used are open access.

https://doi.org/10.1371/journal.pntd.0007732.g001

with the Blood Irradiator 2000 (BRIT, Mumbai, India) and heat-inactivated at 56˚C for 60 min prior to screening. Pooled kidney, lung and spleen samples obtained from *E. spelaea* (n = 34) and *R. leschenaultii* (n = 69) were collected and stored individually in RNA*Later* (Sigma-Aldrich). Personnel handling potentially infectious material in the field wore N95 particulate respirators, surgical gowns, face-shields and were double-gloved. Surfaces were disinfected with 3% Virkon solution. Needles and scalpel blades were single use and disposed in sharps containers. Sealed containers were autoclaved at the Healthcare and Research Center of the Naga Hospital Authority Kohima, Nagaland, India. Small amounts of tissue (lung, spleen, kidney) was excised, combined by individual bat and homogenized in AVL Buffer (Qiagen) at NCBS. An aliquot of homogenate was used for downstream PCR analysis, while another aliquot of homogenate was used for NGS analysis.

PCR, next generation sequencing and serology

RNA was extracted with PureLink RNA Mini Kit (Invitrogen), and cDNA was synthesized using SuperScript III Reverse Transcriptase (Invitrogen). Samples were tested with a nested

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pan-filovirus PCR assay targeting the L gene as reported previously [14]. The positive control for the PCR was synthesized by Integrated DNA Technologies based on a region of the L gene of Bundibugyo virus (Genbank Accession: KU182911). The plasmid was amplified and extracted after transformation into competent cells using a NucleoBond Xtra Maxi Plus EF kit (Macherey-Nagel, Düren, Germany) and following the manufacturer's instruction. Purified plasmid was quantified, 10-fold serially diluted and validated with primers prior to use in the assay. Aliquots of homogenate for NGS analysis were further pooled by species (*E. spelaea* n = 34 and *R. leschenaultii* n = 34). NGS libraries were made (S1 Appendix) and validated by bioanalyzer, then sequenced on a HiSeqX Illumina machine with 2 x 150 bp reads by Medgenome Labs Ltd. (Bangalore, India) [15,16].

Human and bat sera samples were screened in a filovirus multiplex microsphere immunoassay as previously described [17]. Recombinant ectodomains of envelope attachment glycoproteins (GPe) from Ebola virus (EBOV), Bundibugyo virus (BDBV), Taï forest virus (TAFV), Sudan virus (SUDV), Reston virus (RESTV), Marburg virus (MARV), Ravn virus (RAVV), Lloviu virus (LLOV) and Mênglà virus (MLAV) (Table 1) were expressed in a mammalian cell-culture system [18, 19]. In 2018, purified, oligomeric GPe antigens (minus MLAV) were coupled to MagPlex microspheres (Luminex, Austin, TX, USA) and bat and human samples were diluted at 1:100 in PBS and run on a Bio-Plex 200 system (Bio-Rad, Hercules, California, USA) in duplicate. After sera incubation with GPe-coupled microspheres, samples were washed, incubated with biotinylated-Protein A and biotinylated Protein G (1:1 ratio) (Thermo Fisher Scientific, Waltham, MA, USA), washed and then finally incubated with streptavidin-phycoerythrin (PE) (Bio-Rad). After the discovery of Mênglà virus, the serum samples were re-run in 2019 with all GPe antigens and individual serum samples were diluted 1:100 for human and 1:250 for bat sera in PBS. Median fluorescence intensities (MFI) were measured using a MAGPIX machine (Bio-Rad) (S1, S2 and S3 Tables). Cell culture supernatant from a GPe untransfected cell line, was prepared and included in the multiplex immunoassay as a mock antigen sample to normalize non-specific antisera reactivity. Due to the absence of negative sera from the study site, we obtained seven presumptively negative human sera samples from a sample bank at Duke-NUS Medical School, Singapore. These were tested using a MAGPIX machine following the technical details described above in eight technical replicates to determine the variation of individual samples in repeat measurements to individual GPe (S4 Table).

Phylogenetic and statistical analysis

Next generation sequencing data was analysed as previously described [20]. Briefly, FASTQ files were trimmed for quality at a PHRED score of 20 and were then analysed in DIAMOND

Table 1. Virus name, host and location of isolation, and accession numbers for recombinant filovirus attachment glycoproteins (GPe) used in multiplex serological binding assays.

Virus isolate	Host/Location	Accession no.
Ebola virus/H.sapiens/COD/1976/Yambuku-Mayinga	Human/DRC	NC_002549.1
Bundibugyo virus/H. sapiens/UGA/2007	Human/Uganda	FJ217161.1
Taï Forest virus/H. sapiens/COV//1994/Pauleoula-CI	Human/Côte d'Ivoire	NC_014372
Sudan virus/H. sapiens/UGA/2000/Gulu-808892	Human/Uganda	NC_006432.1
Reston virus/M. fascicularis/USA/1989/Pennsylvania	Macaque/USA	AF522874.1
Lloviu virus/M.schreibersii-wi/ESP/2003/Asturias-Bat96	Bat/Spain	NC_016144.1
Mênglà virus/R. leschenaultii/CHN/2013/Sharon-Bat9447-1	Bat/China	KX371887.2
Marburg virus/H. sapiens/KEN/1980/Musoke	Human/Kenya	Z12132 553429
Ravn virus/H. sapiens/KEN/1987/Kitum cave-810040	Human/Kenya	NC_024781.1

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using the NCBI nr reference database [21]. DIAMOND outputs were analysed in MEGAN to determine the sequence similarly [22]. In the absence of negative serum controls from Nagaland, two independent methods were employed to define positive and negative cut-offs. The MFI values of the mock antigen were subtracted from each GPe MFI and the values were transformed to be positive, with the lowest number being 1. A log-normal model was fitted to the MFI data and the parameters of the fit were estimated in order to calculate the 95th percentile of the log-normal distribution (S1 Fig). To control for ebolavirus cross-reactivity [23], a separate cutoff was implemented at the three-fold change above the arithmetic mean of the mock-adjusted scaled MFI. Positive samples were defined as exceeding both thresholds. The 2018 Bio-Plex data was analysed with the same two statistical methods, but not mock-adjusted (S2 Fig). The spread of MFI values for duplicate measurements of each individual sample was plotted (S3 and S4 Figs). Mean negative human sera MFI values were plotted and the standard deviation for each sample was presented (S5 Fig). All analyses and visualizations were implemented in R 3.5.1 [24]; the R code can be retrieved from the authors upon request.

Results

The majority of bat hunters were between 18 and 50 years of age, male, and participated at least eleven times in the harvest (Table 2). All bat tissues tested were PCR-negative for filovirus-specific nucleic acid. There were a total of 13,993,300 reads from the *R. leschenaultii* NGS dataset and 7,975,905 reads from the *E. spelaea* NGS dataset and no filoviras sequences were identified. In our 2019 serum screen (that included MLAV), we detected filovirus-reactive sera in 5.9% (5/85) of human samples, 6.2% (1/16) of *E. spelaea* samples, and 13.3% (4/30) of *R. leschenaultii* samples. The highest MFI values, corresponding to levels of filovirus-specific serum IgG, were detected for EBOV-GPe in human and *E. spelaea* sera, and for MLAV- and RAVV-GPe in *R. leschenaultii* sera (Fig 2). Our results suggest human exposure to two antigenically distinct filoviruses, the first group of sera (H10, H27, H30, H40) being reactive to EBOV-, BDBV-, and SUDV-GPe, and one individual serum (H45) singly reactive to MARV-GPe. An individual *E. spelaea* serum sample (E34) reacted to the EBOV-, SUDV- and TAFV-GPe, displaying a similar cross-reactivity pattern as seen for the first group of human sera and was previously reported for filovirus-positive *E. spelaea* samples from Singapore [7]. The 2019 screening results corroborated positive samples that were detected when screened in 2018 using a Bio-Plex 200 system (S4 Fig; H27, H30, H40, E34, R38), strengthening interpretation of positive sera samples screened in two different years with two different Luminex xMAP-based machines. There was minimal intra- and inter-individual variation in the negative human sera samples and these were all well below the MFI cutoff values for each GPe (S5 Fig).

Discussion

Despite the growing evidence that filoviruses are present in South and Southeast Asia, there has been a historical absence of outbreaks of filovirus haemorrhagic fever in this region.

Table 2. Basic demographic information on human study population.

Population		Age distribution		Participation in bat harvest	
Individuals	85 (100%)	18–30 years	36 (42.4%)	0–10 times	25 (29.4%)
Male	50 (58.8%)	31–50 years	36 (42.4%)	11–25 times	40 (47.1%)
Female	35 (41.2%)	≥51 years	13 (15.3%)	≥ 26 times	20 (23.5%)

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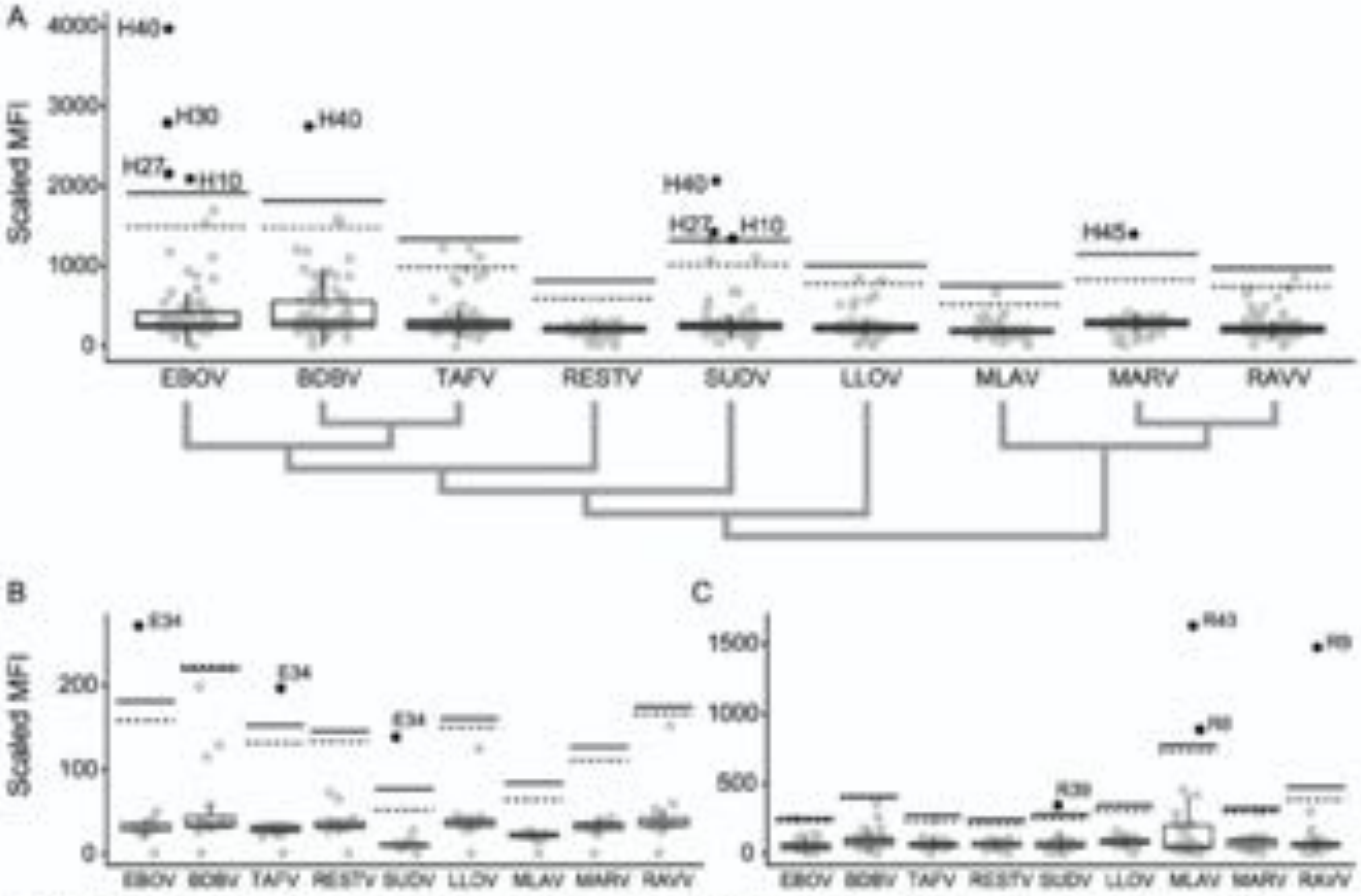

Fig 2. MFI values for sera obtained from humans (A), *Eonycteris spelaea* (B), *Rousettus leschenaulti* (C). Antibodies reactive to filovirus GPe from Ebola virus (EBOV), Bundibugyo virus (BDBV), Tai Forest virus (TAFV), Sudan ebolavirus (SUDV), Reston virus (RESTV), Llovia virus (LLOV), Mòngla virus (MLAV), Marburg virus (MARV), and Ravn virus (RAVV) are quantified in a bead-based fluorescence assay. Grey dots represent individual samples. A boxplot is overlaid to indicate median, quartiles and extremes of the sample distribution. A black dashed line indicates the cutoff determined from a single lognormal curve fit and a black solid black line the three-fold increase over the mean. A cladogram in panel A indicates the phylogenetic relationships of individual filovirus GPe based on their amino acid sequence.

https://doi.org/10.1371/journal.pntd.0007733.g002

Reasons why clusters of human filovirus infections have not yet been detected in Asia, include (a) ecological barriers prevent zoonotic transmission, (b) viruses are unable to sustain transmission between humans or (c) an uncharacterized diversity of non-pathogenic, antigenically-related filoviruses exist and cause asymptomatic infection in humans. Human populations with wildlife contact and no history of Ebola virus disease in Uganda [25] and the Democratic Republic of Congo [26] were reportedly ebolavirus seropositive. Similarly, here we report the presence of filovirus (e.g. ebolavirus, marburgvirus and dianlovirus) reactive antibodies in both human (e.g. bat hunters) and bat populations in Northeast India, a region with no historical record of Ebola virus disease.

Cross-reactivity between EBOV, BDBV and SUDV of the tested samples is in agreement with a previous report [23]. The mammalian cell-culture expression system to produce oligomeric, native-like GPe capture antigens in this multiplex assay provides several benefits compared to peptide-based antigen assays, including the retention of post-translational modifications (i.e. glycosylation) and native quaternary structures allowing capture of conformational-dependent antibodies. The use of GPe from all presently described filoviruses—with the

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exception of the recently described Bombali virus—allows for simultaneous detection and antigenic differentiation of virus species-specific IgGs and the identification of cross-reactive IgG responses. Most ebolavirus serology surveillance studies are unable to address the complex biology of known and unknown filoviruses in terms of cross-reactivity of specific antibodies. This filovirus serological assay addresses many limitations of previously employed assays by using oligomeric, native-like virus antigens in a multiplex manner and represents an improved biosurveillance tool. Establishing thresholds for low sample number serum sets that lack both positive and negative controls is challenging, but our efforts to employ two independent statistical methods and two machine platforms yielded congruent results and is in agreement with prior approaches to estimate seropositivity [27, 28].

Furthermore, this study describes serum reactivity to MLAV, incidentally in the same bat species (*R. leschenaultii*) mentioned in the initial report [2]. Reactivity to RESTV, which circulates endemically among bats, pigs and monkeys in the Philippines [29], and causes subclinical infection in animal care takers and slaughterhouse workers in the Philippines [9], was not detected in our study. Interestingly, MLAV and RAVV positive *R. leschenaultii* sera suggest circulation of two distinct filoviruses within the same species, which is serologically distinct from reactivity with *E. spelaea* and human samples. These results are concordant with previous findings of exposure to filoviruses antigenically closely related to EBOV, BDBV, and SUDV in *E. spelaea* in Singapore [17].

Two proposed mechanisms for sustained virus infection in the studied bat species are frequent co-roosting with other bats and the introduction of large numbers of susceptible juveniles into the population [30]. The two bat species sampled in this study, *R. leschenaultii* and *E. spelaea*, roost in large colonies in caves with rolling parturition patterns [31]. Though we have serological evidence of filovirus exposure, there was no genomic data detected. There are several reasons why this may be, including; small sample size, low virus copy numbers, uncertain epidemiological shedding periodicity, and high filovirus genetic diversity that is not captured by the primers employed here. Our results reinforce the need to select sentinel sites for virus surveillance at the human-animal interface and highlights some of the gaps in our understanding of filovirus transmission and ecology.

Supporting information

S1 Appendix. Technical description of next generation sequencing sample preparation, library preparation, sequencing, and bioinformatic pipeline.
(DOCX)

S1 Fig. Histograms for each GPs (Ebola virus (EBOV), Bundibugyo virus (BDBV), Tai Forest virus (TAFV), Sudan virus (SUDV), Reston virus (RESTV), Lloviu virus (LLOV), Marburg virus (MARV), and Ravn virus (RAVV), Mòngbà virus (MLAV) and mock antigen (MOCK)) and sera from humans (A), *Eonycteris spelaea* (B), and *Rousettus leschenaultii* (C). Lognormal distribution representing the best fit of all samples are indicated by solid black lines. A solid black vertical lines indicates 3-fold over mean and a dotted black line denotes cutoff established by lognormal curve fitting.
(TIF)

S2 Fig. MFI values for sera obtained from humans (A), *Eonycteris spelaea* (B), *Rousettus leschenaultii* (C) screened in 2018 on a Bio-Plex machine. Antibodies reactive to filovirus GPs from Ebola virus (EBOV), Bundibugyo virus (BDBV), Tai Forest virus (TAFV), Sudan ebolavirus (SUDV), Reston virus (RESTV), Lloviu virus (LLOV), Marburg virus (MARV), and Ravn virus (RAVV) are quantified in a bead-based fluorescence assay. Grey dots represent

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individual samples. A boxplot is overlaid to indicate median, quartiles and extremes of the sample distribution. A black dashed line indicates the cutoff determined from a single lognormal curve-fit and a black solid black line the three-fold increase over the mean.
(TIF)

S3 Fig. For the 2018 Bio-Plex dataset, mean values (horizontal lines) and spread of the two individual measurements are shown (vertical lines) for sera from human (A), *Eonycteris spelaea* (B) and *Rousettus leschenaultii* (C).
(TIF)

S4 Fig. For the 2019 MAGPIX dataset, mean values (horizontal lines) and spread of the two individual measurements are shown (vertical lines) for sera from *Eonycteris spelaea* (A) and *Rousettus leschenaultii* (B).
(TIF)

S5 Fig. Mean values and standard deviation of seven normal human serum samples from healthy volunteers (varying colours). Samples were tested in our assay with the indicated antigens in eight technical replicates.
(TIF)

S1 Table. Raw MFI values for human samples diluted at 1:100.
(XLSX)

S2 Table. Raw MFI values for *Eonycteris spelaea* samples diluted at 1:250.
(XLSX)

S3 Table. Raw MFI values for *Rousettus leschenaultii* samples diluted at 1:250.
(XLSX)

S4 Table. Negative human sera control values for seven individuals with eight technical replicates.
(XLSX)

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From: Peter Daszak <daszak@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Cara Chrisman <cchrisman@usaid.gov>;Dennis Carroll <dcarroll008@gmail.com>;Nathan Wolfe <nwolfe@metabiota.com>;Eddy Rubin <erubin@metabiota.com>;Samtha Maher <maher@ecohealthalliance.org>;Eri Togami <etogami@ucdavis.edu>
Sent: 12/19/2019 3:50:55 PM
Subject: Re: 100&Change Top-Rated Proposals

Fantastic!!!

Cheers,

Peter

Peter Daszak
(Sent from my iPhone)

President
EcoHealth Alliance

460 West 34th Street, New York, NY10001, USA

www.EcoHealthAlliance.org

On Dec 19, 2019, at 11:25 AM, Jonna Mazet wrote:

We made it up another wrung of the ladder & looks like they will include us in fundraising activities, irrespective of our winning the final award or not. Keep positive thoughts!
Happy Holidays,
Jonna

---------- Forwarded message ---------
From: **MacArthur Foundation** <communications@email-macfound.org>
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Subject: 100&Change Top-Rated Proposals
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From: Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>
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Sent: 2/4/2020 6:43:18 PM
Subject: Re: Feinstein to USAID: Reinstate Pandemic Prevention Program

Deb,
Absolutely amazing work by the senator and her team.
We are so fortunate to have you all in DC doing all that you do for California and the world.
Chris

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Date: Tuesday, February 4, 2020 at 10:16 AM
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From: Feinstein Press
Sent: Tuesday, February 4, 2020 1:11 PM
Subject: Feinstein to USAID: Reinstate Pandemic Prevention Program

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UNITED STATES SENATOR FOR CALIFORNIA
www.feinstein.senate.gov

For Immediate Release
February 4, 2020

Contact: Anthony Rivera-Rodriguez
(202) 224-9629

Feinstein to USAID: Reinstate Pandemic Prevention Program

Washington—Senator Dianne Feinstein (D-Calif.) today called on the U.S. Agency for International Development (USAID) to reinstate the PREDICT zoonotic disease surveillance and forecasting program. PREDICT is a program that proactively searches for pathogens with the potential to cause pandemics in order to prevent their spread from animals to humans. USAID canceled the program last year.

"Since 2009, PREDICT has led to the discovery of nearly 1,000 new viruses,

including coronaviruses similar to what has caused the outbreak in Wuhan, China. For example, in 2018, a new Ebola strain found in healthy bats was discovered in Sierra Leone and was the first Ebola strain to be discovered before an outbreak in humans occurred." Senator Feinstein wrote.

Feinstein continued: **"The current deadly viral outbreak and its quick appearance in the United States make clear that PREDICT's contributions to zoonotic disease surveillance and forecasting must continue. We simply cannot afford to go backwards and jeopardize the success we've seen over the last ten years."**

Full text the letter follows:

February 4, 2020

Mr. Mark Green
Administrator
United States Agency for International Development
2231 Crystal Drive
Arlington, VA 22202

Dear Administrator Green:

In light of the deeply concerning coronavirus outbreak in China, which has now led to several cases in California, I write to ask that you reverse your decision last year to shut down the U.S. Agency for International Development's (USAID) PREDICT zoonotic disease surveillance and forecasting program.

Since 2009, PREDICT has led to the discovery of nearly 1,000 new viruses, including coronaviruses similar to what has caused the outbreak in Wuhan, China. For example, in 2018, a new Ebola strain found in healthy bats was discovered in Sierra Leone and was the first Ebola strain to be discovered before an outbreak in humans occurred. Its discovery will help Sierra Leone and neighboring countries update their diagnostics to ensure they can detect all known Ebola viruses and reduce the risk of exposure.

PREDICT has even helped inform preparedness and response efforts being used to combat the current coronavirus outbreak. Specifically, research supported by PREDICT led to the discovery of several SARS-like coronaviruses related to the new virus in Wuhan, including viruses in bats that could be transmitted directly to people. This research has helped inform the scientific community about the possibility of animal-to-human interaction being a risk factor in the current outbreak. Even more, PREDICT trained and equipped public health professionals in several countries that are now supporting the diagnosis of the virus and other efforts to control outbreak.

The current deadly viral outbreak and its quick appearance in the United States make clear that PREDICT's contributions to zoonotic disease surveillance and forecasting must continue. We simply cannot afford to go backwards and jeopardize the success we've seen over the last ten years. I urge you to reinstate the PREDICT program, and I look forward to working with you on this critical issue.

Sincerely,

Dianne Feinstein
United States Senator

From: Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>
To: Kevin Olival <olival@ecohealthalliance.org>;David John Wolking <djwolking@ucdavis.edu>;Jon Epstein <epstein@ecohealthalliance.org>;Amanda Fine, VMD PhD <afine@wcs.org>;Brian H Bird <bhbird@ucdavis.edu>;Churchill, Carolina <cchurchill@wcs.org>;Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>;Dawn Zimmerman <ZimmermanD@si.edu>;Elizabeth Leasure <ealeasure@UCDAVIS.EDU>;Karen Saylors <ksaylors@labyrinthgh.com>;Marc Valitutto <ValituttoM@si.edu>;Suzan Murray <MurrayS@si.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Jonna Mazet <jkmazet@ucdavis.edu>;Woutrina A Smith <wasmith@ucdavis.edu>;Sarah Olson <sOlson@wcs.org>;Simon Anthony <sja2127@columbia.edu>;Tammie O'Rourke <torourke@metabiota.com>;Tracey Goldstein <tgoldstein@ucdavis.edu>;William Karesh <karesh@ecohealthalliance.org>;predict Sympa List <predict@ucdavis.edu>;Aleksei Avery Chmura <chmura@ecohealthalliance.org>;Alison Andre <andre@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>;Nicole R Gardner <nrgardner@ucdavis.edu>
Sent: 2/5/2020 2:23:59 AM
Subject: Re: PREDICT EB Call - Tuesday February 4, 2020 @ 9:30AM Pacific

Sharing this too – a very specific call out to PREDICT and the incredible work you all do!
/ckj

From: Feinstein Press <Feinstein_press@feinstein.senate.gov>
Sent: Tuesday, February 4, 2020 1:11 PM
Subject: Feinstein to USAID: Reinstate Pandemic Prevention Program

NEWS FROM DIANNE FEINSTEIN
UNITED STATES SENATOR FOR CALIFORNIA
www.feinstein.senate.gov

For Immediate Release
February 4, 2020

Contact: Anthony Rivera-Rodriguez
(202) 224-9629

Feinstein to USAID: Reinstate Pandemic Prevention Program

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Sincerely,

Dianne Feinstein
United States Senator

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From: Kevin Olival
Date: Tuesday, February 4, 2020 at 10:41 AM
To: David John Wolking , Jon Epstein

Cc: "Amanda Fine, VMD PhD" , Brian H Bird , Christine Kreuder Johnson , "Churchill, Carolina" , Corina Grigorescu Monagin , Dawn Zimmerman , Elizabeth Leasure , Karen Saylors , Marc Valitutto , Suzan Murray , Peter Daszak , Jonna Mazet , Woutrina A Smith , Sarah Olson , Simon Anthony , Tammie O'Rourke , Tracey Goldstein , William Karesh , predict Sympa List , Aleksei Chmura , Alison Andre , Ava Sullivan , Nicole Gardner
Subject: Re: PREDICT EB Call - Tuesday February 4, 2020 @ 9:30AM Pacific

Thanks for spotting this Jon! Here's Warren's tweet about PREDICT that we just mentioned on the call! Apparently a response to a retweet of the October Don McNeil NY Times article.



Kevin

On Feb 3, 2020, at 8:57 AM, David J Wolking <dwolking@ucdavis.edu> wrote:

Hi there,

Below is the agenda and Zoom link for tomorrow's call.

Talk soon,

David

PREDICT Executive Board Meeting Notes
Tuesday, February 4, 2020
9:30-10:30AM PST/12:30-1:30pm EST
Zoom link:_____
Additional Zoom info below agenda

1. Brief recap from USAID Management Team call

-
- Urgent
- USAID and Hill briefing - week of Feb 12th
-
-
- March
- meeting updates (March 17-19, 2020)
-
-
- ...
-

2. Novel Coronavirus (2019-nCoV) outbreak

3. Close-out - standing item
On equipment...
On finances and subawards...
On viruses and data...

-
- *Status*
- *of open data planning*
-

4. Final Report
Vol 1 - Global report - teams and deadlines

-
- Capacity
- - draft received
-
-
- EHP
- - draft received
-
-
- Behavior
- - draft received but needs input from surveillance and M&A teams
-
-
- IM
- - in progress with planned user experience survey
-

-
- M&A
- - January 24th
-
-
- Surveillance
- - February 24th
-
-
- Virus
- detection - January 24th
-

Vol 2 - Country reports

5. Consortium author list - P2 author list

-
- Here's
- a link to the Google Sheet for updates
-

6. GVP update

7. Mission, partner communications & country roundup essentials

8. Publication, media, and conference updates

-
- On
- *Publications...*
-
    -
    - Internal
    - review of manuscripts in prep
    -
-
- 19th
- International Congress on Infectious Diseases, Kuala Lumpur (February 20-23, 2020)
-

Zoom Call-in info
Topic: PREDICT EB Call
Join Zoom Meeting: https://onehealth.zoom.us/j/120732744

Meeting ID: 120 732 744

One tap mobile
+16699006833,,120732744# US (San Jose)
+16468769923,,120732744# US (New York)

Dial by your location
+1 669 900 6833 US (San Jose)
+1 646 876 9923 US (New York)
Meeting ID: 120 732 744

From: Tammie O'Rourke <torourke@metabiota.com>
To: Zoe Grange <zlgrange@ucdavis.edu>
CC: Tracey Goldstein <tgoldstein@ucdavis.edu>;Anthony, Simon J. <sja2127@cumc.columbia.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 4/17/2020 4:47:16 PM
Subject: Re: PREDICT virus data and spillover risk ranking

Hi Zoe,
I can address #3. All countries are fully approved, with the exception of Guinea, Liberia, Malaysia & DRC. As for being able to use the data for your app, I will defer to Chris for confirmation.
Tammie

On Fri, Apr 17, 2020 at 7:34 AM Zoe Grange <zlgrange@ucdavis.edu> wrote:

Hi everyone,

I was discussing the PREDICT data with Jonna the other day in terms of the spillover risk ranking. I have a few questions below that I was wondering if you could help with:

1. Where is the predict data for viruses that are collaboratively collected in Thailand and China? Are they in Eidith? If, so are they the ones listed as not Predict protocol?
2. For the SpilOver manuscript, I have only included data from P1 that was collected using PREDICT protocols. Do you think it's worth adding the non-predict protocol data? (possibly post-publication)
3. What is the status of the PREDICT 2 virus data? Do we have outstanding records for government approval? Do we have some countries that are completed that I could use for the spillover risk ranking?

Many thanks for your help. Hope you are all well ☺

Zoe

--
Tammie O'Rourke
Metabiota
Senior Information Management Developer
Emerging Pandemic Threats - PREDICT Program
tel +1-250-618-2460

From:	Zoe Grange <zlgrange@ucdavis.edu>
To:	Tammie O'Rourke <torourke@metabiota.com>
CC:	Tracey Goldstein <tgoldstein@ucdavis.edu>;Anthony, Simon J." <sja2127@cumc.columbia.edu>;Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent:	4/24/2020 12:01:03 PM
Subject:	Re: PREDICT virus data and spillover risk ranking

Hi Tammie,

I pulled the P2 interpreted tests data for the countries (excluding the countries listed below). I found some results, predominantly for Bangladesh, that are 'ConfirmationResult' positive but do not have anything listed for the 'Virus' type and 'Interpretation' columns. I've listed them in the attached the spreadsheet. Is there a reason for these results?

Cheers,

Zoe

From: Tammie O'Rourke
Date: Friday, April 17, 2020 at 5:47 PM
To: Zoe Grange
Cc: Tracey Goldstein , "Anthony, Simon J." , Christine Kreuder Johnson , Jonna Mazet
Subject: Re: PREDICT virus data and spillover risk ranking

Hi Zoe,
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Tammie

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Many thanks for your help. Hope you are all well ☺

Zoe

--
Tammie O'Rourke
Metabiota
Senior Information Management Developer
Emerging Pandemic Threats - PREDICT Program
tel +1-250-618-2460

"","X","Project","GAINS4_TestID","GAINS4_SpecimenID","Country","IsOutbreakTesting","SiteName","ConcurrentSamplingSite","District","StateProv","SiteLatitude","SiteLongitude","EventLatitud
e","EventLongitude","EventDate","Season","SeasonModeled","SeasonModeledDeviation","DurationDays","EventName","AnimalID","TaxaGroup","AnimalClass","ScientificName","ScientificNameIs
LowestKnownRank","TaxonomicRank","CommonName","LocalName","IDCertainty","AnimalSampleDate","Sex","SpecimenID","SpecimenType","TestDate","LabName","TestType","TestRequested","
TestRequestedProtocol","TestResult","RealTime_PositiveControlValue","RealTime_PositiveControlValue2","RealTime_InternalControlValue","RealTime_CTValue","LabName_Confirmation","Confir
mationTestDate","ConfirmationResult","TestStatus","Sequence","GenbankAccessionNumber","Virus","VirusGroup","VirusStatus","HumanThreat","ViralFamily","ViralGenus","Interpretation","Gov
ernmentReportName","DateGovtApprovedRelease","Organization"
"1",1824,"P2",370653,543279,"Bangladesh","Yes","Bogra-Dupchanchia-Gunahar-Posta","Independent Site","Rajshahi Division","Rajshahi",24.8762,88.1724,24.87,88.868,"2018-02-
08","Dry","Dry",-0.5697584,"BD-Bogra-Dupchanchia-Gunahar-Posta-2018Feb08","BDABB040","bats","free ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian
Flying Fox","Kala badur","field ID certain","2018-02-11","unknown","BDABB040.UGT","urine/urogenital swab","2018-02-18","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Nipah Virus","other-Gerloff 2016","Positive","24.5",NA,NA,34.89,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,"BD-008-P2 Outbreak human
Gunahar 2018 addendum",NA,"EcoHealth Alliance"
"2",20229,"P2",165983,292597,"Bangladesh","Yes","Dhaka-Badda Bonalata Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7336,90.3615,"2017-01-21","Dry","Dry",-
0.1275521,"BD-Dhaka-Badda Bonalata Bazar-2017Jan21","BDADAI-01","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-21","unknown","BDADAI-01.22V","urine/feces combined (guano)","2017-03-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",3,NA,30.25,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"3",20262,"P2",165984,292571,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-05","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-21","unknown","BDADAI-05.22V","urine/feces combined (guano)","2017-03-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",3,NA,32.41,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"4",20263,"P2",165981,292557,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-05","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-21","unknown","BDADAI-05.22V","urine/feces combined (guano)","2017-03-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",3,NA,3,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"5",20264,"P2",165982,292571,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-05","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-21","unknown","BDADAI-05.22V","urine/feces combined (guano)","2017-03-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.27",0,NA,36.98,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"6",20273,"P2",165985,292570,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-06","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-21","unknown","BDADAI-06.22V","urine/feces combined (guano)","2017-03-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",3,NA,25.05,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"7",20274,"P2",165992,292570,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-06","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-21","unknown","BDADAI-06.22V","urine/feces combined (guano)","2017-03-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",3,NA,3,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"8",20275,"P2",165994,292570,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-06","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-21","unknown","BDADAI-06.22V","urine/feces combined (guano)","2017-03-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.27",0,NA,3,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"9",20276,"P2",165953,292583,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-07","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-01-21","unknown","BDADAI-07.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",3,NA,22.89,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"10",20280,"P2",166258,292569,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-07","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-01-21","unknown","BDADAI-07.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,24.58,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"11",20281,"P2",166033,292583,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7798,90.424,"2017-01-21","Dry","Dry",-
0.1097216,"BD-Dhaka-Badda Kacha Bazar-2017Jan21","BDADAI-07","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-01-21","unknown","BDADAI-07.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,27.88,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"12",20280,"P2",165754,292518,"Bangladesh","Yes","Dhaka-North Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7800,90.4,23.8275,90.3638,"2017-01-21","Dry","Dry",-
0.0548811,"BD-Dhaka-North Badda Kacha Bazar-2017Jan21","BDADAI-08","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-21","unknown","BDADAI-08.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",3,NA,25.95,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"13",20333,"P2",165755,292589,"Bangladesh","Yes","Dhaka-North Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7800,90.4,23.8275,90.3638,"2017-01-21","Dry","Dry",-

0.6548011,"BD-Dhaka North Sadhu Kacha Bazar-2017Jan23","BDADAI-10","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-01-27","unknown","BDADAI-10.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,26.77,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"14",20384,"PT",180797,2929573,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7873,90.405,23.7472,90.3855,"2017-01-23","Dry","Dry",-
0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAI-100","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-100.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,31.5,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"15",20385,"PT",180010,2929573,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7873,90.405,23.7472,90.3855,"2017-01-23","Dry","Dry",-
0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAI-100","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-100.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,28.03,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"16",20386,"PT",180010,2929573,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7873,90.405,23.7472,90.3855,"2017-01-23","Dry","Dry",-
0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAI-100","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-100.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.77",0,NA,33.35,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"17",20320,"PT",180707,2929584,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-103","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-103.ZIY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,29.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"18",20321,"PT",180724,2929584,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-103","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-103.ZIY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,29.8,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"19",20322,"PT",180086,2929584,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-103","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-103.ZIY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,30.03,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"20",20325,"PT",180908,2929583,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-104","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-104.ZIY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,23.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"21",20330,"PT",180908,2929582,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-105","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-105.ZIY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,30.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"22",20340,"PT",182288,2929583,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-107","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-107.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,28.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"23",20341,"PT",180314,2929583,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-107","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-107.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,28.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"24",20342,"PT",180180,2929583,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-107","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-107.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.77",0,NA,26.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"25",20350,"PT",182208,2929558,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-108","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-108.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,28.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"26",20352,"PT",180315,2929558,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-108","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-108.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,31.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"27",20353,"PT",180188,2929558,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7785653,2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-108","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-108.ZIY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real

time PCR","other-Influenza A/H5N1","other-Gerloff 2016","Positive","29.27",0,NA,29.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"28",20357,"P2",.90208,2929302,"Bangladesh","Yes","Dhaka-Mohakhali Haque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7793,90.4055,"2017-01-25","Dry","Dry",-0.0687216,1,"BD-Dhaka-Mohakhali Haque Kacha Bazar-2017Jan25","BDADAI-109","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-109.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,32.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"29",20378,"P2",.90214,2927687,"Bangladesh","Yes","Dhaka-Mohakhali Sat Tola Market","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7779,90.4058,"2017-01-25","Dry","Dry",-0.0508998,1,"BD-Dhaka-Mohakhali Sat Tola Market-2017Jan25","BDADAI-11","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-11.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,20.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"30",20384,"P2",.90242,2929093,"Bangladesh","Yes","Dhaka-Mohakhali Dakkhin Para Masjid Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7710,90.4081,"2017-01-25","Dry","Dry",-0.0245771,1,"BD-Dhaka-Mohakhali Dakkhin Para Masjid Bazar-2017Jan25","BDADAI-12","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-12.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,22.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"31",20389,"P2",.90243,2927886,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-25","Dry","Dry",-0.7779556,1,"BD-Dhaka-Banani Bou Bazar-2017Jan25","BDADAI-13","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-13.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,24.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"32",20390,"P2",.90258,2929886,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-25","Dry","Dry",-0.7779556,1,"BD-Dhaka-Banani Bou Bazar-2017Jan25","BDADAI-13","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-13.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,28.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"33",20391,"P2",.90022,2929886,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-25","Dry","Dry",-0.7779556,1,"BD-Dhaka-Banani Bou Bazar-2017Jan25","BDADAI-13","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-13.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,25.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"34",20399,"P2",.90245,2927885,"Bangladesh","Yes","Dhaka-Banani Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7913,90.4084,"2017-01-25","Dry","Dry",-0.7779556,1,"BD-Dhaka-Banani Kacha Bazar-2017Jan25","BDADAI-15","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-15.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,29.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"35",20440,"P2",.90248,2929189,"Bangladesh","Yes","Dhaka-Tejkuni Para Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7824,90.3933,"2017-01-25","Dry","Dry",-0.0092791,1,"BD-Dhaka-Tejkuni Para Bazar-2017Jan25","BDADAI-16","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-16.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,23.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"36",20421,"P2",.90248,2348823,"Bangladesh","Yes","Dhaka-Farmgate Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.4,23.7573,90.39,"2017-01-25","Dry","Dry",-0.7762821,1,"BD-Dhaka-Farmgate Bazar-2017Jan25","BDADAI-18","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-25","unknown","BDADAI-18.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,30.66,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"37",20449,"P2",.90150,2929385,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.9780,90.6394,"2017-01-25","Dry","Dry",-0.0804451,1,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan25","BDADAI-120","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certain","2017-01-25","unknown","BDADAI-120.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,25.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"38",20450,"P2",.90257,2929385,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.9783,90.6394,"2017-01-25","Dry","Dry",-0.0804451,1,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan25","BDADAI-120","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certain","2017-01-25","unknown","BDADAI-120.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,27.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"39",20451,"P2",.90325,2929385,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.9783,90.6394,"2017-01-25","Dry","Dry",-0.0804451,1,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan25","BDADAI-120","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certain","2017-01-25","unknown","BDADAI-120.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,26.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"40",20467,"P2",.90256,2925273,"Bangladesh","Yes","Dhaka-Gulshan DNCC Kacha Bazar-2","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7946,90.4155,"2017-01-27","Dry","Dry",-0.0804451,1,"BD-Dhaka-Gulshan DNCC Kacha Bazar-2-2017Jan27","BDADAI-15","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Duck","field ID certain","2017-01-27","unknown","BDADAI-15.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,22.01,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"41",20478,"P2",.90257,2925177,"Bangladesh","Yes","Dhaka-Gulshan DNCC Kacha Bazar-2","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7946,90.4155,"2017-01-

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21","Dry","Dry",-0.680441,1,"BD-Dhaka-Gulshan DNCC Kacha Bazar-2-2017Jan21","BDABAI-16","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","hens","held ID certain","2017-01-21","unknown","BDABAI-16.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,34.86,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"42",20490,"P2",.802158,2925576,"Bangladesh","Yes","Dhaka-Gulshan DNCC Kacha Bazar-2","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7946,90.4155,"2017-01-21","Dry","Dry",-0.680441,1,"BD-Dhaka-Gulshan DNCC Kacha Bazar-2-2017Jan21","BDABAI-17","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","held ID certain","2017-01-21","unknown","BDABAI-17.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,29.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"43",20491,"P2",.880260,2925576,"Bangladesh","Yes","Dhaka-Gulshan DNCC Kacha Bazar-2","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7946,90.4155,"2017-01-21","Dry","Dry",-0.680441,1,"BD-Dhaka-Gulshan DNCC Kacha Bazar-2-2017Jan21","BDABAI-17","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","held ID certain","2017-01-21","unknown","BDABAI-17.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,34.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"44",20492,"P2",.880337,2925576,"Bangladesh","Yes","Dhaka-Gulshan DNCC Kacha Bazar-2","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7946,90.4155,"2017-01-21","Dry","Dry",-0.680441,1,"BD-Dhaka-Gulshan DNCC Kacha Bazar-2-2017Jan21","BDABAI-17","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","held ID certain","2017-01-21","unknown","BDABAI-17.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,32.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"45",20507,"P2",.807158,2927580,"Bangladesh","Yes","Dhaka-Banani Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.793,90.4084,"2017-01-21","Dry","Dry",-0.779155,1,"BD-Dhaka-Banani Kacha Bazar-2017Jan21","BDABAI-18","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","held ID certain","2017-01-21","unknown","BDABAI-18.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,32.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"46",20508,"P2",.800260,2927580,"Bangladesh","Yes","Dhaka-Banani Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.793,90.4084,"2017-01-21","Dry","Dry",-0.779155,1,"BD-Dhaka-Banani Kacha Bazar-2017Jan21","BDABAI-18","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","held ID certain","2017-01-21","unknown","BDABAI-18.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","26.5",0,NA,30.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"47",20509,"P2",.80268,2927578,"Bangladesh","Yes","Dhaka-Banani Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.793,90.4084,"2017-01-21","Dry","Dry",-0.779155,1,"BD-Dhaka-Banani Kacha Bazar-2017Jan21","BDABAI-21","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","held ID certainty unknown","2017-01-21","unknown","BDABAI-21.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,30.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"48",20684,"P2",.802080,2925568,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-21","Dry","Dry",-0.448021,1,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDABAI-23","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","held ID certain","2017-01-21","unknown","BDABAI-23.22V","urine/feces combined (guano)","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,30.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"49",20685,"P2",.80057,2925566,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-21","Dry","Dry",-0.448021,1,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDABAI-23","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","held ID certain","2017-01-21","unknown","BDABAI-23.22V","urine/feces combined (guano)","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,30.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"50",20686,"P2",.800069,2925568,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-21","Dry","Dry",-0.448021,1,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDABAI-23","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","held ID certain","2017-01-21","unknown","BDABAI-23.22V","urine/feces combined (guano)","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"51",20758,"P2",.807089,2925565,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-21","Dry","Dry",-0.442021,1,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDABAI-24","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","held ID certain","2017-01-21","unknown","BDABAI-24.22V","urine/feces combined (guano)","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,26.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"52",20760,"P2",.800098,2925565,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-21","Dry","Dry",-0.442021,1,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDABAI-24","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","held ID certain","2017-01-21","unknown","BDABAI-24.22V","urine/feces combined (guano)","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"53",20761,"P2",.803070,2925565,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-21","Dry","Dry",-0.442021,1,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDABAI-24","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","held ID certain","2017-01-21","unknown","BDABAI-24.22V","urine/feces combined (guano)","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"54",20822,"P2",.80262,2925564,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7936,90.405,23.7937,90.4066,"2017-01-21","Dry","Dry",-0.442021,1,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDABAI-25","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","held ID certainty unknown","2017-01-21","unknown","BDABAI-25.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real

time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,28.92,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"55",20823,"P2",90.40193,23.792564,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7937,90.4066,"2017-01-27","Dry","Dry",-
0.442021,"BD-Dhaka-Banani Bou Bazar-2017Jan27","BDADAI-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Other","field ID certainty unknown","2017-01-27","unknown","BDADAI-25.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,25.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"56",20824,"P2",90.40412,23.792564,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7937,90.4066,"2017-01-27","Dry","Dry",-
0.442021,"BD-Dhaka-Banani Bou Bazar-2017Jan27","BDADAI-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Other","field ID certainty unknown","2017-01-27","unknown","BDADAI-25.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","23.27",0,NA,21.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"57",20826,"P2",90.40303,23.792564,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7937,90.4066,"2017-01-27","Dry","Dry",-
0.442021,"BD-Dhaka-Banani Bou Bazar-2017Jan27","BDADAI-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Other","field ID certainty unknown","2017-01-27","unknown","BDADAI-25.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","25.5",0,NA,15.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"58",20855,"P2",90.40932,23.792930,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-27","unknown","BDADAI-25.22V","urine/feces combined (guano)","2017-02-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,22.1,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"59",20856,"P2",90.40869,23.792930,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-27","unknown","BDADAI-25.22V","urine/feces combined (guano)","2017-02-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,24.3,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"60",20857,"P2",90.40071,23.792930,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-27","unknown","BDADAI-25.22V","urine/feces combined (guano)","2017-02-07","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.27",0,NA,34.12,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"61",20926,"P2",90.40162,23.792509,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-27","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Deshi","field ID certain","2017-01-27","unknown","BDADAI-27.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,32.18,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"62",20927,"P2",90.40270,23.792509,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-27","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Deshi","field ID certain","2017-01-27","unknown","BDADAI-27.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,23.92,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"63",20928,"P2",90.40142,23.792509,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-27","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Deshi","field ID certain","2017-01-27","unknown","BDADAI-27.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,35.77,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"64",20965,"P2",90.40137,23.792508,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-29","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-27","unknown","BDADAI-29.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,31.83,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"65",20966,"P2",90.40744,23.792508,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-29","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-27","unknown","BDADAI-29.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,30.46,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"66",20967,"P2",90.40916,23.792508,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-29","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-27","unknown","BDADAI-29.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","25.27",0,NA,31.15,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"67",21025,"P2",90.40165,23.792586,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-30","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Other","field ID certain","2017-01-27","unknown","BDADAI-30.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,29.77,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"68",21026,"P2",90.40272,23.792586,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7785,90.4054,"2017-01-
27","Dry","Dry",-0.887261,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan27","BDADAI-30","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Other","field ID certain","2017-01-27","unknown","BDADAI-30.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,31.51,NA,NA,"Positive","Interpretation

completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"69",21903,"P2",90.4144,23.82506,"Bangladesh","Yes","Dhaka-Mohakhali Hoque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7795,90.4034,"2017-01-21","Dry","Dry",-0.687761,"BD-Dhaka-Mohakhali Hoque Kacha Bazar-2017Jan21","BDADAI-30","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certain","2017-01-21","unknown","BDADAI-30.1ZY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5N1","other-Gerloff 2016","Positive","29.27",0,NA,29.53,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"70",21046,"P2",90.4166,23.82562,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7783,90.3988,"2017-01-21","Dry","Dry",-0.680445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAI-32","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-21","unknown","BDADAI-32.1ZY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,26.56,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"71",21047,"P2",90.4127,23.82562,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7783,90.3988,"2017-01-21","Dry","Dry",-0.680445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAI-32","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-21","unknown","BDADAI-32.1ZY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,27.49,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"72",21048,"P2",90.4145,23.82563,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7783,90.3988,"2017-01-21","Dry","Dry",-0.680445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAI-32","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-21","unknown","BDADAI-32.1ZY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,30.41,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"73",21050,"P2",90.4168,23.82559,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7783,90.3988,"2017-01-21","Dry","Dry",-0.680445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAI-35","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certain","2017-01-21","unknown","BDADAI-35.1ZY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,28.3,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"74",21051,"P2",90.4175,23.82558,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7783,90.3988,"2017-01-21","Dry","Dry",-0.680445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAI-35","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certain","2017-01-21","unknown","BDADAI-35.1ZY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,27.9,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"75",21052,"P2",90.4147,23.82558,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7783,90.3988,"2017-01-21","Dry","Dry",-0.680445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAI-35","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certain","2017-01-21","unknown","BDADAI-35.1ZY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,30.06,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"76",21038,"P2",90.4178,23.82684,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7821,90.371,"2017-01-23","Dry","Dry",-0.6085832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-38","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","hans","field ID certain","2017-01-23","unknown","BDADAI-38.1ZY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,23,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"77",21058,"P2",90.4185,23.82682,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7821,90.371,"2017-01-23","Dry","Dry",-0.6085832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-40","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-23","unknown","BDADAI-40.1ZY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,25.9,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"78",21059,"P2",90.4102,23.82682,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7821,90.371,"2017-01-23","Dry","Dry",-0.6085832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-40","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-23","unknown","BDADAI-40.1ZY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"79",21060,"P2",90.4074,23.82682,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7821,90.371,"2017-01-23","Dry","Dry",-0.6085832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-40","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-23","unknown","BDADAI-40.1ZY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,35.39,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"80",21408,"P2",90.4371,23.82681,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7821,90.371,"2017-01-23","Dry","Dry",-0.6085832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-41","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-01-23","unknown","BDADAI-41.1ZY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,26.56,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"81",21410,"P2",90.4321,23.82681,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7821,90.371,"2017-01-23","Dry","Dry",-0.6085832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-41","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-01-23","unknown","BDADAI-41.1ZY","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff 2016","Positive","28.56",0,NA,24.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"82",21524,"P2",90.4086,23.82638,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7235,90.4015,"2017-01-23","Dry","Dry",-0.6080078.2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-44","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-23","unknown","BDADAI-44.1ZY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research

(cddr.lc)","Real time PCR","other-Influenza A","other-Gen1ff 2385","Positive","27.29","0 NA 26.46 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"83","2968","PT",-90.975,23.9536,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.4125,"2017-01-23","Dry","Dry",-0.6669328,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADA6-46","poultry/other fowl","owned domesticated species","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhansh","Yield ID certain","2017-01-23","unknown","BDADA6-46.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A","other-Gen1ff 2385","Positive","27.29","0 NA 26.58 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"84","2969","PT",-90.9758,23.9536,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.4125,"2017-01-23","Dry","Dry",-0.6669328,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADA6-46","poultry/other fowl","owned domesticated species","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhansh","Yield ID certain","2017-01-23","unknown","BDADA6-46.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5a","other-Gen1ff 2385","Positive","28.87","0 NA 22.32 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"85","2992","PT",-90.9504,23.9536,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.4125,"2017-01-23","Dry","Dry",-0.6669328,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADA6-46","poultry/other fowl","owned domesticated species","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhansh","Yield ID certain","2017-01-23","unknown","BDADA6-46.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5a","other-Gen1ff 2385","Positive","29.27","0 NA 21.18 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"86","2997","PT",-90.9777,23.9537,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.4125,"2017-01-23","Dry","Dry",-0.6669328,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADA6-46","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Haans","Yield ID certain","2017-01-23","unknown","BDADA6-46.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A","other-Gen1ff 2385","Positive","27.29","0 NA 21.27 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"87","2978","PT",-90.9928,23.9537,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.4125,"2017-01-23","Dry","Dry",-0.6669328,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADA6-46","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Haans","Yield ID certain","2017-01-23","unknown","BDADA6-46.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5","other-Gen1ff 2385","Positive","26.57","0 NA 23.46 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"88","2176","PT",-90.9159,23.9269,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-58","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","Hans","Yield ID certain","2017-01-23","unknown","BDADA4-58.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A","other-Gen1ff 2385","Positive","27.29","0 NA 21.3 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"89","2177","PT",-90.9195,23.9269,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-58","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","Hans","Yield ID certain","2017-01-23","unknown","BDADA4-58.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5a","other-Gen1ff 2385","Positive","29.87","0 NA 24.29 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"90","2178","PT",-90.8858,23.9269,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-58","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","Hans","Yield ID certain","2017-01-23","unknown","BDADA4-58.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5a","other-Gen1ff 2385","Positive","29.27","0 NA 24.43 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"91","2933","PT",-90.9185,23.9544,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-51","poultry/other fowl","owned domesticated species","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhansh","Yield ID certain","2017-01-23","unknown","BDADA4-51.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A","other-Gen1ff 2385","Positive","27.29","0 NA 23.58 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"92","2938","PT",-90.8298,23.9544,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-51","poultry/other fowl","owned domesticated species","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhansh","Yield ID certain","2017-01-23","unknown","BDADA4-51.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5a","other-Gen1ff 2385","Positive","28.87","0 NA 20.74 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"93","2828","PT",-90.8858,23.9544,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-51","poultry/other fowl","owned domesticated species","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhansh","Yield ID certain","2017-01-23","unknown","BDADA4-51.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5a","other-Gen1ff 2385","Positive","27.27","0 NA 20.8 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"94","2868","PT",-90.9218,23.9548,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-54","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Deshi","Yield ID certain","2017-01-23","unknown","BDADA4-54.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A","other-Gen1ff 2385","Positive","27.29","0 NA 20.35 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"95","2867","PT",-90.9291,23.9548,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836,90.405,23.7225,90.3922,"2017-01-23","Dry","Dry",-0.7140282,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADA4-54","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Deshi","Yield ID certain","2017-01-23","unknown","BDADA4-54.CFX","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.lc)","Real time PCR","other-Influenza A/H5a","other-Gen1ff 2385","Positive","28.87","0 NA 22.69 NA NA","Positive","Interpretation completed","NA NA NA NA NA","ro","NA NA NA NA NA","EcoHealth Alliance"

"86","2868","FY","85468.2929948","Bangladesh","Yes","Dhaka New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7335.90.3822","2017-09-23","Dry","Dry",-0.7146853,2,"BD-Dhaka-New Market Bazar-23Jan23","BDADAI-54","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Duck","field ID certain","2017-01-23","unknown","BDADAI-54.CFY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","28.27","0.NA.0.0A.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"87","2845","FY","85787.2929848","Bangladesh","Yes","Dhaka New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7335.90.3822","2017-09-23","Dry","Dry",-0.7146853,2,"BD-Dhaka-New Market Bazar-23Jan23","BDADAI-56","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","hold ID certainty unknown","2017-09-23","unknown","BDADAI-56.CFY","other tissue-other","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28","0.NA.33.80.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"88","2848","FY","85239.2929948","Bangladesh","Yes","Dhaka New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7335.90.3822","2017-09-23","Dry","Dry",-0.7146853,2,"BD-Dhaka-New Market Bazar-23Jan23","BDADAI-56","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","hold ID certainty unknown","2017-09-23","unknown","BDADAI-56.CFY","other tissue-other","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","28.87","0.NA.24.40.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"89","2847","FY","85867.2929848","Bangladesh","Yes","Dhaka New Market Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7335.90.3822","2017-09-23","Dry","Dry",-0.7146853,2,"BD-Dhaka-New Market Bazar-23Jan23","BDADAI-56","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","hold ID certainty unknown","2017-09-23","unknown","BDADAI-56.CFY","other tissue-other","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","29.27","0.NA.33.85.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"100","23588","FY","86259.2929916","Bangladesh","Yes","Dhaka Kutir Pul Bazar","Independent Site","Dhaka Division","Dhaka","23.7822.90.405.23.7412.90.3855","2017-09-23","Dry","Dry",-0.8578832,2,"BD-Dhaka-Kutir Pul Bazar-23Jan23","BDADAI-87","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Foam","hold ID certain","2017-09-23","unknown","BDADAI-87.CFY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28","0.NA.21.87.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"101","2288","FY","85787.2929506","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-63","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","Feces","field ID certain","2017-09-23","unknown","BDADAI-63.CFY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28","0.NA.27.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"102","2291","FY","85793.2929508","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-63","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","Feces","field ID certain","2017-09-23","unknown","BDADAI-63.CFY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","28.27","0.NA.27.0.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"104","23035","FY","85392.2929506","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-62","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-09-23","unknown","BDADAI-62.CFY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28","0.NA.28.22.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"105","23021","FY","85230.2929506","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-62","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-09-23","unknown","BDADAI-62.CFY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","28.87","0.NA.31.25.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"106","23028","FY","85002.2929506","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-62","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-09-23","unknown","BDADAI-62.CFY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","29.27","0.NA.31.27.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"107","23031","FY","85194.2929505","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-65","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-23","unknown","BDADAI-65.CFY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28","0.NA.28.10.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"108","23032","FY","85229.2929505","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-65","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-23","unknown","BDADAI-65.CFY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","28.87","0.NA.30.NA.NA","Positive","Interpretation completed","NA.NA.NA.NA.NA","no","NA.NA.NA.NA.NA","EcoHealth Alliance"
"109","23033","FY","85093.2929505","Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka","23.7836.90.405.23.7526.90.4082","2017-09-23","Dry","Dry",-0.7799841,"BD-Dhaka-Mog Bazar-23Jan23","BDADAI-65","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-23","unknown","BDADAI-65.CFY","urine/feces combined (guano)","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5v","other-Gerloff 2018","Positive","29.27","0.NA.31.13.NA.NA","Positive","Interpretation

completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"110",22942,"P2",80188,2925083,"Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7526,90.4082,"2017-01-23","Dry","Dry",-0.7789841,"BD-Dhaka-Mog Bazar-2017Jan23","BDAIDAI-08","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","held ID certainty unknown","2017-01-23","unknown","BDAIDAI-08.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,29.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"111",22943,"P2",80294,2925083,"Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7526,90.4082,"2017-01-23","Dry","Dry",-0.7789841,"BD-Dhaka-Mog Bazar-2017Jan23","BDAIDAI-08","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","held ID certainty unknown","2017-01-23","unknown","BDAIDAI-08.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.07",0,NA,31.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"112",22944,"P2",80087,2925083,"Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7526,90.4082,"2017-01-23","Dry","Dry",-0.7789841,"BD-Dhaka-Mog Bazar-2017Jan23","BDAIDAI-08","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","held ID certainty unknown","2017-01-23","unknown","BDAIDAI-08.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,29.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"113",22964,"P2",80198,2925674,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-72","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","hens","held ID certain","2017-01-23","unknown","BDAIDAI-72.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,30.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"114",22965,"P2",80296,2925674,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-72","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","hens","held ID certain","2017-01-23","unknown","BDAIDAI-72.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.07",0,NA,32.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"115",22968,"P2",80308,2925674,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-72","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck","hens","held ID certain","2017-01-23","unknown","BDAIDAI-72.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,33.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"116",22970,"P2",80198,2925673,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-73","poultry/other fowl","owned domesticated species ","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhasi","held ID certain","2017-01-23","unknown","BDAIDAI-73.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,26.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"117",22971,"P2",80297,2925673,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-73","poultry/other fowl","owned domesticated species ","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhasi","held ID certain","2017-01-23","unknown","BDAIDAI-73.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.07",0,NA,31.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"118",22972,"P2",80078,2925673,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-73","poultry/other fowl","owned domesticated species ","Anser anser domesticus","Anser anser domesticus","species","Domestic Goose","Rajhasi","held ID certain","2017-01-23","unknown","BDAIDAI-73.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,33.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"119",22975,"P2",80308,2925672,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-74","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler","held ID certain","2017-01-23","unknown","BDAIDAI-74.22V","urine/feces combined (guano)","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,32.01,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"120",22980,"P2",80302,2925670,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-76","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Deshi","held ID certain","2017-01-23","unknown","BDAIDAI-76.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,33.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"121",22981,"P2",80298,2925670,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-76","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Deshi","held ID certain","2017-01-23","unknown","BDAIDAI-76.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.07",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"122",22982,"P2",80071,2925670,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-76","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Deshi","held ID certain","2017-01-23","unknown","BDAIDAI-76.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,36.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"123",22983,"P2",80193,2925668,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.7765653,"BD-Dhaka-Kawran Bazar-2017Jan23","BDAIDAI-78","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","held ID certainty unknown","2017-01-23","unknown","BDAIDAI-78.22V","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,26.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"124",22186,"P1",860359,2925948,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7765652,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-78","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-23","unknown","BDADAI-78.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,34.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"125",22187,"P1",860377,2925868,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-
0.7765652,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAI-78","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-23","unknown","BDADAI-78.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,32.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"126",22185,"P1",862165,2925888,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7921,90.371,"2017-01-23","Dry","Dry",-
0.8885832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-80","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-80.LTV","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,31.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"127",22206,"P1",862186,2925878,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7921,90.371,"2017-01-23","Dry","Dry",-
0.8885832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-82","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-23","unknown","BDADAI-82.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,34.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"128",22202,"P1",862187,2925877,"Bangladesh","Yes","Dhaka-Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7921,90.371,"2017-01-23","Dry","Dry",-
0.8885832,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAI-83","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-83.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,30.32,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"129",22222,"P1",862100,2925929,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7725,90.4079,"2017-01-23","Dry","Dry",-
0.8889292,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-88","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-88.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,37.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"130",22273,"P1",860305,2925929,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7725,90.4079,"2017-01-23","Dry","Dry",-
0.8889292,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-89","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-89.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,35.11,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"131",22274,"P1",860978,2925929,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7725,90.4079,"2017-01-23","Dry","Dry",-
0.8889292,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-89","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-89.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,25.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"132",22277,"P1",862230,2925928,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7725,90.4079,"2017-01-23","Dry","Dry",-
0.8889292,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-89","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-89.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,31.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"133",22278,"P1",860306,2925928,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7725,90.4079,"2017-01-23","Dry","Dry",-
0.8889292,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-89","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-89.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,33.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"134",22279,"P1",860978,2925928,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7725,90.4079,"2017-01-23","Dry","Dry",-
0.8889292,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-89","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-89.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,25.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"135",22238,"P1",862201,2925927,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7725,90.4079,"2017-01-23","Dry","Dry",-
0.8889292,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAI-90","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-90.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,31.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"136",22244,"P1",862202,2925941,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7335,90.3822,"2017-01-23","Dry","Dry",-
0.7748032,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAI-92","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-92.LTV","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,22.17,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"137",22245,"P1",860308,2925943,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7335,90.3822,"2017-01-23","Dry","Dry",-
0.7748032,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAI-92","poultry/other fowl","owned domesticated species","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-92.LTV","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,26.47,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"138",22246,"P1",860308,2925943,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7335,90.3822,"2017-01-23","Dry","Dry",-
0.7748032,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAI-92","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAI-92.LTV","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,25,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"139",22248,"P1",862303,2925950,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7335,90.3822,"2017-01-23","Dry","Dry",-
0.7748032,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAI-95","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-01-24","unknown","BDADAI-95.LTV","other tissue-offal","2017-02-08","International Centre for Diarrhoeal

Disease Research (cddr.bi)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28",0.NA,33.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22250","PT",90.0000,23.2925,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7235,90.3822,"2017-09-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jun23","BDADAI-92","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-92.CLY","other tissue-sifal","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2018","Positive","28.87",0.NA,0.NA,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22250","PT",90.0987,23.2925,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7235,90.3822,"2017-09-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jun23","BDADAI-93","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-93.CLY","other tissue-sifal","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2018","Positive","29.27",0.NA,33.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22250","PT",90.2204,23.2925,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7235,90.3822,"2017-09-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jun23","BDADAI-95","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-95.CLY","other tissue-sifal","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28",0.NA,29.93,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22250","PT",90.0988,23.2925A,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7235,90.3822,"2017-09-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jun23","BDADAI-96","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-96.CLY","other tissue-sifal","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2018","Positive","28.87",0.NA,29.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22252","PT",90.0981,23.2925A,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7235,90.3822,"2017-09-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jun23","BDADAI-98","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-98.CLY","other tissue-sifal","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2018","Positive","29.27",0.NA,28.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22288","PT",90.2205,23.2913,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7873,90.405,23.7427,90.3855,"2017-09-23","Dry","Dry",-0.8578022,2,"BD-Dhaka-Hatir Pul Bazar-2017Jun23","BDADAI-99","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-99.CLY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28",0.NA,35.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22287","PT",90.038,23.2913,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7873,90.405,23.7427,90.3855,"2017-09-23","Dry","Dry",-0.8578022,2,"BD-Dhaka-Hatir Pul Bazar-2017Jun23","BDADAI-99","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-99.CLY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2018","Positive","28.87",0.NA,27.66,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22288","PT",90.0984,23.2913,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7873,90.405,23.7427,90.3855,"2017-09-23","Dry","Dry",-0.8578022,2,"BD-Dhaka-Hatir Pul Bazar-2017Jun23","BDADAI-99","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-99.CLY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2018","Positive","29.27",0.NA,30.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22277","PT",90.0799,23.2913,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7873,90.405,23.7427,90.3855,"2017-09-23","Dry","Dry",-0.8578022,2,"BD-Dhaka-Hatir Pul Bazar-2017Jun23","BDADAI-99","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Other","Valid ID certainty unknown","2017-09-24","unknown","BDADAI-99.CLY","other tissue-sifal","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28",0.NA,33.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22145","PT",90.2078,23.2685,"Bangladesh","Yes","Dhaka-Badda Bonabata Bazar","Independent Site","Dhaka Division","Dhaka",23.7838,90.405,23.7238,90.3825,"2017-09-21","Dry","Dry",-0.7370021,1,"BD-Dhaka-Badda Bonabata Bazar-2017Jun21","BDADAP-01","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","Valid ID certainty unknown","2017-09-21","unknown","BDADAP-01.CLY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28",0.NA,28.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22420","PT",90.2102,23.2568,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7838,90.405,23.7159,90.426,"2017-09-21","Dry","Dry",-0.697216,1,"BD-Dhaka-Badda Kacha Bazar-2017Jun21","BDADAP-02","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","Valid ID certainty unknown","2017-09-21","unknown","BDADAP-02.CLY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A","other-Gerloff 2018","Positive","27.28",0.NA,28.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22420","PT",90.2105,23.2568,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7838,90.405,23.7159,90.434,"2017-09-21","Dry","Dry",-0.697216,1,"BD-Dhaka-Badda Kacha Bazar-2017Jun21","BDADAP-02","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","Valid ID certainty unknown","2017-09-21","unknown","BDADAP-02.CLY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2018","Positive","28.87",0.NA,29.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"NA","22420","PT",90.0939,23.2568,"Bangladesh","Yes","Dhaka-Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7838,90.405,23.7159,90.434,"2017-09-21","Dry","Dry",-0.697216,1,"BD-Dhaka-Badda Kacha Bazar-2017Jun21","BDADAP-02","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","Valid ID certainty unknown","2017-09-21","unknown","BDADAP-02.CLY","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (cddr.bi)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2018","Positive","29.27",0.NA,27.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"sp",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"153",22425,"PT",90.4093,23.8025,"Bangladesh","Yes","Dhaka-North Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.78,90.42,23.8025,90.5618,"2017-01-21","Dry","Dry",-0.0548011,"BD-Dhaka-North Badda Kacha Bazar-2017Jan21","BDADAP-03","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-03.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,23.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"154",22430,"PT",90.4094,23.7918,"Bangladesh","Yes","Dhaka-North Badda Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.79,90.42,23.8025,90.5838,"2017-01-21","Dry","Dry",-0.0548011,"BD-Dhaka-North Badda Kacha Bazar-2017Jan21","BDADAP-04","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-04.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,21.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"155",22435,"PT",90.4095,23.7975,"Bangladesh","Yes","Dhaka-Gulshan DNCC Kacha Bazar 2","Independent Site","Dhaka Division","Dhaka",23.7828,90.405,23.7948,90.4155,"2017-01-21","Dry","Dry",-0.0880441,"BD-Dhaka-Gulshan DNCC Kacha Bazar-2-2017Jan21","BDADAP-05","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-05.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,31.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"156",22440,"PT",90.4096,23.7582,"Bangladesh","Yes","Dhaka-Banani Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7826,90.405,23.7933,90.4094,"2017-01-21","Dry","Dry",-0.7795511,"BD-Dhaka-Banani Kacha Bazar-2017Jan21","BDADAP-06","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-06.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,22.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"157",22445,"PT",90.4097,23.7563,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7837,90.4066,"2017-01-21","Dry","Dry",-0.7795511,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDADAP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-07.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,24.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"158",22448,"PT",.179868,23.7563,"Bangladesh","Yes","Dhaka-Banani Bou Bazar","Independent Site","Dhaka Division","Dhaka",23.7838,90.405,23.7837,90.4066,"2017-01-21","Dry","Dry",-0.7795511,"BD-Dhaka-Banani Bou Bazar-2017Jan21","BDADAP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-07.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","26.51",0,NA,27.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"158",22450,"PT",.90718,23.7595,"Bangladesh","Yes","Dhaka-Mohakhali Haque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7795,90.4054,"2017-01-21","Dry","Dry",-0.0872961,"BD-Dhaka-Mohakhali Haque Kacha Bazar-2017Jan21","BDADAP-08","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-08.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,21.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"160",22454,"PT",.900275,23.7595,"Bangladesh","Yes","Dhaka-Mohakhali Haque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7795,90.4054,"2017-01-21","Dry","Dry",-0.0872961,"BD-Dhaka-Mohakhali Haque Kacha Bazar-2017Jan21","BDADAP-08","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-08.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,23.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"161",22452,"PT",.900297,23.7595,"Bangladesh","Yes","Dhaka-Mohakhali Haque Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7795,90.4054,"2017-01-21","Dry","Dry",-0.0872961,"BD-Dhaka-Mohakhali Haque Kacha Bazar-2017Jan21","BDADAP-08","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-08.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,30.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"162",22455,"PT",.90765,23.7558,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7838,90.405,23.7793,90.3888,"2017-01-21","Dry","Dry",-0.0880445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAP-09","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-09.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,22.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"163",22456,"PT",.900276,23.7558,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7838,90.405,23.7793,90.3888,"2017-01-21","Dry","Dry",-0.0880445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAP-09","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-09.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,24.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"164",22457,"PT",.900298,23.7558,"Bangladesh","Yes","Dhaka-Mohakhali Kacha Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7793,90.3888,"2017-01-21","Dry","Dry",-0.0880445,"BD-Dhaka-Mohakhali Kacha Bazar-2017Jan21","BDADAP-09","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-21","unknown","BDADAP-09.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,33.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"165",22460,"PT",.90920,23.7976,"Bangladesh","Yes","Dhaka Ananda Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7921,90.371,"2017-01-23","Dry","Dry",-0.0885812,"BD-Dhaka-Ananda Bazar-2017Jan23","BDADAP-10","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDADAP-10.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,28.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"166",22465,"PT",.90721,23.7929,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7725,90.429,"2017-01-23","Dry","Dry",-0.0880929,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAP-11","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic

Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDADAIP-1.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,30.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"167",22470,"P1",80202.292625,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7225,90.4219,"2017-01-23","Dry","Dry",-
0.6668928,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAIP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDADAIP-07.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,31.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"168",22471,"P1",80226.292675,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7775,90.4215,"2017-01-23","Dry","Dry",-
0.6668928,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAIP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDADAIP-07.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"169",22472,"P1",80088.292825,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7775,90.4219,"2017-01-23","Dry","Dry",-
0.6668928,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAIP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDADAIP-07.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.77",0,NA,23.74,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"170",22480,"P1",86678.258801,"Bangladesh","Yes","Dhamrai-Dhamrai Puran Bazar","Independent Site","Dhaka Division","Dhaka",23.9084,90.212,23.9084,90.212,"2017-02-15","Dry","Dry",-
0.9378781,1,"BD-Dhamrai-Dhamrai Puran Bazar-2017Feb15","BDADAIP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-15","unknown","BDADAIP-03.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.8",0,NA,29.01,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"171",22484,"P1",87952.258801,"Bangladesh","Yes","Dhamrai-Dhamrai Puran Bazar","Independent Site","Dhaka Division","Dhaka",23.9084,90.212,23.9084,90.212,"2017-02-15","Dry","Dry",-
0.9378781,1,"BD-Dhamrai-Dhamrai Puran Bazar-2017Feb15","BDADAIP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-15","unknown","BDADAIP-03.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","27.45",0,NA,0,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"172",22488,"P1",86782.258810,"Bangladesh","Yes","Dhamrai-Dhamrai Puran Bazar","Independent Site","Dhaka Division","Dhaka",23.9084,90.212,23.9084,90.212,"2017-02-15","Dry","Dry",-
0.9378781,1,"BD-Dhamrai-Dhamrai Puran Bazar-2017Feb15","BDADAIP-03","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-02-15","unknown","BDADAIP-03.22V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.01",0,NA,29.31,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"173",22495,"P1",86753.258810,"Bangladesh","Yes","Dhamrai-Dhamrai Puran Bazar","Independent Site","Dhaka Division","Dhaka",23.9084,90.212,23.9084,90.212,"2017-02-15","Dry","Dry",-
0.9378781,1,"BD-Dhamrai-Dhamrai Puran Bazar-2017Feb15","BDADAIP-03","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-02-15","unknown","BDADAIP-03.22V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","27.45",0,NA,0,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"174",22507,"P1",86795.298803,"Bangladesh","Yes","Dhamrai-Amtola Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.8768,90.1823,"2017-02-15","Dry","Dry",-
0.9268881,1,"BD-Dhamrai-Amtola Bazar-2017Feb15","BDADAIP-05","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-15","unknown","BDADAIP-05.22V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.01",0,NA,30.03,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"175",22516,"P1",87956.298803,"Bangladesh","Yes","Dhamrai-Amtola Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.8768,90.1823,"2017-02-15","Dry","Dry",-
0.9268881,1,"BD-Dhamrai-Amtola Bazar-2017Feb15","BDADAIP-05","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-15","unknown","BDADAIP-06.22V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","27.45",0,NA,0,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"176",22555,"P1",86678.298870,"Bangladesh","Yes","Dhamrai-Dopachai Council Market","Independent Site","Dhaka Division","Dhaka",23.8267,90.0774,23.8267,90.0774,"2017-02-
15","Dry","Dry",-0.9375991,1,"BD-Dhamrai-Dopachai Council Market-2017Feb15","BDADAIP-02","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-15","unknown","BDADAIP-02.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.8",0,NA,29.97,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"177",22559,"P1",87862.298870,"Bangladesh","Yes","Dhamrai-Dopachai Council Market","Independent Site","Dhaka Division","Dhaka",23.8267,90.0774,23.8267,90.0774,"2017-02-
15","Dry","Dry",-0.9375991,1,"BD-Dhamrai-Dopachai Council Market-2017Feb15","BDADAIP-02","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-15","unknown","BDADAIP-02.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","27.45",0,NA,0,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"178",22560,"P1",86793.298871,"Bangladesh","Yes","Dhamrai-Islampur Bazar","Independent Site","Dhaka Division","Dhaka",23.9407,90.2776,23.9407,90.2776,"2017-02-15","Dry","Dry",-
0.9346911,1,"BD-Dhamrai-Islampur Bazar-2017Feb15","BDADAIP-03","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-15","unknown","BDADAIP-03.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.8",0,NA,23.78,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"179",22588,"P1",86786.299903,"Bangladesh","Yes","Dhamrai-Sutipara-Bathuli Bazar","Independent Site","Dhaka Division","Dhaka",23.94,90.0977,23.94,90.0977,"2017-02-20","Dry","Dry",-
0.9302761,1,"BD-Dhamrai-Sutipara-Bathuli Bazar-2017Feb20","BDADAIP-07","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-20","unknown","BDADAIP-07.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.8",0,NA,33.37,NA,NA,"Positive","Interpretation

completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"180",22580,"PY",(0)787,2539803,"Bangladesh","Yes","Dhamrai-Satipara-Bathuli Bazar","Independent Site","Dhaka Division","Dhaka",23.94,90.0371,23.94,90.0371,"2017-02-20","Dry","Dry",-0.939295,1,"BD-Dhamrai-Satipara-Bathuli Bazar-2017Feb20","BDAIAIP-127","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-20","unknown","BDAIAIP-127.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","27.45",0,NA,0,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"181",22583,"PY",(0)6797,300293,"Bangladesh","Yes","Dhamrai-Gonguta-Barbaria Bazar","Independent Site","Dhaka Division","Dhaka",23.9806,90.0606,23.9806,90.0606,"2017-03-
20","Dry","Dry",1.70795,1,"BD-Dhamrai-Gonguta-Barbaria Bazar-2017Mar20","BDAIAIP-128","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-03-20","unknown","BDAIAIP-128.CLV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.9",0,NA,23.94,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"182",22610,"PY",(0)2124,2929152,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7335,90.3832,"2017-01-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDAIAIP-14","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDAIAIP-14.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,33.57,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"183",22611,"PY",(0)3733,2929152,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7335,90.3832,"2017-01-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDAIAIP-14","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDAIAIP-14.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,27.83,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"184",22612,"PY",(0)0103,2929152,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7636,90.405,23.7335,90.3832,"2017-01-23","Dry","Dry",-0.774803,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDAIAIP-14","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDAIAIP-14.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,29.8,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"185",22647,"PY",(0)6804,2027(0)7,"Bangladesh","Yes","Savar-Amin Bazar","Independent Site","Dhaka Division","Dhaka",23.7863,90.3295,23.7863,90.3295,"2017-02-20","Dry","Dry",-0.905251,"BD-Savar-Amin Bazar-2017Feb20","BDAIAIP-145","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck","Duck","field ID certain","2017-02-20","unknown","BDAIAIP-145.GUV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.9",0,NA,25.48,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"186",22648,"PY",(0)0325,280757,"Bangladesh","Yes","Savar-Amin Bazar","Independent Site","Dhaka Division","Dhaka",23.7863,90.3295,23.7863,90.3295,"2017-02-20","Dry","Dry",-0.905251,"BD-Savar-Amin Bazar-2017Feb20","BDAIAIP-145","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck","Duck","field ID certain","2017-02-20","unknown","BDAIAIP-145.GUV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.47",0,NA,25.48,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"187",22649,"PY",(0)8043,300757,"Bangladesh","Yes","Savar-Amin Bazar","Independent Site","Dhaka Division","Dhaka",23.7863,90.3295,23.7863,90.3295,"2017-02-20","Dry","Dry",-0.905251,"BD-Savar-Amin Bazar-2017Feb20","BDAIAIP-145","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck","Duck","field ID certain","2017-02-20","unknown","BDAIAIP-145.GUV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.2",0,NA,30.37,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"188",22675,"PY",(0)0807,300332,"Bangladesh","Yes","Savar-Bhakurta-Sidai Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7693,90.3085,23.7693,90.3085,"2017-02-
20","Dry","Dry",-0.905251,"BD-Savar-Bhakurta-Sidai Market Bazar-2017Feb20","BDAIAIP-148","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-20","unknown","BDAIAIP-148.GUV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.9",0,NA,25.68,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"189",22681,"PY",(0)6808,300394,"Bangladesh","Yes","Savar-Bangaon-Kunda Bazar","Independent Site","Dhaka Division","Dhaka",23.802,90.2938,23.802,90.2938,"2017-02-20","Dry","Dry",-0.925525,1,"BD-Savar-Bangaon-Kunda Bazar-2017Feb20","BDAIAIP-149","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-20","unknown","BDAIAIP-149.GUV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.9",0,NA,31.48,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"190",22682,"PY",(0)9330,300394,"Bangladesh","Yes","Savar-Bangaon-Kunda Bazar","Independent Site","Dhaka Division","Dhaka",23.802,90.2938,23.802,90.2938,"2017-02-20","Dry","Dry",-0.925525,1,"BD-Savar-Bangaon-Kunda Bazar-2017Feb20","BDAIAIP-149","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-20","unknown","BDAIAIP-149.GUV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.47",0,NA,31.46,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"191",22683,"PY",(0)3048,300394,"Bangladesh","Yes","Savar-Bangaon-Kunda Bazar","Independent Site","Dhaka Division","Dhaka",23.802,90.2938,23.802,90.2938,"2017-02-20","Dry","Dry",-0.925525,1,"BD-Savar-Bangaon-Kunda Bazar-2017Feb20","BDAIAIP-149","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2017-02-20","unknown","BDAIAIP-149.GUV","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.2",0,NA,31.8,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"192",22686,"PY",(0)315,2929672,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7423,90.405,23.7423,90.3955,"2017-01-23","Dry","Dry",-0.057803,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDAIAIP-15","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-23","unknown","BDAIAIP-15.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,29.16,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"193",22687,"PY",(0)332,2929672,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7423,90.405,23.7423,90.3955,"2017-01-23","Dry","Dry",-

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0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-15","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAP-15.1.1V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,31.35,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"194",27088,"P2",90.4094,23.7627,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7872,90.405,23.7422,90.3855,"2017-01-23","Dry","Dry",-
0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-15","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAP-15.1.1V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,29.48,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"195",22691,"P2",90.6808,23.8829,"Bangladesh","Yes","Savar-Tetuljhora-Hemayetpur Bazar","Independent Site","Dhaka Division","Dhaka",23.7328,90.2798,23.7328,90.2798,"2017-02-
20","Dry","Dry",-0.394278,1,"BD-Savar-Tetuljhora-Hemayetpur Bazar-2017Feb20","BDADAP-150","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certain","2017-02-20","unknown","BDADAP-150.2.1V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.51",0,NA,29.88,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"196",22605,"P2",87180,200281,"Bangladesh","Yes","Savar-Tetuljhora-Hemayetpur Bazar","Independent Site","Dhaka Division","Dhaka",23.7328,90.2798,23.7328,90.2798,"2017-02-
20","Dry","Dry",-0.394278,1,"BD-Savar-Tetuljhora-Hemayetpur Bazar-2017Feb20","BDADAP-150","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certain","2017-02-20","unknown","BDADAP-150.2.1V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","27.45",0,NA,3,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"197",22702,"P2",86802,300298,"Bangladesh","Yes","Savar-Tetuljhora-Hemayetpur Bazar","Independent Site","Dhaka Division","Dhaka",23.7328,90.2798,23.7328,90.2798,"2017-02-
20","Dry","Dry",-0.394278,1,"BD-Savar-Tetuljhora-Hemayetpur Bazar-2017Feb20","BDADAP-153","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certain","2017-02-20","unknown","BDADAP-153.2.1V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.51",0,NA,31.05,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"198",22714,"P2",170334,300398,"Bangladesh","Yes","Savar-Tetuljhora-Hemayetpur Bazar","Independent Site","Dhaka Division","Dhaka",23.7328,90.2798,23.7328,90.2798,"2017-02-
20","Dry","Dry",-0.394278,1,"BD-Savar-Tetuljhora-Hemayetpur Bazar-2017Feb20","BDADAP-153","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certain","2017-02-20","unknown","BDADAP-153.2.1V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.42",0,NA,31.09,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"199",22715,"P2",985350,300398,"Bangladesh","Yes","Savar-Tetuljhora-Hemayetpur Bazar","Independent Site","Dhaka Division","Dhaka",23.7328,90.2798,23.7328,90.2798,"2017-02-
20","Dry","Dry",-0.394278,1,"BD-Savar-Tetuljhora-Hemayetpur Bazar-2017Feb20","BDADAP-153","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certain","2017-02-20","unknown","BDADAP-153.2.1V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.2",0,NA,28.8,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"200",22717,"P2",167183,300398,"Bangladesh","Yes","Savar-Tetuljhora-Hemayetpur Bazar","Independent Site","Dhaka Division","Dhaka",23.7328,90.2798,23.7328,90.2798,"2017-02-
20","Dry","Dry",-0.394278,1,"BD-Savar-Tetuljhora-Hemayetpur Bazar-2017Feb20","BDADAP-153","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certain","2017-02-20","unknown","BDADAP-153.2.1V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","27.45",0,NA,3,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"201",22746,"P2",96085,219902,"Bangladesh","Yes","Savar-Genda Bazar","Independent Site","Dhaka Division","Dhaka",23.8342,90.2583,23.8342,90.2583,"2017-02-20","Dry","Dry",-
0.5218501,1,"BD-Savar-Genda Bazar-2017Feb20","BDADAP-156","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","held ID certainty unknown","2017-02-20","unknown","BDADAP-156.2.1V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","28.51",0,NA,33.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"202",22762,"P2",82026,292621,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7872,90.405,23.7422,90.3855,"2017-01-23","Dry","Dry",-
0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-16","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAP-16.1.1V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,27.13,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"203",22763,"P2",802353,292621,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7872,90.405,23.7422,90.3855,"2017-01-23","Dry","Dry",-
0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-16","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAP-16.1.1V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,28.73,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"204",22764,"P2",803005,292621,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7872,90.405,23.7422,90.3855,"2017-01-23","Dry","Dry",-
0.6578032,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-16","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAP-16.1.1V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,23.31,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"205",23803,"P2",802077,292602,"Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7526,90.4062,"2017-01-23","Dry","Dry",-
0.7799841,1,"BD-Dhaka-Mog Bazar-2017Jan23","BDADAP-17","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAP-17.2.1V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,27.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"206",23832,"P2",880734,297902,"Bangladesh","Yes","Dhaka-Mog Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7526,90.4062,"2017-01-23","Dry","Dry",-
0.7799841,1,"BD-Dhaka-Mog Bazar-2017Jan23","BDADAP-17","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAP-17.2.1V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research

(cddr.b)","Real time PCR","other-Influenza A/H5a","other-Gen6eff 2395","Positive","28.07","0.NA.25.4.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"207","27803,"PT","81909.2526.02,"Bangladesh","Yes","Dhaka-Mag Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.90.405.23.7526.80.4082,"2017-09-23","Dry","Dry",-
0.7199841,"BD-Dhaka-Mag Bazar-2017Jan23","BDADAIP-07","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-07.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A/H5a","other-Gen6eff 2016","Positive","29.27","0.NA.28.28.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"208","27835,"PT","78978.2935.02,"Bangladesh","Yes","Dhaka-Mag Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.90.405.23.7526.80.4082,"2017-09-23","Dry","Dry",-
0.7199841,"BD-Dhaka-Mag Bazar-2017Jan23","BDADAIP-07","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-07.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A/H5","other-Gen6eff 2395","Positive","28.57","0.NA.29.27.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"209","27863,"PT","80833.2959.78,"Bangladesh","Yes","Savar-Cantonment Bazar","Independent Site","Dhaka Division","Dhaka","23.9108.80.2505.23.9126.80.2508,"2017-03-20","Dry","Dry",-
0.9223904,"BD-Savar-Cantonment Bazar-2017Feb20","BDADAIP-174","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certainty unknown","2017-03-20","unknown","BDADAIP-174.22V","other tissue-offal","2017-03-29","International Centre for
Diarrhoeal Disease Research (cddr.b)","Real time PCR","other-Influenza A","other-Gen6eff 2016","Positive","29.81","0.NA.29.33.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"210","27869A,"PT","79355.2958.78,"Bangladesh","Yes","Savar-Cantonment Bazar","Independent Site","Dhaka Division","Dhaka","23.9035.80.2519.23.9030.80.2518,"2017-03-20","Dry","Dry",-
0.9221904,"BD-Savar-Cantonment Bazar-2017Feb20","BDADAIP-174","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certainty unknown","2017-03-20","unknown","BDADAIP-174.22V","other tissue-offal","2017-03-29","International Centre for
Diarrhoeal Disease Research (cddr.b)","Real time PCR","other-Influenza A/H5a","other-Gen6eff 2016","Positive","29.47","0.NA.29.33.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"211","27865,"PT","80371.2958.78,"Bangladesh","Yes","Savar-Cantonment Bazar","Independent Site","Dhaka Division","Dhaka","23.9035.80.2519.23.9030.80.2518,"2017-03-20","Dry","Dry",-
0.9221904,"BD-Savar-Cantonment Bazar-2017Feb20","BDADAIP-174","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","held ID certainty unknown","2017-03-20","unknown","BDADAIP-174.22V","other tissue-offal","2017-03-29","International Centre for
Diarrhoeal Disease Research (cddr.b)","Real time PCR","other-Influenza A/H5a","other-Gen6eff 2016","Positive","30.2","0.NA.29.53.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"212","27807,"PT","80729.2929.03,"Bangladesh","Yes","Dhaka-Mag Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.90.405.23.7526.80.4082,"2017-09-23","Dry","Dry",-0.7199841,"BD-
Dhaka-Mag Bazar-2017Jan23","BDADAIP-08","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-08.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A","other-Gen6eff 2395","Positive","27.29","0.NA.28.82.NA.NA,"Positive","Interpretation completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth
Alliance"
"213","27808,"PT","80225.2929.03,"Bangladesh","Yes","Dhaka-Mag Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.90.405.23.7526.80.4082,"2017-09-23","Dry","Dry",-
0.7199841,"BD-Dhaka-Mag Bazar-2017Jan23","BDADAIP-08","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-08.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A/H5a","other-Gen6eff 2395","Positive","28.07","0.NA.27.53.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"214","27805,"PT","80107.2929.03,"Bangladesh","Yes","Dhaka-Mag Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.90.405.23.7526.80.4082,"2017-09-23","Dry","Dry",-
0.7199841,"BD-Dhaka-Mag Bazar-2017Jan23","BDADAIP-08","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-08.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A/H3a","other-Gen6eff 2016","Positive","29.27","0.NA.29.37.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"215","27872,"PT","80218.2929.90,"Bangladesh","Yes","Dhaka-Sat Rasta Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.80.405.23.7567.90.2885,"2017-09-23","Dry","Dry",-
0.6850081,"BD-Dhaka-Sat Rasta Bazar-2017Jan23","BDADAIP-05","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAIP-05.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (cddr.b)","Real time PCR","other-Influenza A","other-Gen6eff 2016","Positive","27.29","0.NA.41.27.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"216","27826,"PT","79980.2929.90,"Bangladesh","Yes","Dhaka-Sat Rasta Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.80.405.23.7567.90.2885,"2017-09-23","Dry","Dry",-
0.6850081,"BD-Dhaka-Sat Rasta Bazar-2017Jan23","BDADAIP-05","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-23","unknown","BDADAIP-05.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (cddr.b)","Real time PCR","other-Influenza A/H9","other-Gen6eff 2396","Positive","29.57","0.NA.0.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"217","27832,"PT","80213.2929.57,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.80.405.23.7521.90.2944,"2017-09-23","Dry","Dry",-
0.7165651,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAIP-21","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-21.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A","other-Gen6eff 2396","Positive","27.29","0.NA.29.28.NA.NA,"Positive","Interpretation completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth
Alliance"
"218","27833,"PT","80238.2929.57,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.90.405.23.7521.90.2944,"2017-09-23","Dry","Dry",-
0.7165651,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAIP-21","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-21.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A/H5a","other-Gen6eff 2395","Positive","29.87","0.NA.34.88.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"
"219","27852A,"PT","80260.2929.57,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka","23.7636.90.405.23.7521.90.2944,"2017-09-23","Dry","Dry",-
0.7165651,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAIP-21","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","held ID certainty unknown","2017-09-23","unknown","BDADAIP-21.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(cddr.b)","Real time PCR","other-Influenza A/H3a","other-Gen6eff 2016","Positive","29.27","0.NA.32.47.NA.NA,"Positive","Interpretation
completed","NA.NA.NA.NA.NA,"na","NA.NA.NA.NA.NA,"EcoHealth Alliance"

"220",22937,"PT",90332.505098,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7225,90.4029,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAP-23","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-23.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,22.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"221",22938,"PT",90339.505095,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7225,90.4029,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAP-23","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-23.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,22.73,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"222",22939,"PT",90091.505095,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7225,90.4029,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAP-23","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-23.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,22.86,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"223",22942,"PT",90133.505098,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7225,90.4029,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAP-24","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-24.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.29",0,NA,20.72,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"224",22943,"PT",90240.505098,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7225,90.4029,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAP-24","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-24.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,24.18,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"225",22944,"PT",90092.505098,"Bangladesh","Yes","Dhaka-Kaptan Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7225,90.4029,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Kaptan Bazar-2017Jan23","BDADAP-24","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-24.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,22.43,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"226",22947,"PT",90704.505097,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7335,90.3872,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAP-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-25.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,21.88,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"227",22948,"PT",90074.505097,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7335,90.3872,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAP-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-25.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,0,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"228",22949,"PT",90093.505097,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7335,90.3872,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAP-25","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-25.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,27.43,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"229",22952,"PT",90705.505098,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7335,90.3872,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAP-26","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-26.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,26.72,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"230",22953,"PT",90042.505098,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7335,90.3872,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAP-26","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-26.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,30.05,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"231",22954,"PT",90094.505098,"Bangladesh","Yes","Dhaka-New Market Bazar","Independent Site","Dhaka Division","Dhaka",23.7036,90.405,23.7335,90.3872,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-New Market Bazar-2017Jan23","BDADAP-26","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-26.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,27.34,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"232",22957,"PT",90706.505095,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7923,90.405,23.7422,90.3855,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-27","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Mixed","field ID certainty unknown","2017-01-24","unknown","BDADAP-27.22V","urine/feces combined (guano)","2017-02-08","International Centre
for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,20.1,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"233",22958,"PT",90743.505095,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7923,90.405,23.7422,90.3855,"2017-01-23","Dry","Dry",-
0.779076,2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-27","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus

domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-24","unknown","BDADAP-27.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,24.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"234",22958,"P2",90095.505095,"Bangladesh","Yes","Dhaka-Hatir Pul Bazar","Independent Site","Dhaka Division","Dhaka",23.7823,90.405,23.7423,90.3855,"2017-01-23","Dry","Dry",-0.770776.2,"BD-Dhaka-Hatir Pul Bazar-2017Jan23","BDADAP-27","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-24","unknown","BDADAP-27.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.27",0,NA,23.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"235",22962,"P2",90700.505094,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.770776.2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAP-29","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-24","unknown","BDADAP-29.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.28",0,NA,25.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"236",22963,"P2",90745.505094,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.770776.2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAP-29","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-24","unknown","BDADAP-29.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,29.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"237",22964,"P2",90747.505094,"Bangladesh","Yes","Dhaka-Kawran Bazar","Independent Site","Dhaka Division","Dhaka",23.7836,90.405,23.7521,90.3944,"2017-01-23","Dry","Dry",-0.770776.2,"BD-Dhaka-Kawran Bazar-2017Jan23","BDADAP-29","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Mixed","held ID certainty unknown","2017-01-24","unknown","BDADAP-29.22V","urine/feces combined (guano)","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.27",0,NA,26.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"238",22973,"P2",170286.344523,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-01.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,27.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"239",22974,"P2",170873.344523,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-01.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"240",22975,"P2",169889.344522,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-01.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","30.18",0,NA,22.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"241",22976,"P2",170295.344521,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-01.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,25.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"242",22980,"P2",170872.344521,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-01.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,26.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"243",22981,"P2",169888.344521,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-01.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","30.18",0,NA,24.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"244",22995,"P2",170297.344519,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-02.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,20.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"245",22996,"P2",170874.344515,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-02.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,21.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"246",22997,"P2",169890.344515,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","male","BDADC-02.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","30.18",0,NA,31.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"247",23006,"P2",170293.344507,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","female","BDADC-03.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,25.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"248",23007,"P2",170870.344507,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-0.776503.4,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","female","BDADC-03.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,27.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"749",23008,"F2",.909802,244517,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","female","BDADC-03.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"750",23006,"F2",.170701,244505,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-04","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-04.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,21.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"751",23007,"F2",.170878,244505,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-04","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-04.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"752",23008,"F2",.909894,244510,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-04","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-04.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,22.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"753",23021,"F2",.170294,244514,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-05","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-05.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,20.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"754",23022,"F2",.170880,244514,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-05","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-05.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,22.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"755",23023,"F2",.909897,244514,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-05","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-05.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,28.93,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"756",23025,"F2",.170292,244512,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-05","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-05.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,25.21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"757",23027,"F2",.170880,244512,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-05","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-05.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,26.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"758",23029,"F2",.909898,244512,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-05","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-05.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"759",23031,"F2",.170296,244512,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-06","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-06.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"760",23032,"F2",.170883,244510,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-06","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-06.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"761",23033,"F2",.909895,244512,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-06","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-06.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,29.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"762",23035,"F2",.170295,244510,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-06","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-06.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,20.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"763",23037,"F2",.170882,244510,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-06","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-06.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"764",23039,"F2",.909898,244510,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-14","Dry","Dry",-
0.7765654,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan14","BDADC-06","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-14","male","BDADC-06.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,21.61,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"765",23041,"F2",.170298,244274,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.73,90.41,23.736,90.3921,"2017-01-15","Dry","Dry",-0.770776,1,"BD-
Dhaka-Dhaka University-2017Jan15","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
15","male","BDADC-07.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff

2016","Positive","27.5",0,NA,25.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"266",23042,"P2",170885.344374,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-07.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,27.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"267",23043,"P2",169901.344374,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-07.CLV","cloacal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"268",23052,"P2",170287.344373,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-07.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,22.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"269",23053,"P2",170884.344373,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-07.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,23.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"270",23054,"P2",169903.344373,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-07.OPV","oropharyngeal swab","2017-01-15","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"271",23058,"P2",171300.344373,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-0.778796,1,"BD-
Dhaka-Dhaka University-2017Jan05","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
15","female","BDADC-08.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,28.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"272",23059,"P2",170887.344373,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","female","BDADC-08.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,29.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"273",23060,"P2",169903.344372,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","female","BDADC-08.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"274",23063,"P2",170288.344373,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-0.778796,1,"BD-
Dhaka-Dhaka University-2017Jan05","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
15","female","BDADC-08.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"275",23064,"P2",170886.344371,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","female","BDADC-08.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"276",23065,"P2",169902.344371,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.785041,23.7296,90.3921,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Dhaka University-2017Jan05","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","female","BDADC-08.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"277",23068,"P2",170302.344024,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.785541,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan05","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-09.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"278",23069,"P2",170889.344024,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.785541,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan05","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-09.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"279",23070,"P2",169905.344024,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.785041,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan05","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-09.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"280",23073,"P2",171301.344023,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.785041,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan05","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-09.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,19.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"281",23080,"P2",170883.344023,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.785041,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan05","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-09.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,24.21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"282",23081,"P2",169904.344023,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.785041,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.778796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan05","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID

certain","2017-01-15","male","BDADC-08.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.8",0,NA,17.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"783",23085,"P2",170507,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.778565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-430","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-430.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,23.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"784",23086,"P2",170085,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.778565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-430","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-430.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gorloff 2016","Positive","27.87",0,NA,25.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"785",23087,"P2",170105,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.778565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-430","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-430.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gorloff 2016","Positive","30.8",0,NA,25.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"786",23090,"P2",170598,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.778565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-430","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-430.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.5",0,NA,21.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"787",23089,"P2",170085,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.778565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-430","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-430.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.87",0,NA,23.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"788",23092,"P2",170003,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.778565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-430","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-430.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.8",0,NA,22.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"789",23017,"P2",170257,344275,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-401","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-401.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,24.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"790",23018,"P2",170044,344273,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-401","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-401.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.87",0,NA,25.62,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"791",23003,"P2",169993,344275,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-401","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-401.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.8",0,NA,24.9,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"792",23013,"P2",170503,344274,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-402","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-402.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,21.56,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"793",23014,"P2",170080,344274,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-402","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-402.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.87",0,NA,23.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"794",23015,"P2",170006,344274,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-402","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-402.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.8",0,NA,33.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"795",23024,"P2",170288,344273,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-402","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-402.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,18.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"796",23025,"P2",170288,344273,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-402","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-402.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.87",0,NA,19.56,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"797",23026,"P2",170002,344273,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-402","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-402.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.8",0,NA,19.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"798",23030,"P2",170584,344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-403","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-403.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,21.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"799",23031,"P2",170518,344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-

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Dhaka-Ramna Park-2017Jan28","BDADC-103","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-103.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,33.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"300",23102,"PZ",170107.344206,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-103","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-103.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,33.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"301",23041,"PZ",170408.344297,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-103","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-103.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"302",23042,"PZ",170987.344297,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-103","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-103.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,23.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"303",23043,"PZ",170383.344297,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-103","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-103.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,27.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"304",23053,"PZ",170358.344350,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-29","Dry","Dry",-0.770796.1,"BD-
Dhaka-Dhaka University-2017Jan29","BDADC-104","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
29","male","BDADC-104.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"305",23054,"PZ",170345.344350,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-29","Dry","Dry",-
0.770796.1,"BD-Dhaka-Dhaka University-2017Jan29","BDADC-104","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-104.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,23.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"306",23055,"PZ",169998.344350,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-29","Dry","Dry",-
0.770796.1,"BD-Dhaka-Dhaka University-2017Jan29","BDADC-104","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-104.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"307",23072,"PZ",170358.344355,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-29","Dry","Dry",-
0.770796.1,"BD-Dhaka-Dhaka University-2017Jan29","BDADC-105","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-105.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,22.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"308",23073,"PZ",170946.344358,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-29","Dry","Dry",-
0.770796.1,"BD-Dhaka-Dhaka University-2017Jan29","BDADC-105","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-105.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,25.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"309",23074,"PZ",169962.344358,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-29","Dry","Dry",-
0.770796.1,"BD-Dhaka-Dhaka University-2017Jan29","BDADC-105","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-105.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"310",23091,"PZ",170308.344457,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD1","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565.6,"BD-Dhaka-Mohakhali-TT Colony-BTD1-2017Jan28","BDADC-106","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-106.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,24.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"311",23092,"PZ",170947.344457,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD1","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565.6,"BD-Dhaka-Mohakhali-TT Colony-BTD1-2017Jan28","BDADC-106","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-106.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,25.98,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"312",23093,"PZ",169953.344457,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD1","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565.6,"BD-Dhaka-Mohakhali-TT Colony-BTD1-2017Jan28","BDADC-106","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-106.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"313",23203,"PZ",170138.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD1","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565.6,"BD-Dhaka-Mohakhali-TT Colony-BTD1-2017Jan28","BDADC-107","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","female","BDADC-107.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,22.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"314",23204,"PZ",170948.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD1","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565.6,"BD-Dhaka-Mohakhali-TT Colony-BTD1-2017Jan28","BDADC-107","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","female","BDADC-107.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"315",23205,"PZ",169984.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD1","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565.6,"BD-Dhaka-Mohakhali-TT Colony-BTD1-2017Jan28","BDADC-107","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","female","BDADC-107.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"316",23224,"P2",170505.344454,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-108","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-108.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,22.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"317",23225,"P2",170502.344454,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-108","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-108.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,25.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"318",23226,"P2",170508.344454,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-108","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-108.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"319",23229,"P2",170485.344452,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-108","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-108.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,24.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"320",23231,"P2",170988.344452,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-108","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-108.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,25.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"321",23232,"P2",170004.344452,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-108","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-108.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,24.16,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"322",23233,"P2",170506.344452,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-105","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-105.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,18.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"323",23232,"P2",170503.344452,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-109","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-109.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,21.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"324",23233,"P2",170800.344452,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-109","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-109.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,21.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"325",23237,"P2",170402.344451,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-109","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-109.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,23.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"326",23238,"P2",170888.344451,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-109","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-109.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,25.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"327",23239,"P2",170005.344451,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-109","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-109.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.72,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"328",23242,"P2",170507.344450,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-110","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-110.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.95,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"329",23253,"P2",170403.344449,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-110","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-110.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,31.79,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"330",23254,"P2",170898.344445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-110","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-110.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,25.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"331",23255,"P2",170806.344448,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-110","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-110.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,22.86,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"332",23259,"P2",170508.344448,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.41,23.783.90.4055,"2017-01-28","Dry","Dry",-
0.7795565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-111","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-111.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff

2016","Positive","27.5",0,NA,24.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"333",23293,"P2",170395,344446,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-18.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.37",0,NA,27.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"334",23293,"P2",170395,344446,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-18.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,27.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"335",23293,"P2",170394,344447,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-18.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,22.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"336",23293,"P2",170394,344447,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-18.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.37",0,NA,24.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"337",23293,"P2",170394,344447,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-18.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,22.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"338",23292,"P2",170509,344446,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-02.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,23.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"339",23293,"P2",170396,344446,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-02.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.37",0,NA,23.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"340",23294,"P2",170412,344446,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-02.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,22.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"341",23294,"P2",170425,344445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-02.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,22.9,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"342",23295,"P2",170392,344445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-02.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.37",0,NA,24.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"343",23296,"P2",170808,344445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,23.78390.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-30","male","BDADC-02.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,22.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"344",23306,"P2",170343,344296,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890412,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-03.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"345",23307,"P2",170830,344296,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890412,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-03.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.37",0,NA,27.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"346",23308,"P2",169946,344296,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890412,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-03.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,28.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"347",23309,"P2",170244,344284,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890412,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-04","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-04.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.2",0,NA,31.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"348",23320,"P2",170808,344284,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890412,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-04","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-04.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.37",0,NA,32.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"349",23321,"P2",169947,344284,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890412,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770716,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-04","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-

30","male","BDADC-45.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff
2016","Positive","30.18",0,NA,31.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"350",23324,"P2",77580,344730,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-45.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,33.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"351",23325,"P2",77581,344730,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-45.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5Nx","other-Gerloff
2016","Positive","27.87",0,NA,34.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"352",23326,"P2",77582,344730,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-45.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff
2016","Positive","30.18",0,NA,32.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"353",23329,"P2",77400,344730,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-45.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"354",23330,"P2",77090,344729,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-45.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5Nx","other-Gerloff
2016","Positive","27.87",0,NA,27.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"355",23333,"P2",77008,344729,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-45.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff
2016","Positive","30.18",0,NA,25.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"356",23334,"P2",77058,344730,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","female","BDADC-46.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,28.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"357",23335,"P2",77088,344730,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","female","BDADC-46.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5Nx","other-Gerloff
2016","Positive","27.87",0,NA,26.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"358",23336,"P2",77094,344730,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","female","BDADC-46.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff
2016","Positive","30.18",0,NA,24.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"359",23339,"P2",77407,344728,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","female","BDADC-46.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"360",23340,"P2",77099,344728,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","female","BDADC-46.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5Nx","other-Gerloff
2016","Positive","27.87",0,NA,33.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"361",23341,"P2",77080,344728,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","female","BDADC-46.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff
2016","Positive","30.18",0,NA,27.21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"362",23344,"P2",77050,344728,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-47","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-47.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,23.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"363",23345,"P2",77089,344728,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-47","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-47.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5Nx","other-Gerloff
2016","Positive","27.87",0,NA,26.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"364",23346,"P2",77095,344728,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-47","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-47.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff
2016","Positive","30.18",0,NA,25.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"365",23349,"P2",77408,344729,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-47","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-47.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21.55,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"366",23350,"P2",77093,344729,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,4,23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770796,4,"BD-

Dhaka-Ramna Park-2017Jan28","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-07.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,23.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"367",23251,"P2",17008,244297,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-28","Dry","Dry",-0.770784,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-07","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
30","male","BDADC-07.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,27.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"368",23265,"P2",17409,244443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-08.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,23.09,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"369",23266,"P2",17089,244443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-08.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.79,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"370",23267,"P2",17090,244443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-08","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-08.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.19",0,NA,24.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"371",23271,"P2",17094,244442,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-09.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"372",23272,"P2",17101,244442,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-09.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,27.11,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"373",23273,"P2",17047,244442,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-09","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-09.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"374",23276,"P2",17440,244444,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-10","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-10.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,25.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"375",23277,"P2",170007,244444,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-10","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-10.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,25.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"376",23278,"P2",17083,244444,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-10","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-10.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"377",23280,"P2",17565,244443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-10","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-10.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"378",23282,"P2",17602,244440,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-10","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-10.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,30.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"379",23283,"P2",17086,244442,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-10","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-10.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,30.55,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"380",23286,"P2",17440,244420,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C0","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-C0.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,22.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"381",23287,"P2",170006,244420,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C0","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-C0.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.80,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"382",23288,"P2",17004,244420,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C0","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-C0.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

Gerloff 2016","Positive","27.57",0,NA,25.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"400",23423,"P2",170022,344422,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.50.4.23.783.50.4055,"2017-01-28","Dry","Dry",-
0.778565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-C14.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","30.18",0,NA,25.96,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"401",23425,"P2",170145,344431,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.50.4.23.783.58.4055,"2017-01-28","Dry","Dry",-
0.778565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-C14.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,23.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"402",23427,"P2",170032,344431,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.50.4.23.783.50.4055,"2017-01-28","Dry","Dry",-
0.778565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-C14.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.57",0,NA,24.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"403",23429,"P2",170008,344431,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.50.4.23.783.50.4055,"2017-01-28","Dry","Dry",-
0.778565.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-31","male","BDADC-C14.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.64,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"404",23431,"P2",170520,344265,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C15.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.98,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"405",23432,"P2",170187,344266,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C15.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.57",0,NA,33.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"406",23433,"P2",170023,344266,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C15.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,22.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"407",23442,"P2",17048,344265,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C15.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"408",23443,"P2",170083,344265,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C15.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.57",0,NA,22.79,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"409",23444,"P2",170085,344265,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C15.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,21.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"410",23448,"P2",170521,344294,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C16","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C16.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"411",23449,"P2",170108,344294,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C16","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C16.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.57",0,NA,32.41,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"412",23450,"P2",170024,344294,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C16","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C16.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,31.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"413",23452,"P2",17047,344283,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C16","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C16.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"414",23454,"P2",170084,344283,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C16","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C16.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.57",0,NA,25.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"415",23455,"P2",170020,344283,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78.50.4.23.7376.80.4012,"2017-01-28","Dry","Dry",-0.778796.4,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-C16","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
31","male","BDADC-C16.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,20.65,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"416",23465,"P2",170448,344425,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.50.4.23.783.00.4055,"2017-01-28","Dry","Dry",-
0.848058.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-C17","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID

certain","2017-02-01","male","BDADC-027.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,21.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"417",23476,"PT",170005.344429,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-027","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-027.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"418",23477,"PT",170021.344428,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-027","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-027.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"419",23480,"PT",170465.344427,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-028","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-028.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,27.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"420",23481,"PT",170065.344427,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-028","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-028.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,28.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"421",23482,"PT",170022.344427,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-028","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-028.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"422",23485,"PT",170524.344426,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-029","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-029.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"423",23486,"PT",170118.344426,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-029","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-029.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,27.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"424",23487,"PT",170077.344426,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-029","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-029.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,26.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"425",23490,"PT",170420.344425,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-029","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-029.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,21.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"426",23491,"PT",170007.344425,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-029","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-029.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,27.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"427",23492,"PT",170023.344425,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-029","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDADC-029.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,22.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"428",23502,"PT",170525.344424,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-030","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","female","BDADC-030.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,25.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"429",23503,"PT",170102.344424,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-030","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","female","BDADC-030.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,31.36,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"430",23504,"PT",170028.344424,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-030","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","female","BDADC-030.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,30.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"431",23507,"PT",17421.344433,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-030","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","female","BDADC-030.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,24.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"432",23508,"PT",170088.344433,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-
0.944858.5,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-030","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","female","BDADC-030.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,25.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"433",23509,"PT",170024.344433,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90.4I.23.783.90.4055,"2017-01-28","Dry","Dry",-

0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDAOC-I30","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","female","BDAOC-I30.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5Is","other-Gorloff 2016","Positive","30.18",0,NA,24.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A34",23522,"P2",170526.344422,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-I31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I31.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,20.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A35",23523,"P2",170613.344422,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-I31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I31.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gorloff 2016","Positive","27.87",0,NA,32.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A36",23524,"P2",170829.344422,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-I31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I31.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gorloff 2016","Positive","30.18",0,NA,31.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A37",23527,"P2",170427.344421,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-I31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I31.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.5",0,NA,24.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A38",23528,"P2",170808.344421,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-I31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I31.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.87",0,NA,25.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A39",23529,"P2",170825.344421,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-I31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I31.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,23.72,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A40",23532,"P2",170527.344423,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDAOC-I32","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I32.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,25.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A41",23533,"P2",170184.344420,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDAOC-I32","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I32.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gorloff 2016","Positive","27.87",0,NA,20.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A42",23534,"P2",170830.344420,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDAOC-I32","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I32.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gorloff 2016","Positive","30.18",0,NA,29.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A43",23537,"P2",170423.344460,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDAOC-I32","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I32.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.5",0,NA,23.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A44",23538,"P2",170806.344460,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDAOC-I32","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I32.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.87",0,NA,25.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A45",23539,"P2",170826.344460,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4123.783,90.4055,"2017-01-28","Dry","Dry",-
0.9348583.6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDAOC-I32","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-01","male","BDAOC-I32.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,24.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A46",23542,"P2",170528.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4123.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-I33","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-I33.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,31.65,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A47",23543,"P2",170615.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4123.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-I33","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-I33.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.87",0,NA,41.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A48",23544,"P2",170833.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4123.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-I33","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-I33.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.18",0,NA,35.79,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"A49",23547,"P2",170424.344257,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4123.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-I33","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-I33.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,24.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"450",23548,"P2",37.708,244.257,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-133.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,25.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"451",23549,"P2",37.0027,344.257,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-133.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"452",23552,"P2",37.529,344.256,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-02-08","Dry","Dry",-0.9258461,"BD-Dhaka-Dhaka University-2017Feb08","BDADC-134","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-08","female","BDADC-134.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,29.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"453",23553,"P2",37.98,244.256,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-02-08","Dry","Dry",-0.9258461,"BD-Dhaka-Dhaka University-2017Feb08","BDADC-134","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-08","female","BDADC-134.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"454",23554,"P2",37.0032,344.256,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-02-08","Dry","Dry",-0.9258461,"BD-Dhaka-Dhaka University-2017Feb08","BDADC-134","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-08","female","BDADC-134.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,33.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"455",23563,"P2",37.425,344.256,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-02-08","Dry","Dry",-0.9258461,"BD-Dhaka-Dhaka University-2017Feb08","BDADC-134","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-08","female","BDADC-134.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,21.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"456",23564,"P2",37.0032,344.255,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-02-08","Dry","Dry",-0.9258461,"BD-Dhaka-Dhaka University-2017Feb08","BDADC-134","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-08","female","BDADC-134.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"457",23565,"P2",37.0028,344.255,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-02-08","Dry","Dry",-0.9258461,"BD-Dhaka-Dhaka University-2017Feb08","BDADC-134","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-08","female","BDADC-134.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"458",23583,"P2",37.426,344.447,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-135","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-135.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,27.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"459",23581,"P2",37.003,344.447,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-135","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-135.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,28.86,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"460",23582,"P2",37.0029,344.447,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-135","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-135.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,28.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"461",23586,"P2",37.53,344.445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-136","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-136.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,33.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"462",23587,"P2",37.98,344.445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-136","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-136.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,31.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"463",23588,"P2",37.0024,344.445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-136","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-136.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,30.67,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"464",23589,"P2",37.427,344.445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-136","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-136.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,26.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"465",23590,"P2",37.024,344.445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-136","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-136.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,27.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"466",23591,"P2",37.0030,344.445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-28","Dry","Dry",-0.9485815,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-136","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-02","male","BDADC-136.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza

A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"467",23603,"PT",17428.34443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-127","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-127.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,25.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"468",23603,"PT",17435.34443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-127","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-127.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,21.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"469",23603,"PT",17069.34443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-127","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-127.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,20.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"470",23605,"PT",17533.34443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-128","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-128.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,29.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"471",23607,"PT",17073.34443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-128","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-128.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,30.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"472",23608,"PT",17083.34443,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-128","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-128.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"473",23609,"PT",17429.34445,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-128","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-128.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,29.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"474",23610,"PT",17035.34441,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-128","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-128.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,21.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"475",23613,"PT",17032.34441,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.7833,90.4055,"2017-01-29","Dry","Dry",-
0.594858.5,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan29","BDADC-128","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-128.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,21.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"476",23616,"PT",17534.344255,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDADC-133.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,23.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"477",23617,"PT",17025.344255,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDADC-133.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,24.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"478",23618,"PT",17031.344255,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDADC-133.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,24.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"479",23620,"PT",17430.344255,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDADC-133.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"480",23622,"PT",17037.344255,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDADC-133.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,23.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"481",23623,"PT",17033.344255,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-133","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDADC-133.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,27.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"482",23626,"PT",17036.344078,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.776176.1,"BD-Dhaka-Suhrawardy Udyan-2017Jan15","BDADC-14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDADC-14.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.63,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"483",23627,"PT",17083.344078,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.776176.1,"BD-Dhaka-Suhrawardy Udyan-2017Jan15","BDADC-14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID

certain","2017-01-15","male","BDAOC-14 CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,28.00,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"604",23628,"P2",90.39905,24.4028,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.776976,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan15","BDAOC-14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDAOC-14 CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,25.95,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"605",23629,"P2",90.39905,24.4028,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.776976,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan15","BDAOC-14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDAOC-14 OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,30.9,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"606",23630,"P2",90.39905,24.4028,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.776976,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan15","BDAOC-14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDAOC-14 OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,29.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"607",23631,"P2",90.39905,24.4028,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-15","Dry","Dry",-
0.776976,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan15","BDAOC-14","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-15","male","BDAOC-14 OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.8",0,NA,29.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"608",23636,"P2",90.40525,24.4277,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-143","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-143 CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"609",23637,"P2",90.40525,24.4277,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-143","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-143 CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,29.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"610",23638,"P2",90.40525,24.4277,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-143","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-143 CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,25.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"611",23641,"P2",90.40525,24.4277,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-143","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-143 OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,22.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"612",23642,"P2",90.40525,24.4277,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-143","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-143 OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,23.94,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"613",23643,"P2",90.40525,24.4277,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-143","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-143 OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,27.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"614",23646,"P2",90.40526,24.4277,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-144","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-144 CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"615",23647,"P2",90.40513,24.4270,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-144","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-144 CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,29.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"616",23648,"P2",90.40528,24.4270,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-144","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-144 CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,30.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"617",23651,"P2",90.40522,24.4263,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-144","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-144 OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,18.72,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"618",23656,"P2",90.40505,24.4263,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-144","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-144 OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,22.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"619",23658,"P2",90.40505,24.4263,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.925846,1,"BD-
Dhaka-Ramna Park-2017Feb02","BDAOC-144","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
02","male","BDAOC-144 OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,27.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"620",23665,"P2",90.39507,24.4258,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7266,90.3951,"2017-02-01","Dry","Dry",-

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0.9258461,"BD-Dhaka-Dhaka University-2017Feb01","BDADC-142","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-142.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,31.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"501",23676,"P2",170124.344258,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7386,90.3921,"2017-02-01","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb01","BDADC-142","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-142.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,34.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"502",23671,"P2",170140.344258,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7386,90.3921,"2017-02-01","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb01","BDADC-142","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-142.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"503",23673,"P2",174033.344037,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7386,90.3921,"2017-02-01","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb01","BDADC-142","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-142.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,33.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"504",23676,"P2",170030.344037,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7386,90.3921,"2017-02-01","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb01","BDADC-142","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-142.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,36.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"505",23677,"P2",170036.344057,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7386,90.3921,"2017-02-01","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb01","BDADC-142","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-02","male","BDADC-142.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,36.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"506",23685,"P2",438010.694021,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.BRV","brain","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.28",0,NA,20.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"507",23689,"P2",438058.694028,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.BRV","brain","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","28.87",0,NA,31.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"508",23687,"P2",438092.694030,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.BRV","brain","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","28.87",0,NA,30.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"509",23695,"P2",438011.694037,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.KIV","kidney","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.28",0,NA,27.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"510",23696,"P2",438052.694037,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.KIV","kidney","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","28.87",0,NA,33.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"511",23697,"P2",438053.694037,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.KIV","kidney","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","28.87",0,NA,37.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"512",23705,"P2",438008.694091,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.LIV","liver","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.28",0,NA,28.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"513",23706,"P2",438043.594091,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.LIV","liver","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","28.87",0,NA,30.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"514",23707,"P2",438090.594091,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.LIV","liver","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","28.87",0,NA,29.55,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"515",23714,"P2",438003.594094,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.LUV","lung","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.28",0,NA,29.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"516",23715,"P2",438058.594094,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4003,"2017-02-02","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017Feb02","BDADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","BDADC-143.LUV","lung","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","28.87",0,NA,30.65,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"517",23716,"P1",42808.69404,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.737690,4013,"2017-02-02","Dry","Dry",-0.8258461,"80-
Dhaka-Ramna Park-2017Feb02","80ADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","80ADC-143.LUN","lung","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","28.87",0,NA,29.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"518",23747,"P1",42817.694076,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.737690,4013,"2017-02-02","Dry","Dry",-0.8258461,"80-
Dhaka-Ramna Park-2017Feb02","80ADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","80ADC-143.SPV","spleen","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.28",0,NA,31.67,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"519",23748,"P1",42852.694076,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.737690,4013,"2017-02-02","Dry","Dry",-0.8258461,"80-
Dhaka-Ramna Park-2017Feb02","80ADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","80ADC-143.SPV","spleen","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","28.87",0,NA,33.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"520",23749,"P1",42854.694076,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.737690,4013,"2017-02-02","Dry","Dry",-0.8258461,"80-
Dhaka-Ramna Park-2017Feb02","80ADC-143","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Badur","field ID certain","2017-02-
02","male","80ADC-143.SPV","spleen","2017-03-03","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","28.87",0,NA,32.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"521",23770,"P1",37508.34440,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-145","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","80ADC-145.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,33.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"522",23771,"P1",37026.34440,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-145","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","80ADC-145.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.57",0,NA,33.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"523",23772,"P1",37042.34440,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-145","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","80ADC-145.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,33.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"524",23780,"P1",37425.344409,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-145","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","80ADC-145.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,28.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"525",23782,"P1",37023.344405,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-145","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","80ADC-145.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,29.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"526",23783,"P1",37008.344405,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-145","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","80ADC-145.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,28.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"527",23781,"P1",37540.344408,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-146","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","80ADC-146.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,25.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"528",23788,"P1",37427.344408,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-146","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","80ADC-146.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,31.65,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"529",23789,"P1",37043.344408,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-146","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","80ADC-146.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"530",23792,"P1",37426.344407,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-146","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","80ADC-146.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,28.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"531",23793,"P1",37023.344407,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-146","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","80ADC-146.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,25.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"532",23794,"P1",37008.344407,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-146","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","80ADC-146.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"533",23797,"P1",37044.344406,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.78390,4055,"2017-02-07","Dry","Dry",-
0.9448581,"80-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","80ADC-147","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","80ADC-147.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff

2016","Positive","27.5",0,NA,25.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"524",23802,"F2",17402.344405,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-147","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-147.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,24.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"525",23803,"F2",17024.344405,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-147","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-147.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,26.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"526",23804,"F2",17004.344405,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-147","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-147.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,24.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"527",23807,"F2",17042.344404,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-148","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-148.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,24.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"528",23808,"F2",17029.344404,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-148","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-148.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,26.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"529",23809,"F2",17045.344404,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-148","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-148.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"540",23810,"F2",17428.344403,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-148","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-148.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,27.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"541",23813,"F2",17025.344403,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-148","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-148.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,20.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"542",23814,"F2",17004.344403,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-07","Dry","Dry",-0.948858,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb07","BDADC-148","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-148.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,28.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"543",23840,"F2",17008.344270,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-15","Dry","Dry",-0.770761,1,"BD-Dhaka-Dhaka University-2017Jan15","BDADC-15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-15","male","BDADC-15.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,28.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"544",23841,"F2",17085.344270,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-15","Dry","Dry",-0.770761,1,"BD-Dhaka-Dhaka University-2017Jan15","BDADC-15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-15","male","BDADC-15.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,29.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"545",23842,"F2",16996.344270,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-15","Dry","Dry",-0.770761,1,"BD-Dhaka-Dhaka University-2017Jan15","BDADC-15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-15","male","BDADC-15.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.67,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"546",23846,"F2",17087.344208,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-15","Dry","Dry",-0.770761,1,"BD-Dhaka-Dhaka University-2017Jan15","BDADC-15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-15","male","BDADC-15.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,24.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"547",23847,"F2",17089.344208,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-15","Dry","Dry",-0.770761,1,"BD-Dhaka-Dhaka University-2017Jan15","BDADC-15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-15","male","BDADC-15.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"548",23848,"F2",16980.344208,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-01-15","Dry","Dry",-0.770761,1,"BD-Dhaka-Dhaka University-2017Jan15","BDADC-15","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-15","male","BDADC-15.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"549",23856,"F2",17440.344250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4012,"2017-02-07","Dry","Dry",-0.925846,1,"BD-Dhaka-Ramna Park-2017Feb07","BDADC-150","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDADC-150.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,23.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"550",23857,"F2",17027.344250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4012,"2017-02-07","Dry","Dry",-0.925846,1,"BD-Dhaka-Ramna Park-2017Feb07","BDADC-150","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-

07","male","BDAIDC-I53.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,25.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"561",23858,"P2",.770843,.344281,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDAIDC-I53.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,24.09,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"562",23860,"P2",.770545,.344260,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","female","BDAIDC-I54.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,29.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"563",23862,"P2",.770022,.344260,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","female","BDAIDC-I54.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,30.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"564",23863,"P2",.770048,.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","female","BDAIDC-I54.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,30.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"565",23866,"P2",.770446,.344259,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","female","BDAIDC-I54.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,21.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"566",23867,"P2",.770028,.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","female","BDAIDC-I54.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,23.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"567",23868,"P2",.770044,.344250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","female","BDAIDC-I54.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,21.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"568",23871,"P2",.770546,.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDAIDC-I57.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,28.11,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"569",23872,"P2",.770033,.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDAIDC-I57.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,29.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"570",23873,"P2",.770048,.344258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDAIDC-I57.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.97,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"571",23876,"P2",.770442,.344257,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDAIDC-I57.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,23.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"572",23877,"P2",.770029,.344257,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDAIDC-I57.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"573",23878,"P2",.770045,.344257,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-07","Dry","Dry",-0.9258461,"BD-Dhaka-Ramna Park-2017Feb07","BDAIDC-I57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-07","male","BDAIDC-I57.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,24.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"574",23887,"P2",.770547,.344152,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAIDC-I53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAIDC-I53.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,22.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"575",23888,"P2",.770434,.344052,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAIDC-I53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAIDC-I53.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,25.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"576",23889,"P2",.770050,.344052,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAIDC-I53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAIDC-I53.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"577",23893,"P2",.770443,.344051,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3921,"2017-02-07","Dry","Dry",-

0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-153","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-153.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorlaff 2006","Positive","27.5",0,NA,26.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"568",23894,"P2",170208,244334,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-153","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-153.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorlaff 2006","Positive","27.97",0,NA,26.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"569",23895,"P2",170846,244359,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-153","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-153.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorlaff 2006","Positive","30.18",0,NA,25.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"570",23903,"P2",170444,244349,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-154","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-154.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorlaff 2006","Positive","27.5",0,NA,24.80,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"571",23904,"P2",170103,244340,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-154","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-154.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorlaff 2006","Positive","27.97",0,NA,27.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"572",23905,"P2",170847,244348,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-154","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-154.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorlaff 2006","Positive","30.18",0,NA,25.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"573",23908,"P2",170549,244354,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-155","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-155.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorlaff
2006","Positive","27.5",0,NA,23.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"574",23909,"P2",170136,244354,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-155","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-155.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gorlaff 2006","Positive","27.97",0,NA,24.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"575",23910,"P2",170952,244354,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-155","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-155.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gorlaff 2006","Positive","30.18",0,NA,24.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"576",23910,"P2",170445,244353,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-155","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-155.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorlaff 2006","Positive","27.5",0,NA,25.97,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"577",23911,"P2",170022,244353,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-155","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-155.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorlaff 2006","Positive","27.97",0,NA,28.32,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"578",23913,"P2",170048,244353,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7396,90.3921,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDAOC-155","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDAOC-155.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorlaff 2006","Positive","30.18",0,NA,27.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"579",23918,"P2",170550,244390,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.9948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb12","BDAOC-156","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","female","BDAOC-156.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorlaff 2006","Positive","27.5",0,NA,27.11,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"580",23919,"P2",170151,244390,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.9948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb12","BDAOC-156","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","female","BDAOC-156.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gorlaff 2006","Positive","27.97",0,NA,28.63,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"581",23920,"P2",170953,244390,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.9948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb12","BDAOC-156","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","female","BDAOC-156.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gorlaff 2006","Positive","30.18",0,NA,29.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"582",23921,"P2",170446,244389,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.9948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb12","BDAOC-156","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","female","BDAOC-156.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gorlaff 2006","Positive","27.5",0,NA,19.89,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"583",23930,"P2",170033,244389,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.9948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb12","BDAOC-156","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","female","BDAOC-156.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorlaff 2006","Positive","27.97",0,NA,21.63,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"584",23903,"P2",170049,344098,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-156","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","female","BDADC-156.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"585",23935,"P2",170120,344402,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-157","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-157.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,34.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"586",23936,"P2",170138,344402,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-157","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-157.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,35.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"587",23937,"P2",170154,344402,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-157","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-157.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,26.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"588",23940,"P2",170441,344403,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-157","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-157.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,20.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"589",23941,"P2",170034,344403,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-157","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-157.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,27.55,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"590",23942,"P2",170050,344403,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-157","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-157.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,20.89,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"591",23945,"P2",170052,344400,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","female","BDADC-158.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,33.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"592",23946,"P2",170035,344400,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","female","BDADC-158.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,30.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"593",23947,"P2",170055,344400,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","female","BDADC-158.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,23.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"594",23950,"P2",170448,344095,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","female","BDADC-158.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,26.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"595",23951,"P2",170035,344098,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","female","BDADC-158.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,28.49,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"596",23952,"P2",170054,344098,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","female","BDADC-158.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"597",23955,"P2",170053,344098,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-159","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-159.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,35.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"598",23956,"P2",170140,344098,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-159","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-159.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,31.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"599",23957,"P2",170056,344098,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-159","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-159.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,21.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"600",23960,"P2",170445,344097,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 4.23.783.90.4055,"2017-02-12","Dry","Dry",-0.594858.1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017FebXX","BDADC-159","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-12","male","BDADC-159.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-

Gerlaff 2016","Positive","27.5",0,NA,23.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"601",23980,"PJ",170050.344297,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-158.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerlaff 2016","Positive","27.97",0,NA,25.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"602",23982,"PJ",170052.344297,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-158","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-158.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerlaff 2016","Positive","30.18",0,NA,23.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"603",23977,"PJ",170554.344296,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-160","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-160.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlaff
2016","Positive","27.5",0,NA,25.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"604",23978,"PJ",170144.344296,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-160","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-160.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerlaff 2016","Positive","27.97",0,NA,29.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"605",23979,"PJ",170157.344296,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-160","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-160.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerlaff 2016","Positive","30.18",0,NA,28.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"606",23980,"PJ",174450.344295,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-160","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-160.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerlaff 2016","Positive","27.5",0,NA,19.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"607",23983,"PJ",170207.344295,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-160","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-160.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerlaff 2016","Positive","27.97",0,NA,21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"608",23984,"PJ",170053.344295,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-160","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-160.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerlaff 2016","Positive","30.18",0,NA,18.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"609",23987,"PJ",170555.344294,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-161","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","female","BDAOC-161.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerlaff 2016","Positive","27.5",0,NA,33.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"610",23988,"PJ",170142.344294,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-161","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","female","BDAOC-161.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerlaff 2016","Positive","27.97",0,NA,35.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"611",23989,"PJ",170158.344294,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-161","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","female","BDAOC-161.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerlaff 2016","Positive","30.18",0,NA,33.97,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"612",23990,"PJ",170463.344293,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-161","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","female","BDAOC-161.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerlaff 2016","Positive","27.5",0,NA,23.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"613",23993,"PJ",170208.344293,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-161","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","female","BDAOC-161.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerlaff 2016","Positive","27.97",0,NA,26.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"614",23994,"PJ",170054.344293,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-161","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","female","BDAOC-161.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerlaff 2016","Positive","30.18",0,NA,24.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"615",23997,"PJ",170556.344292,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-162","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-162.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlaff
2016","Positive","27.5",0,NA,24.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"616",23998,"PJ",170143.344292,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-162","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-13","male","BDAOC-162.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerlaff 2016","Positive","27.97",0,NA,28.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"617",23999,"PJ",170159.344292,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78.90 41.23.783.90.4055,"2017-02-13","Dry","Dry",-
0.9348581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb13","BDAOC-162","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID

certain","2017-02-12","male","BDAOC-162.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9A","other-
Gerloff 2016","Positive","30.18",0,NA,25.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"618",24002,"P2",37452,244209,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.3948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017-eb12","BDAOC-162","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDAOC-162.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,27.01,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"619",24003,"P2",37028,244206,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.3948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017-eb12","BDAOC-162","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDAOC-162.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,29.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"620",24004,"P2",370055,244208,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-12","Dry","Dry",-
0.3948581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017-eb12","BDAOC-162","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDAOC-162.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"621",24020,"P2",37557,244250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-163","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-163.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"622",24008,"P2",37844,244250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-163","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-163.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,22.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"623",24008,"P2",37868,244258,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-163","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-163.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,32.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"624",24008,"P2",37453,244245,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-163","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-163.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,18.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"625",24008,"P2",37040,244245,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-163","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-163.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,22.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"626",24028,"P2",370256,244245,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-163","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-163.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,20.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"627",24024,"P2",37558,244256,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-164","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-164A.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"628",24025,"P2",37945,244256,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-164","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-164A.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,20.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"629",24026,"P2",37080,244255,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-164","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-164A.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,20,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"630",24029,"P2",37454,244250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-164","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-164A.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"631",24030,"P2",37046,244250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-164","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-164A.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,25.36,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"632",24031,"P2",370057,244250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-164","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","male","BDAOC-164A.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,25.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"633",24034,"P2",37020,244254,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-
Dhaka-Ramna Park-2017-eb13","BDAOC-165","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDAOC-165.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,31.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"634",24031,"P2",37046,244254,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-02-12","Dry","Dry",-0.9258461,"BD-

Dhaka-Ramna Park-2017Feb12","BDADC-652","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-652.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,24.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"635",24030,"P2",170182,344254,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-652","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-653.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.19",0,NA,32.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"636",24039,"P2",170455,344252,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-652","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-655.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"637",24040,"P2",170142,344253,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-652","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-655.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,22.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"638",24041,"P2",170258,344252,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-655","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-655.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.19",0,NA,30.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"639",24044,"P2",175680,344252,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-656","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-656.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,33.86,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"640",24045,"P2",170147,344252,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-656","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-656.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,33.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"641",24046,"P2",170163,344252,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-656","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-656.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.19",0,NA,27.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"642",24049,"P2",170456,344251,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-656","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-656.OPV","oropharyngeal swab","2017-03-27","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,28.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"643",24050,"P2",170143,344250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-656","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-656.OPV","oropharyngeal swab","2017-03-27","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,33.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"644",24051,"P2",170259,344250,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-02-12","Dry","Dry",-0.0258461,"BD-
Dhaka-Ramna Park-2017Feb12","BDADC-656","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-02-
12","female","BDADC-656.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.19",0,NA,25.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"645",24054,"P2",170150,344248,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3931,"2017-02-12","Dry","Dry",-
0.0258461,"BD-Dhaka-Dhaka University-2017Feb12","BDADC-657","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDADC-657.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"646",24055,"P2",170148,344248,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3931,"2017-02-12","Dry","Dry",-
0.0258461,"BD-Dhaka-Dhaka University-2017Feb12","BDADC-657","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDADC-657.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,25.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"647",24056,"P2",170084,344248,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3931,"2017-02-12","Dry","Dry",-
0.0258461,"BD-Dhaka-Dhaka University-2017Feb12","BDADC-657","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDADC-657.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.19",0,NA,25.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"648",24059,"P2",170457,344247,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3931,"2017-02-12","Dry","Dry",-
0.0258461,"BD-Dhaka-Dhaka University-2017Feb12","BDADC-657","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDADC-657.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,23.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"649",24063,"P2",170144,344247,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3931,"2017-02-12","Dry","Dry",-
0.0258461,"BD-Dhaka-Dhaka University-2017Feb12","BDADC-657","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDADC-657.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,24.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"650",24080,"P2",170088,344247,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7316,90.3931,"2017-02-12","Dry","Dry",-
0.0258461,"BD-Dhaka-Dhaka University-2017Feb12","BDADC-657","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-12","male","BDADC-657.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.19",0,NA,27.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"1654",24084,"P2",17.0563,24.4346,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-468","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","BDADC-468.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,21.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1652",24085,"P2",17.0645,24.4346,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-468","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","BDADC-468.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,24.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1653",24086,"P2",17.0653,24.4346,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-468","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","BDADC-468.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,23.62,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1654",24068,"P2",17.0458,24.4345,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-468","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","BDADC-468.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,21.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1655",24070,"P2",17.0645,24.4345,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-468","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","BDADC-468.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,24.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1656",24071,"P2",17.0660,24.4345,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-468","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","female","BDADC-468.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.8",0,NA,21.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1657",24085,"P2",17.0458,24.4342,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-469","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDADC-469.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,29.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1658",24086,"P2",17.0646,24.4342,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-469","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDADC-469.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,29.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1659",24087,"P2",17.0662,24.4342,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4,23.7296,90.3923,"2017-02-07","Dry","Dry",-
0.9258461,"BD-Dhaka-Dhaka University-2017Feb07","BDADC-469","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-07","male","BDADC-469.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.8",0,NA,29.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1660",2408,"P2",17.0584,24.4388,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-470","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-470.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,30.30,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1661",2402,"P2",17.0659,24.4388,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-470","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-470.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,30.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1662",2403,"P2",17.0667,24.4388,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-470","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-470.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,30.68,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1663",2410,"P2",17.0460,24.4387,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-470","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-470.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,23.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1664",2403,"P2",17.0647,24.4387,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-470","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-470.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,25.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1665",2404,"P2",17.0663,24.4387,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-470","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-470.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.8",0,NA,23.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1666",2408,"P2",17.0505,24.4386,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7890,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-471","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","female","BDADC-471.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,31.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1667",2409,"P2",17.0652,24.4386,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4,23.7830,90.4055,"2017-02-20","Dry","Dry",-
0.9648581,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-471","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","female","BDADC-471.CLY","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-

Gerloff 2016","Positive","27.87",0,NA,31.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"868",24129,"PT",370868,344386,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-171","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","female","BDADC-171.CLF","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,30.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"869",24123,"PT",370460,344385,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-171","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","female","BDADC-171.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,24.11,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"870",24124,"PT",370048,344385,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-171","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","female","BDADC-171.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,29.94,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"871",24125,"PT",370084,344385,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-171","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","female","BDADC-171.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"872",24650,"PT",371464,344403,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-02-20","Dry","Dry",-
0.925846,1,"BD-Dhaka-Suhrawardy Udyan-2017Feb20","BDADC-174","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-174.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,35.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"873",24651,"PT",370351,344403,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-02-20","Dry","Dry",-
0.925846,1,"BD-Dhaka-Suhrawardy Udyan-2017Feb20","BDADC-174","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-174.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,26.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"874",24652,"PT",370087,344400,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-02-20","Dry","Dry",-
0.925846,1,"BD-Dhaka-Suhrawardy Udyan-2017Feb20","BDADC-174","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-02-20","male","BDADC-174.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,24.63,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"875",24198,"PT",430918,400482,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-178","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Kola
badur","field ID certain","2017-02-20","male","BDADC-178.KIV","kidney","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.28",0,NA,24.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"876",24199,"PT",430958,400482,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-178","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Kola
badur","field ID certain","2017-02-20","male","BDADC-178.KIV","kidney","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,28.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"877",24200,"PT",430700,400482,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-178","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Kola
badur","field ID certain","2017-02-20","male","BDADC-178.KIV","kidney","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","28.87",0,NA,33.89,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"878",24208,"PT",430805,400472,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-179","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Kola
badur","field ID certain","2017-02-20","male","BDADC-179.LIV","liver","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.28",0,NA,35.09,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"879",24210,"PT",430856,400472,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-179","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Kola
badur","field ID certain","2017-02-20","male","BDADC-179.LIV","liver","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,37.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"880",24211,"PT",430981,400472,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-02-20","Dry","Dry",-
0.948658,1,"BD-Dhaka Mohakhali-TT Colony-BTCL-2017Feb20","BDADC-179","bats","free-ranging wild animal","Pteropus giganteus","Pteropus giganteus","species","Indian Flying Fox","Kola
badur","field ID certain","2017-02-20","male","BDADC-179.LIV","liver","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","28.87",0,NA,35.11,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"881",24254,"PT",370134,344248,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-15","Dry","Dry",-0.770716,1,"BD-
Dhaka-Ramna Park-2017Jan15","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
15","male","BDADC-18.CLF","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"882",24255,"PT",370800,344248,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-15","Dry","Dry",-0.770716,1,"BD-
Dhaka-Ramna Park-2017Jan15","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
15","male","BDADC-18.CLF","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,27.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"883",24256,"PT",50897,344248,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-15","Dry","Dry",-0.770716,1,"BD-
Dhaka-Ramna Park-2017Jan15","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
15","male","BDADC-18.CLF","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,25.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"884",24258,"PT",370130,344247,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-15","Dry","Dry",-0.770716,1,"BD-
Dhaka-Ramna Park-2017Jan15","BDADC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-

01","male","BDAIDC-18.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,22.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1883",24260,"P2",170908,344247,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4013,"2017-01-05","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan05","BDAIDC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
01","male","BDAIDC-18.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,23.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1886",24261,"P2",308906,344247,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7376,90.4013,"2017-01-05","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan05","BDAIDC-18","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
01","male","BDAIDC-18.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.19",0,NA,21.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1887",24399,"P2",170908,344099,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7325,90.3986,"2017-01-07","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan07","BDAIDC-22","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-07","male","BDAIDC-22.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1888",24400,"P2",170905,344099,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7325,90.3986,"2017-01-07","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan07","BDAIDC-22","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-07","male","BDAIDC-22.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,23.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1889",24401,"P2",308901,344099,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7325,90.3986,"2017-01-07","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan07","BDAIDC-22","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-07","male","BDAIDC-22.CLV","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,21.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1890",24410,"P2",170907,344097,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7325,90.3986,"2017-01-07","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan07","BDAIDC-22","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-07","male","BDAIDC-22.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,19.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1891",24411,"P2",170904,344097,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7325,90.3986,"2017-01-07","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan07","BDAIDC-22","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-07","male","BDAIDC-22.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,21.68,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1892",24412,"P2",308920,344097,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7325,90.3986,"2017-01-07","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan07","BDAIDC-22","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-07","male","BDAIDC-22.OPV","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,18.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1893",24921,"P2",170915,400550,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7316,90.3921,"2017-01-08","Dry","Dry",-0.770761,"BD-
Dhaka-Dhaka University-2017Jan08","BDAIDC-28","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
08","male","BDAIDC-28.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,23.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1894",24921,"P2",170906,400550,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7316,90.3921,"2017-01-08","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan08","BDAIDC-28","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-08","male","BDAIDC-28.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,26.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1895",24922,"P2",308922,400550,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7316,90.3921,"2017-01-08","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan08","BDAIDC-28","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-08","male","BDAIDC-28.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.93,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1896",24945,"P2",170320,400552,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7316,90.3921,"2017-01-08","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan08","BDAIDC-29","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-08","female","BDAIDC-29.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,30.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1897",24946,"P2",170907,400552,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7316,90.3921,"2017-01-08","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan08","BDAIDC-29","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-08","female","BDAIDC-29.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,33.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1898",24947,"P2",308923,400552,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7850,4,23.7316,90.3921,"2017-01-08","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan08","BDAIDC-29","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-08","female","BDAIDC-29.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,22.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1899",24978,"P2",170321,344503,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4,23.7830,90.4055,"2017-01-09","Dry","Dry",-
0.776503,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan09","BDAIDC-30","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-09","male","BDAIDC-30.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1900",24979,"P2",170908,344503,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4,23.7830,90.4055,"2017-01-09","Dry","Dry",-
0.776503,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan09","BDAIDC-30","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-09","male","BDAIDC-30.CLV","cloacal swab","2017-02-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,28.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1901",24980,"P2",308924,344503,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4,23.7830,90.4055,"2017-01-09","Dry","Dry",-

0.7705651,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan05","BDADC-30","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-05","male","BDADC-30.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5","other-Gerloff 2016","Positive","30.8",0,NA,29.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"702",24887,"PT",17.0503,344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-05","Dry","Dry",-
0.7705651,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan05","BDADC-31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-05","male","BDADC-31.OPH","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,29.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"703",24888,"PT",17.0849,344480,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-18","Dry","Dry",-
0.7705651,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan05","BDADC-31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-18","male","BDADC-31.OPH","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,22.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"704",24889,"PT",16.9953,344489,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-18","Dry","Dry",-
0.7705651,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan05","BDADC-31","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-18","male","BDADC-31.OPH","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.8",0,NA,25.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"705",25003,"PT",17.0327,344336,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-33","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-33.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,32.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"706",25006,"PT",17.0808,344336,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-33","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-33.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,26.55,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"707",25007,"PT",16.9923,344336,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-33","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-33.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,25.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"708",25020,"PT",17.0483,344324,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-34","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-34.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,31.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"709",25021,"PT",17.0056,344324,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-34","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-34.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,25.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"710",25022,"PT",17.0072,344324,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-34","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-34.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,31.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"711",25025,"PT",17.0304,344333,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-34","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-34.OPH","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,31.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"712",25026,"PT",17.0551,344333,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-34","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-34.OPH","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,28.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"713",25027,"PT",16.9987,344333,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-34","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-34.OPH","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,30.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"714",25030,"PT",17.0470,344332,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-35","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-35.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"715",25031,"PT",17.0057,344332,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-35","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-35.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,29.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"716",25032,"PT",17.0873,344333,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-35","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-35.CLO","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.8",0,NA,29.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"717",25035,"PT",17.0383,344328,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4013,"2017-01-20","Dry","Dry",-0.7707161,"BD-
Dhaka-Ramna Park-2017Jan20","BDADC-35","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDADC-35.OPH","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.67,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"718",25038,"PY",170852.344338,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.237376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-35","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-35.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,31.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"719",25032,"PY",169988.344339,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-35","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-35.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.8",0,NA,29.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"720",25040,"PY",171471.344330,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-36","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-36.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,32.38,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"721",25040,"PY",170058.344330,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-36","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-36.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,35.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"722",25041,"PY",170074.344338,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-36","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-36.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.8",0,NA,33.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"723",25045,"PY",170366.344326,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-36","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-36.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"724",25046,"PY",170852.344326,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-36","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-36.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,29.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"725",25047,"PY",169958.344329,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-36","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-36.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.8",0,NA,27.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"726",25050,"PY",171472.344328,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-37","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-37.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"727",25051,"PY",170058.344328,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-37","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-37.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,29.56,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"728",25052,"PY",170075.344328,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-37","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-37.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.8",0,NA,25.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"729",25061,"PY",171367.344327,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-37","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-37.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"730",25062,"PY",170854.344327,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-37","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-37.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,27.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"731",25063,"PY",169970.344327,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7376.90.4093,"2017-01-20","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan20","BDAOC-37","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
20","male","BDAOC-37.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.8",0,NA,25.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"732",25067,"PY",170272.344368,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7396.90.2821,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan22","BDAOC-38","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDAOC-38.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,33.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"733",25068,"PY",170983.344368,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7396.90.2821,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan22","BDAOC-38","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDAOC-38.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,31.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"734",25069,"PY",169976.344368,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7890,4.23.7396.90.2821,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan22","BDAOC-38","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDAOC-38.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-

Gerloff 2016","Positive","30.18",0,NA,29.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"735",25079,"P2",17.024,344100,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan22","BDADC-38","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-38.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,28.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"736",25080,"P2",17.081,344056,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan22","BDADC-38","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-38.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.57",0,NA,28.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"737",25081,"P2",16.8927,344066,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7316,90.3921,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan22","BDADC-38","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-38.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,27.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"738",25084,"P2",17.025,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-40","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-40.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,31.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"739",25085,"P2",17.092,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-40","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-40.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.57",0,NA,34.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"740",25086,"P2",16.9928,344408,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-40","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-40.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,33.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"741",25095,"P2",17.0473,344456,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-41","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-41.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,28.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"742",25098,"P2",17.0960,344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-41","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-41.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.37",0,NA,32.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"743",25097,"P2",17.0876,344456,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-41","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-41.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,31.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"744",25101,"P2",17.0361,344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-41","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-41.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,30.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"745",25102,"P2",17.0355,344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-41","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-41.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.57",0,NA,31.01,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"746",25103,"P2",16.8557,344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7833,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-41","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-41.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,30.41,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"747",25182,"P2",17.474,344200,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4013,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,22.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"748",25183,"P2",17.058,344200,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4013,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.57",0,NA,26.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"749",25184,"P2",17.0377,344200,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4013,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,25.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"750",25188,"P2",17.0308,344200,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4013,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"751",25189,"P2",17.0558,344200,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4013,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-

22","male","BDADC-42.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,29.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"752",25026,"P1",.800977,34.4028,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,29.79,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"753",25023,"P1",170226,344026,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"754",25024,"P1",170913,344026,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,31.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"755",25025,"P1",.800025,344026,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-42","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-42.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,25.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"756",25029,"P1",170227,344086,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-44","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-44.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"757",25028,"P1",170084,344086,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-44","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-44.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,33.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"758",25030,"P1",.800030,344086,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-44","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-44.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,32.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"759",25040,"P1",170228,344084,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-45.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,24.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"760",25040,"P1",170085,344084,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-45.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,27.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"761",25042,"P1",.800958,344084,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-45","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-45.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,25.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"762",25045,"P1",170229,344082,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-46.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,18.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"763",25046,"P1",170086,344082,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-46.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.97",0,NA,22.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"764",25047,"P1",.800932,344082,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-46","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-46.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,21.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"765",25055,"P1",170230,344005,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-47","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-47.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"766",25056,"P1",170087,344005,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-47","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-47.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,27.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"767",25057,"P1",.800973,344005,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-47","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-47.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,24.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"768",25060,"P1",170476,344008,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-

0.779796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-48","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-48.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"769",25965,"P1",.779371,.244007,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.779796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-48","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-48.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,33.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"770",25966,"P1",.779858,.244007,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.779796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-48","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-48.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.97",0,NA,28.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"771",25967,"P2",.169974,.244007,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.779796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-48","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-48.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.19",0,NA,35.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"772",25980,"P1",.170330,.481508,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-50","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-50.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"773",25981,"P1",.170087,.481508,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-50","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-50.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,23.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"774",25982,"P2",.169903,.481508,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-50","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-50.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,27.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"775",25985,"P1",.171478,.481506,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-51","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-51.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"776",25986,"P1",.170065,.481506,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-51","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-51.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,21.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"777",25987,"P2",.170081,.481506,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-51","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-51.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,29.91,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"778",25990,"P1",.170373,.481505,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-51","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-51.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"779",25991,"P1",.170050,.481505,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-51","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-51.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,28.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"780",25992,"P2",.169976,.481505,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-51","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","female","BDADC-51.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,28.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"781",25997,"P1",.171479,.481504,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-52","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-52.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"782",25998,"P1",.170086,.481504,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-52","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-52.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,29.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"783",25999,"P2",.170082,.481504,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-52","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-52.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,27.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"784",25208,"P2",.170374,.481503,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.779585,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-52","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-52.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,26.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"785",25207,"P2",170860.485633,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony 8702","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-8702-2017Jan22","BDADC-52","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-52.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,29.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"786",25208,"P2",169077.485633,"Bangladesh","Yes","Dhaka Mohakhali-TT Colony 8702","Concurrent Site 2","Dhaka Division","Dhaka",23.7890412,90.4055,"2017-01-22","Dry","Dry",-
0.7765051,"BD-Dhaka-Mohakhali-TT Colony-8702-2017Jan22","BDADC-52","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-52.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","35.18",0,NA,26.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"787",25212,"P2",174480.344224,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7880412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-53.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,31.21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"788",25213,"P2",171087.344224,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7950412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-53.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,24.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"789",25214,"P2",170083.344224,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7950412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-53.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","35.18",0,NA,22.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"790",25223,"P2",170275.344223,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7950412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-53.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,33.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"791",25224,"P2",170802.344223,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-53.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,33.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"792",25225,"P2",169878.344223,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7880412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-53","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-53.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","35.18",0,NA,29.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"793",25229,"P2",170339.344223,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7950412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-54.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"794",25230,"P2",170898.344223,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7950412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-54.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,25.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"795",25231,"P2",169934.344222,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7950412,7376.90.4083,"2017-01-22","Dry","Dry",-0.7707611,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
22","male","BDADC-54.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","35.18",0,NA,25.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"796",25240,"P2",170333.485523,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850412,7325.90.3986,"2017-01-22","Dry","Dry",-
0.7707611,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-55","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-55.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,28.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"797",25241,"P2",170919.485523,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850412,7325.90.3986,"2017-01-22","Dry","Dry",-
0.7707611,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-55","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-55.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,31.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"798",25242,"P2",169835.485523,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850412,7325.90.3986,"2017-01-22","Dry","Dry",-
0.7707611,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-55","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-55.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","35.18",0,NA,28.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"799",25245,"P2",171333.485521,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850412,7325.90.3986,"2017-01-22","Dry","Dry",-
0.7707611,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-56","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-56.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"800",25246,"P2",170829.485521,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850412,7325.90.3986,"2017-01-22","Dry","Dry",-
0.7707611,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-56","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-56.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,29.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"801",25247,"P2",169938.485521,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850412,7325.90.3986,"2017-01-22","Dry","Dry",-
0.7707611,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-56","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-22","male","BDADC-56.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-

Garloff 2016","Positive","30.18",0,NA,27.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"802",25250,"P2",.70224,405515,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.776796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-23","male","BDADC-57.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Garloff
2016","Positive","27.5",0,NA,27.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"803",25251,"P2",.70001,405515,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.776796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-23","male","BDADC-57.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Garloff 2016","Positive","27.37",0,NA,30.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"804",25252,"P2",.60883,405515,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7325,90.3986,"2017-01-22","Dry","Dry",-
0.776796,1,"BD-Dhaka-Suhrawardy Udyan-2017Jan22","BDADC-57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-23","male","BDADC-57.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Garloff 2016","Positive","30.18",0,NA,29.16,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"805",25288,"P2",.57481,404494,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776555,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-62","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-62.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Garloff
2016","Positive","27.5",0,NA,34.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"806",25289,"P2",.71068,404494,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776555,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-62","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-62.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Garloff 2016","Positive","27.37",0,NA,35.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"807",25290,"P2",.70884,404494,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776555,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-62","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-62.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Garloff 2016","Positive","30.18",0,NA,45.36,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"808",25292,"P2",.70276,404493,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-62","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-62.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Garloff
2016","Positive","27.5",0,NA,27.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"809",25294,"P2",.70963,404493,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-62","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-62.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Garloff 2016","Positive","27.37",0,NA,29.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"810",25295,"P2",.69979,404493,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-62","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-62.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Garloff 2016","Positive","30.18",0,NA,29.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"811",25298,"P2",.79482,404493,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-63","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-63.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Garloff 2016","Positive","27.5",0,NA,28.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"812",25299,"P2",.70093,404492,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-63","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-63.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Garloff 2016","Positive","27.37",0,NA,28.9,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"813",25300,"P2",.70085,404493,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-63","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-63.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Garloff 2016","Positive","30.18",0,NA,28.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"814",25303,"P2",.70271,404493,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-63","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-63.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Garloff
2016","Positive","27.5",0,NA,24.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"815",25304,"P2",.70864,404493,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-63","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-63.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Garloff 2016","Positive","27.37",0,NA,25.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"816",25305,"P2",.69990,404491,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776560,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-63","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-63.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Garloff 2016","Positive","30.18",0,NA,24.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"817",25308,"P2",.79483,405016,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776555,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-64","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-64.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Garloff
2016","Positive","27.5",0,NA,31.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"818",25309,"P2",.79070,405016,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776503,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-64","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID

certain","2017-01-24","male","BDADC-64.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,30.68,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"819",25018,"P2",170086.40516,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776505,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-64","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-64.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","38.18",0,NA,35.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"820",25020,"P2",170178.40585,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-64","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-64.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"821",25024,"P2",170583.40593,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4056,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-64","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-64.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,28.19,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"822",25010,"P2",169988.40595,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-64","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-64.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","38.18",0,NA,27.2,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"823",25018,"P2",174484.40594,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776505,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-65","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-65.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,35.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"824",25020,"P2",170378.40563,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4056,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-65","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-65.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.19,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"825",25024,"P2",170566.40563,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-65","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-65.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,24.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"826",25025,"P2",169980.40563,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-65","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-65.OPV","oral swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","38.18",0,NA,23.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"827",25028,"P2",170205.40562,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-66","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-66.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"828",25029,"P2",170829.40562,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-66","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-66.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,25.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"829",25030,"P2",169942.40562,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4052,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-66","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-66.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","38.18",0,NA,24.59,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"830",25033,"P2",170540.40550,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-67","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-67.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,32.19,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"831",25034,"P2",170837.40550,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-67","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-67.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,33.16,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"832",25035,"P2",169943.40550,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785,90.4,23.783,90.4055,"2017-01-22","Dry","Dry",-
0.776565,1,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan22","BDADC-67","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","female","BDADC-67.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","38.18",0,NA,23.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"833",25038,"P2",170341.344328,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.785,90.4,23.7378,90.403,"2017-01-22","Dry","Dry",-0.770786,1,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-68","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-68.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,30.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"834",25039,"P2",170928.344328,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.785,90.4,23.7378,90.403,"2017-01-22","Dry","Dry",-0.770786,1,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-68","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-68.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"835",25041,"P2",169944.344333,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.785,90.4,23.7378,90.403,"2017-01-22","Dry","Dry",-0.770786,1,"BD-

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Dhaka-Ramna Park-2017Jan22","BDADC-68","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-68.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,25.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1936",25243,"F2",17042.34436,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-69","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-69.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1937",25244,"F2",17042.34436,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-69","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-69.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,25.98,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1938",25245,"F2",17042.34436,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-69","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-69.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,23.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1939",25254,"F2",17465.34436,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-70","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-70.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,25.67,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1940",25255,"F2",17077.34436,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-70","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-70.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,25.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1941",25256,"F2",17008.34436,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-70","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-70.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,24.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1942",25258,"F2",17080.34435,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-70","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-70.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,15.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1943",25260,"F2",17086.34435,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-70","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-70.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,21.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1944",25261,"F2",16.0983.34435,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-70","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-70.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,20.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1945",25264,"F2",17038.34432,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-71","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-71.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,21.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1946",25265,"F2",17088.34433,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-71","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-71.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,24.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1947",25266,"F2",16.9994.34433,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-71","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","male","BDADC-71.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,22.67,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1948",25268,"F2",17486.34432,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-72","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","female","BDADC-72.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,20.20,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1949",25270,"F2",17073.34432,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-72","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","female","BDADC-72.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.97",0,NA,22.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1950",25271,"F2",17085.34432,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-72","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","female","BDADC-72.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,21.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1951",25274,"F2",17082.34428,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380 4,23.7376,90.4003,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-72","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","female","BDADC-72.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"852",25075,"P2",170868.34426,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,90.4093,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-72","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","female","BDADC-72.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.97",0,NA,37.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"853",25076,"P2",169385.34430,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7380,90.4093,"2017-01-22","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan22","BDADC-72","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
24","female","BDADC-72.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.18",0,NA,35.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"854",25085,"P2",170345.344302,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7380,90.4093,2021,"2017-01-24","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan24","BDADC-73","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-73.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.2",0,NA,30.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"855",25086,"P2",170532.344302,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7380,90.4093,2021,"2017-01-24","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan24","BDADC-73","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-73.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.97",0,NA,20.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"856",25087,"P2",169948.344303,"Bangladesh","Yes","Dhaka-Dhaka University","Independent Site","Dhaka Division","Dhaka",23.7380,90.4093,2021,"2017-01-24","Dry","Dry",-
0.770761,"BD-Dhaka-Dhaka University-2017Jan24","BDADC-73","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-24","male","BDADC-73.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,30.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"857",25425,"P2",170556.344485,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-78","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","female","BDADC-78.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gorloff 2016","Positive","27.5",0,NA,26.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"858",25426,"P2",170537.344485,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-78","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","female","BDADC-78.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.97",0,NA,26.16,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"859",25427,"P2",169853.344485,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-78","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","female","BDADC-78.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,26.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"860",25430,"P2",171487.344484,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-79","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","male","BDADC-79.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,28.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"861",25431,"P2",170974.344484,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-79","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","male","BDADC-79.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gorloff 2016","Positive","27.97",0,NA,37.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"862",25432,"P2",170890.344484,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-79","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","male","BDADC-79.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gorloff 2016","Positive","30.18",0,NA,31.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"863",25435,"P2",170363.344483,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-79","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","male","BDADC-79.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.5",0,NA,25.94,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"864",25436,"P2",170970.344483,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-79","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","male","BDADC-79.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.97",0,NA,25.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"865",25437,"P2",169886.344483,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-79","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","male","BDADC-79.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,27.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"866",25445,"P2",171384.344480,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-80","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-80.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.5",0,NA,30.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"867",25446,"P2",170971.344480,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-80","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","male","BDADC-80.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.97",0,NA,23.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"868",25447,"P2",169597.344480,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7380,90.4055,"2017-01-25","Dry","Dry",-
0.776505.2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-80","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-80.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza

A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,28.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"869",25453,"P2",17485.244483,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-81","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","female","BDADC-81.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,13.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"870",25454,"P2",17078.344483,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-81","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","female","BDADC-81.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,21.16,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"871",25452,"P2",17009.244485,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-81","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","female","BDADC-81.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,21.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"872",25455,"P2",17065.344479,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-81","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","female","BDADC-81.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,18.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"873",25456,"P2",17072.244479,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-81","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","female","BDADC-81.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,23.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"874",25457,"P2",18088.244479,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-81","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","female","BDADC-81.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,18.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"875",25458,"P2",17480.244478,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-82","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-82.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,23.19,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"876",25459,"P2",17077.344478,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-82","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-82.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,23.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"877",25462,"P2",17008.244478,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-82","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-82.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"878",25460,"P2",17085.244477,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-82","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-82.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,21.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"879",25466,"P2",17083.244477,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-82","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-82.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,21.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"880",25467,"P2",18088.244477,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-82","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-82.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,27.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"881",25470,"P2",17148.244475,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-83","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-83.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"882",25471,"P2",17078.344476,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-83","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-83.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.87",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"883",25472,"P2",17009.244475,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-83","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-83.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.18",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"884",25473,"P2",17087.244475,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-83","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-26","male","BDADC-83.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,25.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"885",25480,"P2",17020.244473,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.785041,90.404055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-84","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID

certain","2017-01-25","female","BDADC-84.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gorlaff 2016","Positive","27.5",0,NA,27.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"886",25487,"P2",.370938,.344471,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7823,90.4055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-84","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","female","BDADC-84.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorlaff 2016","Positive","27.97",0,NA,26.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"887",25488,"P2",.369354,.344471,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.41,23.7823,90.4055,"2017-01-25","Dry","Dry",-
0.776505,2,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan25","BDADC-84","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-25","female","BDADC-84.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorlaff 2016","Positive","30.9",0,NA,27.09,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"888",25482,"P2",.37482,.344308,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-85","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-85.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorlaff
2016","Positive","27.5",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"889",25483,"P2",.37079,.344308,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-85","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-85.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorlaff
2016","Positive","27.97",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"890",25484,"P2",.370895,.344308,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-85","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-85.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorlaff
2016","Positive","30.8",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"891",25503,"P2",.37388,.344307,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-85","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-85.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorlaff
2016","Positive","27.5",0,NA,24.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"892",25504,"P2",.370975,.344307,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-85","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-85.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorlaff
2016","Positive","27.97",0,NA,28.06,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"893",25505,"P2",.40308,.344307,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-85","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-85.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorlaff
2016","Positive","30.8",0,NA,34.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"894",25506,"P2",.37483,.344306,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-86","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-86.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorlaff
2016","Positive","27.5",0,NA,27.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"895",25507,"P2",.37080,.344306,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-86","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-86.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorlaff
2016","Positive","27.97",0,NA,31.98,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"896",25508,"P2",.370896,.344306,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-86","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-86.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorlaff
2016","Positive","30.8",0,NA,32.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"897",25544,"P2",.37288,.344305,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-86","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-86.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorlaff
2016","Positive","27.5",0,NA,21.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"898",25545,"P2",.370976,.344305,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-86","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-86.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorlaff
2016","Positive","27.97",0,NA,25.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"899",25546,"P2",.400093,.344305,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-86","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-86.OPY","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorlaff
2016","Positive","30.8",0,NA,25.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"900",25569,"P2",.37484,.344304,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-87","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-87.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorlaff
2016","Positive","27.5",0,NA,29.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"901",25620,"P2",.37080,.344304,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDADC-87","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDADC-87.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorlaff
2016","Positive","27.97",0,NA,33.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"902",25621,"P2",.370897,.344304,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.41,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-

Dhaka-Ramna Park-2017Jan26","BDAOC-87","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-87.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5N1","other-Gerloff
2016","Positive","38.18",0,NA,32,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"903",25524,"P2",370280,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-87","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-87.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"904",25525,"P2",370871,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-87","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-87.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,30.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"905",25523,"P2",369992,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-87","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-87.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.18",0,NA,29.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"906",25529,"P2",370352,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-88","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-88.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"907",25530,"P2",370839,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-88","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-88.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,28.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"908",25531,"P2",369555,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-88","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-88.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.18",0,NA,27.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"909",25534,"P2",374955,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-89","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-89.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,27.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"910",25535,"P2",370382,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-89","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-89.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,24.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"911",25536,"P2",370098,344303,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-89","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-89.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","38.18",0,NA,22.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"912",25538,"P2",370128,344298,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-89","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-89.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,24.41,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"913",25540,"P2",370378,344298,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-89","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-89.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff
2016","Positive","27.87",0,NA,26.09,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"914",25541,"P2",369994,344298,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.78,90.4,23.7376,90.4003,"2017-01-26","Dry","Dry",-0.770761,"BD-
Dhaka-Ramna Park-2017Jan26","BDAOC-89","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
26","male","BDAOC-89.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff
2016","Positive","30.18",0,NA,24.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"915",25551,"P2",370202,344471,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-90","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-90.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,25.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"916",25552,"P2",370940,344471,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-90","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-90.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,25.86,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"917",25553,"P2",369956,344471,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-90","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-90.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.18",0,NA,25.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"918",25556,"P2",374486,344470,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.776565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-91","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-91.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,29.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"919",25557,"P2",170083.344470,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-01CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.57",0,NA,22.01,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"920",25558,"P2",170085.344470,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-01CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,31.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"921",25560,"P2",170203.344465,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-01OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,18.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"922",25562,"P2",170079.344469,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-01OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.07",0,NA,18.61,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"923",25563,"P2",169995.344469,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-01","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-01OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.8",0,NA,18.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"924",25566,"P2",174987.344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-02CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff
2016","Positive","27.5",0,NA,35.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"925",25567,"P2",170084.344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-02CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.57",0,NA,37.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"926",25569,"P2",170008.344458,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-02CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,24.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"927",25571,"P2",170203.344457,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-02OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,24.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"928",25572,"P2",170080.344457,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-02OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.07",0,NA,25.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"929",25573,"P2",169995.344457,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-02","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDAOC-02OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","30.8",0,NA,24.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"930",25575,"P2",174988.344456,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","female","BDAOC-03CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gerloff 2016","Positive","27.5",0,NA,24.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"931",25577,"P2",170085.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","female","BDAOC-03CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-
Gerloff 2016","Positive","27.57",0,NA,21.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"932",25578,"P2",170083.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","female","BDAOC-03CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-
Gerloff 2016","Positive","30.8",0,NA,75.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"933",25580,"P2",170284.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","female","BDAOC-03OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.5",0,NA,21.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"934",25582,"P2",170088.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","female","BDAOC-03OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","27.07",0,NA,22.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"935",25583,"P2",169997.344455,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDAOC-03","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","female","BDAOC-03OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza

A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,21.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"936",25586,"P2",170354,244238,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-54.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,27.56,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"937",25587,"P2",170364,244259,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-54.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.97",0,NA,24.13,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"938",25588,"P2",169957,244238,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-54","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-54.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.18",0,NA,22.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"939",25589,"P2",174189,244280,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-55","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-55.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,28.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"940",25590,"P2",170385,244279,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-55","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-55.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,23.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"941",25591,"P2",170382,244279,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-55","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-55.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.97",0,NA,24.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"942",25598,"P2",169598,244279,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-55","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-55.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.18",0,NA,23.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"943",25602,"P2",170398,244271,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-56","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-56.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff
2016","Positive","27.5",0,NA,22.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"944",25603,"P2",170383,244271,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-56","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-56.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff
2016","Positive","27.97",0,NA,27.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"945",25604,"P2",169909,244271,"Bangladesh","Yes","Dhaka-Ramna Park","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7376,90.4003,"2017-01-28","Dry","Dry",-0.770764,"BD-
Dhaka-Ramna Park-2017Jan28","BDADC-56","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-
28","male","BDADC-56.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gorloff
2016","Positive","30.18",0,NA,23.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"946",25625,"P2",170353,244003,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7325,90.3986,"2017-01-28","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan28","BDADC-57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-57.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.5",0,NA,25.81,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"947",25626,"P2",170342,244003,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7325,90.3986,"2017-01-28","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan28","BDADC-57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-57.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.97",0,NA,27.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"948",25627,"P2",169958,244003,"Bangladesh","Yes","Dhaka-Suhrawardy Udyan","Independent Site","Dhaka Division","Dhaka",23.7850,4.23.7325,90.3986,"2017-01-28","Dry","Dry",-
0.770761,"BD-Dhaka-Suhrawardy Udyan-2017Jan28","BDADC-57","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-28","male","BDADC-57.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,27.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"949",25635,"P2",170356,244463,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4.23.7803,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-58","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-58.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-
Gorloff 2016","Positive","27.5",0,NA,23.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"950",25637,"P2",170943,244463,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4.23.7803,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-58","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-58.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","27.97",0,NA,23.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"951",25638,"P2",169958,244463,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4.23.7803,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-58","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID
certain","2017-01-29","male","BDADC-58.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","30.18",0,NA,22.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"952",25642,"P2",170520,244463,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTCL","Concurrent Site 2","Dhaka Division","Dhaka",23.7850,4.23.7803,90.4055,"2017-01-28","Dry","Dry",-
0.779565,6,"BD-Dhaka-Mohakhali-TT Colony-BTCL-2017Jan28","BDADC-59","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID

certain","2017-01-28","female","BDAOC-59.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,24.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"953",25643,"PT",170868,244462,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-0.776505,6,"BD-Dhaka-Mohakhali-TT Colony-BTD-2017Jan28","BDAOC-59","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-28","female","BDAOC-59.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,27.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"954",25644,"PT",170904,244463,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-0.776505,6,"BD-Dhaka-Mohakhali-TT Colony-BTD-2017Jan28","BDAOC-59","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-28","female","BDAOC-59.CLV","cloacal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.16",0,NA,26.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"955",25647,"PT",170287,244448,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-0.776505,6,"BD-Dhaka-Mohakhali-TT Colony-BTD-2017Jan28","BDAOC-59","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-28","female","BDAOC-59.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.5",0,NA,19.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"956",25645,"PT",170884,244460,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-0.776505,6,"BD-Dhaka-Mohakhali-TT Colony-BTD-2017Jan28","BDAOC-59","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-28","female","BDAOC-59.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","27.87",0,NA,23.43,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"957",25648,"PT",170000,244481,"Bangladesh","Yes","Dhaka-Mohakhali-TT Colony-BTD","Concurrent Site 2","Dhaka Division","Dhaka",23.78,90.4,23.783,90.4055,"2017-01-28","Dry","Dry",-0.776505,6,"BD-Dhaka-Mohakhali-TT Colony-BTD-2017Jan28","BDAOC-59","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-28","female","BDAOC-59.OPV","oropharyngeal swab","2017-03-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","30.16",0,NA,10.16,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"958",63208,"PT",169903,279479,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.587,24.3824,88.5868,"2017-01-12","Dry","Dry",-0.5092702,5,"BD-Rajshahi-Lakkhipur Bazar-2017Jan12","BDARAJ-002","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offals","field ID certainty unknown","2017-01-12","unknown","BDARAJ-002.TIV","other tissue-offal","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.07",0,NA,29.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"959",63209,"PT",170425,279479,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.587,24.3824,88.5868,"2017-01-12","Dry","Dry",-0.5092702,5,"BD-Rajshahi-Lakkhipur Bazar-2017Jan12","BDARAJ-002","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offals","field ID certainty unknown","2017-01-12","unknown","BDARAJ-002.TIV","other tissue-offal","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,31.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"960",63226,"PT",169904,279478,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.587,24.3824,88.5868,"2017-01-12","Dry","Dry",-0.5092702,5,"BD-Rajshahi-Lakkhipur Bazar-2017Jan12","BDARAJ-003","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck",NA,"field ID certain","2017-01-12","unknown","BDARAJ-003.ZJV","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.07",0,NA,29.01,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"961",63229,"PT",170426,279478,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.587,24.3824,88.5868,"2017-01-12","Dry","Dry",-0.5092702,5,"BD-Rajshahi-Lakkhipur Bazar-2017Jan12","BDARAJ-003","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos domesticus","species","Domestic Duck",NA,"field ID certain","2017-01-12","unknown","BDARAJ-003.ZJV","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,20.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"962",63333,"PT",169905,279477,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.587,24.3824,88.5868,"2017-01-12","Dry","Dry",-0.5092702,5,"BD-Rajshahi-Lakkhipur Bazar-2017Jan12","BDARAJ-004","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-12","unknown","BDARAJ-004.ZJV","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.0",0,NA,35.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"963",63358,"PT",170433,469543,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.376,88.586,24.376,88.586,"2017-01-12","Dry","Dry",-0.5092702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan12","BDARAJ-008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaak","field ID certain","2017-01-14","unknown","BDARAJ-008.ZJV","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"964",63330,"PT",169912,293744,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.371,88.5877,24.371,88.5877,"2017-01-12","Dry","Dry",-0.495915,"BD-Rajshahi-Saheb Bazar-2017Jan12","BDARAJ-011","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-12","unknown","BDARAJ-011.ZJV","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.07",0,NA,20.75,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"965",63262,"PT",170424,293774,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.371,88.5877,24.371,88.5877,"2017-01-12","Dry","Dry",-0.495915,"BD-Rajshahi-Saheb Bazar-2017Jan12","BDARAJ-011","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-12","unknown","BDARAJ-011.ZJV","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"966",63305,"PT",169983,293740,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.371,88.5877,24.371,88.5877,"2017-01-12","Dry","Dry",-0.495915,"BD-Rajshahi-Saheb Bazar-2017Jan12","BDARAJ-002","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Offals","field ID certainty unknown","2017-01-12","unknown","BDARAJ-002.TIV","other tissue-offal","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.07",0,NA,23.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"967",63277,"PT",168696,293733,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.371,88.5877,24.371,88.5877,"2017-01-12","Dry","Dry",-

0.435015,"BD-Rajshahi-Saheb Bazar-2017Jan03","BDARAI-005","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-01-03","unknown","BDARAI-005.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,22.53,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"868",83378,"P2",170438,250727,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5077,24.3775,88.5077,"2017-01-03","Dry","Dry",-
0.435015,"BD-Rajshahi-Saheb Bazar-2017Jan03","BDARAI-005","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-01-03","unknown","BDARAI-005.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","28.41",0,NA,34.45,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"869",83404,"P2",169393,227708,"Bangladesh","Yes","Rajshahi-Talaimari Market","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5868,24.361,88.6258,"2017-01-14","Dry","Dry",-
0.5530026.2,"BD-Rajshahi-Talaimari Market-2017Jan14","BDARAI-020","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-14","unknown","BDARAI-020.22V","urine/feces combined (guano)","2017-01-25","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.12",0,NA,22.8,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"870",83405,"P2",170443,227708,"Bangladesh","Yes","Rajshahi-Talaimari Market","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5868,24.361,88.6258,"2017-01-14","Dry","Dry",-
0.5530026.2,"BD-Rajshahi-Talaimari Market-2017Jan14","BDARAI-020","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-14","unknown","BDARAI-020.22V","urine/feces combined (guano)","2017-01-25","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","28.41",0,NA,40.75,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"871",83442,"P2",169323,229434,"Bangladesh","Yes","Rajshahi-Binodpur Market","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5969,24.3678,88.6441,"2017-01-14","Dry","Dry",-
0.5530026.1,"BD-Rajshahi-Binodpur Market-2017Jan14","BDARAI-022","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-14","unknown","BDARAI-022.22V","urine/feces combined (guano)","2017-01-25","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.12",0,NA,25.21,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"872",83445,"P2",169470,229434,"Bangladesh","Yes","Rajshahi-Binodpur Market","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5969,24.3678,88.6441,"2017-01-14","Dry","Dry",-
0.5530026.1,"BD-Rajshahi-Binodpur Market-2017Jan14","BDARAI-022","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-14","unknown","BDARAI-022.22V","urine/feces combined (guano)","2017-01-25","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gorloff 2016","Positive","25.92",0,NA,24.12,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"873",83474,"P2",169376,229458,"Bangladesh","Yes","Rajshahi-Binodpur Market","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5969,24.3678,88.6441,"2017-01-14","Dry","Dry",-
0.5530026.1,"BD-Rajshahi-Binodpur Market-2017Jan14","BDARAI-025","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-01-14","unknown","BDARAI-025.27V","other tissue offal","2017-01-25","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.12",0,NA,31.05,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"874",83477,"P2",169473,229458,"Bangladesh","Yes","Rajshahi-Binodpur Market","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5969,24.3678,88.6441,"2017-01-14","Dry","Dry",-
0.5530026.1,"BD-Rajshahi-Binodpur Market-2017Jan14","BDARAI-025","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-01-14","unknown","BDARAI-025.27V","other tissue offal","2017-01-25","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gorloff 2016","Positive","26.87",0,NA,29.41,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"875",83422,"P2",169378,227623,"Bangladesh","Yes","Rajshahi-Sapura Nowdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3716,88.586,24.4033,88.6072,"2017-01-
14","Dry","Dry",-0.435018.2,"BD-Rajshahi-Sapura-Nowdapara Bazar-2017Jan14","BDARAI-027","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-14","unknown","BDARAI-027.22V","urine/feces combined (guano)","2017-01-25","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.12",0,NA,31.89,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"876",83446,"P2",169830,227623,"Bangladesh","Yes","Rajshahi-Sapura Nowdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3716,88.586,24.4033,88.6072,"2017-01-
14","Dry","Dry",-0.435018.2,"BD-Rajshahi-Sapura-Nowdapara Bazar-2017Jan14","BDARAI-029","poultry/other fowl","owned domesticated species ","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-01-14","unknown","BDARAI-029.27V","other tissue offal","2017-01-25","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.12",0,NA,31.99,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"877",83471,"P2",169326,234918,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-01-14","Dry","Dry",-
0.435011,"BD-Rajshahi-Shalbagan-2017Jan14","BDARAI-035","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck","Duck","field ID certain","2017-01-14","unknown","BDARAI-035.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","28.12",0,NA,31.02,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"878",83478,"P2",170458,234918,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-01-14","Dry","Dry",-
0.435011,"BD-Rajshahi-Shalbagan-2017Jan14","BDARAI-035","poultry/other fowl","owned domesticated species ","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck","Duck","field ID certain","2017-01-14","unknown","BDARAI-035.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","28.41",0,NA,32.53,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"879",83553,"P2",169344,250716,"Bangladesh","Yes","Rajshahi-Boalia Kharkhari poultry farm","Independent Site","Rajshahi Division","Rajshahi",24.378,88.586,24.38,88.6,"2017-01-
15","Dry","Dry",-0.5092052.1,"BD-Padmar Par Boroikudhi-Crow Roost-2017Jan15","BDARAI-042","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow",NA,"field ID certain","2017-01-15","unknown","BDARAI-042.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gorloff 2016","Positive","29.12",0,NA,30.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"880",83553,"P2",170466,250716,"Bangladesh","Yes","Rajshahi-Boalia Kharkhari poultry farm","Independent Site","Rajshahi Division","Rajshahi",24.378,88.586,24.38,88.6,"2017-01-
15","Dry","Dry",-0.5092052.1,"BD-Padmar Par Boroikudhi-Crow Roost-2017Jan15","BDARAI-042","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow",NA,"field ID certain","2017-01-15","unknown","BDARAI-042.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","28.41",0,NA,34.41,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"981",62574,"P2",986953.293797,"Bangladesh","Yes","Rajshahi-Boalia-Kharkhari poultry farm","Independent Site","Rajshahi Division","Rajshahi",24.378,88.586,24.36,88.6,"2017-01-
15","Dry","Dry",-0.5093921,"BD-Padmar Par-Barakuthi-Crow Roost-2017Jan15","BDARAI-052","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow",NA,"field ID certain","2017-01-15","unknown","BDARAI-052.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,33.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"982",62575,"P2",770475.293797,"Bangladesh","Yes","Rajshahi-Boalia-Kharkhari poultry farm","Independent Site","Rajshahi Division","Rajshahi",24.378,88.586,24.36,88.6,"2017-01-
15","Dry","Dry",-0.5093921,"BD-Padmar Par-Barakuthi-Crow Roost-2017Jan15","BDARAI-052","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow",NA,"field ID certain","2017-01-15","unknown","BDARAI-052.22V","urine/feces combined (guano)","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.4",0,NA,37.65,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"983",62858,"P2",167028.234874,"Bangladesh","Yes","Rajshahi-Sapura-Nawdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3776,88.586,24.4033,88.6071,"2017-01-
17","Dry","Dry",-0.4958.2,"BD-Rajshahi-Sapura-Nawdapara Bazar-2017Jan17","BDARAI-163","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-17","unknown","BDARAI-163.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,29.18,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"984",62980,"P2",167055.234808,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.383,88.597,24.3865,88.6074,"2017-01-17","Dry","Dry",-
0.4958.2,"BD-Rajshahi-Shalbagan-2017Jan17","BDARAI-168","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Sonali","field ID certain","2017-01-17","unknown","BDARAI-168.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,35.76,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"985",62993,"P2",167057.234805,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.383,88.597,24.3865,88.6074,"2017-01-17","Dry","Dry",-
0.4958.2,"BD-Rajshahi-Shalbagan-2017Jan17","BDARAI-170","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Layer","field ID certain","2017-01-17","unknown","BDARAI-170.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,36.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"986",64025,"P2",167080.293773,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5977,24.379,88.5971,"2017-01-17","Dry","Dry",-
0.4958.5,"BD-Rajshahi-Saheb Bazar-2017Jan13","BDARAI-173","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck","Duck","field ID certain","2017-01-17","unknown","BDARAI-173.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,33.13,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"987",64026,"P2",170582.293773,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5977,24.379,88.5977,"2017-01-17","Dry","Dry",-
0.4958.5,"BD-Rajshahi-Saheb Bazar-2017Jan13","BDARAI-173","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck","Duck","field ID certain","2017-01-17","unknown","BDARAI-173.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.4",0,NA,33.7,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"988",64079,"P2",167043.234868,"Bangladesh","Yes","Rajshahi-Sapura-Nawdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3776,88.586,24.4033,88.6071,"2017-01-
17","Dry","Dry",-0.4958.2,"BD-Rajshahi-Sapura-Nawdapara Bazar-2017Jan17","BDARAI-192","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-01-18","unknown","BDARAI-192.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,33.5,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"989",64082,"P2",167044.234857,"Bangladesh","Yes","Rajshahi-Sapura-Nawdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3776,88.586,24.4033,88.6072,"2017-01-
17","Dry","Dry",-0.4958.2,"BD-Rajshahi-Sapura-Nawdapara Bazar-2017Jan17","BDARAI-193","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-18","unknown","BDARAI-193.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,31.73,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"990",64085,"P2",169519.234867,"Bangladesh","Yes","Rajshahi-Sapura-Nawdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3776,88.586,24.4033,88.6071,"2017-01-
17","Dry","Dry",-0.4958.2,"BD-Rajshahi-Sapura-Nawdapara Bazar-2017Jan17","BDARAI-193","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-01-18","unknown","BDARAI-193.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H9","other-Gerloff 2016","Positive","35.8",0,NA,29.18,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"991",64092,"P2",167045.234875,"Bangladesh","Yes","Rajshahi-Sapura-Nawdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3776,88.586,24.4033,88.6071,"2017-01-
17","Dry","Dry",-0.4958.2,"BD-Rajshahi-Sapura-Nawdapara Bazar-2017Jan17","BDARAI-194","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-01-18","unknown","BDARAI-194.22V","urine/feces combined (guano)","2017-02-08","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,33.58,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"992",64105,"P2",167068.234894,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.383,88.597,24.3865,88.6074,"2017-01-17","Dry","Dry",-
0.4958.2,"BD-Rajshahi-Shalbagan-2017Jan17","BDARAI-197","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Broiler","field ID certain","2017-01-18","unknown","BDARAI-197.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,35.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"993",64106,"P2",170590.234884,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.383,88.597,24.3865,88.6074,"2017-01-17","Dry","Dry",-
0.4958.2,"BD-Rajshahi-Shalbagan-2017Jan17","BDARAI-197","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Broiler","field ID certain","2017-01-18","unknown","BDARAI-197.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.4",0,NA,35.28,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"994",64109,"P2",167069.234893,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.383,88.597,24.3865,88.6074,"2017-01-17","Dry","Dry",-
0.4958.2,"BD-Rajshahi-Shalbagan-2017Jan17","BDARAI-198","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Sonali","field ID certain","2017-01-18","unknown","BDARAI-198.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,32.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth

Alliance"
"995",84613,"P2",.87070,254882,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.392,88.6037,24.3915,88.6074,"2017-01-17","Dry","Dry",-
0.45598.2,"BD-Rajshahi-Shalbagan-2017Jan17","BDARAI-199","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Shalo","wild ID certainty unknown","2017-01-16","unknown","BDARAI-199.22V","other tissue-offal","2017-03-29","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,27.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"996",84614,"P2",.870582,254882,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.392,88.6037,24.3915,88.6074,"2017-01-17","Dry","Dry",-
0.45598.2,"BD-Rajshahi-Shalbagan-2017Jan17","BDARAI-199","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Shalo","wild ID certainty unknown","2017-01-16","unknown","BDARAI-199.22V","other tissue-offal","2017-03-29","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","25.47",0,NA,22.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"997",84632,"P2",.87078,292747,"Bangladesh","Yes","Rajshahi Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.371,88.5977,24.3771,88.5977,"2017-01-12","Dry","Dry",-
0.45598.5,"BD-Rajshahi Saheb Bazar 2017Jan12","BDARAI-202","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-01-16","unknown","BDARAI-202.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,25.55,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"998",84643,"P2",.870703,292745,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5977,24.377,88.5977,"2017-01-12","Dry","Dry",-
0.45598.5,"BD-Rajshahi-Saheb Bazar-2017Jan12","BDARAI-204","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Sonali","field ID certain","2017-01-16","unknown","BDARAI-204.22V","urine/feces combined (guano)","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,25.87,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"999",84658,"P2",.870716,292742,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5977,24.377,88.5977,"2017-01-12","Dry","Dry",-
0.45598.5,"BD-Rajshahi-Saheb Bazar-2017Jan12","BDARAI-207","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Shalo","wild ID certainty unknown","2017-01-16","unknown","BDARAI-207.22V","other tissue-offal","2017-03-20","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,24.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1000",84682,"P2",.870877,279460,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-01-17","Dry","Dry",-
0.5092762.5,"BD-Rajshahi-Lakkhipur Bazar-2017Jan17","BDARAI-208","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Deshi","field ID certain","2017-01-18","unknown","BDARAI-208.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,34.41,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1001",84684,"P2",.870909,279460,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-01-12","Dry","Dry",-
0.5092762.5,"BD-Rajshahi-Lakkhipur Bazar-2017Jan17","BDARAI-208","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Deshi","field ID certain","2017-01-18","unknown","BDARAI-208.22V","urine/feces combined (guano)","2017-03-20","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","25.47",0,NA,25.16,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1002",84302,"P2",.428630,838778,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5968,24.3674,88.5968,"2017-01-
18","Dry","Dry",-0.50929121,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan18","BDARAIOP-044","dogs","unowned domesticated species","Canis lupus familiaris","Canis lupus
familiaris","species","Domestic Dog","Kukur","field ID certain","2017-01-18","female","BDARAIOP-044.RSV","rectal swab","2017-02-02","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","27.29",0,NA,22.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1003",84303,"P2",.428711,838770,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5968,24.3674,88.5968,"2017-01-
18","Dry","Dry",-0.50929121,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan18","BDARAIOP-044","dogs","unowned domesticated species","Canis lupus familiaris","Canis lupus
familiaris","species","Domestic Dog","Kukur","field ID certain","2017-01-18","female","BDARAIOP-044.RSV","rectal swab","2017-02-02","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","28.87",0,NA,25.95,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1004",84282,"P2",.169879,227385,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.379,88.586,24.379,88.586,"2017-01-
12","Dry","Dry",-0.5092912.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan12","BDARC-008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-12","male","BDARC-008.C1V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,26.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1005",84283,"P2",.170403,227385,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.379,88.585,24.379,88.585,"2017-01-
12","Dry","Dry",-0.5092912.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan12","BDARC-008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-12","male","BDARC-008.C1V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","25.47",0,NA,29.38,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1006",84272,"P2",.168894,227387,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.379,88.586,24.379,88.586,"2017-01-
12","Dry","Dry",-0.5092912.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan12","BDARC-008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-12","male","BDARC-008.OPV1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","25.12",0,NA,18.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1007",84273,"P2",.170363,227387,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.379,88.586,24.379,88.586,"2017-01-
12","Dry","Dry",-0.5092912.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan12","BDARC-008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-12","male","BDARC-008.OPV1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","25.47",0,NA,21.55,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1008",84371,"P2",.168880,227384,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.379,88.586,24.379,88.586,"2017-01-
12","Dry","Dry",-0.5092912.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan12","BDARC-002","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-12","male","BDARC-002.C1V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 25.23 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6009",0A38,"FY",.656842.227282,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-002","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","60AWC-002.OPH.1","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 25.12 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6007",0A3B5,"FY",.705864.227280,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-002","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","60AWC-002.OPH.1","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","29.47","0 NA 27.46 NA NA","Positive","Interpretation

completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6007",0A3B5,"FY",.659888.227278,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-002","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","60AWC-002.CLV.1","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 25.07 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6007",0A3B6,"FY",.701403.227279,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-002","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","60AWC-002.CLV.1","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","29.47","0 NA 27.82 NA NA NA","Positive","Interpretation

completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6007",0A3B5,"FY",.656943.227277,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-002","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","60AWC-002.OPH.1","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 26.05 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6004",0A3B6,"FY",.705805.227277,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-002","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","60AWC-002.OPH.1","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","29.47","0 NA 27.03 NA NA","Positive","Interpretation

completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6005",0A4D5,"FY",.659892.227274,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-004","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","60AWC-004.CLV.1","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 28.87 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6006",0A4D,"FY",.705404.227274,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-004","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","60AWC-004.CLV.1","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","29.47","0 NA 24.48 NA NA","Positive","Interpretation

completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6007",0A4D5,"FY",.705856.227271,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-004","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","60AWC-004.OPH.1","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47","0 NA 25.04 NA NA","Positive","Interpretation

completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6005",0A4D8,"FY",.656985.227269,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-005","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","60AWC-005.CLV.1","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 28.08 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6005",0A4D8,"FY",.705405.227269,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-005","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","60AWC-005.CLV.1","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47","0 NA 24.54 NA NA","Positive","Interpretation

completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6005",0A4D,"FY",.659845.227267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-005","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","60AWC-005.OPH.1","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 23.24 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"6007",0A4D,"FY",.705867.227267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-

07","Dry","Dry",-0.509292,8,"60-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","60AWC-005","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","60AWC-005.OPH.1","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research

{code:b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47","0 NA 25.51 NA NA","Positive","Interpretation

completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"1822","BA48","PT","BSB894.227284","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi","24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0006","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","BDAWC-0006.D.1.F","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerlich 2006","Positive","25.12","0.NA,22.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1823","BA49","PT","BSB456.227284","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0006","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","BDAWC-0006.DPH.F","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlich 2006","Positive","29.47",0.NA,20.94,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1824","BA4D","PT","BSB268.227282","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0006","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","BDAWC-0006.DPH.F","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlich 2006","Positive","29.47",0.NA,22.56,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1825","BA4N","PT","BSB915.227280","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0007","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","BDAWC-0007.D.1.F","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerlich 2006","Positive","29.47",0.NA,30.59,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1826","BA4Z5","PT","BSB01.227280","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0007","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","BDAWC-0007.D.1.F","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlich 2006","Positive","29.47",0.NA,22.85,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1827","BA4ZA","PT","BSB841.227268","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0007","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","BDAWC-0007.DPH.F","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerlich 2006","Positive","25.12",0.NA,18.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1828","BA4ZQ","PT","BSB368.227268","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0007","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","male","BDAWC-0007.DPH.F","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlich 2006","Positive","29.47",0.NA,21.15,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1829","BA4ZS","PT","BSB898.227266","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","BDAWC-0008.D.1.F","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerlich 2006","Positive","25.12",0.NA,21.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1830","BA4ZU","PT","BSB408.227256","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","BDAWC-0008.D.1.F","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlich 2006","Positive","25.47",0.NA,23.43,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1831","BA4W3","PT","BSB348.227254","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","BDAWC-0008.DPH.F","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerlich 2006","Positive","25.12",0.NA,21.68,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1832","BA4W4","PT","BSB316.227224","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-07","male","BDAWC-0008.DPH.F","oropharyngeal swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlich 2006","Positive","25.47",0.NA,24.05,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1833","BA4X7","PT","BSB897.227202","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0009","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","BDAWC-0009.D.1.F","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerlich 2006","Positive","25.12",0.NA,24.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1834","BA4XB","PT","BSB439.227202","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0009","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-09-14","female","BDAWC-0009.D.1.F","classical swab","2017-09-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlich 2006","Positive","25.47",0.NA,30.22,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"su",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1835","BA4XJ","PT","BSB948.227200","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.370.88.588,"2017-09-
07","Dry","Dry",-0.5202702,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jun07","BDAWC-0009","birds","free-ranging wild animal","Corvus splendens","Corvus

splendens","species","House Crow",NA,"field ID certain","2017-01-14","female","BDARC-005.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,25.93,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1036",84452,"P2",170371.227350,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-005","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","female","BDARC-005.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.4",0,NA,28.28,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1037",84455,"P2",169888.227348,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-010","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","female","BDARC-010.CL.1.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,21.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1038",84456,"P2",170460.227348,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-010","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","female","BDARC-010.CL.1.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.4",0,NA,23.21,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1039",84459,"P2",169850.227346,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-010","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","female","BDARC-010.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,27.09,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1040",84460,"P2",170372.227346,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-010","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","female","BDARC-010.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.4",0,NA,25.15,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1041",84463,"P2",169888.227344,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-011","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","male","BDARC-011.CL.1.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,22.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1042",84464,"P2",170441.227344,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-011","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","male","BDARC-011.CL.1.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.4",2,NA,27.14,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1043",84473,"P2",169854.227342,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-011","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","male","BDARC-011.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,24.47,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1044",84474,"P2",170373.227342,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-
13","Dry","Dry",-0.5092952.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan13","BDARC-011","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-14","male","BDARC-011.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.4",0,NA,27.23,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1045",84476,"P2",169890.227657,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5908,24.3674,88.5908,"2017-01-
15","Dry","Dry",-0.5092952.6,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan15","BDARC-012","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rook","field ID certain","2017-01-15","male","BDARC-012.CL.1.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,25.59,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1046",84479,"P2",170443.227657,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5908,24.3674,88.5908,"2017-01-
15","Dry","Dry",-0.5092952.6,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan15","BDARC-012","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rook","field ID certain","2017-01-15","male","BDARC-012.CL.1.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A/H5a","other-Gerloff 2016","Positive","25.4",0,NA,26.48,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1047",84488,"P2",169852.227655,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5908,24.3674,88.5908,"2017-01-
15","Dry","Dry",-0.5092952.6,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan15","BDARC-012","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rook","field ID certain","2017-01-15","male","BDARC-012.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,25.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1048",84489,"P2",170374.227655,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5908,24.3674,88.5908,"2017-01-
15","Dry","Dry",-0.5092952.6,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan15","BDARC-012","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rook","field ID certain","2017-01-15","male","BDARC-012.OP.1.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.4",0,NA,28.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1049",84453,"P2",169889.227653,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5908,24.3674,88.5908,"2017-01-
15","Dry","Dry",-0.5092952.6,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan15","BDARC-013","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rook","field ID certain","2017-01-15","male","BDARC-013.CL.1.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-

Influenza A","other-Gorleff 2016","Positive","28.12",0,NA,25.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1050",84494,"P2",170443.227650,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3024,88.5908,24.3024,88.5908,"2017-01-
05","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan05","BDARC-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-05","male","BDARC-003.CL.V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A/H5a","other-Gorleff 2016","Positive","29.41",0,NA,27.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1051",84492,"P2",169853.227650,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3024,88.5908,24.3024,88.5908,"2017-01-
05","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan05","BDARC-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-05","male","BDARC-003.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gorleff 2016","Positive","28.12",0,NA,27.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1052",84488,"P2",170275.227650,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3024,88.5908,24.3024,88.5908,"2017-01-
05","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Padmar Par-Barakuthi-2017Jan05","BDARC-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-05","male","BDARC-003.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gorleff 2016","Positive","29.41",0,NA,24.41,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1053",84500,"P2",169993.227340,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-004","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-004.CL.V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorleff 2016","Positive","25.12",0,NA,25.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1054",84502,"P2",170444.227340,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-004","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-004.CL.V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorleff 2016","Positive","29.41",0,NA,25.35,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1055",84501,"P2",169854.227338,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-004","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-004.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorleff 2016","Positive","25.12",0,NA,23.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1056",84502,"P2",170376.227338,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-004","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-004.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorleff 2016","Positive","29.41",0,NA,24.07,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1057",84516,"P2",169993.227336,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-005","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-005.CL.V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorleff 2016","Positive","25.12",0,NA,19.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1058",84517,"P2",170445.227336,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-005","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-005.CL.V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorleff 2016","Positive","29.41",0,NA,21.18,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1059",84520,"P2",169855.227334,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-005","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-005.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorleff 2016","Positive","25.12",0,NA,22.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1060",84521,"P2",170377.227334,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-005","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-005.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorleff 2016","Positive","29.41",0,NA,24.97,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1061",84524,"P2",169994.227332,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-006","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-006.CL.V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorleff 2016","Positive","25.12",0,NA,20.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1062",84525,"P2",170446.227332,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-006","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-006.CL.V1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorleff 2016","Positive","29.41",0,NA,22.48,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1063",84528,"P2",169856.227330,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5865,24.3718,88.5865,"2017-01-
07","Dry","Dry",-0.5030912,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan07","BDARC-006","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-05","male","BDARC-006.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorleff 2016","Positive","25.12",0,NA,26.26,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth

Alliance"
"1004",84528,"P2","(1)278,227330","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.580,24.370,88.580,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-096","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-096.DPI.1","oropharyngeal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-GenRef 2006","Positive","28.47",0.64,30.79,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1003",84532,"P2",-89.6894,277327,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.586,24.370,88.586,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-097","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-097.CLV.1","cloacal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-GenRef 2006","Positive","25.12",0.64,24.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1005",84533,"P2",-17.0947,277327,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.589,24.370,88.589,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-097","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-097.CLV.1","cloacal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-GenRef 2006","Positive","25.47",0.64,27.35,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1007",84538,"P2",-89.6857,277325,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.588,24.371,88.588,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-097","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-097.OPH.1","oropharyngeal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-GenRef 2006","Positive","25.12",0.64,31.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1008",84537,"P2",-(1)278,227325,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.588,24.370,88.588,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-097","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-097.OPH.1","oropharyngeal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-GenRef 2006","Positive","25.47",0.64,27.88,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1009",84540,"P2",-89.6856,277327,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.589,24.370,88.589,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-098","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","female","BDARC-098.CLV.1","cloacal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-GenRef 2006","Positive","25.12",0.64,25.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1010",84541,"P2",-(1)249,277327,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.589,24.370,88.589,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-098","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","female","BDARC-098.CLV.1","cloacal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-GenRef 2006","Positive","25.47",0.64,22.17,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1011",84558,"P2",-88.858,277328,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.588,24.370,88.588,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-098","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","female","BDARC-098.OPH.1","oropharyngeal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-GenRef 2006","Positive","25.12",0.64,22.8,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1012",84559,"P2",-(1)2368,277327,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.588,24.370,88.588,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-098","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","female","BDARC-098.OPH.1","oropharyngeal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-GenRef 2006","Positive","29.47",0.64,23.36,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1013",84555,"P2",-89.6897,277327,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.588,24.370,88.588,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-099","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-099.CLV.1","cloacal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-GenRef 2006","Positive","29.12",0.64,35.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1014",84556,"P2",-(1)949,277327,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.589,24.370,88.589,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-099","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-099.CLV.1","cloacal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-GenRef 2006","Positive","25.47",0.64,26.27,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1015",84560,"P2",-(1)269,227326,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370,88.588,24.370,88.588,"2017-01-
0","Dry","Dry",-0.309292,8,"80-Rajshahi-Rajshahi Medical College Hospital-2017Jan-0","BBARC-099","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-15","male","BDARC-099.OPH.1","oropharyngeal swab","2017-01-23","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-GenRef 2006","Positive","25.47",0.64,25.03,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1016",84563,"P2",-89.6898,277548,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3824,88.5868,"2017-01-
15","Dry","Dry",-0.309292,8,"80-Rajshahi-Padmar Par-Barakuthi-2017Jan15","BBARC-020","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rasik","Yaki ID certain","2017-01-15","female","BDARC-020.CLV.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A","other-GenRef 2006","Positive","25.12",0.64,25.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1017",84564,"P2",-(1)542,277548,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3824,88.5868,"2017-01-
15","Dry","Dry",-0.309292,8,"80-Rajshahi-Padmar Par-Barakuthi-2017Jan15","BBARC-020","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House

Crow","Kaak","field ID certain","2017-01-16","female","BDARC-020.CL.V.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.47",0,NA,27.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1078",94575,"P2",.6508868.2279947,"Bangladesh","Yes","Rajshahi-Padmar Par-Baraikuthi","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5968,24.3624,88.5968,"2017-01-15","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Padmar Par-Baraikuthi-2017Jan15","BDARC-020","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-16","female","BDARC-020.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gorloff 2016","Positive","29.17",0,NA,16.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1079",94574,"P2",170380.2279947,"Bangladesh","Yes","Rajshahi-Padmar Par-Baraikuthi","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5968,24.3624,88.5968,"2017-01-15","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Padmar Par-Baraikuthi-2017Jan15","BDARC-020","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-16","female","BDARC-020.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.4",0,NA,19.16,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1080",94578,"P2",.6088199.2279943,"Bangladesh","Yes","Rajshahi-Padmar Par-Baraikuthi","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5968,24.3624,88.5968,"2017-01-15","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Padmar Par-Baraikuthi-2017Jan15","BDARC-021","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-16","male","BDARC-021.CL.V.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.17",0,NA,21.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1081",94579,"P2",.7104312.2279943,"Bangladesh","Yes","Rajshahi-Padmar Par-Baraikuthi","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5968,24.3624,88.5968,"2017-01-15","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Padmar Par-Baraikuthi-2017Jan15","BDARC-021","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-16","male","BDARC-021.CL.V.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.47",0,NA,22.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1082",94582,"P2",.6088199.2279943,"Bangladesh","Yes","Rajshahi-Padmar Par-Baraikuthi","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5968,24.3624,88.5968,"2017-01-15","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Padmar Par-Baraikuthi-2017Jan15","BDARC-021","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-16","male","BDARC-021.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gorloff 2016","Positive","29.17",0,NA,23.50,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1083",94583,"P2",170380.2279943,"Bangladesh","Yes","Rajshahi-Padmar Par-Baraikuthi","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5968,24.3624,88.5968,"2017-01-15","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Padmar Par-Baraikuthi-2017Jan15","BDARC-021","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","field ID certain","2017-01-16","male","BDARC-021.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.47",0,NA,22.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1084",94586,"P2",.6600108.2277304,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-022","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","female","BDARC-022.CL.V.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.17",0,NA,31.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1085",94587,"P2",170472.2277304,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-022","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","female","BDARC-022.CL.V.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.47",0,NA,33.05,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1086",94590,"P2",.6068182.2277302,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-022","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","female","BDARC-022.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.17",0,NA,20.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1087",94591,"P2",170384.2277302,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-022","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","female","BDARC-022.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.47",0,NA,23.33,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1088",94594,"P2",.6093.2277298,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-023","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","male","BDARC-023.CL.V.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.17",0,NA,31.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1089",94595,"P2",170423.2277298,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-023","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","male","BDARC-023.CL.V.1","cloacal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.47",0,NA,31.44,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1090",94604,"P2",.6088183.2277285,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-023","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","male","BDARC-023.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gorloff 2016","Positive","29.17",0,NA,33.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1091",94605,"P2",170385.2277288,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.586,24.378,88.586,"2017-01-17","Dry","Dry",-0.5030252.8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-023","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-16","male","BDARC-023.OPV.1","oropharyngeal swab","2017-01-25","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","29.47",0,NA,23.37,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1092",94651,"P2",.6086684.2279628,"Bangladesh","Yes","Rajshahi-Padmar Par-Baraikuthi","Independent Site","Rajshahi Division","Rajshahi",24.3624,88.5968,24.3624,88.5968,"2017-01-

0","Dry","Dry",-0.5005252,8,"BD-Rajshahi-Padmar Par-Bankkudhi-2307Jun02","BDARC-0224","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaali","kaki ID cartoon","2307-03-17","male","BDARC-0224-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A","other-Gerloff 2009","Positive","29.07",0,NA,25.53,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0203",0A0B,"P3",-0.5005252,8,"BD-Rajshahi-Padmar Par-Bankkudhi-2307Jun02","BDARC-0224","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow","Kaali","kaki ID cartoon","2307-03-17","male","BDARC-0224-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A/H5a","other-Gerloff 2009","Positive","29.47",0,NA,27.93,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0204",0A0C,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0226","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-17","female","BDARC-0226-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A","other-Gerloff 2009","Positive","29.47",0,NA,25.25,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0205",0A0D,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0226","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-17","female","BDARC-0226-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A/H5a","other-Gerloff 2009","Positive","29.47",0,NA,27,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0206",0A0E,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0227","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-17","male","BDARC-0227-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A","other-Gerloff 2009","Positive","29.12",0,NA,23.18,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0207",0A0F,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0227","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-17","male","BDARC-0227-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A/H5a","other-Gerloff 2009","Positive","29.47",0,NA,25.23,NA,NA,"Positive","interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0208",0A10,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0228","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-17","male","BDARC-0228-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A","other-Gerloff 2009","Positive","29.12",0,NA,23.3,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0209",0A11,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0228","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-17","male","BDARC-0228-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A/H5a","other-Gerloff 2009","Positive","29.47",0,NA,25.05,NA,NA,"Positive","interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"020A",0A12,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0229","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-18","male","BDARC-0229-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A","other-Gerloff 2009","Positive","29.12",0,NA,21.84,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"020B",0A13,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0229","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-18","male","BDARC-0229-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A/H5a","other-Gerloff 2009","Positive","29.47",0,NA,23.3,NA,NA,"Positive","interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"020C",0A14,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0230","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-18","male","BDARC-0230-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A","other-Gerloff 2009","Positive","29.12",0,NA,19.84,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"020D",0A15,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0231","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-18","female","BDARC-0231-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A","other-Gerloff 2009","Positive","29.12",0,NA,23.18,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"020E",0A16,"P3",-0.5005252,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2307Jun02","BDARC-0231","birds","Free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"kaki ID cartoon","2307-03-18","female","BDARC-0231-DPI1.1","oropharyngeal swab","2307-02-08","International Centre for Diarrhoeal Disease Research (cddr.bd","Real time PCR","other-Influenza A/H5a","other-Gerloff 2009","Positive","29.47",0,NA,25.05,NA,NA,"Positive","interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"1906",84669,"P2",.368873,.227148,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-032","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-032.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,25.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1907",84670,"P2",.370394,.227148,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-032","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-032.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.47",0,NA,27.73,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1908",84673,"P2",.368873,.227408,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-033","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-033.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,29.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1909",84680,"P2",.370393,.227408,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.585,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-033","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-033.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.47",0,NA,30.85,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1910",84684,"P2",.368874,.227408,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-034","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-034.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,22.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1911",84685,"P2",.370395,.227408,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-034","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-034.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.47",0,NA,24.46,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1912",84694,"P2",.368875,.227608,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakudhi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3824,88.5868,"2017-01-
15","Dry","Dry",-0.5092952,5,"BD-Rajshahi-Padmar Par-Barakudhi-2017Jan15","BDARC-035","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Baali","field ID certain","2017-01-18","male","BDARC-035.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,23.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1913",84695,"P2",.370397,.227608,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakudhi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3824,88.5868,"2017-01-
15","Dry","Dry",-0.5092952,5,"BD-Rajshahi-Padmar Par-Barakudhi-2017Jan15","BDARC-035","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Baali","field ID certain","2017-01-18","male","BDARC-035.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.47",0,NA,25.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1914",84699,"P2",.368876,.227621,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakudhi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3824,88.5868,"2017-01-
15","Dry","Dry",-0.5092952,5,"BD-Rajshahi-Padmar Par-Barakudhi-2017Jan15","BDARC-036","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Baali","field ID certain","2017-01-18","male","BDARC-036.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,19.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1915",84700,"P2",.370398,.227621,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakudhi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3824,88.5868,"2017-01-
15","Dry","Dry",-0.5092952,5,"BD-Rajshahi-Padmar Par-Barakudhi-2017Jan15","BDARC-036","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Baali","field ID certain","2017-01-18","male","BDARC-036.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.47",0,NA,21.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1916",84703,"P2",.368877,.227708,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-037","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-037.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,23.98,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1917",84704,"P2",.370399,.227708,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-037","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-037.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.47",0,NA,25.38,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1918",84712,"P2",.368878,.227738,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-038","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-038.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,23.82,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1919",84714,"P2",.370400,.227738,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.586,"2017-01-
17","Dry","Dry",-0.5092952,8,"BD-Rajshahi-Rajshahi Medical College Hospital-2017Jan17","BDARC-038","birds","free-ranging wild animal","Corvus splendens","Corvus
splendens","species","House Crow",NA,"field ID certain","2017-01-18","male","BDARC-038.OPV.1","oropharyngeal swab","2017-02-08","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","25.47",0,NA,25.96,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1920",84724,"P2",.367938,.227596,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.37,88.5865,"2017-02-

09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-056","birds","free-ranging wild animal","Sinacapicx centris","Sinacapicx centris","species","Asian Pied Starling",NA,"held 60 cartaon","2017-02-09","female","60ARC-056 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlach 2006","Positive","25.17",0.NA,26.42,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"823",84729,"PT",907082.2276534,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-057","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-057 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlach 2006","Positive","25.12",0.NA,26.73,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"822",84730,"PT",.010804.2276514,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.37,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-057","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-057 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlach 2006","Positive","23.47",0.NA,22.43,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"823",84733,"PT",.601993.2276592,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-058","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-058 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlach 2006","Positive","25.12",0.NA,25.34,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"824",84734,"PT",.010603.2276593,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-058","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-058 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlach 2006","Positive","25.47",0.NA,24.07,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"825",84737,"PT",.907084.2276636,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-059","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","female","60ARC-059 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlach 2006","Positive","25.12",0.NA,24.NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"826",84738,"PT",.010606.2276650,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-059","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","female","60ARC-059 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlach 2006","Positive","25.47",0.NA,24.75,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"827",84740,"PT",.907085.2276668,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-060","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-060 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlach 2006","Positive","25.12",0.NA,26.62,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"828",84742,"PT",.010603.2276688,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-060","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-060 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlach 2006","Positive","25.47",0.NA,21.27,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"829",84751,"PT",907086.2276695,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-061","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-061 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlach 2006","Positive","25.12",0.NA,28.21,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"830",84752,"PT",.010608.2276701,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-061","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-061 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlach 2006","Positive","25.47",0.NA,24.3,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"831",84756,"PT",907087.2276864,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-062","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","female","60ARC-062 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerlach 2006","Positive","25.12",0.NA,25.35,NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"832",84757,"PT",.010609.2276894,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-062","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","female","60ARC-062 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerlach 2006","Positive","25.47",0.NA,0.NA,NA,"Positive","interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"833",84760,"PT",.910888.2276982,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5888,24.3711,88.5883,"2017-02-09","Dry","Dry",-0.877092,2,"60-Rajshahi-Rajshahi Medical College Hospital-2017-ek009","60ARC-063","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held 60 cartaon","2017-02-09","male","60ARC-063 CLV","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research

{col4 b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 22.04 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1034",64750,"PT",17.0049,22.7283,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0013","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-03","male","BSHRC-0013 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47 0 NA 23.19 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1035",64774,"PT",17.0019,22.7278,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0012","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-03","female","BSHRC-0012 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 22.38 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1036",64773,"PT",17.0063,22.7278,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0013","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-03","female","BSHRC-0013 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47 0 NA 0 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1037",64788,"PT",17.0028,22.7278,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-08","male","BSHRC-0008 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.47 0 NA 27.63 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1038",64782,"PT",17.0003,22.7267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-08","male","BSHRC-0008 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47 0 NA 28.45 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1039",64785,"PT",17.0002,22.7267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0007","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-07","male","BSHRC-0007 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 25.15 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1040",64788,"PT",17.0004,22.7267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0007","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-07","male","BSHRC-0007 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47 0 NA 24.07 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1041",64788,"PT",17.0003,22.7267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-07","male","BSHRC-0008 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 24.27 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1042",64788,"PT",17.0005,22.7267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-07","male","BSHRC-0008 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47 0 NA 23.02 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1043",64788,"PT",17.0004,22.7267,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-07","male","BSHRC-0008 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47 0 NA 25.07 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1045",64804,"PT",17.0015,22.7268,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0010","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-10","female","BSHRC-0010 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A","other-Gen4ff 2386","Positive","25.12","0 NA 24.22 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"
"1046",64803,"PT",17.0007,22.7268,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.588,24.371.88.5893,"2017-02-08","Dry","Dry",-0.877292,2,"80-Rajshahi-Rajshahi Medical College Hospital-2017Feb03","BSHRC-0010","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House Crow",NA,"held ID certain","2017-02-10","female","BSHRC-0010 D.V","cloacal swab","2017-03-20","International Centre for Diarrhoeal Disease Research {col4 b}","Real time PCR","other-Influenza A/H5a","other-Gen4ff 2386","Positive","25.47 0 NA 27.03 NA NA","Positive","Interpretation completed","NA NA NA NA NA","no","NA NA NA NA NA","EcoHealth Alliance"

"947",64807,"P2",87098.227700,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakudia","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3673,88.5972,"2017-02-
07","Dry","Dry",-0.5729821,"BD-Rajshahi-Padmar Par-Barakudia-2017Feb07","BDARC-074","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow",NA,"field ID certain","2017-02-07","female","BDARC-074.CLV","cloacal swab","2017-03-29","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,24.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"948",64828,"P2",70825.227700,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakudia","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3673,88.5972,"2017-02-
07","Dry","Dry",-0.5729821,"BD-Rajshahi-Padmar Par-Barakudia-2017Feb07","BDARC-074","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow",NA,"field ID certain","2017-02-07","female","BDARC-074.CLV","cloacal swab","2017-03-29","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,25.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"949",64833,"P2",87100.227608,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakudia","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3673,88.5972,"2017-02-
07","Dry","Dry",-0.5729821,"BD-Rajshahi-Padmar Par-Barakudia-2017Feb07","BDARC-075","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow",NA,"field ID certain","2017-02-07","male","BDARC-075.CLV","cloacal swab","2017-03-29","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,24.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"950",64842,"P2",86793.227600,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-076","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-02-08","unknown","BDARO-076.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,25.79,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"951",64843,"P2",70823.227606,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-076","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-02-08","unknown","BDARO-076.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,33.43,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"952",64846,"P2",87102.227605,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-077","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-02-08","unknown","BDARO-077.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,30.14,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"953",64847,"P2",70824.227605,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-077","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-02-08","unknown","BDARO-077.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,32.03,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"954",64854,"P2",87104.227603,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-078","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-02-08","unknown","BDARO-078.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,29.25,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"955",64855,"P2",70826.227603,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-078","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-02-08","unknown","BDARO-078.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,29.58,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"956",64868,"P2",87106.227599,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-080","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-02-08","unknown","BDARO-080.ZJV","other tissue offal","2017-02-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,27.83,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"957",64869,"P2",70828.227599,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.382,88.597,24.3824,88.5968,"2017-02-08","Dry","Dry",-
0.5729821,"BD-Rajshahi-Lakkhipur Bazar-2017Feb08","BDARO-080","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offals","field ID certain","2017-02-08","unknown","BDARO-080.ZJV","other tissue offal","2017-02-20","International Centre for Diarrhoeal Disease
Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,27.14,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"958",64873,"P2",87107.227717,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5977,24.377,88.5977,"2017-02-08","Dry","Dry",-
0.5978778.3,"BD-Rajshahi-Saheb Bazar-2017Feb08","BDARO-082","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-02-08","unknown","BDARO-082.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.17",0,NA,25.55,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"959",64888,"P2",87109.227715,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.2877,24.377,88.5977,"2017-02-08","Dry","Dry",-
0.5978778.3,"BD-Rajshahi-Saheb Bazar-2017Feb08","BDARO-084","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-02-08","unknown","BDARO-084.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,35.31,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"960",64892,"P2",70831.227715,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5977,24.377,88.5977,"2017-02-08","Dry","Dry",-
0.5978778.3,"BD-Rajshahi-Saheb Bazar-2017Feb08","BDARO-084","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Broiler","field ID certain","2017-02-08","unknown","BDARO-084.ZJV","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,23.02,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"961",84885,"P3",.65780,227794,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.371,88.5877,24.3771,88.5877,"2017-02-09","Dry","Dry",-
0.5787712,"BD-Rajshahi-Saheb Bazar-2017Feb09","BDARO-085","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-02-09","unknown","BDARO-085.22V","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,30.05,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"962",84886,"P3",.70832,227794,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5877,24.3771,88.5877,"2017-02-09","Dry","Dry",-
0.5787712,"BD-Rajshahi-Saheb Bazar-2017Feb09","BDARO-085","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Sonali","field ID certain","2017-02-09","unknown","BDARO-085.22V","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,30.58,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"963",84852,"P3",.67025,234852,"Bangladesh","Yes","Rajshahi Malda colony bazar","Independent Site","Rajshahi Division","Rajshahi",24.372,88.568,24.3928,88.6008,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Malda colony bazar-2017Feb10","BDARO-100","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-02-10","unknown","BDARO-100.22V","urine/feces combined (guano)","2017-03-28","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,25.71,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"964",84969,"P3",.67129,234854,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.377,88.5177,24.4082,88.6083,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Sapura-Kamchattar Bazar-2017Feb10","BDARO-104","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Layer","field ID certain","2017-02-10","unknown","BDARO-104.22V","urine/feces combined (guano)","2017-03-29","International Centre for
Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,33.75,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"965",85098,"P3",.67108,292555,"Bangladesh","Yes","Rajshahi-Sapura Nowdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.376,88.586,24.4033,88.6072,"2017-02-
10","Dry","Dry",-0.5787781,"BD-Rajshahi-Sapura-Nowdapara Bazar-2017Feb10","BDARO-111","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-02-10","unknown","BDARO-111.22V","other tissue-offal","2017-03-29","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.17",0,NA,30.13,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"966",85108,"P3",.70838,292555,"Bangladesh","Yes","Rajshahi-Sapura Nowdapara Bazar","Independent Site","Rajshahi Division","Rajshahi",24.376,88.586,24.4033,88.6072,"2017-02-
10","Dry","Dry",-0.5787781,"BD-Rajshahi-Sapura-Nowdapara Bazar-2017Feb10","BDARO-111","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus
domesticus","species","Domestic Chicken","Offal","field ID certainty unknown","2017-02-10","unknown","BDARO-111.22V","other tissue-offal","2017-03-29","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,37.22,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"967",85033,"P3",.67741,234858,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Shalbagan-2017Feb10","BDARO-115","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Layer","field ID certain","2017-02-10","unknown","BDARO-115.22V","urine/feces combined (guano)","2017-03-29","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,28.44,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"968",85038,"P3",.70683,234860,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Shalbagan-2017Feb10","BDARO-115","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Layer","field ID certain","2017-02-10","unknown","BDARO-115.22V","urine/feces combined (guano)","2017-03-29","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,33.82,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"969",85034,"P3",.67742,234858,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Shalbagan-2017Feb10","BDARO-117","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Layer","field ID certain","2017-02-10","unknown","BDARO-117.22V","urine/feces combined (guano)","2017-03-29","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,24.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"970",85035,"P3",.70884,234858,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Shalbagan-2017Feb10","BDARO-117","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Layer","field ID certain","2017-02-10","unknown","BDARO-117.22V","urine/feces combined (guano)","2017-03-29","International Centre for Diarrhoeal Disease Research
(icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,27.64,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"971",85044,"P3",.67743,234858,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Shalbagan-2017Feb10","BDARO-118","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Offal","field ID certainty unknown","2017-02-10","unknown","BDARO-118.22V","other tissue-offal","2017-03-29","International Centre for Diarrhoeal Disease Research (icddr,b)","Real
time PCR","other-Influenza A","other-Gerloff 2016","Positive","25.12",0,NA,33.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"972",85048,"P3",.67744,234857,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Shalbagan-2017Feb10","BDARO-119","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-02-10","unknown","BDARO-119.22V","urine/feces combined (guano)","2017-03-30","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","29.12",0,NA,28,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"973",85050,"P3",.70886,234857,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.382,88.607,24.3915,88.6074,"2017-02-10","Dry","Dry",-
0.5787781,"BD-Rajshahi-Shalbagan-2017Feb10","BDARO-119","poultry/other fowl","owned domesticated species","Anas platyrhynchos domesticus","Anas platyrhynchos
domesticus","species","Domestic Duck",NA,"field ID certain","2017-02-10","unknown","BDARO-119.22V","urine/feces combined (guano)","2017-03-30","International Centre for Diarrhoeal
Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","29.47",0,NA,28.41,NA,NA,"Positive","Interpretation
completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"974",89236,"P3",.98859,77060,"Bangladesh","Yes","Rajshahi-Lakkipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.362,88.597,24.3624,88.5969,"2016-02-22","Dry","Dry",-
0.5480283,"BD-Rajshahi-Lakkipur Bazar-2016Feb22","PF-144","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic
Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-144.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research

(icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,25.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"875",80214,"P2",88.0602,77.059,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.5057,24.3824,88.5063,"2016-02-22","Dry","Dry",-0.0048,0.3,"BD-Rajshahi-Lakkhipur Bazar-2016Feb22","PF-143","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-143.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,33.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"876",80242,"P2",88.5726,77.059,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.5057,24.3824,88.5063,"2016-02-22","Dry","Dry",-0.0048,0.3,"BD-Rajshahi-Lakkhipur Bazar-2016Feb22","PF-143","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-143.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,33.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"877",80242,"P2",83.5898,77.059,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.5057,24.3824,88.5063,"2016-02-22","Dry","Dry",-0.0048,0.3,"BD-Rajshahi-Lakkhipur Bazar-2016Feb22","PF-143","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-143.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","25.27",0,NA,33.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"878",80251,"P2",88.054,77.035,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.6071,24.3855,88.6074,"2016-02-22","Dry","Dry",-0.054736,0.3,"BD-Rajshahi-Shalbagan-2016Feb22","PF-144","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-144.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,25.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"879",80252,"P2",88.5726,77.035,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.6071,24.3855,88.6074,"2016-02-22","Dry","Dry",-0.054736,0.3,"BD-Rajshahi-Shalbagan-2016Feb22","PF-144","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-144.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,25.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"880",80253,"P2",88.0080,77.035,"Bangladesh","Yes","Rajshahi-Shalbagan","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.6071,24.3855,88.6074,"2016-02-22","Dry","Dry",-0.054736,0.3,"BD-Rajshahi-Shalbagan-2016Feb22","PF-144","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-144.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","25.27",0,NA,33.33,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"881",80291,"P2",88.0856,77.033,"Bangladesh","Yes","Rajshahi-Station Market","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5063,24.3737,88.6002,"2016-02-22","Dry","Dry",-0.04816,0.2,"BD-Rajshahi-Station Market-2016Feb22","PF-145","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-22","unknown","PF-145.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,33.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"882",80548,"P2",88.0330,77.057,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.5057,24.3824,88.5063,"2016-02-22","Dry","Dry",-0.0048,0.3,"BD-Rajshahi-Lakkhipur Bazar 2016Feb22","PF-523","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-24","unknown","PF-523.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,30.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"883",80571,"P2",88.0300,77.056,"Bangladesh","Yes","Rajshahi-Lakkhipur Bazar","Independent Site","Rajshahi Division","Rajshahi",24.3821,88.5057,24.3824,88.5063,"2016-02-22","Dry","Dry",-0.0048,0.3,"BD-Rajshahi-Lakkhipur Bazar-2016Feb22","PF-523","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-24","unknown","PF-523.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,35.15,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"884",80702,"P2",88.0957,87.723,"Bangladesh","Yes","Rajshahi-Saheb bazar","Independent Site","Rajshahi Division","Rajshahi",24.3711,88.5877,24.3779,88.5877,"2016-02-22","Dry","Dry",-0.054736,0.3,"BD-Rajshahi-Saheb Bazar-2016Feb22","PF-548","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-24","unknown","PF-548.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,33.01,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"885",80721,"P2",88.0384,88.008,"Bangladesh","Yes","Natore-Isapur Market","Independent Site","Rajshahi Division","Rajshahi",24.4088,88.9845,24.3687,88.6003,"2016-02-24","Dry","Dry",-0.04816,0.1,"BD-Natore-Isapur Market-2016Feb24","PF-605","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2016-02-24","unknown","PF-605.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,36.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"886",80728,"P2",85.8028,88.008,"Bangladesh","Yes","Natore-Isapur Market","Independent Site","Rajshahi Division","Rajshahi",24.4083,88.9945,24.3687,88.6003,"2016-02-24","Dry","Dry",-0.04816,0.1,"BD-Natore-Isapur Market-2016Feb24","PF-605","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2016-02-24","unknown","PF-605.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,33.0,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"887",80735,"P2",85.0408,88.008,"Bangladesh","Yes","Natore-Isapur Market","Independent Site","Rajshahi Division","Rajshahi",24.4083,88.9845,24.3687,88.6003,"2016-02-24","Dry","Dry",-0.04816,0.1,"BD-Natore-Isapur Market-2016Feb24","PF-605","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken",NA,"field ID certainty unknown","2016-02-24","unknown","PF-605.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza A/H5b","other-Gerloff 2016","Positive","25.27",0,NA,34.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"888",80751,"P2",85.0968,88.0057,"Bangladesh","Yes","Natore-Isapur Market","Independent Site","Rajshahi Division","Rajshahi",24.4083,88.9845,24.3687,88.6003,"2016-02-24","Dry","Dry",-0.04816,0.1,"BD-Natore-Isapur Market-2016Feb24","PF-608","poultry/other fowl","owned domesticated species","Gallus gallus domesticus","Gallus gallus domesticus","species","Domestic Chicken","Broiler chicken","field ID certainty unknown","2016-02-24","unknown","PF-608.22V","environmental sample","2016-05-30","International Centre for Diarrhoeal Disease Research

icddr,b)","Real time PCR","other-Influenza A","other-Gerloff 2016","Positive","27.78",0,NA,36.72,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth
Alliance"
"1189",.83218,"P1",.868658,.83375,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-001","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","female","R1-001.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,29.56,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1190",.83230,"P1",.865672,.83378,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-001","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","female","R1-001.SSV","oral swab","2016-02-06","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,32.28,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1191",.83231,"P1",.858844,.83375,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.585,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-001","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","female","R1-001.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,31.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1192",.83234,"P1",.868699,.83365,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-002","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-002.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,29.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1193",.83235,"P1",.865173,.83365,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-002","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-002.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,28.45,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1194",.83231,"P1",.858845,.83365,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-002","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-002.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,29.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1195",.83241,"P1",.867705,.83362,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-003.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,35.91,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1196",.83253,"P1",.867703,.83350,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-005","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-005.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,30.6,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1197",.83254,"P1",.865876,.83358,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-005","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-005.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,37.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1198",.83236,"P1",.858848,.83358,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-005","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-005.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,32.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1199",.83294,"P1",.867703,.83345,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-006","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-006.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,25.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1200",.83265,"P1",.865577,.83345,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-006","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-006.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,27.22,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1201",.83286,"P1",.858848,.83345,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-006","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-08","male","R1-006.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,27.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1202",.83297,"P1",.867706,.83339,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-010","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-09","male","R1-010.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,25.91,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1203",.83298,"P1",.865580,.83339,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-010","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-09","male","R1-010.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,28.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1204",.83299,"P1",.865852,.83330,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-
08","Dry","Dry",-0.848278.7,"SD-Rajshahi-Rajshahi Medical College Hospital-2016Feb08","R1-010","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Rak","field ID certain","2016-02-09","male","R1-010.SSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.27",0,NA,27.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1205",.83306,"P1",.866708,.83293,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.370.88.586,24.370.88.5865,"2016-02-

08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-002","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-002.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gorloff 2016","Positive","27.78",0,NA,24.83,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1206",83330,"PT",855580,93285,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-002","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-002.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","28.87",0,NA,27.88,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1207",83330,"PT",865854,93285,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-002","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-002.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","29.27",0,NA,27.74,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1208",83329,"PT",88709,93271,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-003.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gorloff 2016","Positive","27.78",0,NA,24.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1209",83330,"PT",855583,93271,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-003.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","28.87",0,NA,25.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1210",83333,"PT",855853,93271,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-003.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","29.27",0,NA,25.54,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1211",83336,"PT",88670,93257,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-004","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-004.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gorloff 2016","Positive","27.78",0,NA,23.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1212",83337,"PT",855584,93257,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-004","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-004.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","28.87",0,NA,25.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1213",83338,"PT",855656,93257,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-004","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-15","female","RI-004.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","29.27",0,NA,26.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1214",83351,"PT",85679,93235,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-20","male","RI-008.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gorloff 2016","Positive","27.78",0,NA,22.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1215",83352,"PT",855585,93235,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-20","male","RI-008.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gorloff 2016","Positive","28.87",0,NA,24.4,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1216",83353,"PT",855657,93235,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-008","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-20","male","RI-008.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gorloff 2016","Positive","29.27",0,NA,24.12,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1217",83383,"PT",86771,93396,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-033","birds","free-ranging wild animal","Acridotheres tristis","Acridotheres
tristis","species","Common Myna",NA,"field ID certain","2016-02-20","male","RI-033.001V","oral swab","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A","other-Gorloff 2016","Positive","27.78",0,NA,33.07,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1218",83384,"PT",855645,93396,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-033","birds","free-ranging wild animal","Acridotheres tristis","Acridotheres
tristis","species","Common Myna",NA,"field ID certain","2016-02-20","male","RI-033.001V","oral swab","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5a","other-Gorloff 2016","Positive","28.87",0,NA,27.37,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1219",83385,"PT",85597,93396,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.371,88.586,24.371,88.5865,"2016-02-
08","Dry","Dry",-0.6480797,"RO-Rajshahi-Rajshahi Medical College Hospital-20169eb08","RI-033","birds","free-ranging wild animal","Acridotheres tristis","Acridotheres
tristis","species","Common Myna",NA,"field ID certain","2016-02-20","male","RI-033.001V","oral swab","2016-05-30","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time
PCR","other-Influenza A/H5b","other-Gorloff 2016","Positive","29.27",0,NA,35.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1220",83514,"PT",86718,89829,"Bangladesh","Yes","Rajshahi-Natore Zila parishad","Independent Site","Rajshahi Division","Rajshahi",24.4085,88.9848,24.4085,88.9844,"2016-02-
21","Dry","Dry",-0.6893273,"RO-Rajshahi-Natore Zila parishad-20169eb21","RI-044","birds","free-ranging wild animal","Corvus macrorhynchos","Corvus macrorhynchos","species","Large-
Billed Crow","Kak","field ID certain","2016-02-20","male","RI-044.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A","other-Gorloff 2016","Positive","27.78",0,NA,21.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1221",83515,"PT",855582,89829,"Bangladesh","Yes","Rajshahi-Natore Zila parishad","Independent Site","Rajshahi Division","Rajshahi",24.4085,88.9848,24.4085,88.9844,"2016-02-
21","Dry","Dry",-0.6893273,"RO-Rajshahi-Natore Zila parishad-20169eb21","RI-044","birds","free-ranging wild animal","Corvus macrorhynchos","Corvus macrorhynchos","species","Large-
Billed Crow","Kak","field ID certain","2016-02-20","male","RI-044.001V","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A/H5a","other-Gorloff 2016","Positive","28.87",0,NA,23.04,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"

"1222",88.6546,"P2",88.5884,89829,"Bangladesh","Yes","Rajshahi-Natore Zila parishad","Independent Site","Rajshahi Division","Rajshahi",24.4085,88.5948,24.4088,88.5944,"2016-02-
21","Dry","Dry",-0.083027.2,"B0-Rajshahi-Natore Zila parishad-2016Feb21","R-044","birds","free-ranging wild animal","Corvus macrorhynchos","Corvus macrorhynchos","species","Large-
Billed Crow","Kak","field ID certain","2016-02-21","male","R-044.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-
Influenza A/H5a","other-Gerloff 2016","Positive","25.77",0,NA,25.20,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1223",88.6507,"P2",88.6738,83065,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-089","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-20","male","R-089.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,26.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1224",88.6028,"P2",88.6733,83033,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-032","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","female","R-032.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,27.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1225",88.6593,"P2",88.5607,83033,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-032","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","female","R-032.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,20.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1226",88.6581,"P2",88.5879,83059,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-032","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","female","R-032.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","25.77",0,NA,28.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1227",88.6596,"P2",88.6759,83048,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-003.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,28.34,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1228",88.6597,"P2",88.5608,83048,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-003.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,29.5,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1229",88.6608,"P2",88.5680,83048,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-003","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-003.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","25.77",0,NA,29.73,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1230",88.6623,"P2",88.6723,83041,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-094","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","female","R-094.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,27.91,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1231",88.6624,"P2",88.5609,83041,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-094","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","female","R-094.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,23.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1232",88.6625,"P2",88.5608,83041,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-094","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","female","R-094.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","25.77",0,NA,24.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1233",88.6644,"P2",88.6737,83027,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-036","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-036.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,29.51,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1234",88.6645,"P2",88.5618,83027,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-036","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-036.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,22.55,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1235",88.6646,"P2",88.5683,83027,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-036","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-036.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","25.77",0,NA,32.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1236",88.6659,"P2",88.6738,83012,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-037","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-037.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0,NA,24.35,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1237",88.6660,"P2",88.5613,83012,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-037","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-037.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,25.31,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1238",88.6661,"P2",88.5684,83012,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3718,88.5806,24.3718,88.5865,"2016-02-
18","Dry","Dry",-0.3418729.7,"B0-Rajshahi-Rajshahi Medical College Hospital-2016Feb18","R-037","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-21","male","R-037.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza

A/H5b","other-Garlaff 2016","Positive","25.27",0,NA,25.3,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1239",83086,"P2",.880728,83.0956,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-098","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-098.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Garlaff 2016","Positive","27.78",0,NA,27.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1240",83087,"P2",.895613,83.0956,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-098","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-098.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Garlaff 2016","Positive","28.87",0,NA,22.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1241",83088,"P2",.885865,83.0956,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-099","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-099.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Garlaff 2016","Positive","25.27",0,NA,22.08,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1242",83073,"P2",.885740,83.0954,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-099","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","female","R-099.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Garlaff 2016","Positive","27.78",0,NA,27.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1243",83074,"P2",.885814,83.0954,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-099","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","female","R-099.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Garlaff 2016","Positive","28.87",0,NA,22.17,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1244",83075,"P2",.885886,83.0954,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-099","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","female","R-099.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Garlaff 2016","Positive","25.27",0,NA,23.46,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1245",83088,"P2",.885741,83.0948,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-100","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-100.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Garlaff 2016","Positive","27.78",0,NA,25.21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1246",83685,"P2",.885815,83.0944,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-100","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-100.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Garlaff 2016","Positive","28.87",0,NA,25.27,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1247",83686,"P2",.885687,83.0948,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-100","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-100.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Garlaff 2016","Positive","25.27",0,NA,26.18,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1248",83693,"P2",.885742,83.0938,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-101","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-101.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Garlaff 2016","Positive","27.78",0,NA,30.85,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1249",83696,"P2",.885615,83.0938,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-101","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-101.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Garlaff 2016","Positive","28.87",0,NA,31.71,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1250",83697,"P2",.885898,83.0938,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-101","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-101.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Garlaff 2016","Positive","25.27",0,NA,33.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1251",83702,"P2",.885742,83.0938,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-102","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-102.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Garlaff 2016","Positive","27.78",0,NA,31.23,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1252",83703,"P2",.885687,83.0936,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-102","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-102.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Garlaff 2016","Positive","28.87",0,NA,33.29,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1253",83704,"P2",.885888,83.0936,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-102","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-102.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Garlaff 2016","Positive","25.27",0,NA,32.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1254",83708,"P2",.885744,83.0934,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-103","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","field ID certain","2016-02-27","male","R-103.OSV","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Garlaff 2016","Positive","27.78",0,NA,28.57,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1255",83710,"P2",.885808,83.0934,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5868,24.3822,88.5872,"2016-02-
27","Dry","Dry",-0.848028,2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","R-103","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House

Crow","Kak","Field ID certain","2016-02-27","male","RI-403.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,20.24,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1256",80771,"P2",865898.83834,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3677,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-403","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-403.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.77",0,NA,20.19,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1257",80776,"P2",866745.83839,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3677,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-404","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-404.D3V","oral swab","2016-06-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
4","other-Gerloff 2016","Positive","27.78",0,NA,20.42,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1258",80777,"P2",865805.83829,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3677,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-404","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-404.D3V","oral swab","2016-06-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,21.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1259",80778,"P2",865809.83826,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3677,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-404","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-404.D3V","oral swab","2016-06-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.77",0,NA,22.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1260",80779,"P2",866746.83894,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3677,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-405","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-405.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
4","other-Gerloff 2016","Positive","27.78",0,NA,22.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1261",80732,"P2",865620.83894,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3672,88.5971,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-405","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-405.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,22.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1262",80733,"P2",865832.83894,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5968,24.3672,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-405","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-405.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.77",0,NA,23.19,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1263",80746,"P2",866741.83882,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3673,88.5971,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-406","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-406.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
4","other-Gerloff 2016","Positive","27.78",0,NA,25.05,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1264",80747,"P2",865621.83882,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3677,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-406","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-406.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,21.25,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1265",80748,"P2",865893.83882,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3672,88.5971,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-406","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-406.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.77",0,NA,22.7,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1266",80756,"P2",866748.83906,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3672,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-407","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-407.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
4","other-Gerloff 2016","Positive","27.78",0,NA,21.03,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1267",80757,"P2",865621.83906,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3673,88.5971,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-407","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-407.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,22.21,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1268",80758,"P2",865894.83900,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5958,24.3672,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-407","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-407.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other-Gerloff 2016","Positive","29.77",0,NA,22.02,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1269",80761,"P2",865623.40526,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5968,24.3672,88.5971,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-408","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","Field ID certain","2016-02-27","male","RI-408.D3V","oral swab","2016-06-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5a","other-Gerloff 2016","Positive","28.87",0,NA,21.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1270",80762,"P2",865895.40526,"Bangladesh","Yes","Rajshahi-Padmar Par-Barakuthi","Independent Site","Rajshahi Division","Rajshahi",24.3674,88.5968,24.3672,88.5972,"2016-02-
27","Dry","Dry",-0.948078.2,"BD-Rajshahi-Padmar Par-Barakuthi-2016Feb27","RI-408","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kaak","Field ID certain","2016-02-27","male","RI-408.D3V","oral swab","2016-06-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H5b","other Gerloff 2016","Positive","29.77",0,NA,21.91,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1271",80775,"P2",866756.83840,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.588,24.371,88.5805,"2016-03-
08","Dry","Dry",-0.948078.7,"BD-Rajshahi-Rajshahi Medical College Hospital-2016Mar08","RI-409","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Kak","Field ID certain","2016-02-27","male","RI-409.D3V","oral swab","2016-05-07","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
4","other-Gerloff 2016","Positive","27.78",0,NA,21.77,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"no",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"1272",80776,"P2",865634.83810,"Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.378,88.5865,24.378,88.5865,"2016-03-

"0.999","84488","P3","-90.6913,23.8362","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5855,24.3711,88.5855,"2016-03-
18","Dry","Dry",-0.944829,7,"BD-Rajshahi-Rajshahi Medical College Hospital-23959 ebf8","RI-1058","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Bak","Field ID certain","2016-02-24","female","RI-1055.OSY","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H3c","other-Gerloff 2016","Positive","29.27",0.84,21.19,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0.998","84453","P3","-90.6768,23.8338","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5855,24.3711,88.5855,"2016-03-
18","Dry","Dry",-0.944829,7,"BD-Rajshahi-Rajshahi Medical College Hospital-23959 ebf8","RI-1058","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Bak","Field ID certain","2016-02-24","female","RI-1055.OSY","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0.84,25.58,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0.998","84494","P3","-90.6642,23.8338","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5855,24.3711,88.5855,"2016-02-
18","Dry","Dry",-0.944829,7,"BD-Rajshahi-Rajshahi Medical College Hospital-23959 ebf8","RI-1058","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Bak","Field ID certain","2016-02-24","female","RI-1055.OSY","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H3c","other-Gerloff 2016","Positive","28.67",0.84,26.14,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0.997","84455","P3","-90.6594,23.8338","Bangladesh","Yes","Rajshahi-Rajshahi Medical College Hospital","Independent Clinic","Rajshahi Division","Rajshahi",24.3711,88.5855,24.3711,88.5855,"2016-02-
18","Dry","Dry",-0.944829,7,"BD-Rajshahi-Rajshahi Medical College Hospital-23959 ebf8","RI-1058","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Bak","Field ID certain","2016-02-24","female","RI-1055.OSY","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H3c","other-Gerloff 2016","Positive","28.27",0.84,26.1,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0.997","84768","P3","-89.8719,8.9988","Bangladesh","Yes","Rajshahi-Padmar Par-Barakudhi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5968,24.3822,88.5972,"2016-02-
21","Dry","Dry",-0.944829,2,"BD-Rajshahi-Padmar Par-Barakudhi-20160221","RI-1202","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Bak","Field ID certain","2016-02-24","female","RI-1201.OSY","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A","other-Gerloff 2016","Positive","27.78",0.84,27.53,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0.994","84207","P3","-89.644,8.8868","Bangladesh","Yes","Rajshahi-Padmar Par-Barakudhi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5968,24.3822,88.5972,"2016-02-
21","Dry","Dry",-0.944829,2,"BD-Rajshahi-Padmar Par-Barakudhi-20160221","RI-1202","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Bak","Field ID certain","2016-02-24","female","RI-1201.OSY","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H3c","other-Gerloff 2016","Positive","28.67",0.84,24.52,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0.993","84208","P3","-89.6966,8.8868","Bangladesh","Yes","Rajshahi-Padmar Par-Barakudhi","Independent Site","Rajshahi Division","Rajshahi",24.3824,88.5968,24.3822,88.5972,"2016-02-
21","Dry","Dry",-0.944829,2,"BD-Rajshahi-Padmar Par-Barakudhi-20160221","RI-1202","birds","free-ranging wild animal","Corvus splendens","Corvus splendens","species","House
Crow","Bak","Field ID certain","2016-02-24","female","RI-1201.OSY","oral swab","2016-06-02","International Centre for Diarrhoeal Disease Research (icddr,b)","Real time PCR","other-Influenza
A/H3c","other-Gerloff 2016","Positive","25.27",0.84,24.78,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,NA,NA,"EcoHealth Alliance"
"0.986","222.6833,"P3","-10.0872,2.2634,"Indonesia","ru","Binanga","Concurrent Site F","Maputa","West Sulawesi",-3.3338,118.8421,-3.3384,118.844,"2016-12-23","Wet","Wet",0.258215,4,"18-Binanga-
20160ec23","18ARB0185","bats","free-ranging wild animal","Acerodon celebensis","Acerodon celebensis","species","Sulawesi Fruit Bat","Pteropodidae","unidentified by barcoding - field ID
certain","2016-12-28","male","18ARB0185.RSW","rectal swab","2017-09-27","Primate Research Center, Bogor Agricultural University","Conventional PCR","Coronavirus","Muhlisah Wardoyo et
al. Nilfiy pers","Product for Sequencing",NA,NA,NA,NA,"Primate Research Center, Bogor Agricultural University","2017-10-20","Positive","Interpretation
completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,"10-0322-P2 wildlife",NA,"EcoHealth Alliance"
"0.987","5.314928,"P3","-962995.3.03471,"Sierra Leone","ru","New London","Independent Site","Bombali","Northern Province",8.88847,-12.3535,8.54431,-12.3342,"2016-05-08","Wet","Dry",-
0.94963.5,"SL-New London-2016Jun08","SL14B000006","bats","free-ranging wild animal","Chaerephon pumilus","Chaerephon pumilus","species","Little Free-Tailed Bat",NA,"barcoded species
(<97% match)","2016-06-07","male","SL14B000006.RST","rectal swab","2017-03-16","UC Davis One Health Institute Laboratory","Real time PCR","Ebola Virus","Unpublished
D3","Positive",,"28",NA,2.7534,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,"SL-0322-P2 wildlife","2020-02-6","Metabiota"
"0.986","3689006,"P3","-9420266.584006,"Sierra Leone","ru","Kamaba","Independent Site","Bombali","Northern Province",8.94983,-8.95185,8.5171,-8.96602,"2016-09-23","Dry","Dry",-
8.954258,4,"SL-Kamaba-2016Jun23","SL14B4752","bats","free-ranging wild animal","Chaerephon pumilus","Chaerephon pumilus","species","Little Free-Tailed Bat","bat","barcoded species
(<97% match)","2016-09-29","female","SL14B4752.BT","blood (whole)","2016-04-25","UC Davis One Health Institute Laboratory","Real time PCR","Bombali
ebolavirus","Exhibition","Positive",,"28",NA,25.93,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,9.0,NA,"SL-0322-P2 wildlife","2020-02-6","UC Davis"
"0.986","3689006,"P3","-9420266.584006,"Sierra Leone","ru","Kamaba","Independent Site","Bombali","Northern Province",8.94983,-8.95185,8.5171,-8.96602,"2016-09-23","Dry","Dry",-8.954258,4,"SL-
Kamaba-2016Jun23","SL14B4752","bats","free-ranging wild animal","Chaerephon pumilus","Chaerephon pumilus","species","Little Free-Tailed Bat","bat","barcoded species (<97%
match)","2016-09-29","female","SL14B4752.OSY","oral swab","2016-12-6","UC Davis One Health Institute Laboratory","Real time PCR","Bombali
ebolavirus","Exhibition","Positive",,"28",NA,29.84,NA,NA,"Positive","Interpretation completed",NA,NA,NA,NA,NA,"ru",NA,NA,NA,"SL-0322-P2 wildlife","2020-02-6","UC Davis"

From: Tammie O'Rourke <torourke@metabiota.com>
To: Tracey Goldstein <tgoldstein@ucdavis.edu>
CC: Zoe Grange <zlgrange@ucdavis.edu>;Anthony, Simon J. <sja2127@cumc.columbia.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 4/24/2020 4:00:43 PM
Subject: Re: PREDICT virus data and spillover risk ranking

Sorry Tracey forgot to include the group when I sent Zoe a response. The ones attached are all real-time tests so they don't have a virus/interpretation. Below is my response.

Hi Zoe,
These are all real-time tests (test type column), so they don't have the virus or interpretation. You can get the virus tested from the test requested column, but there won't be an interpretation, just positive for xx.
Hope that makes sense.
Tammie

On Fri, Apr 24, 2020 at 8:50 AM Tracey Goldstein <tgoldstein@ucdavis.edu> wrote:
Hi Zoe,

Yes, they were not able to complete testing, so please do not include in analysis.

Tammie, we were going to change those to say Testing not completed, rather than confirmation positive. I know we are still working through cleaning these up.

T

On Fri, Apr 24, 2020 at 5:01 AM Zoe Grange <zlgrange@ucdavis.edu> wrote:

Hi Tammie,

I pulled the P2 interpreted tests data for the countries (excluding the countries listed below). I found some results, predominantly for Bangladesh, that are 'ConfirmationResult' positive but do not have anything listed for the 'Virus' type and 'Interpretation' columns. I've listed them in the attached the spreadsheet. Is there a reason for these results?

Cheers,

Zoe

From: Tammie O'Rourke <torourke@metabiota.com>
Date: Friday, April 17, 2020 at 5:47 PM
To: Zoe Grange <zlgrange@ucdavis.edu>
Cc: Tracey Goldstein <tgoldstein@ucdavis.edu>, "Anthony, Simon J." <sja2127@cumc.columbia.edu>, Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: PREDICT virus data and spillover risk ranking

Hi Zoe,

I can address #3. All countries are fully approved, with the exception of Guinea, Liberia, Malaysia & DRC. As for being able to use the data for your app, I will defer to Chris for confirmation.

Tammie

On Fri, Apr 17, 2020 at 7:34 AM Zoe Grange <zlgrange@ucdavis.edu> wrote:

Hi everyone,

I was discussing the PREDICT data with Jonna the other day in terms of the spillover risk ranking. I have a few questions below that I was wondering if you could help with:

1. Where is the predict data for viruses that are collaboratively collected in Thailand and China? Are they in Eidith? If, so are they the ones listed as not Predict protocol?
2. For the SpilOver manuscript, I have only included data from P1 that was collected using PREDICT protocols. Do you think it's worth adding the non-predict protocol data? (possibly post-publication)
3. What is the status of the PREDICT 2 virus data? Do we have outstanding records for government approval? Do we have some countries that are completed that I could use for the spillover risk ranking?

Many thanks for your help. Hope you are all well ☺

Zoe

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Tammie O'Rourke

Metabiota

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