From: Andrew Clements <aclements@usaid.gov>
Sent: Tue, 9 Oct 2018 08:51:23 -0700
Subject: Re: PREDICT ATF Equipment Request (Year 5, Request No. 2)
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: "predict@ucdavis.edu" <predict@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, David John Wolking <djwolking@ucdavis.edu>, Hannah R Chale <hrchale@ucdavis.edu>, Alisa Pereira <apereira@usaid.gov>

Hi Liz,
I approved this ATF equipment request.

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 Oct 9, 2018, at 5:23 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Andrew. Please find attached an After-the-Fact equipment request for Smithsonian. They purchased a VetScan iSTAT in Year 2, but they did not obtain the required AOR prior approval. They also erroneously reported the expense as Other Direct Costs in their April 2016 invoice, so the purchase was not caught during our HQ invoice review process. Per Smithsonian, this product was purchased in anticipation of wildlife surveillance activities to be conducted. At the time of purchase, the Smithsonian PREDICT team had experienced a change in global staff with the hiring of three new team members to implement the projects while also losing two team members at the same time. During this transition, a brief lapse in protocol occurred while new team members learned project needs in pursuing product purchases. This error was identified during a recent internal review of Smithsonian's PREDICT project inventory, and we now seek to rectify the situation with your ATF approval. If you have any questions or need any additional information to approve, please let me know.
>
> Thanks,
> Liz
>
> *Elizabeth Leasure*
> *Financial Operations Manager*
> *One Health Institute*
> REDACTED *(cell)*
> *530-754-9034 (office)*
> *Skype: ealeasure*
>
> <ATF PREDICT Equipment Request_Year 5_No. 2_10.9.18_final.pdf>

From: Andrew Clements <aclements@usaid.gov>
Sent: Tue, 9 Jun 2020 01:14:33 -0700
Subject: Re: REQUEST FOR REPORT ON TAXATION OF FOREIGN ASSISTANCE
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, "predictmgt@usaid.gov" <predictmgt@usaid.gov>, predict Sympa List <predict@ucdavis.edu>

Thanks. I shared it with Tamar.

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 8, 2020, at 11:21 PM, 'Elizabeth Leasure' via PREDICTMGT <predictmgt@usaid.gov> wrote:

> Hi Andrew. We actually have that report ready to go (see attached), we just wanted to make sure the Mission used the appropriate channel to request it.
>
> Thanks,
> Liz
>
> *Elizabeth Leasure*
> *Financial Operations Manager*
> *One Health Institute*
> REDACTED *(cell)*
> *530-754-9034 (office)*
> *Skype: ealeasure*
>
> ---
>
> **From:** Andrew Clements <aclements@usaid.gov>
> **Sent:** Monday, June 8, 2020 2:02 PM
> **To:** Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
> **Cc:** Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>; Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>; Jonna Mazet <jkmazet@ucdavis.edu>; predictmgt@usaid.gov
> **Subject:** Fwd: REQUEST FOR REPORT ON TAXATION OF FOREIGN ASSISTANCE
>
> See request below. If you can make the deadline tomorrow without dropping anything else, fine. Otherwise, I told them they wouldn't get it tomorrow so don't kill yourself over this. Anytime by the end of this week would be fine.
>
> *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:** Tamar Bah <tbah@usaid.gov>
> **Date:** June 8, 2020 at 9:06:14 PM GMT+2
> **To:** aclements@usaid.gov
> **Cc:** Ewa Piotrowska <epiotrowska@usaid.gov>, isimmons@usaid.gov
> **Subject: Fwd: REQUEST FOR REPORT ON TAXATION OF FOREIGN ASSISTANCE**
>
> Hello Andrew,

Please kindly provide us with the Tax on Foreign Assistance regarding Predict for FY18. This is an urgent data call from Washington through our Program Office here.

Predict asked me to refer to you. It is due tomorrow. Please fill out the excel sheet and send back to us.

Thanks!

Sent from my iPhone
Begin forwarded message:

From: Izetta Minko-Moreau <isimmons@usaid.gov>
Date: April 6, 2020 at 11:47:28 GMT
To: Lamine Bangoura <lbangoura@usaid.gov>, Souro Kamano <skamano@usaid.gov>, Tamar Bah <tbah@usaid.gov>
Cc: Eliane Mbounga <embounga@usaid.gov>, Pierre Balamou <pbalamou@usaid.gov>
Subject: Fwd: REQUEST FOR REPORT ON TAXATION OF FOREIGN ASSISTANCE

Please contact your partners regarding this request.

Izetta Y. S. Minko-Moreau

Health Office Director, USAID/ Guinea
Mobile
Direct: REDACTED

"*Managing your time without setting priorities is like shooting randomly and calling whatever you hit the target.*" Peter Turla

---------- Forwarded message ---------
From: **Ewa Piotrowska** <epiotrowska@usaid.gov>
Date: Mon, Mar 30, 2020 at 11:36 AM
Subject: REQUEST FOR REPORT ON TAXATION OF FOREIGN ASSISTANCE
To: Izetta Simmons <isimmons@usaid.gov>, Taisha Jones <tajones@usaid.gov>, Mark Koenig <mkoenig@usaid.gov>, Maladho Balde <mbalde@usaid.gov>, Binta Ann <bann@usaid.gov>, Jonta Williams <mariewilliams@usaid.gov>, Albert Asante <aasante@usaid.gov>, Bernadette Daluz <bdaluz@usaid.gov>, Madeleine Soumah <msoumah@usaid.gov>, Aissatou Conde <aconde@usaid.gov>
Cc: Andrew Williams <ANDWILLIAMS@usaid.gov>, Arafan Kourouma <akourouma@usaid.gov>, Jeff Bryan <jbryan@usaid.gov>, Miriam Lutz <mlutz@usaid.gov>

Hi everyone,

Is our foreign assistance taxed in any way in Guinea or Sierra Leone, and if so, is there a reimbursement process? There's a congressional requirement to report on the amount taxed and the amount reimbursed, if any. Right now we are asked to report on taxes withheld and reimbursed for fiscal year 2018 (Oct 1 2017 - Sep 30 2018).

Please check with your teams and send OFM and me any taxed, reimbursed, and non-reimbursed amounts for FY 2018. This is due to Washington on April 10, but we'll need to coordinate with our Embassies to respond, so please respond by next Wednesday, April 8.

If taxes are assessed against our assistance and full reimbursement was not provided by 9/30/2019, we are required to withhold 200% of the non-reimbursed amount from our FY 2019 assistance allocated for the central government.

Instead of reading the whole cable below, here's the action request:
Posts and Bureaus are required to collect information on the total amount of value added taxes (VAT), customs duties, and other taxes assessed during FY 2018 by a foreign government or entity against assistance financed by foreign assistance funds and report this information to regional bureaus in Washington, including any reimbursements received. If there is an effective agreement in place for reimbursement of taxes or if the host government does not charge taxes, this should be likewise noted.

If you enjoy reading guidance documents, you can find more detailed information on this process in the attachment.

Thanks very much!
Ewa

Ewa Piotrowska
Supervisory Program Officer
USAID/Guinea and Sierra Leone
REDACTED

From: SMART Core <svcsmartbtsewssprec2@state.gov>
Sent: Wednesday, March 25, 2020 12:37 AM
Subject: REQUEST FOR REPORT ON TAXATION OF UNITED STATES FOREIGN ASSISTANCE

UNCLASSIFIED

Action Office:	ALDACS, DAO, POL, AID_EXEC, ECON, FMO
Info Office:	AID_LES_INFO, FMM_LES_INFO, FMO_LES_INFO, MGT_INFO, AIDEX_INFO, ECON_LES_INFO, FMO_INFO

MRN:	20 STATE 32468
Date/DTG:	Mar 25, 2020 / 250023Z MAR 20
From:	SECSTATE WASHDC
Action:	MOGADISHU, AMEMBASSY *ROUTINE*; ALL DIPLOMATIC AND CONSULAR POSTS COLLECTIVE *ROUTINE*
E.O.:	13526

TAGS: AFIN, EFIN, ECON, EAID, PREL

Subject: REQUEST FOR REPORT ON TAXATION OF UNITED STATES FOREIGN ASSISTANCE

FROM JAMES L. RICHARDSON, DIRECTOR OF THE OFFICE OF U.S. FOREIGN ASSISTANCE
TO ALL COMS, ASSISTANT SECRETARIES, ASSISTANT ADMINISTRATORS, USAID MISSION DIRECTORS, AND AGENCY HEADS AT POST

This cable contains action requests in Paragraphs 6, 8, 9, 10

1. This is a reporting action for all Posts/Missions and Washington offices that received foreign assistance funds, per section 7013 of the Department of State, Foreign Operations, and Related Programs Appropriations Act, 2018 (Div. K, P.L. 115-141)(FY 2018 SFOAA).

2. Section 7013 of the FY 2018 SFOAA requires U.S. government departments and agencies providing assistance appropriated under titles III through VI of the SFOAA to take certain actions to prevent taxation of U.S. foreign assistance funds or to obtain reimbursement of taxes paid. If taxes were assessed during FY 2018 (October 1, 2017 to September 30, 2018) against foreign assistance funds appropriated in the FY 2018 SFOAA or in prior Acts, section 7013 requires the withholding of 200% of any unreimbursed taxes from the following fiscal year's foreign assistance allocation to that country's central government.

3. CHANGES IN APPLICATION: Historically, this provision has applied only to taxes assessed in a particular fiscal year on funds that were appropriated in that same fiscal year. Due to the timeline on which funds are typically obligated, this has resulted in the withholding requirement having very limited application. In FY 2017, however, section 7013(b) was broadened to include all taxes assessed during FY 2017 regardless of whether the foreign assistance funds subject to taxation were appropriated in the FY 2017 SFOAA or in a prior-year appropriations act. This is a significant change that continues in the FY 2018 SFOAA and will likely result in larger amounts of taxation being captured by the provision than in prior years. For this reason, it is particularly important that Posts/Missions and Washington offices respond to the action requests below by the stated reporting dates. Additional guidance will be provided later to address taxation assessed in FY 2017.

Action Required

6. Posts and Bureaus are required to collect information on the total amount of value added taxes (VAT), customs duties, and other taxes assessed during FY 2018 by a foreign government or entity against assistance financed by foreign assistance funds and report this information to regional bureaus in Washington, including any reimbursements received. If there is an effective agreement in place for reimbursement of taxes or if the host government does not charge taxes, this should be likewise noted in the reporting template. Detailed Guidance and sample templates are posted on SharePoint at the DOS VAT guidance link at https://usdos.sharepoint.com/sites/F/SitePages/Home.aspx or the USAID VAT guidance link at https://pages.usaid.gov/F/vat-guidance.

7. Even if an Embassy reported previously that either no assistance is charged VAT or customs duties, or that there was an effective regime for reimbursement in place, a report is required for FY 2018.

8. Please provide the name of the Point of Contact (POC) at post for this action by March 31, 2020, to your regional bureau POC listed in the guidance posted on SharePoint at https://usdos.sharepoint.com/sites/F/SitePages/Home.aspx or the USAID VAT guidance link at

https://pages.usaid.gov/F/vat-guidance.

9. Special Washington reporting offices are required to report on taxes assessed on funds that were not executed by Post since Post may not be aware of VAT, customs duties, or other taxes assessed on these funds. Special Washington reporting offices will report this information directly to the F POC.

10. Taxes reported from Embassies and Special Washington reporting offices must be submitted as described in the detailed guidance. Reports received without the required information in the appropriate format will be returned for correction.

11. It is important that we receive responses from all Embassies and Special Washington reporting offices. This provision is of extremely high interest to the Congress, which mandates that the Secretary submit a report on how the relevant departments or agencies are implementing this provision of law. Congress has also asked about the number of Embassies reporting compared to the number that should be reporting. Furthermore, sec. 7031(a) of the FY 2018 SFOAA conditions the provision of government-to-government assistance on whether or not the recipient government is in compliance with the principles in section 7013.

12. State Department regional bureaus are responsible for providing consolidated reporting from the embassies to the POC in the Office of U.S. Foreign Assistance (F), at F-RA-Execution@state.gov.

13. Special Washington reporting offices are responsible for submitting a report directly to the F POC at F-RA-Execution@state.gov.

14. Embassies should refer questions to the relevant State bureau or other agency point of contact regarding the appropriate format for reporting and for clarification of the accounts/programs subject to reporting. Regional bureau and special Washington reporting offices will refer questions to the F POC if necessary.

15. For detailed guidance, reporting formats, and other helpful information go to https://usdos.sharepoint.com/sites/F/SitePages/Home.aspx or the USAID VAT guidance link at https://pages.usaid.gov/F/vat-guidance, or contact the F POC, at F-RA-Execution@state.gov.

16. REPORTING DATES:

(A) [April 10, 2020]– EMBASSY REPORTS DUE TO DEPARTMENT REGIONAL BUREAUS: Embassies are required to consolidate country data by total taxes assessed and total reimbursements received by account and provide this information to the State regional bureau POC listed in the guidance.

(B) [April 10, 2020]– SPECIAL WASHINGTON REPORTING OFFICES REPORTS DUE TO F - Special Washington reporting offices should consolidate the information by country/account and submit this information to the F POC, at F-RA-Execution@state.gov.

(C) [April 24, 2020]- REGIONAL BUREAU REPORTS DUE TO F – Using data provided by Posts/Missions, Department of State regional bureaus should consolidate the reports by country/account for each country and submit this information to the F POC at F-RA-Execution@state.gov. *Bureaus are responsible for keeping the F POC informed of the status of determination requests.*

MINIMIZE CONSIDERED

Signature: Pompeo

Drafted By:	F:Bowe, Avon T
Cleared By:	EUR-IO/EX/FM:Buckneberg Preston, Jody
	WHA/PPC:Fralish, Teresa M
	AF/EX:Reynolds, Christopher R
	F/RA:VandenAssem, Christian W
	F/RA:Mosley, R Andrew
	EAP/EX:LaMontagne, David M
	P:Mohamoud, Safia
	D:Hammad, Hammad B
	NEA-SCA/EX:Al-Laham, Eliza F
	WHA/EX:Pan, Angela P
	SES\DostalCJ
Approved By:	F:Richardson, James L
Released By:	F:Bowe, Avon T
XMT:	BASRAH, AMCONSUL; CARACAS, AMEMBASSY; SANAA, AMEMBASSY; ST PETERSBURG, AMCONSUL; VLADIVOSTOK, AMCONSUL; ALEXANDRIA, AMCONSUL

Action Post:	AMEMBASSY CONAKRY
Dissemination Rule:	DISP_ALDAC, AID_LES_INFO, DAO_ACTION, FMM_LES_INFO, FMO_LES_INFO, POL, AID_EXEC, ECON, MGT_INFO, AID_EXEC_Info, FMO, ECON_LES_INFO, FMO_INFO

UNCLASSIFIED

<VAT Report_FY18_Guinea_6.8.2020.xlsx>

From: Andrew Clements <aclements@usaid.gov>
Sent: Mon, 9 Jan 2017 13:34:40 +0100
Subject: Re: PREDICT Management Team Agenda - Monday January 9, 2017 @ 10AM PST
To: "William B. Karesh" <karesh@ecohealthalliance.org>
Cc: David Wolking <djwolking@ucdavis.edu>, Alisa Pereira <apereira@usaid.gov>, Cassandra Louis Duthil <clouisduthil@usaid.gov>, Chris Johnson <ckjohnson@ucdavis.edu>, 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>, PREDICTMGT <predictmgt@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>, Ava Sullivan <sullivan@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>, Amanda Fuchs <fuchs@ecohealthalliance.org>, Catherine Machalaba <machalaba@ecohealthalliance.org>, Evelyn Luciano <luciano@ecohealthalliance.org>, Molly Turner <turner@ecohealthalliance.org>, Taylor Elnicki <telnicki@metabiota.com>

Thanks, Billy. Safe travels.

Do you have anything to add on the status of discussions with FAO related to coordinated surveillance with Predict? Especially, now that FAO will be focusing more on country-identified endemic zoonotic diseases in the GHSA countries in Africa.

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 Jan 6, 2017, at 11:32 PM, William B. Karesh <karesh@ecohealthalliance.org> wrote:

> Dear all,
> I'll be winging my way to SFO at the time of the Monday call so I'll have to miss it.

A few short updates on partnerships:

1) GHSA event at State Dept well attended, nice farewell talks given by Secr. Kerry, NSA Susan Rice and Administrator Smith. Only 7% of the speakers (me) mentioned that over 60% of the diseases mentioned arise from animals and that failing to invest more upstream will only lead us back to the 20th Century and continue to overburden public health systems.
2) FAO coordination moving along as expected.
3) P-2 team visit to CDC last week went well - Jonna, Chris or Tracey can update the group.
4) P&R offering to help with One Health assessment work - will cover details at meeting in California
5) "One Health in Action" booklet done with P&R just back from the printers in English and French, copies will be brought to meeting in California
6) One Health Economics workshop with World Bank all set for January 30 - Feb 2, LaToya Armstrong will be participating as well as P&R, WHO and FAO.

BK

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

EcoHealth Alliance
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New York, NY 10001 USA

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+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 Jan 4, 2017, at 7:56 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi there,
Attached and below is the call-in information and agenda for PREDICT's Management Team call next Monday January 9, 2017 at 10AM PST/1PM EST.

I'll follow-up with the calendar reminder next.

Best,

David

PREDICT Management Team Agenda

Monday, January 9, 2017

10:00am PST/1:00pm EST

REDACTED **Access code** REDACTED

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

Standing items

USAID Updates

1. **Administrative items**
    a. Annual report feedback
    b. CIPs for GHSA Phase 2 countries (DRC and Rwanda request)
    c. Senior behavioral surveillance coordinator update
    d. Metabiota travel situation and ITA for DRC

e. Yellow fever plans and carry-over in DRC

f. GHSA M&E

2. **Mission communication round-up**

a. Indonesia

b. Ethiopia

c. Uganda

d. CIV

e. Sierra Leone

f. Guinea

g. Liberia

3. **Semi-annual Consortium meeting, January 10-11 in Pacifica, CA:** last call for agenda comments, feedback, or questions (agenda will be shared before the call)

4. **FAO collaboration/coordination updates (Billy)**

5. **Other coordination and engagement priorities (Billy)**

<PREDICT MT Agenda (1.9.17) Final.docx>

Sent: Wed, 25 Jan 2017 06:21:54 -0800
Subject: Re: Liberia REDISSE workplan
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Alisa Pereira <apereira@usaid.gov>
Cc: "Andrew (GH/HIDN) Clements" <AClements@usaid.gov>

Thanks -- that's great,
J

On Wednesday, January 25, 2017, Alisa Pereira <apereira@usaid.gov> wrote:

Jonna-

I suggested Billy for this role since he is the donor liaison and to take pressure off an already strained field team.

Please advise if you agree or prefer someone else to play this role.

Thanks

Sent from my iPhone

Begin forwarded message:

From: Kendra Chittenden <kchittenden@usaid.gov>
Date: January 25, 2017 at 7:39:04 AM EST
To: "William B. Karesh, D.V.M" <Karesh@ecohealthalliance.org>
Cc: PREDICTMGT <predictmgt@usaid.gov>, Jim Desmond <desmond@ecohealthalliance.org>, Jon Epstein <epstein@ecohealthalliance.org>, Monica Dea <mdea@usaid.gov>, Mildred Howard <mphoward@usaid.gov>, "Louise Flynn ([redacted]
Subject: Fwd: Liberia REDISSE workplan

Billy,
I wanted to share the REDISSE workplan and ask for your assistance to ensure that PREDICT's activities -- particularly current and planned support to LIBR are adequately captured. Additionally - since PREDICT has a great perspectives on the gaps in lab capacity and workforce to provide input or recommendations that help to best leverage REDISSE resources to address the issues.

Garba and John Dogba (NOHTA) with Monica Dea are all participating in the meetings in Liberia this week. The meeting came up quickly and we know Jim is still out so we appreciate your help to add PREDICT input & recommendations.

The Gov't of Liberia and REDISSE asked for all feedback by Feb 3rd so we'd like to request that our **EPT partners send feedback by Jan 30th** because Monica is working with other EPT partners and CDC and DOD to integrate all USG feedback.

Thanks for your help!! Kendra

---------- Forwarded message ----------
From: **Kendra Chittenden** <kchittenden@usaid.gov>
Date: Mon, Jan 23, 2017 at 4:13 PM
Subject: Liberia REDISSE workplan
To: PREDICTMGT <predictmgt@usaid.gov>
Cc: Andrew Clements <aclements@usaid.gov>, Alisa Pereira <apereira@usaid.gov>

PREDICT team-
This is the draft REDISSE workplan that Monica Dea shared with us and was going to share with partners.

The meeting is this week in Monrovia. Liberia is a phase 2 country so this is the beginning of the process (unlike Sierra Leone and Guinea which are in the final workplan approvals). Liberia was suppose to be a phase 1 country but this was pushed back & the workplan was adjusted not only for the delayed timeline but also because the total amount will be $15 M (not $30 M as initially offered in phase 1).

John Dogba, NOHTA, and Garba from FAO will be in the meeting as will Monica Dea from USAID. If PREDICT has an opportunity to participate this week that is terrific. if not the has asked USAID to send comments so we can pass your input along.

The lead for REDISSE in Liberia is--

Shunsuke (Shun) Mabuchi (smabuchi@worldbank.org)

Kendra
--

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

--

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

--

From: Jon Epstein <epstein@ecohealthalliance.org>
Sent: Thu, 2 Feb 2017 14:47:41 -0500
To: predict-outbreak@ucdavis.edu
Cc: Mindy Rostal <rostal@ecohealthalliance.org>, Emily Hagan <hagan@ecohealthalliance.org>, Peter Daszak <daszak@ecohealthalliance.org>, "William B. Karesh, D.V.M" <karesh@ecohealthalliance.org>, Ariful Islam <arif@ecohealthalliance.org>
Subject: [predict] [predict-outbreak] Bangladesh outbreak update: Feb 2nd
Crow die off_PREDICT Bangladesh_Dhaka_Feb 2 2017.docx

Jonna,
Attached is the Feb 2 update for Dhaka. We noticed that the total #crows sampled listed in the Feb 1 report had an error (listed as 148, instead of 140). Sorry about that, but today's total is correct.

We've finished sample collection in Dhaka, but some labwork and behavioral analyses are still pending. Once we complete these, our engagement will be completed. I'm not sure if this still warrants daily updating, but let us know what USAID would like at this point.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH

Vice President for Science and Outreach

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

1.212.380.4467 (direct)
REDACTED (mobile)

web: ecohealthalliance.org

Twitter: @epsteinjon

USAID | PREDICT
FROM THE AMERICAN PEOPLE

PREDICT Outbreak Rapid Report

Today's Date: February 2, 2017
Cumulative day of the outbreak investigation: 19
Working Title of Investigation: *Crow_dieoff_Bangladesh_Dhaka_2017*

Please describe the disease signs and symptoms and species affected (humans, domesticated animals, wildlife:
On 14th January, the PREDICT field team (team members who were not directly involved in investigating the crow die-off in Rajshahi) was sampling bats and observed unusual mortality of crows (*Corvus splendens*) on the premises of Mohakhali Wireless, Dhaka City. The team observed the crows suddenly falling from trees; and clinical signs of: circling, inability to fly, lethargy, torticollis, tremors, and diarrhea. No history or clinical signs were reported or noted in other domesticated animals or people.

Location	
Country:	Bangladesh
District:	Dhaka (This is 245km from Rajshahi)
Village/Town:	Dhaka city: Wireless Mohakhali, Ramna Park, Sohrawardi uddan, Dhaka University, and Modumoti Model Town
GPS Coordinates (if known):	*Mohakhali Wireless* N23 47.010 E90 24.289 *Ramna Park:* N23 44.347 E90 23.969 *Dhaka University:* N2344.087 E9023.499
Date that first case(s) of illness occurred (if known or estimate):	January 14, 2017
Date that PREDICT was first notified of outbreak:	January 14, 2017

Key Information	Description of Findings/Actions/Outcomes
How many affected individuals?	Human: Suspected__0__ Confirmed__0__Deaths__0__ Domestic animal: Suspected__0__ Confirmed__0__Deaths__0__ Wild animal: Suspected__148__ Confirmed__0__Deaths_148__
How was outbreak first noticed?	The PREDICT-2 team was conducting routine bat sampling in Dhaka. On January 14, 2017, Country Coordinator, Dr. Ariful Islam, reported observing 4 sick or dying crows on the premises of a telecommunications company where PREDICT was also conducting bat sampling. The Country Coordinator notified the Director of the Institute of Epidemiology, Disease Control & Research (IEDCR) about a second crow die-off (*see also PREDICT's report on the concurrent Rajshahi outbreak*) on the premises of the telecommunication company, Mohakhali Wireless. The Director of IEDCR then informally and verbally requested the PREDICT-2 team to extend their Rajshahi outbreak response efforts to also investigate the crow die-off in

	Dhaka. When asked, local residents stated that the crow die-off had started in the beginning of January. IEDCR expressed interest in understanding the geographical distribution, cause and extent of this outbreak and find any epidemiological links between these two outbreak sites (Dhaka and Rajshahi).
Where was the first reported case? What is/was the extent of geographic spread? Include comments on the apparent speed of spread.	The crow die-off was first observed at Mohakhali wireless. An additional 4 crow roosts were observed by the PREDICT team that also had evidence of crow morbidity and mortality approximately 7km from Mohakhali at Ramna Park, Suhrawardy Uddan, Modumoti Model Town and Dhaka University. The team searched Dhaka city for other crow roosts and observed apparently healthy crows at 7 additional roosts. Discussions with local residents and additional field observations indicated there was no further evidence of crow mortality events or unusual illness at these other roosts.
Has the country requested support from PREDICT (include date of request)?	The Director of IEDCR requested PREDICT's support in this outbreak on January 14, 2017, as part of the official request for the ongoing Rajshahi outbreak. The director of IEDCR officially acknowledged the outbreak on January 15, 2017.
If so, which government agency requested PREDICT support?	Institute of Epidemiology, Disease Control and Research (IEDCR) and One Health Secretariat of Bangladesh under Ministry of Health and Family Welfare, Government of the people's Republic of Bangladesh.
When was PREDICT response initiated (date)?	January 14, 2017
Are other EPT partners involved in the response (which ones and how)?	On 18 January, IEDCR provided an update of the investigation at the National Influenza Technical Steering Committee coordination meeting. FAO and P&R were present. On the 25th, there was a second meeting to discuss the outbreak and FAO presented data from ongoing, routine live bird market (LBM) surveillance.
What type of assistance did PREDICT initially provide? Which PREDICT personnel were involved?	PREDICT was engaged at the start of outbreak response, since the team reported the unusual deaths and clinical signs. At IEDCR's request, the team immediately collected crow samples and provided technical advice to IEDCR. The team surveyed nearby crow roosts (within 7 km) and found 4 additional sites where crows had clinical signs and mortality. The PREDICT team visited 14 live bird markets and sampled poultry offal. These markets are in Dhaka close to the outbreak site and are not under routine surveillance by FAO. PREDICT conducted wild bird and feral dog sampling; environmental crow and poultry fecal sample collection; qualitative interviews; transported personnel; transported samples from the field to the PREDICT lab at icddr,b and the DLS National Laboratory – The Central Disease Investigation Laboratory (CDIL). Diagnostic analyses are being conducted by the Ministry of Livestock and Fisheries reference lab as well as the reference lab at the Bangladesh Livestock Research Institute (BLRI) and icddr,b. The PREDICT team included Dr. Ariful Islam, PREDICT-2 country coordinator; one veterinary research officer; one anthropologist; one field research assistant; and two field technicians who have wildlife expertise. At icddr,b, lab testing was overseen by PREDICT Bangladesh lab lead, Dr. Zia Rahman and conducted by 2 research officers.
When was the first official acknowledgement of the outbreak (by which government agency or other reputable body and date)?	The Director Institute of Epidemiology, Disease Control & Research (IEDCR) first officially acknowledged the crow die-off on January 15, 2017. The response was initiated by the Director of IEDCR on January 14, 2017. In

When was a response initiated and by whom? Which agencies were involved? Who was in charge of the national response?	this outbreak response, the Ministry of Health & Family Welfare, Ministry of Forest and Environment, and Ministry of Fisheries and Livestock were each involved as part of the Government of Bangladesh response. iccdr,b was involved as a PREDICT lab partner to support preliminary sample testing. For the Dhaka crow die-off investigation, the Bangladesh Livestock Research Institute (BLRI) and the Central Diagnostic Investigation Laboratory (CDIL) serve as official reference labs (under Ministry of Fisheries and Livestock) and are performing confirmatory testing for a subset of samples screened at icddr,b. BLRI and CDIL will report the official laboratory results on behalf of the Government of Bangladesh, once diagnostic testing is completed. Prof. Dr. Meerjady Sabrina Flora, Director, IEDCR is in charge of the national response.
Was the cause of the outbreak confirmed by a laboratory? If so, give details, including cause, species, specimen types tested and dates of testing if known.	The etiology of outbreak was preliminarily identified by laboratory testing, and confirmatory testing is on-going. Note: The PREDICT team has been actively sampling sick or dead crows in Dhaka from Jan 14th, and the outbreak remains active. Below is a detailed daily summary of PREDICT field activities and samples submitted to lab partners for analysis.
Where was the laboratory testing performed (name of laboratory)?	icddr,b, Bangladesh Livestock Research Institute(BLRI), and Central Disease Investigation laboratory (CDIL)
Number of days between initiation of government response and lab confirmation of laboratory results.	Confirmed diagnostic results from the Government of Bangladesh have not been released.
Summary of the Outbreak:	**To be filled after active outbreak activity has ceased**
Working name of the outbreak (e.g., Yellow Fever - DRC)	Crow die-off Dhaka
Total number of cases:	Human: Suspected__0____ Confirmed__0___Deaths__0__ Domestic animal: Suspected__0____ Confirmed__0___Deaths__0___ Wild animal: Suspected___148__ Confirmed_0___Deaths_148
Summary of PREDICT Team response activities during the outbreak.	Since January 14, 2017, after receiving a verbal request from the Director of IEDCR (the official acknowledgement of the die-off was on the 15th of January), the PREDICT team has been continuing its field investigations and has sampled than 148 crows and collected 81 live bird market environmental samples, 40 poultry offal samples, 6 feral dog samples and captured 13 wild birds that are co-roosting with crows (species ID pending). We submitted all the samples to icddr,b lab and a subset of samples were submitted to BLRI for confirmatory testing. Additional testing and laboratory systems strengthening also ongoing at CDIL. The qualitative team performed their observational and informal interviews in the outbreak area, live bird markets and poultry farms. The PREDICT team has continued to sample wild crows, as of January 31st, at three of the sites with ongoing crow mortality: Wireless Mohakhali, Ramna Park, Sohrawardi uddan. The anthropology team has one more field site visit and then then will finalize their report. Laboratory diagnostics are ongoing.

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PREDICT Response Timeline

Working Title of Investigation: *Crow_dieoff_Bangladesh_Dhaka_2017*

Key Events:

Date	Day #	Notification or Action Taken
January 14, 2017	1	First notification of unusual disease activity by PREDICT team
(See Rajshahi report)		CC notification to PREDICT lead partner
January 14, 2017	1	Unofficial request from the government for the PREDICT team
January 14, 2017	1	First deployment of PREDICT teams to outbreak field site – PREDICT team was already deployed to the site sampling bats
January 14, 2017	1	First specimen collection
January 14, 2017	1	First specimens delivered to laboratory
January 15, 2017	2	Invitation to assist from government received by PREDICT team
January 15, 2017	2	First Outbreak Taskforce meeting attended by PREDICT CC or PREDICT team members
January 15, 2017	2	First samples (12 oral and cloacal swab samples in VTM) collected from 6 crows and submitted to icddr,b laboratory and preliminary testing completed. These samples were screened by real time PCR for the M gene, H5, H7, and H9. The preliminary results were sent to IEDCR on same day.
January 16, 2017	3	First report of preliminary results to government (Department of Livestock Services and the Forest Dept.) and taskforce by IEDCR
January 18, 2017	5	Additional samples from 27 crows submitted for testing to both icddr,b and BLRI for testing
January 22, 2017	9	Additional preliminary testing completed at icddr,b for confirmation at BLRI; supplemental testing methods begun on Predict-collected samples at Central Disease Investigation Laboratory (CDIL) supporting larger lab system
January 26, 2017	13	PREDICT submitted an additional 165 samples consisting of 78 crow samples (cloacal and oropharyngeal), 41 poultry offal samples (from the 14 live bird markets), 40 environmental fecal samples and 6 feral dog samples to the PREDICT lab at icddr,b.
January 30, 2017	17	PREDICT's anthropologist performed observational and informal interviews at one live bird market neighboring Mohakhali outbreak site. The team sampled 12 dead crows from two locations (7 from Mohakhali wireless, and 5 from Ramana Park) and safely packed and shipped carcasses to CDIL for safe disposal. 12 swab samples from the crows were shipped to icddr,b lab for testing. PREDICT team also found 7 new crow roosts with apparently healthy crows and no history of crow die-off according to local residents. The anthropology team has one more field site visit and then then will finalize their report. Additional biological sample and behavioral data collection by Predict (ongoing as usual Predict scope of work). Laboratory diagnostics are ongoing
January 31, 2017	18	PREDICT collected observational behavioral data and conducted informal interviews with vendors at a live bird market neighboring Ramna Park outbreak site. The team sampled 9 dead crows from two locations (7 from Mohakhali Wireless, and 2 from Ramna Park) and safely packed and shipped the carcasses to CDIL for disposal via incineration. Cloacal and oropharyngeal swab samples from 9 crows were shipped to icddr,b lab for preliminary testing. Laboratory diagnostics are ongoing.

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		The PREDICT team identified 5 additional crow roosts with apparently healthy crows and no history of recent crow die-off according to local residents.
February 1st, 2017	19	PREDICT collected observational behavioral data and conducted informal interviews with vendors at a live bird market neighboring Sohrawardi Uddan outbreak site. The team sampled 8 dead crows from three locations (6 from Mohakhali Wireless, 1 Sohrawardi Uddan and 1 from Ramna Park) and safely packed and shipped the carcasses to CDIL for disposal via incineration. Cloacal and oropharyngeal swab samples collected from the 8 crows were shipped to icddr,b lab for preliminary testing. Laboratory diagnostics are ongoing. The PREDICT team identified three additional crow roosts with apparently healthy crows and no history of recent crow die-off according to local residents. A regular meeting of all USAID Mission partners, including PREDICT, will take place on February 6, 2017. The Mission Director will be updated on all PREDICT-2 activities as well as on PREDICT's engagement with the Government of Bangladesh in the investigation of the crow die-off. The PREDICT Country Coordinator updated P&R, FAO, CDIL, IEDCR regarding recent activities.
February 2, 2017		The team sampled 8 dead crows from three locations (4 from Mohakhali Wireless, 2 Sohrawardi Uddan and 2 from Ramna Park) and safely packed and shipped the carcasses to CDIL for disposal via incineration. Cloacal and oropharyngeal swab samples collected from the 8 crows and were shipped to icddr,b lab for preliminary testing. Laboratory diagnostics are ongoing. The team also found a recently dead Indian flying fox (*Pteropus medius*) at a crow die-off site in Sohrawardi Uddan. Bat was necropsied and samples were shipped to icddr,b lab for influenza testing. This concludes the crow sampling in Dhaka. The PREDICT Country Coordinator updated DLS, CDIL, IEDCR regarding recent activities.
PENDING		First notification to USAID of government cleared confirmatory laboratory results

From: Jon Epstein <epstein@ecohealthalliance.org>
Sent: Mon, 13 Mar 2017 04:39:08 +0545
To: Dan Schar <dschar@usaid.gov>, "Sudarat Damrongwatanapokin D.V.M., Ph" <sdamrongwatanapokin@usaid.gov>
Cc: Andrew Clements <AClements@usaid.gov>, predict@ucdavis.edu, Evelyn Luciano <luciano@ecohealthalliance.org>, Molly Turner <turner@ecohealthalliance.org>, Tom Hughes <tom.hughes@ecohealthalliance.org>, Peter Daszak <daszak@ecohealthalliance.org>, Emma Lane <lane@ecohealthalliance.org>, "Alisa Pereira (GH/HIDN)" <apereira@usaid.gov>
Subject: [predict] potential outbrief visit to RDMA on March 22nd?

Dear Dan and Sudarat,
I hope you're well. I was wondering if you are available and would like to meet for an out brief following my Malaysia visit, on March 22nd? I could fly to NY via Bangkok. Tom would also be able to join for the meeting and we could update on IDEEAL, as well.

Please let me know if the timing works.

Cheers,
Jon

--

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)
REDACTED (mobile)

web: ecohealthalliance.org

Twitter: @epsteinjon

From:	Andrew Clements <aclements@usaid.gov>
To:	predict@ucdavis.edu <predict@ucdavis.edu>
CC:	predictmgt@usaid.gov <predictmgt@usaid.gov>;spaige@usaid.gov <spaige@usaid.gov>;Andrea Long-Wagar <alongwagar@usaid.gov>
Sent:	3/21/2017 11:37:02 AM
Subject:	[predict] Fwd: PRO/EDR> Undiagnosed rash - Cameroon: (EN) fatalities, RFI

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: March 21, 2017 at 7:16:31 PM GMT+1
To: promed-post@promedmail.org, promed-edr-post@promedmail.org
Subject: PRO/EDR> Undiagnosed rash - Cameroon: (EN) fatalities, RFI
Reply-To: promedNOREPLY@promedmail.org

UNDIAGNOSED RASH - CAMEROON: (EXTREME NORTH) FATALITIES, REQUEST FOR INFOMRATION
****
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: Sat 18 Mar 2017
Source: Cameroon Online [edited]
<http://www.cameroononline.org/spotted-fever-claims-16-lives-cameroon/>

At least 16 people, mostly children under the age of 5 have died in Far North Cameroon of a mysterious disease that affected a total of 54 people, sources said. The Disease Control and Epidemics Director (DLMEP) at the Ministry of Public Health, Dr. Etoundi Mballa said "We are dealing with a curious disease the symptoms of which suggest that it is atypical eruptive fever". He added: "Investigations are ongoing".

He said that officials of the Ministry of Public Health were of the view that the important was to know whether it is an infectious disease "and so far we know that is not something that contaminates." The fever which appeared in 6 health districts of Mayo-Tsanaga, in the Far North continues to claim victims.

Its frequent clinical manifestations are persistent fever, skin rashes, anemia, hepatosplenomegaly and lymphadenopathy.

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

[The etiology of this outbreak with a case fatality rate (CFR) of almost 30 percent is unclear. Bacterial diseases such as typhoid fever and leptospirosis might be considered but in general the CFR is quite high for those diseases. One of the viral hemorrhagic fevers could be considered by mosquito-borne viruses such as dengue. ProMED would appreciate more information about this outbreak from knowledgeable sources. - Mod.LL

A HealthMap/ProMED-mail map can be accessed at:
<http://healthmap.org/promed/p/36202>.]

[See Also:
2016

Undiagnosed skin rash - Liberia: (Monrovia) RFI
http://promedmail.org/post/20161201.4668562
Undiagnosed skin rash - South Africa: (NL) RFI
http://promedmail.org/post/20161021.4575989
Undiagnosed rash - USA: (CA) airborne lepidopterism susp, RFI
http://promedmail.org/post/20160930.4527849
Undiagnosed skin rash - USA: (NC) RFI
http://promedmail.org/post/20160725.4366693
Undiagnosed rash outbreak - Dominican Republic (02): (AL) comment
http://promedmail.org/post/20160513.4218972
Undiagnosed rash outbreak - Dominican Republic: (AL) itchy rash, children, RFI http://promedmail.org/post/20160511.4215147
2015

Undiagnosed outbreak - Sudan (05): (ND) fever, rash, refugee camp, children, RFI http://promedmail.org/post/20151110.3780916
2004

Undiagnosed rash illness - Ecuador (Carchi): RFI
http://promedmail.org/post/20041117.3087]
.....sb/ll/ao/mpp
###
****

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Dennis Carroll <dcarroll@usaid.gov>
Sent: 4/11/2017 9:07:20 AM
Subject: Re: GVP.CUGH. Session_9 April (dc).pptx - Invitation to edit

Thanks, Dennis -- that one worked great,
J

On Tue, Apr 11, 2017 at 8:53 AM, Dennis Carroll (via Google Slides) <drive-shares-noreply@google.com> wrote:

Dennis Carroll has invited you to **edit** the following presentation:

GVP.CUGH. Session_9 April (dc).pptx

Unl pro

All, here is the power point in its entirety from the CUGH presentation. You should be able to access, edit and save on your own drive. Let me know if there are any issues

d

Google Slides: Create and edit presentations online.
Google Inc. 1600 Amphitheatre Parkway, Mountain View, CA 94043, USA
You have received this email because someone shared a presentation with you from Google Slides.

Logo for Google Slides

From: Dennis Carroll <dcarroll@usaid.gov>
Sent: Tue, 11 Apr 2017 12:55:47 -0400
Subject: Re: GVP.CUGH. Session_9 April (dc).pptx - Invitation to edit
To: Jonna Mazet <jkmazet@ucdavis.edu>
Cc: Peter Daszak <daszak@ecohealthalliance.org>, Eddy Rubin <erubin@metabiota.com>, Catherine Machalaba <machalaba@ecohealthalliance.org>, "Ana S. Ayala" <asa58@law.georgetown.edu>

Thanks sister

d

Dr Dennis Carroll
Director, Emerging Threats Program
U.S. Agency for International Development
Office: (202) 712-5009
Mobile: REDACTED

> On Apr 11, 2017, at 12:18 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
>
> Thanks, Dennis!
> A couple of edits, as the reformatting made the Bat CoV slide incorrect
> (some text can't be read and arrows point to wrong viruses). I deleted that
> slide for simplicity (so don't use it if you have it) and cleaned up one
> other.
> Great being together and doing the panel!
> Good luck with your presentation, Ana, & fabulous seeing you,
> Jonna
>
> On Tue, Apr 11, 2017 at 8:53 AM, Dennis Carroll (via Google Slides) <
> drive-shares-noreply@google.com> wrote:
>
>> Dennis Carroll <dcarroll@usaid.gov> has invited you to *edit* the
>> following presentation:
>> GVP.CUGH. Session_9 April (dc).pptx
>>
<https://docs.google.com/a/ucdavis.edu/presentation/d/1M0Z2p9raJaav9JY0gtotOmCWo75ZVWKQe7vl7-1cp78/edit?usp=sharing_eil&ts=58ecfbeb>
>> [image: Unknown profile photo]All, here is the power point in its
>> entirety from the CUGH presentation. You should be able to access, edit and
>> save on your own drive. Let me know if there are any issues
>>
>> d
>> Open in Slides
>>
<https://docs.google.com/a/ucdavis.edu/presentation/d/1M0Z2p9raJaav9JY0gtotOmCWo75ZVWKQe7vl7-1cp78/edit?usp=sharing_eip&ts=58ecfbeb>
>> Google Slides: Create and edit presentations online.
>> Google Inc. 1600 Amphitheatre Parkway, Mountain View, CA 94043, USA
>> You have received this email because someone shared a presentation with
>> you from Google Slides. [image: Logo for Google Slides]
>> <https://drive.google.com>
>>
> <GVP.CUGH. Session_9 April (dc jm rev).pptx>

From: Dennis Carroll <dcarroll@usaid.gov>
Sent: Tue, 11 Apr 2017 16:32:49 -0400
Subject: Re: GVP.CUGH. Session_9 April (dc).pptx - Invitation to edit
To: Catherine Machalaba <machalaba@ecohealthalliance.org>
Cc: "Ana S. Ayala" <Ana.Ayala@law.georgetown.edu>, Eddy Rubin <erubin@metabiota.com>, Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>

Catherine, its still a mess. Let me work with people here to find a less corruptible way of sending the file.

d

On Tue, Apr 11, 2017 at 2:33 PM, Catherine Machalaba <machalaba@ecohealthalliance.org> wrote:

> Thank you to Dennis for sending to the group! (and my apologies for the delay while offline in transit all day).
> I compared this set to my slides to my version from Sunday, and some of the formatting and animation on slides 6, 17, 31, 49 and 52 does not display correctly- Dennis, this might be what you're seeing too? It might be an issue with converting across Google slides to PowerPoint-- Is it OK if try adding in those slides again, and then uploading the slides to a DropBox folder that I will invite this group to?

Kind regards,
Catherine

Catherine Machalaba, MPH
Health and Policy Program Coordinator

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

1.212.380.4472 (direct)
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1.212.380.4465 (fax)
www.ecohealthalliance.org

Science Officer, Future Earth oneHEALTH Project

Chair, Veterinary Public Health Special Primary Interest Group, American Public Health Association

Program Officer, IUCN SSC Wildlife Health Specialist Group

> On Apr 11, 2017, at 2:17 PM, Ana S. Ayala <Ana.Ayala@law.georgetown.edu> wrote:

Yes. It seems to be working fine on presentation mode.

On Tue, Apr 11, 2017 at 2:08 PM Dennis Carroll <dcarroll@usaid.gov> wrote:

> Did you put it in presentation mode and run the slides?

Dr Dennis Carroll
Director, Emerging Threats Program
U.S. Agency for International Development
Office: (202) 712-5009
Mobile: REDACTED

On Apr 11, 2017, at 1:35 PM, Ana S. Ayala <Ana.Ayala@law.georgetown.edu> wrote:

> That's strange. For what is worth, I can see them fine on my computer.

Ana S. Ayala, J.D., LL.M.
Director, Global Health Law LL.M. Program
O'Neill Institute for National and Global Health Law

Georgetown University Law Center
(202) 662-9462 | (202) 662-4045 fax
Ana.Ayala@law.georgetown.edu
www.oneillinstitute.org

On Tue, Apr 11, 2017 at 1:21 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:

> Wow, Jonna just opened your version up and ran it. A LOT of corrupted slides. Not sure what happened along the way. Take another look

On Tue, Apr 11, 2017 at 12:18 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> Thanks, Dennis!
> A couple of edits, as the reformatting made the Bat CoV slide incorrect (some text can't be read and arrows point to wrong viruses). I deleted that slide for simplicity (so don't use it if you have it) and cleaned up one other.
> Great being together and doing the panel!
> Good luck with your presentation, Ana, & fabulous seeing you,
> Jonna

On Tue, Apr 11, 2017 at 8:53 AM, Dennis Carroll (via Google Slides) <drive-shares-noreply@google.com> wrote:

> Dennis Carroll has invited you to **edit** the following presentation:
>
> GVP.CUGH. Session_9 April (dc).pptx
>
> All, here is the power point in its entirety from the CUGH presentation. You should be able to access, edit and save on your own drive. Let me know if there are any issues
>
> d
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> Open in Slides
>
> Google Slides: Create and edit presentations online.
> Google Inc. 1600 Amphitheatre Parkway, Mountain View, CA 94043, USA
> You have received this email because someone shared a presentation with you from Google Slides.

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

Office: 202-712-5009
Mobile: REDACTED

--
Sent from Gmail Mobile

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

Office: 202-712-5009
Mobile: REDACTED

Sent: Thu, 11 May 2017 11:02:20 -0700
Subject: Re: Bat communication material
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Leilani Francisco <francisco@ecohealthalliance.org>
Cc: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>

Hi Leilani,
What time do you want to print? I know Chris wants to give you comments prior, but she (and I) have been in meetings all morning.
Thanks for your continued good work,
Jonna

On Wed, May 10, 2017 at 4:49 PM, Leilani Francisco <francisco@ecohealthalliance.org> wrote:

Hi team,

Thank you for all of your feedback on the communication plan.

Please find attached an updated version containing tracked changes.

This version includes feedback from Jon, Tracey, and from the call today with Jonna, Chris, and Peter.

I will plan to print this out tomorrow in the early afternoon to bring to the USAID meeting on Friday.

I look forward to your thoughts.

Best,

Leilani

From: Leilani Francisco [mailto:francisco@ecohealthalliance.org]
Sent: Monday, May 8, 2017 2:25 PM
To: 'Tracey Goldstein' <tgoldstein@ucdavis.edu>; 'Aiah Gbakima' <[redacted]>; 'Karen Saylors' <ksaylors@metabiota.com>; 'Eddy Rubin' <erubin@metabiota.com>; 'Jonna Mazet' <jkmazet@ucdavis.edu>
Subject: RE: Bat communication material

Hello everyone,

Please find attached a next pass at the communication campaign strategy. I've attached:

- A version containing all of the tracked changes, comments, and responses
- A clean version

This version includes feedback from Karen, Jason, Aiah, and myself.

I look forward to your thoughts.

Best,

Leilani

From: [redacted] **On Behalf Of** Tracey Goldstein
Sent: Friday, April 28, 2017 5:39 PM
To: Leilani Francisco <francisco@ecohealthalliance.org>
Cc: Aiah Gbakima <[redacted]>; Karen Saylors <ksaylors@metabiota.com>; Eddy Rubin <erubin@metabiota.com>; Jonna Mazet <jkmazet@ucdavis.edu>

Subject: Re: Bat communication material

Hi Leilani.

Sorry for the delay getting this to you. Quite a few comments and suggestions attached - please let me know if you would like to chat further.

Best, Tracey

On Wed, Apr 26, 2017 at 7:19 AM, Leilani Francisco <francisco@ecohealthalliance.org> wrote:

> Hello everyone,
>
> Please find attached the latest version of the document which now includes updates from Karen, Aiah, and Billy.
>
> Tracey,
>
> Does everything look ok to you? Did you have any updates you'd like to add?
>
> Best,
>
> Leilani

From: Leilani Francisco [mailto:francisco@ecohealthalliance.org]
Sent: Thursday, April 20, 2017 1:26 PM
To: 'Aiah Gbakima' <[redacted]>; 'Karen Saylors' <ksaylors@metabiota.com>
Cc: 'Tracey Goldstein' <tgoldstein@ucdavis.edu>; 'Eddy Rubin' <erubin@metabiota.com>; 'Jonna Mazet' <jkmazet@ucdavis.edu>
Subject: RE: Bat communication material

Hi Aiah and Karen,

Many thanks for the helpful videoconference yesterday.

Please find attached an updated version of the plan which incorporates the table, our discussion yesterday, and some additional resources.

I look forward to your edits and feedback.

Best,

Leilani

From: Leilani Francisco [mailto:francisco@ecohealthalliance.org]
Sent: Tuesday, April 18, 2017 4:05 PM
To: 'Aiah Gbakima' <REDACTED>
Cc: 'Tracey Goldstein' <tgoldstein@ucdavis.edu>; 'Eddy Rubin' <erubin@metabiota.com>; 'Karen Saylors' <ksaylors@metabiota.com>; 'Jonna Mazet' <jkmazet@ucdavis.edu>
Subject: RE: Bat communication material

Thanks Aiah, no worries, you did send the correct one.

Karen and I have just a few follow up questions for you. I'll get in touch directly to set up a time.

Best,

Leilani

From: Aiah Gbakima [mailto:REDACTED]
Sent: Tuesday, April 18, 2017 1:19 PM
To: Leilani Francisco <francisco@ecohealthalliance.org>
Cc: Tracey Goldstein <tgoldstein@ucdavis.edu>; Eddy Rubin <erubin@metabiota.com>; Karen Saylors <ksaylors@metabiota.com>; Jonna Mazet <jkmazet@ucdavis.edu>

Subject: Re: Bat communication material

I hope I did send the correct one. In any case, here is what I was planning on sending over to you all. If the same, please ignore it.

Best,

Aiah

On Tue, Apr 18, 2017 at 4:41 PM, Leilani Francisco <francisco@ecohealthalliance.org> wrote:

> Many thanks for the below and for all of the very helpful updates to the table.
>
> Karen and I will be talking at 3PM US EDT and will circle back with any questions.
>
> Best,
>
> Leilani

From: Aiah Gbakima [mailto:[redacted]
Sent: Saturday, April 15, 2017 2:13 PM
To: Jonna Mazet <jkmazet@ucdavis.edu>
Cc: Leilani Francisco <francisco@ecohealthalliance.org>; Tracey Goldstein <tgoldstein@ucdavis.edu>; Eddy Rubin <erubin@metabiota.com>; Karen Saylors <ksaylors@metabiota.com>

Subject: Re: Bat communication material

We may need to a one-time intervention since most houses in the areas where the positive bats come from have fairly good houses. The only pressing need will be wire meshes around the outside/under the roof to keep the bats out of their roofs.

What will be necessary for a long time solution will be to teach them on how they can keep the bats out of their houses themselves. Along that line, we have to ask the district councils to include those expenditures in their annual budgets going forward. That way, we teach them to help themselves.

The intial task should be ours since this is one thing that they asked us to do: get the bats out of their houses. We can also use local carpenters to do this job and we may ask local building material stores to donate materials to support these

efforts. We will continue to populate the table until we get it right because we need to have a plan for community enagement before we meet the President since he will surely ask about our next steps. Have wondefrul and safe easter.

Aiah

On Fri, Apr 14, 2017 at 8:01 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> Looking good so far -- thanks for working on it!
>
> My only concern with what you have so far is the exclusion devise, given that all houses may or may not have doors and windows that are closable and that the bats are about as big as your smallest finger. So unless we were to cover the entire houses (every crack and crevice) with a devise, I'm not sure how those would be feasible and thus worth our time in further development/consideration. I guess as one tool in a tool kit for houses with just one or two problem areas, but I'm not sure that should be our emphasis in the emergency phase. Think about keeping small mice out of a house for frame of reference. If we're thinking a way out for entrapped bat, once all cracks and crevices are sealed by other means, it may be worth a bit more consideration, but I don't think USAID will be able to fund a device for every home, so we should also consider that in advance of messaging.
>
> Otherwise support further development of the strategies described.
>
> Have a nice weekend,
>
> Jonna
>
> On Fri, Apr 14, 2017 at 11:09 AM, Leilani Francisco <francisco@ecohealthalliance.org> wrote:
>
> > Dear Proff,
> >
> > It was a pleasure meeting and talking with you today.
> >
> > Thank you for all of the helpful information that you shared.
> >
> > Please find attached an updated strategy table which now contains information from our discussion.
> >
> > Thanks for being willing to review and add detail to this after the holiday.
> >
> > Please feel free to get in touch with any questions.
> >
> > Best regards,
> >
> > 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: Karen Saylors [mailto:ksaylors@metabiota.com]
Sent: Thursday, April 13, 2017 3:37 PM
To: Jonna Mazet <jkmazet@ucdavis.edu>
Cc: Tracey Goldstein <tgoldstein@ucdavis.edu>; Eddy Rubin <erubin@metabiota.com>; Leilani Francisco <francisco@ecohealthalliance.org>; Aiah Gbakima <REDACTED>

Subject: Rc: Bat communication matcrial

Hi Jonna.

Leilani and I just spoke and we will follow up with Aiah tomorrow and get back to this team with a plan as soon as possible.

Thanks,

Karen

From: <REDACTED> on behalf of Jonna Mazet <jkmazet@ucdavis.edu>
Date: Thursday, April 13, 2017 at 10:03 AM
To: Karen Saylors <ksaylors@metabiota.com>
Cc: Tracey Goldstein <tgoldstein@ucdavis.edu>, Eddy Rubin <erubin@metabiota.com>, Leilani Francisco <francisco@ccohcalthalliancc.org>, Aiah Gbakima <REDACTED>
Subject: Re: Bat communication material

Thanks, Karen,

This information will be helpful in contributing to the overall plan.

I apologize if there was a miscommunication or if I was ambiguous, but I was really hoping for was for you to work with Aiah and Leilani to develop more of an outline of all of the different parts of the communication plan that need to be in place and when, rather than the content of the messaging. Like I said, though, the info will still be a useful contribution. The rest of the development and finalization of that content will happen with the overall team, and I know Leilani has a group pulling all of the literature from the WA outbreak and communication pieces that worked and didn't work for other bat-reservoir outbreaks, as well as for birds in avian influenza situations.

I know you have spoken with Leilani this week, and things are developing.

You have a ton on your plate, with the shipments and other organizational details to get things on track in SL and elsewhere. I don't want to overwhelm your To Do list with every little detail, so please do reach out for confirmation before developing intensive written materials and plans that may or may not be the immediate priority.

What I hope you can do is work with Leilani and Aiah to gather intel regarding our team's capacity on the ground, as well as that of potential partners, regarding feasible plans for how the schedule and staffing of all of the different communication steps will work. We very much also what other groups from within the country may have the best experience/success in communicating about Ebola in the country. Of course all of this information compilation must be done stealthily to avoid leaks, so no information should be shared about the finding, just identification of the best practices that have worked locally and pitfalls to avoid based on lessons learned.

So specifically, I am interested in the following (for each -- feasible and optimal timing, staff options, etc.):

- Community information sharing:
    - what are options and optimal timing (e.g. a single meeting with community leaders first, then follow-up meetings in each community OR individual meetings in certain districts occurring simultaneously (could we even staff that -- maybe with partners if that is preferred, but then we would need a training plan for those teams))
    - Specific staffing plans and mechanisms for this piece
- Mechanisms to provide support for communities for any recommended interventions
    - supplies & procurement/distribution
    - instructions
- Press
    - press release for in-country & FAQs
    - press release for global community
    - preferred feature article for release at same time in-country
    - potential for high-level international press piece to support overall philosophy of finding viruses early
- Additional pieces depending on how long we have to plan and prepare (e.g. linking messages with a publication, damage control if things go wrong, etc.)

I look forward to receiving a check-list and outline for these pieces that can form the structure for a living document that we can flesh out as we continue to develop pieces and strategies. I'm fine with Leilani gathering the information from you two and compiling and constructing the plan, recognizing that your attentions are needed elsewhere on many priority issues at the moment.

Please keep any ideas and products from this request to only the distribution list on this email for now.

Thank you,

Jonna

On Tue, Apr 11, 2017 at 4:09 PM, Karen Saylors <ksaylors@metabiota.com> wrote:

Hi Tracey and Jonna.

Here is a layman's Bat Communication Strategy for your review. I've shared it with no one beyond this group, so it doesn't contain Sierra Leone-specific language or references at this point.

Please let me know if you have suggestions or further orientation.

Thanks,

Karen

From: [redacted] on behalf of Tracey Goldstein <tgoldstein@ucdavis.edu>
Date: Tuesday, April 11, 2017 at 12:57 PM
To: Karen Saylors <ksaylors@metabiota.com>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Eddy Rubin <erubin@metabiota.com>
Subject: Re: Bat communication material

Hi Karen,

As we discussed on the call, please do not share any documents with the in country team - we are not ready for that, we need a comprehensive plan. Please send your thoughts to me and Jonna and we can go from there.

Thank you, Tracey

On Tue, Apr 11, 2017 at 10:49 AM, Karen Saylors <ksaylors@metabiota.com> wrote:

Good morning.

Based on your request on Friday, I'm working on bat communication material for Sierra Leone. I'll share a draft with Aiah and James tonight for them to flesh out, [redacted]

I have a question for you about this document:

—who is the target audience? Is it village-level communities where we are doing animal sampling or are we aiming for wider national media coverage? In following up on questions from Dennis and Jonna, Eddy asked me yesterday whether Prof is prepping recommendations intended for a SL major newspaper piece to be released simultaneously or immediately after the country's press release, so I assume we are aiming for a national audience, but please confirm. I know that on Friday, Aiah was talking specifically about how to frame these findings to the communities PREDICT is working in, so I want to orient the draft correctly so that he differentiates between local and national messages.

I'll work with Aiah to get you a document by early Thursday morning unless you tell me you need it more urgently.

Thanks,

Karen

--

Tracey Goldstein, PhD
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School of Veterinary Medicine
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Phone: (530) 752-0412
Fax: (530) 752-3318
E-mail: tgoldstein@ucdavis.edu

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Aiah A. Gbakima, MSPH, Ph.D., GCOR

Country Director, Metabiota Inc, Sierra Leone

Country Coordinator, USAID/Predict Program, Sierra Leone

Mobile: REDACTED

Skype: REDACTED

--

Aiah A. Gbakima, MSPH, Ph.D., GCOR

Country Director, Metabiota Inc, Sierra Leone

Country Coordinator, USAID/Predict Program, Sierra Leone

Mobile: REDACTED

Skype REDACTED

--

Tracey Goldstein, PhD

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Sent: Mon, 22 May 2017 08:02:04 -0700
Subject: Re: Quick & Timely: Cote d'Ivoire
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Molly Turner <turner@ecohealthalliance.org>
Cc: Peter Daszak <daszak@ecohealthalliance.org>, Billy Karesh <karesh@ecohealthalliance.org>, Melinda Rostal <rostal@ecohealthalliance.org>

Thanks,
Jonna

On Mon, May 22, 2017 at 7:54 AM, Molly Turner <turner@ecohealthalliance.org> wrote:

> Hi Jonna,
> Initially the lead will be Peter but we'll be looking to hire a francophone country lead here in the office.

Best,
Molly

On Mon, May 22, 2017 at 10:28 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> Good morning,
> I'm having a quick call with the CdI Mission in 30 minutes. Have you decided who will be the lead for the country. I believe Billy will take on RoC, but I didn't get an idea of who will be the initiating contact/global lead for CdI.
> I will tell them this morning that the transition from MB to EHA will begoin this week. Just strikes me that since Zandra knows you, she will likely ask me who will be in charge. I'll also gather intel for you on her perspective of in-country team strengths and weaknesses.
> Have a nice day,
> Jonna

--
Molly Turner
Federal Grants Coordinator

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To: lkramer@usaid.gov, jkamau@primateresearch.org, [redacted], VodzakME@si.edu, ZimmermanD@si.edu, predict@ucdavis.edu, david.mutonga@thepalladiumgroup.com, [redacted], rechalar@usaid.gov, spaige@usaid.gov, aclements@usaid.gov
From: [redacted]
Sent: Tue, 11 Jul 2017 17:19:59 +0300
Subject: [predict] Settled in IPR

Dear all,

I am delighted to let you know that I moved to IPR and I am now well accommodated in the PREDICT office since yesterday. Many thanks to all of you that made this possible. It is a quiet and nice working environment.

Regards.

Tom

From:	Andrew Clements <aclements@usaid.gov>
To:	Katherine Leasure <kaleasure@ucdavis.edu>
CC:	PREDICTMGT <predictmgt@usaid.gov>;Predict inbox <predict@ucdavis.edu>
Sent:	7/12/2017 12:56:31 PM
Subject:	[predict] Re: Change to Approved ITA - B. Watson to UK/Norway

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 5:53 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Hi Andrew. EcoHealth Alliance has submitted an amendment to the previously approved ITA for Brooke Watson. Our apologies for the late notification; they just received the request from Dennis Carroll for Brooke's participation in an additional presentation in Norway. I have included below the amended ITA request for Ms. Watson, as well as the previously approved ITA for reference. Please let me know if you have any questions. Thanks!

AMENDED ITA:
EcoHealth Alliance would like to request travel approval for Ms. Brooke Watson to travel from New York, New York, USA to London, United Kingdom from July 9-13, 2017 for meetings with partners and potential partners for the Global Virome Project. She will then fly from London, England to Oslo, Norway from July 13-14, 2017 for meetings with the CEPI (Coalition for Epidemic Preparedness Innnovations) Executive Board in support of the Global Virome Project. [**$2,100 airfare/$427 (London), $271 (Oslo) max daily per diems]*
Trip purpose: UK - Ms. Brooke Watson will assist USAID EPT PREDICT-2 Director, Dennis Carroll, for meetings at the Welcome Trust, the Coalition for Epidemic Preparedness Innovations (CEPI), the London School of Hygiene and Tropical Medicine (LSHTM), Chattham House, and the Lancet. Ms. Watson will travel in Peter Daszak's stead and represent EcoHealth Alliance and the Science & Technology Thematic Area of the Global Virome Project. She will provide research and presentation support, as needed, and will answer any questions related to the modeling strategy for global sampling for the Global Virome Project. Norway - Ms. Watson will assist USAID EPT PREDICT-2 Director, Dennis Carroll, during a meeting with the Coalition for Epidemic Preparedness Innovations (CEPI) Executive Board. She will provide research and presentation support as needed, and will answer any questions related to the modeling strategy for global sampling for the Global Virome Project.

PREVIOUSLY APPROVED ITA:
EcoHealth Alliance would like to request travel approval for Ms. Brooke Watson to travel from New York, New York, USA to London, United Kingdom from July 9-15, 2017 for meetings with partners and potential partners for the Global Virome Project. *[*$1,650 airfare/$427 (London) max daily per* diem]

Trip purpose: Ms. Brooke Watson will assist USAID EPT PREDICT-2 Director, Dennis Carroll, for meetings at the Welcome Trust, the Coalition for Epidemic Preparedness Innovations (CEPI), the London School of Hygiene and Tropical Medicine (LSHTM), Chattham House, and the Lancet. Ms. Watson will travel in Peter Daszak's stead and represent EcoHealth Alliance and the Science & Technology Thematic Area of the Global Virome Project. She will provide research and presentation support, as needed, and will answer any questions related to the modeling strategy for global sampling for the Global Virome Project.

Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
530-752-7526

530-752-3318 FAX
kaleasure@ucdavis.edu

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From: "Katherine Leasure" <kaleasure@ucdavis.edu>
To: "'PREDICTMGT'" <predictmgt@usaid.gov>
Cc: <predict@ucdavis.edu>, "'Jonna Mazet'" <jkmazet@ucdavis.edu>
Subject: PREDICT International Travel Requests
Sent: Thu, 27 Jul 2017 13:08:19 -0700

Please find below international travel requests for your review and approval. Please let me know if you have any questions. Thanks!!

1. Epstein (Bangladesh, India): $1400 airfare/$290 (Dhaka), $400 (Delhi) max daily per diems
2. Latinne (Indonesia): $2200 airfare/$146 (North Sulawesi) max daily per diem
3. Islam (Latvia): $1600 airfare/$344 (Riga) max daily per diem

Travel Requests –

1. EcoHealth Alliance would like to request travel approval for Dr. Jon Epstein to travel from Kuala Lumpur, Malaysia to Dhaka, Bangladesh from August 19-22, 2017, and Delhi, India from August 22-24, 2017 to meet with Country Coordinators, government officials and the USAID local missions for workplanning meetings.

Trip purpose: Bangladesh - Dr. Epstein will meet with government officials in Dhaka, and the area's PREDICT Country Coordinator. Dr. Epstein will also meet with the mission to discuss future workplanning with FAO in attendance. India – Dr. Epstein plans to fly from Dhaka to Delhi on August 22 to meet with the India mission, Country Coordinator, and Senior Management team from PREDICT-2 India.

2. EcoHealth Alliance would like to request travel approval for Dr. Alice Latinne to travel from New York, NY, USA to North Sulawesi, Indonesia from August 19, 2017 to September 2, 2017 for field work with in-country partners.

Trip purpose: In North Sulawesi, Dr. Alice Latinne will assist the PREDICT Indonesia team in field sampling (rodents and bats), and ensure correct implementation of new rodent sampling protocols.

3. EcoHealth Alliance would like to request travel approval for Ariful Islam to travel from Dhaka, Bangladesh to Riga, Latvia from September 9-15, 2017 for the ESWI 2017 Influenza Conference Meeting.

Trip purpose: The European Scientific Working group on Influenza is hosting the ESWI Influenza Conference 2017; the group and the conference aim to enhance public health protection against influenza and is the largest European scientific conference entirely dedicated to influenza. During this year, PREDICT Bangladesh participated in multiple disease outbreaks relating to influenza. Ariful Islam will represent PREDICT Bangladesh at this conference and through the presentation of three posters from the PREDICT Bangladesh team that have been accepted at the ESWI 2017 conference featuring data from the outbreaks and public health emergency response to outbreaks. This is a forum to engage the influenza community and participate is scientific policy discussions beneficial to PREDICT Bangladesh and PREDICT globally.

Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
530-752-7526
530-752-3318 FAX
kaleasure@ucdavis.edu

From: Andrew Clements <aclements@usaid.gov>
Sent: Tue, 1 Aug 2017 16:08:30 +0200
Subject: Heads up on additional in-country interviews as part of EPT-2 evaluation
To: Jonna Mazet <jkmazet@ucdavis.edu>, David J Wolking <djwolking@ucdavis.edu>, matthew lebreton <[redacted]>, Dr Prime Mulembakani <pmulembakani@metabiota.com>, Karen Saylors <ksaylors@metabiota.com>
Cc: "Pereira, Alisa (GH/HIDN)" <apereira@usaid.gov>, Ashna Kibria <akibria@usaid.gov>, Shana Gillette <sgillette@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>

There was a phone call yesterday with the evaluation team to talk about how to capture information on the EPT-2 response to outbreaks. Cameroon and DRC were chosen to be representatives to get an in-country perspective. The following is the plan for collecting this information:

- Jean-Felly (USAID/DRC) and Mounkaila (USAID/Cameroon) will each convene a group in their respective countries to discuss specific outbreaks — H5N1 and monkeypox in Cameroon and yellow fever in DRC — and EPT2 support to the responses.
- Groups will likely be made up of USAID, PREDICT, FAO, CC and possibly government or academic representatives.
- Dr. Daniel Lucey will lead the discussion for the EPT-2 evaluation team and will provide a phone conference line for the discussion.
- The discussion will take place as soon as feasible and before August 28th when the team is expected to leave for Vietnam and Thailand.

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: 1-571-345-4253
E-mail: aclements@usaid.gov

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

From: "William B. Karesh" <karesh@ecohealthalliance.org>
To: [redacted]
Cc: Jonna Mazet <jkmazet@UCDAVIS.EDU>, Renata Curi Hauegen <[redacted], Gian Luca Burci <[redacted]
[redacted], Sam Halabi <sfh9@georgetown.edu>, Cara Chrisman <cchrisman@usaid.gov>
Subject: Re: GVP MOU
Sent: Fri, 29 Sep 2017 15:23:53 +0000
GVP Partners Policy 27 Sept 17.docx
ATT00001.htm

Hi [redacted]
Attached is the most current version of the GVP partnerships agreement.

As you use it to develop an MOU please make sure you share a draft of the MOU with the GVP ELSI team (Gian Luca and Sam copied here) and the GVP Partnership team (Renata and me copied here) to run through the partnership process.

All the Best,

Billy

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

Global Virome Project

The Global Virome Project is a global cooperative scientific initiative to massively lower risk of harm from future viral outbreaks over 10 years.

Partnerships Policy

Partners of the Global Virome Project (GVP) share these core values:

Strengthen and Build up national capabilities for prevention, detection and response for emerging viral threats in all partner countries on an unprecedented scale: GVP partners actively support the concept that a better understanding of the vast number of viruses that may result in emerging infectious diseases or contribute to improved health outcomes can significantly help to prevent or reduce the occurrence and impacts of epidemics and pandemics.

Value of Science: GVP partners are committed to advancing the understanding of the interaction of viruses, hosts and their shared environments and use sound science to guide decision making and policy

Embrace an international scope, while fostering local ownership: GVP partners value collaborative approaches as this forms the basis for leveraging the strengths of the partners, extending abilities, and engaging diverse audiences and stakeholders.

Promote equitable access to data and benefits and foster transparency: GVP partners are committed to share scientific findings, methods, and techniques with other partners and the global community.

Guiding Principles

The Global Virome Project is guided by a commitment to:

- Valuing partnerships that improve outcomes and lead to strengthening both global and local capacity for future efforts;
- Openly sharing information discovered from the work of the GVP among partners;
- Basing decisions and actions on the best available evidence and science;
- Focusing efforts where the need is high and where local partners are willing to engage;
- Building upon existing programs, experiences and networks when possible, and creating new ones when necessary;
- Developing, utilizing, and/or promoting multi-disciplinary solutions and

approaches that reduce or eliminate adverse impacts to the health of people, animals and the environment; and
- Respecting the unique strengths, experience, expertise, and various levels of participation of GVP partners.

Partnership in the Global Virome Project provides:

- The opportunity to participate in the largest global initiative to identify viruses with the potential to cause epidemics and pandemics and those with potential to be used to prevent epidemics and pandemics.

- The opportunity to benefit from the knowledge and experience accumulated/acquired by the founding teams/professional of GVP through previous projects, as Predict.

- Prepared rational, support services and operational management of the project

- Guidance from a highly qualified Scientific or Strategic Committee

- Take advantage of an international network of skilled team of specialists and complementary expertises

- External recognition of partner organization's principles, values, and achievements.

- Rights to mention GVP partnership in grant and funding proposals, publications, etc.

- Access to a broad domestic and international network of experts, students and volunteers associated with the GVP.

- Networking opportunities among peers and opportunity to leverage expertise and strengths of GVP partners to enhance efforts.

Criteria for partnership:

GVP partnership is open to all organizations actively working towards the advancement of our guiding principles and core values; and who also meet the following criteria:

- Partnership is open to non-profit or for profit organizations, government agencies, academic institutions and inter-governmental bodies.

- Partner organizations must be currently engaged in work that contributes to the goals of the GVP.

- Partners will agree to:

    - Comply with national laws and regulations and international treaties relevant and applicable to the work they are conducting as part of the GVP.
    - Obtain appropriate ethical approvals for human and animal studies if required for the work they are conducting as part of the GVP.
    - GVP Intellectual property rights and material transfer agreements
    - Make viral genomic sequence data publically available within 90 days of discovery.
    - Collect and make available meta-data GVP determines relevant to sample collection and analyses.
    - Be legally responsible and liable for all activities undertaken in their work.

New Partners

- Potential new partners must express their interest in joining the GVP in writing to the GVP Governance, Advisory and Partnerships working group (GAP). Potential partners should indicate ways in which they will work to advance the efforts of the GVP.

- The GAP or other participants in the GVP may proactively invite organizations to join the GVP.

- The GAP will periodically carry out a partnership assessment based on the criteria outlined above.

- Organizations that comply with all the above criteria will be offered partnership.

Termination of Partnership

- GVP partnerships will be reviewed and renewed every 3 years using a January 1st calendar year basis.

- Organizations may terminate their partnership at any time upon written notification to GVP

- GVP shall have the right to terminate, for good and sufficient reasons, the partnership of any organization

Financial Relationships

- There is no payment or partnership fee required to participate.
- The GVP provides no assurance or guarantee of funding to partners
- The GVP encourages and will help facilitate when possible, approaches with and among partners in fund-raising efforts to support collaborative work.

Sent: Sun, 22 Oct 2017 12:00:10 -0700
Subject: Re: Ecology and Evolution of Infectious Diseases
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: "Janzen, Daniel H" <djanzen@sas.upenn.edu>
Cc: "Hallwachs, Winnie" <whallwac@sas.upenn.edu>, Dennis Carroll <dcarroll@usaid.gov>, REDACTED
REDACTED, Peter Daszak <daszak@ecohealthalliance.org>, Brooke Genovese <bgenovese@ucdavis.edu>, Brooke Watson <watson@ecohealthalliance.org>, Cara Chrisman <cchrisman@usaid.gov>

Ha -- good on you! Maybe we should test you as a sentinel for novel viruses ;)
I think I sent you the updated 2-pager back in September. I'll find that email and re-forward it.
Have a good one,
Jonna

On Sun, Oct 22, 2017 at 9:48 AM, Janzen, Daniel H <djanzen@sas.upenn.edu> wrote:

22 Oct 2017
ACG (yes, am here in ACG now)

Right now, all I need is your advert 1-2 pager that has the logo diagram on it but with the wording corrected. I have an older version that you sent way back when.
This has been a slow trudge because I am having to do a lot of biopolitics dancing around the whole genome stuff. Barcoding took years for acceptance too, but now barcoding is accepted protocol (politically, despite the few scientific luddites). The underlying problem is that the more things one shows that one can do with a wild genome and its info, the more worried about the "loss" of the genome (by making it public) that the species-rich countries become. Possessive nationalism, no surprise for the Pleistocene playbook. Needless to say, they have two centuries+ of being ripped off by the developed countries, so it is an uphill slog. It took me all this time to get a first meeting with the government and non-gov world in CR, starting on 8 Dec 2016 in Cancun in the CBD Cop13. I am still surviving on those surveyor's stakes stuck in the ground back then. Wish us all luck and Godspeed. Ambassador Macaya has been a Godsend for it all.

And, money talks. Not for corrupt officials, but for getting a government to perk up its ears as to "possibility" that the project being discussed will have fuel. Makes a difference in a starving country. The world tends to forget that a tropical country the size of West Virginia does not have big pots of cash just sitting around looking for a worthwhile thing to spend it on.

Will report after 3 November.

Apologize for slow.

But we do have Liomys salvini (Heteromys salvini) happily running around the living room floor last night picking up the popcorn that I put out for them (as well as stealing what I brought home from the grocery store)n, and the Glossophaga soricini are happily hanging in the rafters of the refrigerator room. They are not going anywhere but their populations certainly do fluctuate (and one wonders if severe population fluctuations are not a form of virus cleansing of the genome, if it is that only certain individuals in the population have a given asymptomatic virus).

Smile. Dan and Winnie

On Oct 22, 2017, at 10:17 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Hi Dan,
Let me know if you'd like to do a call to catch up or if we can provide any visuals that would be fhelpful for your talk.
Thanks for all that you do,
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
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+1-530-752-3630
onehealthinstitute.net

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

On Sun, Oct 22, 2017 at 7:08 AM, Janzen, Daniel H <djanzen@sas.upenn.edu> wrote:

> Thanks, that is the kind of thing (bureaucratic nightmare) I would be deep into if I was doing this or depending on NSF.
> The GVP people are on it.

Very fashionable these days.

It will be in my 2nov talk here IF Edgar and Patricia get their act together to organize it.

> On Oct 22, 2017, at 8:02 AM, Eric Palola <palola@gdfcf.org> wrote:

FYI,

NSF track rfp….. caught my eye in possible relation to Global Virome Project.

https://www.nsf.gov/funding/pgm_summ.jsp?pims_id=5269&WT.mc_id=USNSF_39&WT.mc_ev=click

Eric

Eric Palola
Executive Director
Guanacaste Dry Forest Conservation Fund
palola@gdfcf.org
802-343-2929
www.gdfcf.org
www.facebook.com/gdfcf

Sent: Fri, 17 Nov 2017 20:19:51 -0800
Subject: Re: Update briefing on Global Virome Project
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Dennis Carroll <dcarroll@usaid.gov>
Cc: Peter Daszak <daszak@ecohealthalliance.org>, Brooke Watson <watson@ecohealthalliance.org>, Eddy Rubin <erubin@metabiota.com>, Nathan Wolfe <nwolfe@metabiota.com>, REDACTED

Fantastic!
J

On Thu, Nov 16, 2017 at 12:46 PM, Dennis Carroll <dcarroll@usaid.gov> wrote:

not to share

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

Office: 202-712-5009
Mobile: REDACTED

Sent: Thu, 21 Dec 2017 10:54:45 -0800
Subject: Re: Transitioning to Behavioral Scientist Position at USDA APHS
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Leilani Francisco <francisco@ecohealthalliance.org>
Cc: Peter Daszak <daszak@ecohealthalliance.org>

First I'm hearing of it! Perhaps they won't refill.
Happy Holidays,
Jonna

On Thu, Dec 21, 2017 at 10:53 AM, Leilani Francisco <francisco@ecohealthalliance.org> wrote:

That's a surprise.

Do we know if anyone will be taking her place?

Thanks for sending!

Leilani

From: REDACTED [mailto: REDACTED **On Behalf Of** Jonna Mazet
Sent: Thursday, December 21, 2017 1:47 PM
To: Peter Daszak <daszak@ecohealthalliance.org>; Leilani Francisco <francisco@ecohealthalliance.org>
Subject: Fwd: Transitioning to Behavioral Scientist Position at USDA APHS

FYI,

J

---------- Forwarded message ----------
From: **Shana Gillette** <sgillette@usaid.gov>
Date: Thu, Dec 21, 2017 at 10:25 AM
Subject: Transitioning to Behavioral Scientist Position at USDA APHS
To: "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Cc: Andrew <aclements@usaid.gov>, Alisa Pereira <apereira@usaid.gov>

Dear Jonna and Chris,

Tomorrow will be my last day in the office as a USDA PASA for the Foreign Agricultural Service at USAID. I have accepted a position as the behavioral scientist for USDA APHIS in Hyattsville, Maryland and I start on January 22nd.

Although tomorrow is my last day in the office, I will be teleworking from January 10-19th, so please let me know if you have any questions/concerns that need to be addressed before I leave.

I have really enjoyed working with the PREDICT team and I look forward to seeing PREDICT results in the news in the next two years.

Warm Regards,

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

Work Mobile: 571-243-3424

Personal Cell REDACTED

Email: sgillette@usaid.gov

Sent: Thu, 21 Dec 2017 10:56:14 -0800
Subject: Re: Transitioning to Behavioral Scientist Position at USDA APHS
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Shana Gillette <sgillette@usaid.gov>
Cc: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Andrew <aclements@usaid.gov>, Alisa Pereira <apereira@usaid.gov>

Dear Shana,
Oh wow -- I hope congratulations are in order!
We will certainly miss you and your wisdom that have helped to shape the project. We will happily keep you updated if you are interested.
I hope to work with you again in your new position.
Please let us know if there is anything we can do to help the transition go smoothly.
Happy Holidays,
Jonna

On Thu, Dec 21, 2017 at 10:25 AM, Shana Gillette <sgillette@usaid.gov> wrote:

> Dear Jonna and Chris,
> Tomorrow will be my last day in the office as a USDA PASA for the Foreign Agricultural Service at USAID. I have accepted a position as the behavioral scientist for USDA APHIS in Hyattsville, Maryland and I start on January 22nd.
>
> Although tomorrow is my last day in the office, I will be teleworking from January 10-19th, so please let me know if you have any questions/concerns that need to be addressed before I leave.
>
> I have really enjoyed working with the PREDICT team and I look forward to seeing PREDICT results in the news in the next two years.
>
> Warm Regards,
> 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
Work Mobile: 571-243-3424
Personal Cell: REDACTED
Email: sgillette@usaid.gov

Sent: Wed, 3 Jan 2018 14:16:09 -0800
Subject: Fwd: Two attendees who need invites to the GVP meeting
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Katie Leasure <kaleasure@ucdavis.edu>
Cc: Eri Togami <etogami@ucdavis.edu>, Hongying Li <li@ecohealthalliance.org>

FYI,
J

---------- Forwarded message ----------
From: **Peter Daszak** <daszak@ecohealthalliance.org>
Date: Wed, Jan 3, 2018 at 1:46 PM
Subject: Two attendees who need invites to the GVP meeting
To: "jkmazet@ucdavis.edu" <jkmazet@ucdavis.edu>
Cc: [redacted], "kaleasure@ucdavis.edu" <kaleasure@ucdavis.edu>, Brooke Watson <watson@ecohealthalliance.org>, Hongying Li <li@ecohealthalliance.org>, "George F Gao [redacted]
<[redacted]

Happy New Year Jonna and [redacted]

The good news is that George Gao will be going to the PMAC meeting. I'm going to book his flight directly because I'm flying through Beijing and Hongying will be trying to get us on the same plane from Beijing to Bangkok so we can start our conversations.

However, apologies that I didn't email earlier, but the previous co-chair of the GVP Metadata Platform WG, Di (Dylan) Liu is moving to another institute and will be unable to continue in that capacity. George Gao recommended another scientist, Dr. Juncai Ma, to replace Dylan's position at the Metadata Platform WG, and attend the GVP side meeting at PMAC. He's the director of the World Data Center for Microorganisms (WDCM) at the Chinese Academy of Sciences. Dennis and I met him in Beijing in September where he presented their current work on the Global Catalogue of Microorganisms (GCM) and Global Sequencing for Type Strains, as well as some tentative ideas for the GVP data platform. He would be a perfect replacement.

In addition, George would like to bring the director of laboratory management from China CDC (Dr. Qiang Wei) to the meeting to help the project operations later, so I wanted to make sure an invitation can be extended to them for their travel approval and visa application as soon as possible. (Please copy Hongying Li li@ecohealthalliance.org, so she can help coordinate.)

There addresses are below. I know space is limited, but I do think it's really important to have a good turnout from China:

Dr. Juncai MA

Director, World Data Center for Microorganisms(WDCM)

Institute of Microbiology, Chinese Academy of Sciences

[redacted]

Tel: [redacted]

FAX: + REDACTED

REDACTED

Dr. Wei Qiang

Professor/Director

Office of labortory Management

Chinese Center for Disease Control and Prevention,China

REDACTED

REDACTED

Let me know if you have any questions and thanks very much!

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: REDACTED
To: Eddy Rubin <erubin@metabiota.com>, Peter Daszak <daszak@ecohealthalliance.org>, Brooke Watson <watson@ecohealthalliance.org>, Dennis Carroll <dcarroll@usaid.gov>, Nathan Wolfe <nwolfe@metabiota.com>, "Sacchetti, Ben" <Sacchetti.Ben@bcg.com>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: Agenda
Sent: Thu, 25 Jan 2018 03:45:34 +0000
GVP side meeting agenda_ET_JM.docx

This is the correct version – thanks!

REDACTED

From: REDACTED
Sent: Wednesday, January 24, 2018 7:34 PM
To: Eddy Rubin <erubin@metabiota.com>; Peter Daszak <daszak@ecohealthalliance.org>; 'Brooke Watson' <watson@ecohealthalliance.org>; 'Dennis Carroll' <dcarroll@usaid.gov>; Nathan Wolfe <nwolfe@metabiota.com>; Sacchetti, Ben <Sacchetti.Ben@bcg.com>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Agenda

Hi core team,

Jonna and I worked on getting the agenda on paper reflecting Dennis and Ben's input (attached). We have been receiving requests from participants for the agenda and background documents, so hoping to distribute the agenda as soon as possible.

The only missing information is as follows:

- Moderator for open session –Dennis or Peter or Eddy or Jonna?
- Confirmed panelists: David Nabarro, Peter Bogner and Juncai Ma. – Ben, is this correct?

Best,

REDACTED

REDACTED
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

Global Virome Project
PMAC side-meeting, closed session

Monday January 29, 2018, 9.00am-12.30pm

Meeting objectives

1. Update on establishment of GVP partnership
2. Review progress in refining GVP strategic and operational way forward
3. Discuss plans for "Open Session" in the afternoon

Agenda

Time	Agenda item	Presenters/facilitators
8:30 – 9:00	Registration	All participants
9:00 – 9:15	**1. Introduction** • Welcoming remarks and Introductions • Review of meeting agenda & objectives	Dennis Carroll
9:15 – 9:40	**2. A Year in Review: Overview on outreach, organizational structure, evolving launch strategy** • Introductions • Publications, articles • Update on NGO status	Dennis Carroll
9:40 – 10:10	**3. Overarching strategic and operational vision** Thematic group updates • Science and technology • Implementation • Governance	Peter Daszak Jonna Mazet Dennis Carroll
10:10 – 10:30	Break	
10:30 – 11:30	**4. Progress report** • Investment case • Resource mobilization • Organization & governance	Boston Consulting Group
11:30 – 12:00	**5. Perspectives from China and/or Thailand** • Rationale for interest in GVP • Status updates and next steps	Country representatives
12:00 – 12:20	**6. Plan for Open Session**	
12:20 – 12:30	**7. Closing remarks**	

Global Virome Project

PMAC side-meeting, open session

Monday January 29, 2018, 14.00-17.30

Meeting objective

To introduce the rationale, evidence and strategic approach for GVP and its goal of building a world safe from emerging viral threats.

Agenda

Time	Agenda item	Presenters/facilitators
13:30 – 14:00	Registration	All participants
14:00 – 14:10	**1. Introduction** • Welcoming remarks • Review of meeting agenda & objectives	Dennis Carroll
14:10 -15:50	**2. What is the Global Virome Project?** • The Challenge • Proof-of-concept • Solution • Global Health Impact • Way-forward vision: 10 year vision, path to launch	Dennis Carroll Jonna Mazet Peter Daszak Eddy Rubin
15:50 – 16:10	Break	
16:10 – 17:15	**3. Panel discussion: GVP from the perspective of key stakeholders**	Moderator Panelists
17:15 – 17:30	**4. Closing remarks**	Dennis Carroll

Sent: Wed, 21 Feb 2018 20:26:46 -0800
Subject: Re: two variables for viral ranking website - happy to help ID data, etc.
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: "Kevin Olival, PhD" <olival@ecohealthalliance.org>
Cc: Peter Daszak <daszak@ecohealthalliance.org>

Thanks -- we'll let you know if we need an assist. We have strategies that we're trying at the moment (that have been informed by some M&A team inquiries). Toph didn't have better data sets for us to try.
More soon,
J

On Wed, Feb 21, 2018 at 10:12 AM, Kevin Olival, PhD <olival@ecohealthalliance.org> wrote:

> Hi Jonna,
> Per the EB call today, please let us know what the two viral ranking variables are holding up the viral ranking, and maybe the M&A team here could help! Happy to check around.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

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

1.212.380.4478 (direct)
REDACTED (mobile)
1.212.380.4465 (fax)
www.ecohealthalliance.org

From:	Jonna Mazet <jkmazet@ucdavis.edu>
To:	Kevin Olival, PhD <olival@ecohealthalliance.org>
CC:	Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;Predict inbox <predict@ucdavis.edu>;Anna Willoughby <willoughby@ecohealthalliance.org>
Sent:	2/27/2018 2:20:47 PM
Subject:	Re: Transcribed flip-chart notes from Brussels intervention modeling session

Thanks!
J

On Tue, Feb 27, 2018 at 1:59 PM, Kevin Olival, PhD <olival@ecohealthalliance.org> wrote:
Jonna, CKJ, and Peter,

Here are the transcribed flip chart notes from the 'Bat and other modeling intervention project' session in Brussels. I have pictures of each completed flip chart if you're interested too! Just wanted to make sure you had this.

Cheers,
Kevin

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Sent: Wed, 7 Mar 2018 19:52:25 +0700
To: Hongying Li <li@ecohealthalliance.org>
Cc: Andrew Clements <aclements@usaid.gov>, "Pereira, Alisa (GH/HIDN)" <apereira@usaid.gov>, predict@ucdavis.edu, Ava Sullivan <sullivan@ecohealthalliance.org>, 博士石正丽 <[redacted]>, Hu Ben <[redacted]>, 刘军 <[redacted]>, 张云智 <[redacted]>, 朱光剑 <[redacted]>, [redacted], Daniel Schar <dSchar@usaid.gov>, Anchalee Jatapai <ajatapai@usaid.gov>
Subject: [predict] Fwd: PREDICT2 Y4Q1 Mission/Partner Update_China
Y4Q1 PREDICT Partner Updates_China.pdf

Dear Hongying Li,
Thank you very much for sharing P2 China Y4Q1 report with RDMA.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
[redacted]
E-mail: sdamrongwatanapokin@usaid.gov
Tel: [redacted], Fax: [redacted]

---------- Forwarded message ----------
From: **Hongying Li** <li@ecohealthalliance.org>
Date: Tue, Mar 6, 2018 at 9:26 PM
Subject: PREDICT2 Y4Q1 Mission/Partner Update_China
To: Dan Challender <[redacted]>, Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Cc: Andrew Clements <aclements@usaid.gov>, apereira@usaid.gov, predict@ucdavis.edu, Ava Sullivan <sullivan@ecohealthalliance.org>, 博士石正丽 <[redacted]>, Hu Ben <[redacted]>, 刘军 <[redacted]>, 张云智 <[redacted]>, 朱光剑 <[redacted]>, [redacted]

This email is sent on behalf of Dr. Zhengli Shi, PREDICT in-Country Coordinator of China
Dear Dan and Sudarat,

Attached please find the PREDICT 2 Y4Q1 Mission/Partner Updates from China. It will also be shared to all of our in-country partners in China on behalf of PREDICT, and I wanted to make sure you have a copy. Please feel free to let me know if you have any question.

Warmest Regards,

Zhengli SHI, Ph.D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
[redacted]
[redacted]
[redacted]
Tel & Fax: [redacted]
Email: [redacted]

USAID | PREDICT
FROM THE AMERICAN PEOPLE

January 31, 2018

Dear Partner,

The PREDICT project, part of USAID's Emerging Pandemic Threats program (EPT), is developing a global early warning system to detect, track, and predict the emergence of new zoonotic pathogens from wildlife that could pose a threat to human health. In China, PREDICT is implemented by EcoHealth Alliance in close partnership with Wuhan Institute of Virology (WIV) of Chinese Academy of Sciences, Food and Agriculture Organization of the United Nations (FAO), Institute of Microbiology of Chinese Academy of Sciences, Yunnan Institute of Endemic Diseases Control & Prevention, Institute of Pathogenic Microbiology of Guangdong Center for Disease Control and Prevention (GDCDC), Guangdong Provincial Institute of Public Health (GDIPH), and in cooperation with local stakeholders and communities.

Below is the summary of PREDICT achievements and progress during Year 4 from October 2017 to January 2018.

Please direct all correspondence to the PREDICT China Country Coordinator and the Global Point of Contact:

Dr. Zhengli Shi
PREDICT China Country Coordinator
Email: REDACTED
Phone: REDACTED
Address: [redacted]

Hongying Li
EcoHealth Alliance
Email: li@ecohealthalliance.org
Phone: +1 9175732178
Address: 460 West 34 Street, New York, NY 10001, USA

PREDICT-2 China Continuing Plans

Implement concurrent biological and behavioral surveillance activities at high-risk animal-human interfaces for disease emergence, amplification, and spread at selected sites, and continue working with government and community to apply PREDICT findings into local policy-making and behavior changes programs in Year 4 and Year 5.

Continuing Activities

- Conduct concurrent biological and behavioral surveillance of targeted human and wild animal populations at selected sites.
- RT-PCR assays for Coronavirus, Paramyxovirus, Influenza virus, Filovirus and Bunyavirus.
- Optimize assays to distinguish high priority viruses including SARS-like Coronavirus, MERS-like Coronavirus, Filoviruses, Flaviviruses, Henipaviruses, and Bunyaviruses.
- Conduct expanded pathogen characterization of viruses identified under PREDICT1 & 2 (in wildlife and humans) from key viral families such as Coronaviruses, Paramyxoviruses, Filoviruses, Flaviviruses, and Influenza viruses.
- Pilot serological tests of collected human samples for SARS-like Coronavirus with developed ELISA.
- Maintain laboratory and field standard operating procedures including cold-chain, receiving specimens, biosafety, and biosecurity systems.
- Provide PREDICT laboratory results reports to government partners to maintain communication channels, inform of findings for discussion, and request approval to release data.
- Enhance data sharing and communication processes with state and federal partner agencies as appropriate to strengthen data platforms and improve the ease of dissemination of relevant animal, human, epidemiological, and ecological data.
- Provide support during outbreaks for planning, logistics, field investigation, sampling, and diagnostic testing, if requested.
- Pilot the behavioral change interventions at high-risk bats-human interfaces at selected PREDICT sites.

PREDICT China Summary of Activities & Progress from 01 October 2016 to 31 January 2018.

Surveillance and Field Activities

- Year 4 field sampling schedule was developed and discussed with PREDICT global and in-country teams.

Diagnostics Activities and Cold Chain

- A total of 1,084 bat samples (oral & rectal swabs) collected in Year 2 from 542 bats have been tested for Coronavirus, Paramyxovirus, Influenza virus, Filovirus and Bunyavirus, with results submitted to EIDITH for interpretation. Y3 bat samples are being tested at Wuhan Institute of Virology.
- A total of 218 samples were tested from 218 humans. Samples were tested for the following 5 viral families/genera: Coronaviruses, Flaviviruses, Paramyxoviruses, Filoviruses, and Influenza virus. Government approval has been obtained for the reporting of these test results. One known strain of Influenza A virus was detected in one human sample.

Capacity Building

- PREDICT/China team coordinated *The 1st International Workshop on Biosafety Laboratory Management and Experimental Techniques* at Wuhan Institute of Virology on 18-28 October, 2017, where PREDICT in-country staff from Thailand, as well as 20 other participants from Asian and African countries were invited to attend and receive trainings on laboratory practice for high-level biosafety laboratories.

Other Activities

- PREDICT/China in-country field coordinator Dr. Guangjian Zhu attended PREDICT all-country meeting in Brussels. A poster from the PREDCIT China team was presented at the meeting.
- An article from the PREDICT China team was published in the journal *Plos Pathogen* titled “Discovery of A Rich Gene Pool of Bat SARS-related Coronaviruses”, which provides further insight into bat SARS-related CoVs.

From: Jaber Belkhiria <jabelkhiria@ucdavis.edu>
Sent: Wed, 21 Mar 2018 08:09:44 -0700
To: Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>
Cc: David John Wolking <djwolking@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>
Subject: [predict] Re: FW: Emerging Pandemic Threat Program Evaluation report posted on DEC

First time for me.
J

On Wed, Mar 21, 2018 at 6:29 AM, Corina Grigorescu Monagin <cgmonagin@ucdavis.edu> wrote:

Have we seen this before?

C

From: Philippe Mutwa <pmutwa@usaid.gov>
Date: Wednesday, March 21, 2018 at 5:51 AM
To: "Kinzer, Michael" <KinzerM@state.gov>, "Ting, Jim Y" <TingJY@state.gov>, "Balaconis, John G Maj USAF DTRA J3-7 (US)" <john.g.balaconis.mil@mail.mil>, "Casse, Aminata G" <CasseAG@state.gov>, "Duerr, Cynthia K (APHIS/USDA)" <cynthia.k.duerr@aphis.usda.gov>, "Campbell, Laura (DAKAR/HEALTH)" <lcampbell@usaid.gov>, Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>, REDACTED <REDACTED>, rianatou Bada Alambedji <REDACTED>, Savadogo Madi <savadogo.madi@ohcea.org>, "Kabore, Youssouf (FAOSN)" <youssouf.kabore@fao.org>
Subject: Emerging Pandemic Threat Program Evaluation report posted on DEC

Dear Colleagues:

I'm sharing with you the USAID Emerging Threats Program (EPT-2/GHSA) evaluation report. The team worked on this program evaluation since June 2017, and was published this month (March 2018). Senegal did participate in online surveys.

Warm regards,

Philippe

--

Philippe R. Mutwa, MD, PhD

Global Health Security Agenda Advisor

USAID I U.S. Agency for International Development

REDACTED

Office Phone: REDACTED | Mobile phone: REDACTED

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:	4/15/2018 12:26:26 AM
Subject:	Re: PREDICT International Travel Requests

Australia travel approved.

DRC 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 Apr 14, 2018, at 1:33 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. Zambrana-Torrelio (Australia): $2100 airfare/$310 (Canberra) max daily per diem
2. Saylors (DRC): $2300 airfare/$394 (Kinshasa) max daily per diem

Travel Requests –

1. EcoHealth Alliance would like to request travel approval for Dr. Carlos Zambrana-Torrelio to travel from Newark, New Jersey, USA to Canberra, Australia from April 29 to May 5, 2018 to participate in the symposium "Advancing the frontiers of ecological modelling to predict the risk of emerging infectious diseases and guide sustainable development" organized by CSIRO.

Trip purpose: Dr. Zambrana-Torrelio will be traveling to Canberra, Australia to participate in a three-day meeting on disease emergence. The first day of the meeting will be an open symposium where Dr. Zambrana-Torrelio will present work on Hotspots and disease modeling from the PREDICT project as well as the current status of the Global Virome Project. The following days will be discussions on the implementation of future forecasts for the emergence infectious disease hotspots model.

2. Metabiota would like to request travel approval for Dr. Karen Saylors to travel from San Francisco, California, USA to Kinshasa, Democratic Republic of Congo from April 30 to May 5, 2018 to meet with Metabiota PREDICT DRC team.

Trip purpose: To meet with the Metabiota PREDICT DRC team to provide supervisory support and oversight of PREDICT operations. **Dr. Saylors will be traveling to DRC for a non-USAID funded project. Costs will be shared between the two projects.*

Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
530-752-7526
530-752-3318 FAX
kaleasure@ucdavis.edu

--

From: [redacted]
To: Latoya Armstrong <laarmstrong@usaid.gov>
Cc: Cara Chrisman <cchrisman@usaid.gov>, Dennis Carroll <dcarroll@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: Japan outreach list
Sent: Tue, 24 Apr 2018 16:00:28 +0000

Hi LaToya,

That sounds good, and I'm glad the list is helpful. I'll keeps my eye out for the event confirmation.

Best,

[redacted]
Fellow
One Health Institute
School of Veterinary Medicine
University of California, Davis

From: Latoya Armstrong [mailto:laarmstrong@usaid.gov]
Sent: Tuesday, April 24, 2018 4:50 AM
To: [redacted]
Cc: Cara Chrisman <cchrisman@usaid.gov>; Dennis Carroll <dcarroll@usaid.gov>; Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: Japan outreach list

[redacted]

Thanks so much for these suggestions. This is great. A number of these we've also been in contact with in the past, but no longer have the latest contact information.

You'll see that I've copied you on a separate note back to our USAID office in Tokyo on next steps.

Let's connect on a draft note (in Japanese) to go out to several of those listed in your note and once we have details on date for Dennis's event fully confirmed by the Embassy.

Very pleased to be working with you.

cheers,
LaToya

On Mon, Apr 23, 2018 at 4:37 PM, [redacted] wrote:
Hi LaToya,

It was great connecting with you over the phone this morning. Here are my outreach ideas for Japan, with my thoughts and notes in blue.

Academia

- Tokyo University – I'm not sure about specifics but I believe there is frequent interaction between Tokyo U and the government. Many policy makers are Tokyo U graduates.
    - Institute of Medical Science (IMS, 東京大学医科学研究所) – Perhaps the most relevant research institute within Tokyo University. I know the director. Focuses on molecular science, epidemiology, emerging infectious diseases etc.
    - Prominent Ebola/influenza researcher based at the Laboratory of Virology at IMS: Dr. Kawaoka Yoshihiro

(河岡義裕), who is a virologist.

- Others?

- Nagasaki University Institute of Tropical Medicine (長崎大学熱帯医学研究所) – most prominent tropical medicine group in medical community
- Hokkaido Univcrsity – most prominent vetcrinary school, most prominent zoonoscs/Onc Hcalth institution in Japan
  - Research Center for Zoonosis Control –where zoonoses research is based
    - Dr. Hiroshi Kida (喜田宏) – veterinarian, zoonoses expert, director of center
    - Dr. Ayato Takada (高田礼人) – veterinarian, zoonoses expert, head of global epidemiology at the center
- Dr. Kohei Makita – One health expert, connections with FAO rome, based in Rakuno University (veterinary college)
- Japan Society of Tropical Medicine(日本熱帯医学会) –I'm not sure how large/authoritative they are in the academic world.

Private

Private companies that are interested in investing in global health are listed in the figure below.

Global Health Innovative Technology Fund (GHIT fund:グローバルヘルス技術振興基金) website. https://www.ghitfund.org/hww/businessmodel/jp

Names of companies that I can make out:

- Astellas pharma
- Otsuka pharma
- Eisai pharma
- Sysmex
- Fujifilm
- Merck

- Johnson&Johnson Japan
- GSK Japan

There may be more companies if you look at them one-by-one.

Public

- Ministry of Foreign Affairs
    - Japan International Cooperation-MOFA affiliated, USAID partner

- Ministry of Health, Labour, and Welfare
    - National Institute for Infectious Diseases - MOHLW affiliated but don't work closely. They are more technical. My former boss at WHO was seconded from this organization

- National Center for Global Health and Medicine（国立研究開発法人　国際国立医療研究センタ* - Independent but public institution
    - Dr. Norio Ohmagari – prominent global health physician in the global health world. I briefly met him at a WHO meeting in Manila.

- Ministry of Environment – usually less involved in health, main work is in radiation related issues, climate change etc. Lower priority.

Others

World Organization for Animal Health (OIE) Regional Representation for Asia and the Pacific – based in Tokyo University. I have two contacts here.
World Health Organization Kobe Center – less relevant, because they do not work on EIDs. EID folks from Japan are represented in the WHO western pacific regional office in Manila.

I hope this is helpful, and I'm looking forward to exploring more.

Best,
REDACTED

--

LaToya Armstrong
Senior Policy and Donor Engagement Advisor
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From: Brooke Genovese <bgenovese@ucdavis.edu>
To: James Bangura [redacted]
Cc: Brian H Bird <bhbird@gmx.ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: [iOHC] Latest Conference Program
Sent: Thu, 26 Apr 2018 16:20:39 +0000
OHP_5OHC_programme.pdf

Hi James,

I'm sending along the latest (and final) program for the International One Health Congress in Saskatoon, Canada. You're likely getting the emails from the conference list serve, but just in case! The session you're co-chairing with Jonna is on page 18.

-Brooke

THE 5TH INTERNATIONAL

ONE HEALTH PLATFORM

one health CONGRESS

Canada
SASKATOON 22-25 June
2018

OHS ONE HEALTH SCIENCE

AMR ANTIMICROBIAL AGENTS AND RESISTANCE

SPI SCIENCE POLICY INTERFACE

Programme

FRIDAY 22 JUNE 2018

11:00-12:00	**CONGRESS PRESS BRIEFING**	SALON C-D

CONGRESS CO-CHAIRS: **Prof. Ab Osterhaus** *and* **Prof. John Mackenzie**

The congress press briefing is open for members of the press attending the congress. Congress co-chairs Prof. Ab Osterhaus and Prof. John Mackenzie will provide an overview of the congress programme, highlighting key lectures and elaborating on major topics. The scope and objectives of the congress will be put in the wider framework of the threats of emerging and re-emeriging diseases and the challenges the world faces when addressing antimicrobial resistance. Members of the press receive detailed information about speakers' backgrounds and expertises and on how to contact them during the congress. The press briefing will not be recorded and can therefore not be shared with journalists who are not attending the congress.

12:00-14:30	**SPECIAL PLENARY SESSION-open to non-congress attendees**	SALON A-B

Chronic Wasting Disease-lessons learned from the BSE crisis

CHAIR: **Adriano Aguzzi**, *director Insitute of Neuropathology, University Hospital Zürich, Switzerland*

1. First evidence of intracranial and peroral transmission of Chronic Wasting Disease into Cynomolgus macaques: a work in progress
   Stephanie Czub, *Canadian Food Insprection Agency, Alberta, Canada*
2. Battling Chronic Wasting Disease in Norway: an update on management and disease development after two years on the map
   Carlos Gonçalo das Neves, *Head of Food Safety & Emerging Health Threats, Norwegian Veterinary Institute, Norway*
3. Detection of prions associated to Chronic Wasting Disease in animal blood and in association to environmental materials
   Claudio Soto, *Director the George and Cynthia Mitchell Center, University of Texas/USDA, USA*
4. Investigations of Chronic Wasting Disease strains and transmission barriers
   Glenn Telling, *Prion Research Center, Colorado State University, USA*
5. BSE, CWD and alternatively folded forms of the cellular 1 prion protein, PrPc
   David Westaway, *Centre for Prions and Protein Folding Diseases, University of Alberta, Canada*
6. Why do we have a prion protein?
   Adriano Aguzzi, *director Insitute of Neuropathology, University Hospital Zürich, Switzerland*

14:30-15:00	COFFEE BREAK

15:00-17:00	**SPECIAL PLENARY SESSION**	SALON A-B

available

FRIDAY 22 JUNE 2018

17:00-18:30 — **SPECIAL PLENARY SESSION** — SALON A-B

Potential impact of vaccination on antibiotic usage and antibiotic resistance: the influenza case

CHAIRS: **Surbhi Malhotra-Kumar**, *University of Antwerp, Belgium*
Ab Osterhaus, *RIZ Hannover, Germany*

1. Quantifying the problem of antibiotic resistance
   Surbhi Malhotra-Kumar, *University of Antwerp, Belgium*
2. The role of diagnostics and viral vaccines in reducing antibiotic resistance
   Speaker to be confirmed
3. Assessing the full economic value of vaccines in reducing AMR
   Jonathan Rushton, *Professor of Animal Health and Food Systems Economics, University of Liverpool, UK*
4. Vaccination and antibiotic resistance in developing countries
   Speaker to be confirmed
5. The influenza case: a systematic literature review on the impact of influenza vaccination on antibiotic use
   Marco Goeijenbier, *Erasmus Medical Center Rotterdam, The Netherlands*

18:30-20:00 — **OPENING CEREMONY** — THEATRE

- Welcome by the congress chairs

OPENING LECTURES:

1. **Theresa Tam**, *Chief Public Health Officer of Canada*
2. **Jaspinder Komal**, *acting Chief Veterinary Officer of Canada*

KEYNOTE ADDRESS:

- One Health for a Challenged World by Nobel Laureate by
  Peter Doherty, *University of Melbourne, Australia*

20:00-22:00 — **WELCOME RECEPTION**

SATURDAY 23 JUNE 2018

07:30-9:00 **BREAKFAST PLENARY SESSION** — SALON A-B

Tuberculosis: A One-health problem in underserved communities

Organized by the University of Saskatchewan

09:15-10:15 **KEYNOTE LECTURES** — THEATRE

1. One Health as a Pillar of Policy, **Bill Karesh**, *Ecohealth Alliance*
2. Past, present and future of AMR, **Giuseppe Cornaglia**, *University of Verona, Italy*

10:15-10:45 COFFEE BREAK

10:45-12:30 **PARALLEL SESSIONS**

ONE HEALTH SCIENCE 1 — SALON A-B

Pathogen discovery

CHAIR: **Linfa Wang**, *Duke-NUS Medical School, Singapore*

CO-CHAIR: **Peng ZHOU**, *Chinese Academy of Sciences*

1. Plagiorchis sp. in small mammals of Senegal: an emerging food-borne trematodiasis?
   Stefano Catalano, *Royal Veterinary College, University of London*
2. Zika Virus Exposure In Malaysia; A Preliminary Study On Seroprevalence Among Local Population
   Wan Nabilatul Huda Wan Ghazali, *Institute For Medical Research, Malaysia*
3. A new concept for de-novo detection of viral pathogens with adaptive diagnostics and integrated data analysis approaches results in the recent discovery of two novel viruses
   Leonie Franziska Forth, *Friedrich-Loeffler-Institut, Germany*
4. Novel orthobunyavirus identified in an African child with severe encephalopathy
   Arthur Wouter Dante Edridge, *Academic Medical Center, The Netherlands*
5. Seroprevalence of West Nile virus in wild birds in Bangladesh
   Ausraful Islam, *ICDDR,B-Bangladesh*

10:45-12:30 **ONE HEALTH SCIENCE 2** — SALON C-D

Surveillance and early detection

CHAIR: **Ab Osterhaus**, *RIZ Hannover, Germany*

CO-CHAIR: **Nistara Randhawa**, *One Health Institute UC Davis, USA*

1. One Health-oriented outbreak response in Cameroon: A case study of the 2016 Monkeypox outbreak response in Cameroon
   Moctar Mouiche, *MOSAIC, Cameroon*
2. Zoonotic Enteric Parasites in Humans, Animals, and Drinking Water in Mongolian Households and Their Associated Risk Factors
   Anu Davaasuren, *The National Center for Communicable Diseases, MOH, Ulaanbaatar, Mongolia*
3. Evidence of silent infection of domestic pigs with Highly Pathogenic Avian Influenza H5N1 and H1N1pdm09 in 'hot spot' Nigeria: Is a pandemic virus already in the pipeline?
   Clement Adebajo Meseko, *National Veterinary Research Institute, Nigeria*
4. Phylogenetic analysis of viruses detected in mosquitoes, horses and humans supports epidemiological data indicating two different geographical origins for epidemics of encephalitis due to Murray Valley encephalitis virus
   David William Smith, *PathWest Laboratory Medicine WA, Australia*
5. Prevalence and characterization of Brucella spp. in slaughter animals in Gauteng Province abattoirs and assessment of zoonotic risk factors posed to abattoir workers
   Francis Babaman Kolo, *University of Pretoria, South Africa*

SATURDAY 23 JUNE 2018

10:45-12:30

ANTIMICROBIAL AGENTS AND RESISTANCE — GALLERY C-D

Use of antibiotics in human and animals, in food and agriculture and the link to AMR and environmental impact

CHAIR: **Jorgen Schlundt,** *Nanyang Technological University, Singapore*

CO-CHAIR: **Jaap Wagenaar**, *Utrecht University, The Netherlands*

1. Reduced and responsible use of antibiotics in food-producing animal in The Netherlands
   Christianne J.M. Bruschke, *Ministry of Agriculture, Nature and Food Quality, The Netherlands*
2. Antimicrobial resistance in wildlife species: the potential for sentinel surveillance in a ONE HEALTH perspective
   Carlos G. Das Neves, *Norwegian Veterinary Institute, Norway*
3. Comparative human exposure to antimicrobial-resistant Campylobacter species, Escherichia coli, Salmonella enterica from food animals using integrated assessment modelling: A farm to fork approach
   Colleen Patricia Murphy, *Public Health Agency of Canada*
4. Assessing Impacts of Antibiotic Therapy in Neonatal Dairy Calves on Gut and Animal Health
   Olivia Char Lottes, *Washington State University, USA*
5. Prevalence and Antimicrobial Resistance profile of Salmonella spp. in retail meats of Super Shop: a food safety risk
   Mohammed Abdus Samad, *Bangladesh Livestock Research Institute, Bangladesh*

10:45-12:30

SCIENCE POLICY INTERFACE — GALLERY A-B

The IMPACTS of Zoonotic Diseases – Why should OH be of importance to policy makers? Lessons learnt from One Health crises.

CHAIR: **John Mackenzie**, *Curtin University, Australia*

CO-CHAIR: **Casey Barton-Beravesh**, *CDC, USA*

1. New World Screwworm Eradication in South Florida – A One Health Success Story
   Lisa Conti, *One Health Initiative*
2. Ebola: what went wrong and where do we go now?
   Speaker to be confirmed
3. Rift Valley Fever as a public health emergency
   Pierre Formenty, *Team lead – Viral Haemorrhagic Fevers (VHF), World Health Organization*
4. Lessons learned from the H1N1 influenza pandemic: are we prepared for a new outbreak
   Speaker to be confirmed

12:30-14:00 LUNCH

SPECIAL PLENARY SESSION — SALON A-B

PREDICT Project

SATURDAY 23 JUNE 2018

14:00-15:45 **PARALLEL SESSIONS**

ONE HEALTH SCIENCE 1 — SALON A-B

Diagnostics

CHAIR: **Martyn Jeggo**, *Geelong Centre for Emerging Infectious Diseases, Australia*

CO-CHAIR: **Dang Xuan Sinh**, *Center for Public Health and Ecosystem Research, Hanoi, Vietnam*

1. Recombinant techniques to address the challenges in development of assays for diagnosis and surveillance of emerging zoonotic diseases
   Felicity Jane Burt, *University of the Free State, South Africa*
2. Comparison of two RdRp PCR assays for the detection of MERS related Coronaviruses
   Sininat Petcharat, *King Chulalongkorn Memorial Hospital, Thailand*
3. The accuracy of pre-vaccination screening for Q fever and the extent of exposure – Bayesian latent class analysis
   Solomon Meseret Woldeyohannes, *University of Queensland, Australia*
4. Reproducibility of results and performance of TB diagnostics in East Africa Public Health Laboratory Networking Project sites in Kenya: Implication on Policy Resolution for Strategic TB Diagnosis
   Willie Abela Githui, *Kenya Medical Research Institute*
5. Development of lateral flow immunochromatographic test for multiple detection of Salmonella Species in poultry food product
   Rafik Sayed, *Central laboratory for evaluation of veterinary biologics, Egypt*

14:00-15:45

ONE HEALTH SCIENCE 2 — SALON C-D

Intervention strategies

CHAIR: **Sarah Cleaveland**

CO-CHAIR: **Rachel Hopper**, *Liverpool School of Tropical Medicine, UK*

1. Adapting the determinants of health perspectives to developing and implementing integrated priorities to address social and ecological expectations for fisheries and community health
   Craig Stephen, *University of Saskatchewan, Canada*
2. Control versus elimination of Taenia solium in eastern Zambia: Preliminary assessment of a two-year interventional program in the Katete and Sinda districts in the Eastern Province of Zambia
   Emma Clare Hobbs, *Institute of Tropical Medicine, Antwerp, Belgium*
3. An integrated human-animal health approach to reduce the disease burden of psittacosis
   Lenny Hogerwerf, *National Institute for Public Health and the Environment, The Netherlands*
4. Factors associated with improved uptake of Johne's Disease control mechanisms on Australian dairy farms: Regulatory insights from evolving control strategies
   Paul Douglas Burden, *University of Calgary, Canada*
5. Harm reduction: A strategy for One Health action in the face of uncertainty and conflict
   Christa Gallagher, *Ross University School of Veterinary Medicine. St. Kitts and Nevis*

SATURDAY 23 JUNE 2018

14:00-15:45 **ANTIMICROBIAL AGENTS AND RESISTANCE** — GALLERY C-D

Genomic epidemiology / evolution of AMR transmission

CHAIR: **Robert Skov**, *MVZ Synlab, Leverkusen, Germany*

CO-CHAIR: **Jesper Larsen**, *Statens Serum Institut, Denmark*

1. The human resistome within the Dutch pork production chain, a metagenome-wide study among farmers and slaughterhouse workers
   Liese Van Gompel, *Utrecht University, The Netherlands*
2. Genomic and evolutionary analysis of Clostridium difficile sequence type 11: a genetically diverse lineage of significant One Health importance
   Daniel R Knight, *University of Western Australia, Australia*
3. Whole genome sequencing reveals limited contribution of non-intensive chicken farming to extended-spectrum beta-lactamase producing Escherichia coli colonization in humans in southern Vietnam
   Trung Nguyen Vinh, *Oxford University Clinical Research Unit, Vietnam*
4. Associations between antimicrobial use and the fecal resistome on broiler farms in nine European countries
   Roosmarijn Luiken, *Utrecht University, The Netherlands*
5. Epidemic clones of community-acquired methicillin-resistant Staphylococcus aureus in slaughter pigs, Cuba
   Michel Baez Arias, *National Centre of Animal and Plant Health (CENSA), Cuba*

14:00-15:45 **SCIENCE POLICY INTERFACE** — GALLERY A-B

Addressing zoonotic diseases at the animal-human-ecosystem interface. What are the threats? How to be prepared?

CHAIR: **Ab Osterhaus**, *RIZ Hannover, Germany*

1. Avian Influenza Surveillance in Live Birds Markets in Thailand
   Ong-orn Prasarnphanich, *United States Centers for Disease Control and Prevention Southeast Asia Regional Office*
2. Challenges in Complexity: How Brucellosis Thrives in the Science-Policy Interface Space
   Darrell Abernethy, *Faculty of Veterinary Science, University of Pretoria*
3. Achieving Rabies Zero by 2030
   Waqas Ahmad, *University of Veterinary and Animal Sciences, Pakistan*
4. Future Earth's Top Ten Challenges for One Health
   Peter Daszak and William B. Karesh, *EcoHealth Alliance*

15:45-16:15 COFFEE BREAK

SATURDAY 23 JUNE 2018

16:15-18:00 **PARALLEL SESSIONS**

ONE HEALTH SCIENCE 1 — SALON A-B

Social science and politics

CHAIR: **Jonathan Rushton**, *University of Liverpool, UK*

CO-CHAIR: **Mieghan Bruce**, *Murdoch University, Australia*

1. Antimicrobials In Society: A One Health Approach in Kampala, Uganda
   Laurie Denyer Willis, *London School of Hygiene and Tropical Medicine, UK*
2. (Re)Claiming Water Stewardship in a Changing Climate – Learning from the Margins
   Corinne J Schuster-Wallace, *McMaster University, Canada*
3. MAN-IMAL: An experimental One Health degree program around animal-man-food
   Francois Meurens, *Oniris-Nantes Atlantic National College of Veterinary Medicine, France*
4. Human Behavioural Research at the Animal-Human Interface: Hunting and Trading of Bushmeat in Lao PDR
   Soubanh Silithammavong, *Metabiota, USA*
5. Evaluation Of One Health-Ness: Insights Into Interdisciplinary And Cross–Sectoral Integration
   Simon Rüegg, *University of Zurich, Switzerland*

16:15-18:00

ONE HEALTH SCIENCE 2 — SALON C-D

Pathogenesis 1

CHAIR: **Marietjie Venter**, *University of Pretoria, SA*

CO-CHAIR: **Felicity Burt**, *University of the Free State, South Africa*

1. Cytokine patterns in Hemorrhagic Fever with Renal syndrome and Crimean-Congo Hemorrhagic Fever
   Katerina Tsergouli, *Aristotle University of Thessaloniki, Greece*
2. Replication of naturally occurring MERS-CoV protein 4a deletion variants in vitro and in vivo
   Mart Matthias Lamers, *Erasmus MC, The Netherlands*
3. The effect of antiretroviral naïve HIV-1 infection on the ability of Natural Killer cells to produce IFN-γ upon exposure to Plasmodium falciparum- infected Erythrocytes
   Carole Stephanie Sake Ngane, *University of Yaoundé I, CIRCB, Cameroon*
4. Chronic ethion exposures and endotoxin interaction induce pulmonary damage and genotoxicity in mice
   To be confirmed
5. Dynamic interaction of rabies virus with endosomes and end binding partners (EB3 and p140cap) of Cytoskeleton
   Waqas Ahmad, *University of Veterinary and Animal Sciences, Jhang Campus, Pakistan*

SATURDAY 23 JUNE 2018

14:00-15:45

ANTIMICROBIAL AGENTS AND RESISTANCE — GALLERY C-D

Real life applications of whole genome sequencing

CHAIR: **Surbhi Malhotra-Kumar**, *University of Antwerp, Belgium*

1. Comparative Genomics of Vancomycin-Resistant Enterococcus spp. isolated from Wastewater Treatment Plants
   Haley Ann Sanderson, *Queen's University, Canada*
2. Integrating whole genome sequencing data into quantitative microbial risk assessment modeling: a case study for Salmonella Heidelberg resistant to third-generation cephalosporins in Canadian broiler chicken production
   Lucie Collineau, *Public Health Agency of Canada*
3. Whole Genome Sequence Profiling of Antibiotic Resistant Staphylococcus aureus isolates from Livestock and Farm Attendants in Ghana
   Beverly Egyir, *Noguchi Memorial Institute for Medical Research, Ghana*
4. Phenotypic and genomic analysis of antimicrobial resistant E. coli isolated from ready-to-eat food in Singapore
   Siyao Guo, *Nanyang Technological University Food Technology Centre, Singapore*
5. Antibiotic use and biosecurity in pig farming are determinants for antimicrobial resistance, a metagenome-wide association study in nine European countries
   Liese van Gompel, *Utrecht University, The Netherlands*

14:00-15:45

SCIENCE POLICY INTERFACE — GALLERY A-B

The drivers of emerging zoonotic diseases

CHAIR: **Moira McKinnon**, *Medical practitioner, Canberra, Australia*

1. The migration, climate change, and vector-borne disease nexus
   Kanya C. Long, *World Bank*
2. AMR containment and Prevention considering the Drivers of EID in Thailand
   Suwit Wibulpolprasert, *Ministry of Public Health, Thailand*
3. The Long and Hard Road to Evidence Based policy
   Bonnie Henry, *Provincial Health Officer British Columbia, Canada*
4. Communicating the evidence to policy makers and populations. Who is the right audience?
   Speaker to be confirmed

18:00-19:30

POSTER SESSION

- Opportunity for congress delegates to interact with poster authors
- Wine and cheese, offered by the organizers

SUNDAY 24 JUNE 2018

07:30-9:00

BREAKFAST PLENARY SESSION — SALON A-B

Global Perspectives on Health and Security and the Future of Biological Threat Reduction

Organized by the Weapons Threat Reduction Program, Global Affairs Canada

09:15-10:15

KEYNOTE LECTURES — THEATRE

1. Lecture title to be confirmed, **Michael Ryan**, *World Health Organization*
2. From zoonoses to pandemics: lessons learned from HIV,
   Mark Feinberg, *International AIDS Initiative*

10:15-10:45 COFFEE BREAK

10:45-12:30

PARALLEL SESSIONS

ONE HEALTH SCIENCE 1 — SALON A-B

Drivers for emerging diseases 1

CHAIR: **Rita Colwell**, *Johns Hopkins University Bloomberg School of Public Health, USA*

CO-CHAIR: **Antar Jutla**, *West Virginia University, USA*

1. Quantifying the health, economic, and ecosystem impacts of land-use change as a driver of disease emergence in Southeast Asia
   Carlos Zambrana-Torrelio, *EcoHealth Alliance, USA*
2. Impacts of urbanization and conversion of rainforests into large industrial oil palm plantations on the ecology of Aedes vectors in arbovirus foci, Côte d'Ivoire
   Julien Zahouli Bi Zahouli, *Centre Suisse de Recerches SCientifiques en Côte d'Ivoire, Ivory Coast*
3. The use of a nationwide pig movement network to predict the spatial risk of Nipah virus outbreaks in Thailand
   Anuwat Wiratsudakul, *Faculty of Veterinary Science, Mahidol University, Thailand*
4. Ecosystem Change and Zoonoses Emergence
   Barry John McMahon, *University College Dublin, Ireland*
5. Identification of molecular determinants of aquatic and terrestrial morbillivirus cross-species infections
   Wendy Karen Jo Lei, *University of Veterinary Medicine Hannover, Germany*

SUNDAY 24 JUNE 2018

10:45-12:30

ONE HEALTH SCIENCE 2

SALON C-D

One health in underprivileged communities

CHAIR: **Mark Rweyemamu**, *Director of the Southern African Centre for Infectious Diseases and Surveillance (SACIDS)*

CO-CHAIR: **Rafael Maciel de Freitas**, *Instituto Oswaldo Cruz, Brazil*

1. Molecular detection and characterization of Anaplasma phagocytophilum strains associated with different hosts in Bushbuckridge, Mpumalanga, South Africa
   Agatha Onyemowo Kolo, *University of Pretoria, South Africa*
2. Assessment of aerosolization of Avian Influenza A associated with market hygiene and practices and potential occupational exposure of live bird market workers in Bangladesh
   Mahbubur Rahman, Institute of Epidemiology, *Disease Control and Research, Bangladesh*
3. Transformation within Indigenous Lived Experiences and the Journey from a Pedagogy of Oppression to a Pedagogy of Hope and Freedom
   Anne Poelina, *the University of Notre Dame, Australia*
4. Tackling the second deadliest Neglected Tropical Disease: Predicting and reducing the impact of snakebite on human and animal health through One Health analyses of hotspots and access to care
   Rafael Ruiz de Castaneda, *Institute of Global Health, Faculty of Medicine, University of Geneva, Switzerland*
5. What will it take to eliminate rabies in Africa?
   S Mwangi Thumbi, *Washington State University, Kenia*

10:45-12:30

ANTIMICROBIAL AGENTS AND RESISTANCE

GALLERY C-D

Prevalence and surveillance of resistance

CHAIR: **Gerard Wright**, *M.G. DeGroote Institute for Infectious Disease Research, Canada*

CO-CHAIR: **Georgina Cox**, *University of Guelph, Canada*

1. Temporal Changes in Antibiotic Resistance in Common Bottlenose Dolphins (Tursiops truncatus), a Sentinel Species
   Adam M Schaefer, *Florida Atlantic University, USA*
2. Antimicrobial Resistance in Salmonella enterica Isolates from Wildlife in Virginia
   Karen Gruszynski, *Lincoln Memorial University, USA*
3. Antibiotic resistance and epidemiology of Campylobacter recovered from humans, animals and environmental sources in Ghana
   Akosua Bonsu Karikari, *University for Development Studies, School of Medicine and Health Sciences, Ghana*
4. A longitudinal evaluation of Salmonella Typhimurium AMR prevalence and transmission using whole genome sequencing and phenotyping in a poultry population with no antimicrobial selection pressure
   Helen Kathleen Crabb, *the University of Melbourne, Australia*
5. Urban Wildlife and the Epidemiology of Antimicrobial Resistance in Nairobi
   James Hassel, *University of Liverpool, UK*

SUNDAY 24 JUNE 2018

10:45-12:30

SCIENCE POLICY INTERFACE — GALLERY A-B

Resistance to antibiotics and antivirals: challenges for policy makers and scientists

CHAIR: **Laura H. Kahn**, *Princeton University, USA*

CO-CHAIR: **Christianne Bruschke**, *Chief Veterinary Officer, The Netherlands*

1. Antimicrobial Resistance and One Health solutions
   Joergen Schlundt, *University of Singapore*
2. Antimicrobial resistance: Canada's science and policy challenges
   Aline Dimitri, *Canadian Food Inspection Agency, Canada*
3. The Nordic countries strategy for AMR: challenges at "high latitudes" for policy makers, scientists and society
   Carlos Gonçalo das Neves, *Norwegian Veterinary Institute, Norway*
4. WHO guidelines on use of medically important antimicrobials in food-producing animals
   Scott McEwen, *University of Guelph, Canada*

12:30-14:00 LUNCH

SPECIAL PLENARY SESSION — SALON A-B

Neglected Zoonotic Diseases in Resource-Poor, Marginalised and Under-Served Communities: Challenges in Infectious Disease Control

CHAIR: **Martyn Jeggo**, *Geelong Centre for Emerging Infectious Diseases, Australia*

1. Where we left off: main conclusions of the 2014 International meeting on the control of Neglected Zoonotic Diseases
   Speaker to be confirmed
2. Combatting Neglected Zoonotic Diseases at the human/animal interface: an overview
   Ab Osterhaus, *RIZ Hannover, Germany*
3. Challenges and opportunities to preventing and responding to outbreaks of helminth/bacterial/viral infections in livestock
   Speaker to be confirmed
4. Need to acquire community support to implementing effective control programmes
   Speaker to be confirmed

SUNDAY 24 JUNE 2018

14:00-15:45 **PARALLEL SESSIONS**

ONE HEALTH SCIENCE 1 — SALON A-B

Drivers for emerging diseases 2

CHAIR: **Peter Daszak**, *President of the EcoHealth Alliance*

CO-CHAIR: **Ottorino Cosivi**, *WHO-Brazil*

1. Leveraging viral phylodynamics to inform spatiotemporal transmission of viral infectious diseases in Africa: 2009 Influenza A/H1N1 in Africa
   Fredrick Nzabanyi Nindo, *University of Cape Town, South Africa*
2. Risk of pneumonia among residents living near goat and poultry farms
   Pim Martijn Post, *Dutch National Institute for Public Health and the Environment (RIVM), The Netherlands*
3. Effect of Habitat Modification on Risk of Scrub Typhus, An Emerging Infectious Disease in Bhutan
   Tandin Zangpo, *Khesar Gyalpo University of Medical Sciences of Bhutan*
4. A One Health Understanding of the Rodent Meat Value Chain in the Mekong Delta, Vietnam: Implications for Zoonotic Disease Risk Mitigation (Wellcome Trust VIZIONS)
   Jason Euren, *Metabiota, USA*
5. Climate variability and infectious diseases nexus: Evidence from Sweden
   Mwenya Mubanga, *Uppsala University, Sweden*

14:00-15:45

ONE HEALTH SCIENCE 2 — SALON C-D

Pathogenesis 2

CHAIR: **Malik Peiris**, *University of Hong Kong*

CO-CHAIR: **Wendy Karen Jo Lei**, *Research Center for Emerging Infections and Zoonoses, Hannover, Germany*

1. Species specific binding of the MERS-coronavirus S1A protein
   W Widagdo, *Erasmus MC, The Netherlands*
2. Using Bioluminescent Salmonella Strains to Study Host-Pathogen Interaction in Chicken will Allow One-Health-Approach
   Dinesh Hirantha Wellawa, *Vaccine and Infectious Disease Organization, Canada*
3. Influenza A viruses activate host PI3K/Akt survival pathway for pro-viral advantage in chicken but not in duck cells
   Sanjeeva Kumar, *University of Nottingham, UK*
4. Environmental CO2 Modification of Innate Immune responses to LPS and Organic Dust
   David Schneberger, *University of Saskatchewan, Canada*
5. Rabies virus interrupts cofilin pathway and induces depolymerization of actin in hippocampal region
   Waqas Ahmad, *University of Veterinary and Animal Sciences, Jhang Campus, Pakistan*

SUNDAY 24 JUNE 2018

14:00-15:45 **ANTIMICROBIAL AGENTS AND RESISTANCE** — GALLERY C-D

Novel strategies for amr interventions / preparedness

CHAIR: **Laura H. Kahn**, *Princeton University, USA*

CO-CHAIR: **Reema Persad-Clem**, *UC Berkeley, USA*

1. Operationalising One Health Approaches to Surveillance for Antimicrobial Resistance
   Joanna Susan Mckenzie, *Massey University, New Zealand*
2. #AMR: Exploring the role of social media in addressing antimicrobial resistance
   M9egan Lesley Moore, *University of Saskatchewan, Canada*
3. Development of 2-Aminoimidazole Compounds that Enhance Antibiotic Activities to Reduce Antibiotic Usage
   Malcolm Thomas, *Agile Sciences, Inc, USA*
4. A novel participatory strategy to reduce antimicrobial use in agricultural systems
   Mark Bryan, *VetSouth Limited Winton, New Zealand*
5. Can inhibition of transmission of KPC and CTX-M producing plasmids reduce the spread of AMR?
   Michelle M.C. Buckner, *University of Birmingham, UK*

14:00-15:45 **SCIENCE POLICY INTERFACE** — GALLERY A-B

One health and global health security-disaster risk reduction

CHAIR: **William B. Karesh**, *EcoHealth Alliance*

CO-CHAIR: **Trevor Smith**, *Deputy Executive Director and General Counsel, Global Affairs Canada*

1. The Global Health Security Agenda
   Speaker to be confirmed
2. The Weapons of Mass Destruction Threat Reduction Program
   Trevor Smith, *Deputy Executive Director and General Counsel, Global Affairs Canada*
3. Objectives and achievements of the Defense Threat Reduction Agency
   Lance Brooks, *Division Chief Cooperative Bio Engagement Program, Department of Defense, USA*
4. The Role of Private Industry
   Speaker to be confirmed

15:45-16:15 COFFEE BREAK

SUNDAY 24 JUNE 2018

16:15-18:00 **PARALLEL SESSIONS**

ONE HEALTH SCIENCE 1 — SALON A-B

Vaccines 1

CHAIR: **George Gao**, *Deputy Director-General CDC China*

CO-CHAIR: **Volker Gerdts**, *University of Saskatchewan, Canada*

1. Portfolio Approach, Development and Stockpile of MERS-CoV Vaccines: A Case Study
   Simone Blayer, *CEPI, UK*
2. Protective non-specific effect of rabies vaccine in humans, dogs and cattle: One Health implications
   Anne Conan, *Ross University School of Veterinary Medicine, Saint Kitts and Nevis*
3. Brucellosis in the changing peri-urban dairy systems of West Africa
   Laura Ann Craighead, *RVC, UK*
4. A Cimaza Case Study – Highlighting Effectiveness of Comics/Animations in Enhancing Science Literacy and in Particular the Science Behind Vaccines and Viral Diseases
   Susan Obeid, *CIMAZA, Belgium*
5. A systematic review of strategies for reducing missed opportunities for vaccination
   Anelisa Jaca, *South African Medical Research Council, South Africa*

16:15-18:00

ONE HEALTH SCIENCE 2 — SALON C-D

Infectious diseases from an ecohealth perspective 1

CHAIR: **Craig Stephen**, *University of Saskatchewan, Canada*

CO-CHAIR: **Patrick Leighton**, *University of Montreal, Canada*

1. Integrating Ecosystem Approaches to Health: A One Health Investigation of Rift Valley Fever Virus
   Melinda K Rostal, *EcoHealth Alliance, USA*
2. The Other Side of One Health: A Brucellosis story
   Barbara Akorfa Glover, *University of Pretoria, South Africa*
3. One ring to rule them all: Uniting human, animal, and environmental data using the Checklist for One Health Epidemiological Reporting of Evidence (COHERE)
   Peter M. Rabinowitz, *Center for One Health Research, University of Washington, USA*
4. Ecohealth Project at the community level: Disease Research and development at the human-domestic animal and wildlife interface, Uganda
   Innocent Bidason Rwego, *University of Minnesota, Uganda*
5. "Whenever I see a fruit bat, I think Hendra" – Attitudes and risk perception of Australian horse owners towards flying foxes in relation to Hendra virus
   Anke Wiethoelter, *University of Melbourne, Australia*

SUNDAY 24 JUNE 2018

14:00-15:45

ANTIMICROBIAL AGENTS AND RESISTANCE

GALLERY C-D

Alternative approaches to tackling resistant infections

CHAIR: **Britta Lassman**, *International Society for Infectious Diseases*

CO-CHAIR: **Mohamed Sirdar**, *University of Pretoria, South Africa*

1. Antibiotics usage by pastoralists in livestock in North-central Nigeria: The socio-cultural drivers for antibiotic resistance emergence and public health implications
   Nma Bida Alhaji, *Niger State Government, Nigeria*
2. Extent of dispensing prescription-only medications without a prescription in community drug retail outlets in Addis Ababa, Ethiopia: a simulated-patient study
   Begashaw Melaku Gebresillassie, *University of Gondar, Ethiopia*
3. Towards a Global Database of Emerging Antibiotic Resistance
   Brooke Watson, *EcoHealth Alliance, USA*
4. Current Patterns of Antibiotic Resistance in High Density Livestock-Human Populations in Western Kenya
   Steven Alan Kemp, *University of Liverpool, UK*
5. Antimicrobial use behaviours, the economics of animal disease and perceptions of antimicrobial policy in pig production in Vietnam
   Lucy Alice Coyne, *University of Liverpool, UK*

14:00-15:45

SCIENCE POLICY INTERFACE

GALLERY A-B

Making one health operational: the barriers to change and glimmers of hope

CHAIR: **Robert Salerno**, *DAI Global Health*

1. Introduction to the session's concept and objectives
   Robert Salerno, *session chair*
2. A decade of implementing One Health in Kenya: Translating research into practice
   Peninah Munyua, *Kenya CDC*
3. One Health Secretariat: A Formalized coordinating Entity for Operationalizing One Health in Bangladesh
   Meerjady Sabrina Flora, *IEDCR, Bangladesh*
4. Making One Health operational within the Caribbean Region
   Chris Oura, *University of the West Indies, Trinidad*
5. Characterizing the interventions of the private sector extractive industries during the Ebola virus disease crisis in West Africa
   Sambe Duale, *USAID Emerging Pandemic Threats 2 Program*
6. Tripartite Guidance: Taking One Health Approaches to Address Zoonotic Diseases in Countries: A "Glimmer of Hope"
   Elizabeth Mumford, *World Health Organization*
7. Panel discussion and open Q&A

SUNDAY 24 JUNE 2018

18:00-19:30 **SPECIAL PLENARY SESSION** — SALON A-B

Emerging and re-emerging infectious diseases: assessment, preparedness and eradication

CHAIRS: **Mike Ryan**, *the World Health Organization*
William B. Karesh, *EcoHealth Alliance*

1. Introducing emerging and re-emerging infectious diseases / The threat of an Influenza Pandemic
   Ab Osterhaus, *RIZ Hannover, Germany*
2. Eradication of infectious diseases: past, present and future
   Nick Juleff, *Senior Program Officer Animal Health portfolio, Bill & Melinda Gates Foundation*
3. Risk reduction of health emergencies and impact of climate change on health: implications of relevant international frameworks
   Chadia Wannous, *Towards a Safer World Network for Pandemic Preparedness (TASW)*
4. Strengthening global biological security
   Speaker: to be confirmed
5. Community-based surveillance for early detection of EID
   Speaker: to be confirmed
6. Health emergency challenges from the animal health pharma perspective
   Speaker: to be confirmed
7. Health emergency challenges from the human health pharma perspective
   Speaker: to be confirmed

20:00-23:00 **FAREWELL DINNER** — REMAI MODERN ART GALLERY

MONDAY 25 JUNE 2018

08:00-10:00	**BREAKFAST PLENARY SESSION**	SALON A-B
10:00-10:30	COFFEE BREAK	
10:30-12:15	**PARALLEL SESSIONS**	

ONE HEALTH SCIENCE 1 — SALON A-B

Vaccines 2

CHAIR: **Lorne Babiuk**, *University of Alberta, Canada*

CO-CHAIR: **Teresia Maina**, *University of Saskatchewan, Canada*

1. Development of a highly pathogenic avian H7N9 influenza disease model in mouse
   Shelby Layne Landreth, *University of Saskatchewan, Canada*
2. A trial to assess the thermotolerance of an inactivated rabies vaccine
   Felix John Lankester, *Washington State University, Tanzania*
3. Acceptance Of Heterologous Prime-Boost Vaccination Regimens – An Assessment
   Sabrina Ivol, *Janssen Vaccines & Prevention, The Netherlands*
4. Identifying Genomic Predictors of Vaccine Response in Swine
   Peris Mumbi Munyaka, *University of Alberta, Canada*
5. Q fever vaccine failure rate, duration of longevity of immunity and associated demographic factors in Australia
   Solomon Meseret Woldeyohannes, *University of Queensland, Australia*

10:30-12:15

ONE HEALTH SCIENCE 2 — SALON C-D

Infectious diseases from an ecohealth perspective 2

CHAIR: **Jonna Mazet**, *UC Davis, USA*

CO-CHAIR: **James Bangura**, *UC Davis One Health Institute, Freetown, Sierra Leone*

1. The role of mainland-island bat movement in the dissemination of viruses of public health concern in the Caribbean
   Janine Seetahal, *The University of the West Indies, Trinidad & Tobago*
2. Nematode co-infections, environmental factors and weather impact infection with the zoonotic bacterium, Bartonella tribocorum, in urban Norway rats (Rattus norvegicus)
   Jamie Lee Rothenburger, *University of Calgary Faculty of Veterinary Medicine, Canada*
3. Environmental Change Increases Human-Macaque Interactions and the Risk of Zoonotic Disease Spillover
   Ariful Islam, *Institute of Epidemiology, Disease Control and Research, Bangladesh*
4. Explaining variation in human and animal zoonotic infection risk in northern Tanzania: defining agro-ecological systems and their contribution to risk
   William Anson de Glanville, *University of Glasgow, UK*
5. Building collaborative capacity to evaluate zoonotic viral sharing among bats, primates, and people in Tanzania
   Elizabeth VanWormer, *University of Nebraska, Lincoln, USA*

MONDAY 25 JUNE 2018

10:30-12:15 | **ANTIMICROBIAL AGENTS AND RESISTANCE** | GALLERY C-D

Rapid diagnostics

CHAIR: **Rafael Canton**, *University hospital of Madrid, Spain*

CO-CHAIR: **Moon Tay Yue Feng**, *Nanyang Technological University, Singapore*

1. Analysis of single nucleotide polymorphism in KatG gene in isoniazid resistant Mycobacterium Tuberculosis
   Muhammad Arif, *University of Malakand, Pakistan*
2. Exploiting the potential of flow cytometry in rapid antimicrobial susceptibility testing
   Timothy John Jay Inglis, *University of Western Australia, Australia*
3. Novel and Rapid Multiplex Allele-Specific PCR (MAS-PCR) Test for Rapid Detection of MDR and XDR-TB from the Sputum of Lung TB Patients in Makassar, Indonesia
   Muhammad Nasrum Massi, *Hasanuddin University, Indonesia*
4. Presence of oqxA and oqxB genes in a multidrug resistant Salmonella Typhimurium isolate recovered from swine in Brazil
   Daniel F. Monte, *University of São Paulo, Brazil*

10:30-12:15 | **SCIENCE POLICY INTERFACE** | GALLERY A-B

One health in underserved, resource-poor and marginalized communities / funding needs and funding mechanisms / funding policies for one health

CHAIR: **Marietjie Venter**, *University of Pretoria, SA*

1. One Health in Africa: a concept with global benefits
   Speaker to be confirmed
2. First Nations of Canada and the One Health approach
   Addie Pryce, *Assembly of First Nations, Canada*
3. One Health, rabies response and more-than-human considerations in Indigenous communities in Northern Australia
   Chris Degeling, *University of Wollongong, Australia*

12:15-13:45 | **PLENARY SESSION** | THEATRE

Late breakers

CHAIR: **John Mackenzie**, *Curtin University, Australia*

Submission of late breaker abstracts until 15 May 2018

13:45-14:00 | **CLOSING CEREMONY** | THEATRE

MONDAY 25 JUNE 2018

14:00-14:30	LUNCH
14:30-15:30	**PRESS CONFERENCE - LIVE STREAM** SALON C-D Prof. John Mackenzie, Prof. Ab Osterhaus and other key contributors to the congress will share the main outcomes on aspects of emerging and re-emerging infectious diseases and antimicrobial resistance. They will inform members of the press about the development of a "White Paper" - established during the congress. The White Paper will provide in-depth descriptions of the major One Health challenges and threats. It will openly state what is going wrong on a societal level, what is lacking and what the gaps are in order to make the world a safer place when it comes to One Health issues. The White Paper will come with a clear call for actions, a roadmap that describes what needs to be done - better and more. The press conference will be live streamed. The accompanying press statement will be distributed to members of the press globally.
15:30-	**GUIDED EXCURSIONS**

From: Andrew Clements <aclements@usaid.gov>
Sent: Wed, 23 May 2018 03:28:56 -0700
Subject: Re: PREDICT Workplan & Budget for USAID/Jordan Y4 funds
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: PREDICTMGT <predictmgt@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, David John Wolking <djwolking@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>, Hannah R Chale <hrchale@ucdavis.edu>

Hi Liz,
No issues from me or the Mission so consider it approved.

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 May 22, 2018, at 10:51 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Andrew. Just following up on this. If you have any questions or need anything else to approve, please let me know.
>
> Thanks!
> Liz
>
> *Elizabeth Leasure*
> *Financial Operations Manager*
> *One Health Institute*
> REDACTED *(cell)*
> *530-754-9034 (office)*
> *Skype: ealeasure*
>
> ---
>
> **From:** predict-request@ucdavis.edu <predict-request@ucdavis.edu> **On Behalf Of** Elizabeth Leasure
> **Sent:** Thursday, May 3, 2018 3:32 PM
> **To:** Andrew Clements <aclements@usaid.gov>
> **Cc:** PREDICTMGT <predictmgt@usaid.gov>; Jonna Mazet <jkmazet@ucdavis.edu>; David John Wolking <djwolking@ucdavis.edu>; predict@ucdavis.edu; Hannah R Chale <hrchale@UCDAVIS.EDU>
> **Subject:** [predict] PREDICT Workplan & Budget for USAID/Jordan Y4 funds
>
> Hi Andrew. Please find attached for your review/approval a workplan and budget for the $200K in USAID/Jordan funds received for PREDICT Y4 activities. Let me know if you have any questions.
>
> Thanks!
> Liz
>
> *Elizabeth Leasure*
> *Financial Operations Manager*
> *One Health Institute*
> REDACTED *(cell)*
> *530-754-9034 (office)*
> *Skype: ealeasure*

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: PREDICTMGT <predictmgt@usaid.gov>;isimmons@usaid.gov <isimmons@usaid.gov>;bhaberer@usaid.gov <bhaberer@usaid.gov>;Jean-Felly Numbi <jnumbi@usaid.gov>;Linda Mobula <mmobula@usaid.gov>
CC: PREDICT-outbreak <predict-outbreak@ucdavis.edu>;Karen Saylors <ksaylors@metabiota.com>;Brian Bird <bhbird@ucdavis.edu>
Sent: 6/10/2018 12:21:17 PM
Subject: UPDATE PREDICT DRC EVD outbreak 10 June 2018

And another for today,
Jonna

PREDICT Outbreak or Health Event Rapid Report

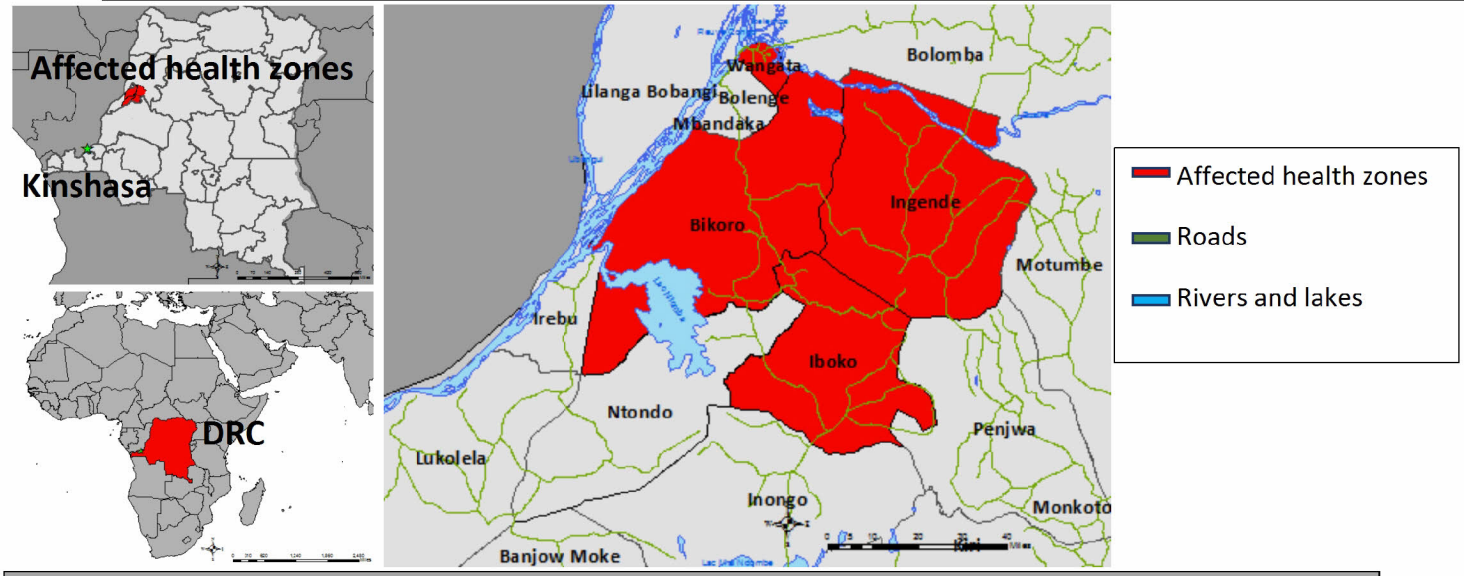
Today's Date: June 10, 2018
Working Title of Investigation: Ebola virus disease outbreak in Equateur province, DR Congo.
Cumulative day of the outbreak investigation: 36 days

Please describe the disease signs and symptoms and species affected (humans, domesticated animals, wildlife:

Between April 3 and May 7, 2018, 17 successive deaths were recorded in the health district of Ikoko Impenge, in the health zone of Bikoro (Equateur Province). Seventeen individuals were linked through family relationships. Patients presented with the following symptoms prior to their death: fever, diarrhea, abdominal pain, vomiting, muscle and joint pain, and hemorrhagic symptoms.

On May 4, an alert for suspected Viral Hemorrhagic Fever in the Bikoro health zone was received at the MOH Office of Disease Control.

On May 8, two out of five individuals tested were confirmed as Ebola virus (species, *Zaire ebolavirus)* by RT-PCR at INRB. As of May 12, additional possible EVD cases continue to be identified in the affected area.



Location	
Country:	Democratic Republic of the Congo
District:	Equateur
Village/Town:	IKOKO IMPENGE / Health zone of BIKORO
GPS Coordinates (if known):	Latitude : -0.749997 ; Longitude : 18.1166662
Date that first case(s) of illness occurred (if known or estimate):	April 03, 2018
Date that PREDICT was first notified of outbreak:	May 07, 2018

<table>
<tr><th>Key Information</th><th>Description of Findings/Actions/Outcomes</th></tr>
<tr><td>How many affected individuals?</td><td>
<table>
<tr><th></th><th>Suspected</th><th>Confirmed</th><th>Deaths</th><th>Total affected</th></tr>
<tr><td>Humans</td><td>14</td><td>38</td><td>28</td><td>66</td></tr>
<tr><td>Domestic Animals</td><td>0</td><td>0</td><td>0</td><td>0</td></tr>
<tr><td>Wild Animals</td><td>0</td><td>0</td><td>0</td><td>0</td></tr>
</table>
</td></tr>
<tr><td>How was outbreak first noticed?</td><td>Ikoko Impenge health district notified the Bikoro Health Zone of 1 death with viral hemorrhagic fever-like symptoms.</td></tr>
<tr><td>Where was the first reported case? What is/was the extent of geographic spread? Include comments on the apparent speed of spread.</td><td>

A cluster in week 11 (12-18 March 2018) in Bikoro area, Equateur, DRC, including 19 cases including 17 deaths, 15 deaths of which were in the community, raised the alert of suspected VHF.
Symptoms observed include fever, vomiting, abdominal pain, eye redness, and diarrhea, and were not alleviated by antibiotic and antimalarial treatment.
The first reported case was at IKOKO IMPENGE Health District. Between April 3 and May 7, 2018, 17 deaths were recorded among people with family relationships, from a total of 27 total cases, according to MOH. (According to WHO reports, investigations identified 135 cases retrospectively, going back as far as January 2018 in the Igende zone, 60km from Bikoro, so there is some conflicting information circulating.)
The first case in Bikoro was a policeman who arrived from Igende area. He died in a health centre in Ikoko Impenge village, Bikoro area.
Following the first case's funeral, 11 family members developed symptoms and 7 died. The deceased all had either attended the funeral or acted as caregivers.
Five patients were sampled and tested for EVD, of which two were found positive for EVD by RT-PCR at INRB in Kinshasa on 8 May 2018.

</td></tr>
<tr><td>Has the country requested support from PREDICT (include date of request)?</td><td>The DRC requested unspecified support from PREDICT on May 7, 2018. On Tuesday, May 8, MOH requested that PREDICT conduct additional testing of the 5 samples stored at INRB, which USAID approved on the same day. The PREDICT lab</td></tr>
</table>

	team received samples and initiated testing on Wednesday, May 9. On May 9, a list of unmet needs was developed at the outbreak response meeting with MOH and partners. Late on May 11, PREDICT received a formal request from the Government through INRB regarding support for outbreak response activities. In response to the list of unmet needs provided by the laboratory commission, PREDICT provided 150 PPE, a Smartcycler PCR machine and accompanying computer, and two gloveboxes. On May 12, INRB requested PPE and sampling kits from PREDICT to send to the outbreak sites. USAID quickly approved this, so Metabiota ordered these with the plan to express them to DRC. On May 16, the MOH (INRB) officially asked PREDICT for a space in a -80 freezer to store Ebola vaccines. The mobile lab in Bikoro is functional (with RT-PRC, rapid tests, and GeneExpert up and running) as is the Mbandaka MOH-INRB lab
If so, which government agency requested PREDICT support?	Ministry of Health through the National Institute of Biomedical Research (INRB)
When was PREDICT response initiated (date)?	Tuesday, May 8, 2018
Are other EPT partners involved in the response (which ones and how)?	No
What type of assistance did PREDICT initially provide? Which PREDICT personnel were involved?	PREDICT is running the PREDICT protocol testing on patient specimens, using PREDICT virus family primers with the intent of finding filoviruses or other viral families, as well as identifying sequences for further elucidation of species and strain. (Previously INRB testing of five patients' whole blood specimens for EVD found two to be positive for Ebola virus (*Zaire ebolavirus)* by RT-PCR at INRB in Kinshasa on May 7 2018.) On May 12, the K-Plan mobile lab (previously acquired through USAID support) was deployed to the outbreak site in

	Bikoro and Iboko. The INRB team arrived that Saturday morning in Mbandaka, the capital of Equator Province, for preparation.
When was the first official acknowledgement of the outbreak (by which government agency or other reputable body and date)? When was a response initiated and by whom? Which agencies were involved? Who was in charge of the national response?	The first official acknowledgement of the outbreak was by the MOH Office of Disease Control on May 6, 2018. A joint investigation team was deployed by MOH, WHO and MSF, and according to MOH, another team from the MOH Office of Disease Control and WHO deployed today to Mbandaka (capital of Equateur province) to lead case investigations. Background on area: Ikoko Impenge health area covers 15km and includes 5 villages, all of which have reported suspected cases. This area of DRC has not suffered previous documented Ebola outbreaks. Ikoko Impenge health area is not covered by mobile telephone networks, but is accessible by road. It lies 128km from Mbandaka, the capital of Equateur province, however the road is under renovation and the current route is 280km. An airstrip is present 8km from Bikoro, which is 30km from Ikoko.
Was the cause of the outbreak confirmed by a laboratory? If so, give details of the initial confirmation (cause, species, specimen types tested and dates of testing if known).	INRB testing of five patients' whole blood specimens for EVD found two to be positive for Ebola virus (*Zaire ebolavirus)* by RT-PCR at INRB in Kinshasa on May 7 2018.
Where was the laboratory testing performed (name of laboratory)?	INRB
Number of days between initiation of government response and lab confirmation of laboratory results.	1 day
Summary of the Outbreak or Event:	**To be filled after active outbreak or event activity has ceased**
Working name of the outbreak:	
Total number of cases:	

	Suspected:	**Confirmed:**	**Deaths:**
Humans			
Domestic Animals			
Wild Animals			

Summary of PREDICT Team response activities during the outbreak.	

PREDICT Outbreak or Health Event Response Daily Activities/Timeline

Working Title of Investigation: Ebola virus outbreak DRC Equateur April-May 2018

Key Events:

Date	Day #	Notification or Action Taken
April 3, 2018	-34	First suspect case in family cluster
May 6, 2018	1	Head Office of Disease Control officially acknowledges the outbreak.
May 7, 2018	2	The government, through the INRB, verbally requests PREDICT support. Specific details of request pending. Confirmation of Ebola virus by RT-PCR at the INRB laboratory. Of five samples tested, two were positive for *Zaire ebolavirus*.
May 8, 2018	3	MOH verbally requests for PREDICT to conduct PREDICT protocol testing of samples at INRB. Written approval from USAID AOR communicated to PREDICT DRC team. Samples transferred to PREDICT lab. Official Statement of the Ebola Virus Epidemic released by the Congolese Government (Ministry of Health). Developed road map and response plan. An investigative mission led by the director of the Office of Disease Control (DGLM) planned for Wednesday May 9, 2018 in the province of Equateur. **Monitoring report:** • New cases registered: 4 (in the health center) • On five previous cases monitored, three were released. There are two active cases in the General Hospital. • Total of active and monitored cases: 6 (among which 4 are suspected cases). • Laboratory confirmed cases : 2 • Deaths : 17 • Total notified cases: 23
May 9, 2018	4	PREDICT lab analysis of clinical specimens following PREDICT virus-family

		level protocols is in progress. PREDICT Country Coordinator met with MOH and partners on response plan and development of list of unmet needs. An investigative mission led by Office of Disease Control (DGLM) was deployed today May 9 to the province of Equateur. **Monitoring report:** • New cases registered: 4 • Total of active and monitored cases: 10 (among which 8 are suspected cases). • Confirmed cases : 2 • Deaths: 17 • Total cases under investigation: 27
May 10, 2018	5	Four new suspected cases and one death were reported in the health zone of Iboko, near the Bikoro health zone. The deceased case was a health professional who had symptoms suggestive of Ebola virus disease. **Monitoring report:** • Deaths: 18 cases • Suspected cases: 12 cases • Confirmed cases: 2 cases • Total notified cases: 32 cases (in Bikoro and Iboko) Identified actions: • Identification of positive cases • Contact tracing • Active monitoring • Sensitization seminars of all the Chief Medical officers in the health zones of Equator Province.
May 11, 2018	6	Late on May 11, the PREDICT DRC team received a formal request from the Government, through INRB regarding support for response activities. In response to the list of unmet needs provided by the laboratory commission, PREDICT provided 150 PPE, a Smartcycler and accompanying computer, and two gloveboxes. The K-Plan mobile lab (previously acquired through USAID support) will be deployed to the outbreak site in Bikoro and Iboko tomorrow (May 12, 2018). There is a significant and urgent need for sampling kits on sites of the outbreak.

		According to the WHO, all conditions are met for the vaccine to arrive in Kinshasa next week (week of May 14 to 20, 2018). **Monitoring report**: • New suspected cases : 2 (one in Iboko and the other in Bikoro) • There are three community alert cases in Mbandaka of new reports of ill individuals in the community requiring follow-up. • Deaths : 18 • Suspected cases: 14 (9 in Bikoro, 5 in Iboko) • Confirmed cases: 2 • Total notified cases: 34 (in Bikoro and Iboko)
May 12, 2018	7	In preparation for this deployment, the INRB Team arrived in Mbandaka, the capital of Equator Province. The Minister of Health and Ministry of Health officials arrived this morning to the sites of the epidemic. The INRB Team is in Bikoro. The K-Plan mobile lab was shipped this morning to Bikoro via Mbandaka. The Director General of the WHO arrives tonight in Kinshasa. **Monitoring report**: • New suspected cases : 2 (in Wangata, one of three health zones of Mbandaka) • After re-evaluation of the situation, the number of suspected cases was revised downward to Bikoro (8 suspected cases) and Iboko (2 suspected cases). • Deaths: 18 • Suspected cases: 12 (8 in Bikoro, 2 in Iboko, 2 in Wangata) • Confirmed cases: 2 • Cases previously suspected but tested negative: 3 • Total notified cases: 35 in 4 health zones (Bikoro , Iboko, Wangata and Ingende; this count includes the 3 laboratory-negative cases).
May 13, 2018	8	Director General of the WHO, MOH and representative of WHO DRC visit Mbandaka and Bikoro. **Monitoring report**: • New suspected cases : 5 (2 in Bikoro ; 3 in Iboko) • Deaths: 20 (17 in Bikoro; 3 in Iboko) • Suspected cases: 17 (10 in Bikoro, 5 in Iboko, 2 in Wangata) • Confirmed cases: 2

		• Cases previously suspected but tested negative: 3 • Total notified cases: 42 in 4 health zones (Bikoro , Iboko, Wangata and Ingende; this count includes the 3 laboratory-negative
May 14, 2018	9	Cold chain for vaccination is being deployed on site. **Monitoring report:** • New suspected cases : 3 (in Bikoro) • Deaths: 20 (17 in Bikoro; 3 in Iboko) • Suspected cases: 20 (13 in Bikoro, 5 in Iboko, 2 in Wangata) • Confirmed cases: 2 • Cases previously suspected but tested negative: 3 • Total notified cases: 45 in 4 health zones (Bikoro , Iboko, Wangata and Ingende); this count includes the 3 laboratory-negative
May 15, 2018	10	USAID approved the request in support for outbreak response. Previously, the analysis made on the five samples at the PREDICT lab cost $111.35 At the end of all analysis, this amount may reach $276.69 **Monitoring report:** • New suspected cases : 3 (in Wangata) • Deaths: 20 (18 in Bikoro; 2 in Iboko) • Suspected cases: 20 (14 in Bikoro, 3 in Iboko, 3 in Wangata) • Confirmed cases: 2 • Cases previously suspected but tested negative: 3 • Total notified cases: 42 in 4 health zones (Bikoro , Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 16, 2018	11	5412 doses of vaccines against EVD arrived in Kinshasa. The MOH (INRB) officially asked PREDICT for a space in a -80 freezer to store the vaccines. A vaccination committee will be set up to coordinate vaccination activities. In view of the spread of the outbreak in several health zones, a reassessment of laboratory needs is being made by the Laboratory commission. This changing state of need will integrate all affected health areas. **Monitoring report:** • New suspected cases : 2 (1 in Bikoro and another in Wangata)

		• Deaths: 23 (20 in Bikoro; 3 in Iboko) • Probable cases: 20 (18 in Bikoro; 2 in Iboko) • Suspected cases: 21 (15 in Bikoro, 3 in Iboko, 3 in Wangata) • Confirmed cases: 3 • Cases previously suspected but tested negative: 3 • Total notified cases: 44 in 4 health zones (Bikoro , Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 17, 2018	12	Vaccination at the sites of the outbreak will begin on Monday, May 21, 2018. Vaccination will target health professionals working in the hospitals, contacts of the confirmed cases, and contacts of the case contacts. In view of the importance of the outbreak, the laboratory and research commission reassessed the needs for assistance. In order to circumvent the difficulties related to customs clearance, the chairman of the commission, Pr Muyembe, suggested that some materials be bought in Kinshasa. Six specimen collected on May 16 should arrive tonight in Kinshasa from Mbandaka. The laboratory in Bikoro is fully functional. Rapid diagnostic test and RT-PCR will be used. In Mbandaka, the GeneXpert is set up, but electricity is a problem . **Monitoring report:** • New suspected cases : 0 • Deaths: 24 (21 in Bikoro; 3 in Iboko) • Probable cases: 21 (19 in Bikoro; 2 in Iboko) • Suspected cases: 1 (health zone has not been specified) • Confirmed cases: 14 (13 in Bikoro ; 1 in Wangata) • Contact case: 532 (330 in Bikoro; 120 in Iboko; 52 in Wangata; 30 in Ntondo) • Cases previously suspected but tested negative: 3 • Total notified cases: 45 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative cases. Please note that the total notified cases (45) does not match the sum of the suspected, confirmed and deceased cases, but these are the numbers MOH is reporting.

		The WHO situation report (May 16 version) indicates a total of 44 notified cases and 23 deaths.
May 18, 2018	13	A new MOH team arrived in Mbandaka this morning. **Monitoring report:** • New suspected cases : 4 (in Iboko) • Deaths: 25 (20 in Bikoro; 4 in Iboko ; 1 in Wangata) • Probable cases: 21 (19 in Bikoro; 2 in Iboko) • Suspected cases: 4 (in Iboko) • Confirmed cases: 17 (8 in Bikoro ; 5 in Iboko; 4 in Wangata) • Followed contact cases: 429 (274 in Bikoro; 73 in Iboko; 52 in Wangata; 30 in Ntondo) • Total notified cases: 42 in 4 health zones (Bikoro , Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals. Please note that the total notified cases (42) does not match the sum of the suspected, confirmed and deceased cases, but these are the numbers MOH is reporting. The WHO situation report (May 17 version) indicates a total of 45 notified cases and 24 deaths.
May 19, 2018	14	Free health care will be provided in epidemic health zones (areas where there are confirmed cases) and in health zones close to the epidemic zone. In total, seven health zones have been identified. In Mbandaka , 62 frontline health care and laboratory workers (11 in Wangata, 24 in Bolenge and 27 at the Ebola Treatment Center) have been identified to receive the vaccine. An additional 3000 doses are expected to reach Kinshasa on May 19, 2018. The shipping of vaccines to Mbandaka will begin on May 20, 2018. **Monitoring report:** • Deaths: 26 (22 in Bikoro; 3 in Iboko ; 1 in Wangata) • Probable cases: 21 (19 in Bikoro; 2 in Iboko) • Suspected cases: 3 (2 in Iboko; 1 in Wangata) • Confirmed cases: 21 (10 in Bikoro ; 7 in Iboko; 4 in Wangata) • Followed contact cases: 501 (279 in Bikoro; 75 in Iboko; 117 in Wangata; 30 in Ntondo) • Total notified cases: 45 in 4 health zones (Bikoro , Iboko, Wangata and Ingende); this count does not include the 3

		• laboratory-negative individuals.
May 20, 2018	15	On May 19, a confirmed female case from Wangata left the Ebola treatment center in Mbandaka. An alert case in Kinshasa was tested negative for Ebolavirus by RT-PCR at INRB. 560 doses of vaccine arrived in Mbandaka. **Monitoring report:** • Deaths: 26 (22 in Bikoro; 3 in Iboko ; 1 in Wangata) • Probable cases: 21 (19 in Bikoro; 2 in Iboko) • Suspected cases: 6 (6 in Iboko) • Confirmed cases: 22 (10 in Bikoro ; 8 in Iboko; 4 in Wangata) • Followed contact cases: 511 (273 in Bikoro; 95 in Iboko; 113 in Wangata; 30 in Ntondo) • Total notified cases: 49 in 4 health zones (Bikoro , Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 21, 2018	16	The vaccination campaign (rVSV-ZEBOV) started today in the epidemic zones. The PREDICT laboratory analyzed four confirmed positive specimens from Mbandaka, which previously tested positive by the geneXpert platform. One of the four specimens tested positive for filovirus RNA using the PREDICT virus-family consensus PCR protocol, this initial result will be confirmed by genetic sequencing. The PREDICT lab also tested the two positive confirmed specimens from Bikoro. One sample was positive for filovirus using the PREDICT virus-family level consensus PCR protocol which will also be confirmed by genetic sequencing. **Monitoring report:** • Deaths: 27 (22 in Bikoro; 3 in Iboko ; 2 in Wangata) • Probable cases: 21 (19 in Bikoro; 2 in Iboko) • Suspected cases: 2 (in Wangata) • Confirmed cases: 28 (10 in Bikoro ; 14 in Iboko; 4 in Wangata) • Followed contact cases: 561 (301 in Bikoro; 115 in Iboko; 115 in Wangata; 30 in Ntondo) • Total notified cases: 51 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-

		• negative individuals. Please note: the WHO situation report (May 20 version) indicates a total of 49 notified cases and 26 deaths.
May 22, 2018	17	Two patients left the Wangata Ebola Treatment Center. Both were found later, including one individual who had died after returning to their home. One death in Wangata (from May 20) was reported as non-EVD. 33 people were vaccinated (rVSV-ZEBOV) including 10 hospital health personnel in Wangata, 22 case contacts and the Director of the Expanded Vaccination Program. **Monitoring report:** • Deaths: 27 (23 in Bikoro; 3 in Iboko ; 1 in Wangata) • Probable cases: 21 (19 in Bikoro; 2 in Iboko) • Suspected cases: 9 (6 in Iboko; 3 in Wangata) • Confirmed cases: 28 (10 in Bikoro; 14 in Iboko; 4 in Wangata) • Followed contact cases: 561 (321 in Bikoro; 114 in Iboko; 112 in Wangata; 30 in Ntondo) [note the total should be 577] • Total notified cases: 58 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 23, 2018	18	Another 3,800 doses of vaccines have been received in Mbandaka. The total number of doses delivered and available for administration in the outbreak sites is 4,360. **Monitoring report:** • Deaths: 30 (24 in Bikoro; 3 in Iboko ; 3 in Wangata) • Probable cases: 22 (20 in Bikoro; 2 in Iboko) • Suspected cases: 16 (2 in Bikoro; 8 in Iboko; 6 in Wangata) • Confirmed cases: 30 (10 in Bikoro; 16 in Iboko; 4 in Wangata) • Followed contact cases: 587 (344 in Bikoro; 111 in Iboko; 102 in Wangata; 30 in Ntondo) • Total notified cases: 68 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 24, 2018	19	As part of WASH and communication efforts, MOH did a training on safe burial practices, and has begun disinfecting houses of those who have

		died. They are providing psychosocial support to victims, family members, and medical staff, as well as sensitization to cultural, religious, and opinion leaders. The Minister of Health said today that safe burials are regarded as inhumane, so there is a lot of communication that must accompany this, and that we must learn lessons from West Africa on how best to roll this out to communities. **Monitoring report:** • Deaths: 23 (16 in Bikoro; 4 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 8 (2 in Bikoro; 5 in Iboko; 1 in Wangata) • Confirmed cases: 31 (10 in Bikoro; 17 in Iboko; 4 in Wangata) • Followed contact cases: 927 (445 in Bikoro; 302 in Iboko; 180 in Wangata) ; this represents 85% contact trace coverage rate of known contacts. • Total notified cases: 52 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals. 560 additional vaccine doses were sent to outbreak site today, with 4000 supplemental doses expected later this week. Vaccination of traditional medicine practitioners began today in the affected areas.
May 25, 2018	20	*Informational update and details on INRB initiated animal sampling field activities:* As part of an ecological study, two members of INRB Team were sent to Bikoro. Their objective is to capture and sample bats in order to research potential Ebola virus reservoirs. One of the INRB field-team members, has been trained by PREDICT on animal sampling protocols and regularly works with the PREDICT team to sample wild animals in bushmeat markets and with hunters and trappers. The INRB animal sampling team intends to conduct field sampling until June 9, 2018. The PREDICT team has no direct involvement in these activities at this time. *VSV-ZEBOV vaccine:* Of the 180 contacts registered in Mbandaka, 154 people have been vaccinated.

		PREDICT laboratory testing: PREDICT conducted laboratory testing following virus family level consensus PCR protocols of two previously INRB tested Ebola-positive specimens sent from the outbreak sites. PCR products from one of these two specimens were obtained by the PREDICT laboratory testing methods, and were shipped Friday to Germany for sequencing. **Monitoring report:** • Deaths: 24 (16 in Bikoro; 5 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 6 (3 in Bikoro; 2 in Iboko; 1 in Wangata) • Confirmed cases: 35 (10 in Bikoro; 21 in Iboko; 4 in Wangata) • Followed contact cases: 948 (483 in Bikoro; 296 in Iboko; 129 in Wangata; 40 in Ntondo) ; this represents 86% contact trace coverage rate of known contacts. • Total notified cases: 54 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 26, 2018	21	**VSV-ZEBOV vaccine:** 56 people (registered contacts and health staff) were vaccinated in Mbandaka. To date, a total of 210 people have been vaccinated. **Monitoring report:** • Deaths: 25 (16 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 6 (2 in Bikoro; 3 in Iboko; 1 in Wangata) • Confirmed cases: 35 (10 in Bikoro; 21 in Iboko; 4 in Wangata) • Followed contact cases: 922 (478 in Bikoro; 296 in Iboko; 148 in Wangata) ; this represents 84% contact trace coverage rate of known contacts. • Total notified cases: 54 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 27, 2018	22	**VSV-ZEBOV vaccine:** 108 people (registered contacts and health staff) were vaccinated in Mbandaka. To date, a total of 318 people have been vaccinated. **Contact Tracing:** The Director General of the Directorate of Disease

		Control reported the extension of the case investigation zone to Kiri Health Zone, Bandundu Province. A woman died in Iboko between May 5-10 and the corpse was returned to Kiri, where it was handled by 14 people. The woman's daughter also died. These exposed contacts will be investigated by a team of MOH experts, scheduled for tomorrow (May 28). Please note that the number of contact cases followed was not announced. However, the Epidemiological Surveillance Commission reports 201 new contacts registered. **Monitoring report:** • Deaths: 25 (16 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 8 (2 in Bikoro; 5 in Iboko; 1 in Wangata) • Confirmed cases: 35 (10 in Bikoro; 21 in Iboko; 4 in Wangata) • Total notified cases: 56 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 28, 2018	23	**VSV-ZEBOV vaccine***:* 50 people (registered contacts) were vaccinated in Mbandaka. To date, a total of 368 people have been vaccinated. **Contact Tracing:** An investigation will be conducted in Kiri on May, 29. The Surveillance Commission mentioned 15 contact cases in Kiri, which is not consistent with their announcement on May 27. **Monitoring report:** • Deaths: 25 (16 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 6 (1 in Bikoro; 4 in Iboko; 1 in Wangata) • Confirmed cases: 35 (10 in Bikoro; 21 in Iboko; 4 in Wangata) • Followed contact cases: 736 (265 in Bikoro; 317 in Iboko; 154 in Wangata) ; this represents 74% contact trace coverage rate of known contacts. • Total notified cases: 54 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the 3 laboratory-negative individuals.
May 29, 2018	24	**VSV-ZEBOV vaccine:** 94 people were vaccinated (58 in Mbandaka ; 20 in Bikoro; 16 in Iboko). To date, a total of 462 people have been

		vaccinated.(462 in Mbandaka; 20 in Bikoro; 16 in Iboko) **Contact Tracing:** MOH experts went to kiri for an investigative mission. **Monitoring report:** • Deaths: 25 (16 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 3 (2 in Bikoro; 1 in Wangata) • Confirmed cases: 35 (10 in Bikoro; 21 in Iboko; 4 in Wangata) • Followed contact cases: 528 (112 in Bikoro; 262 in Iboko; 154 in Wangata) ; this represents 55% contact trace coverage rate of known contacts. • Total notified cases: 51 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals. Please note that 5 suspecetd cases were tested negative (4 in Iboko; 1 in Wangata). New suspeceted cases : 2 (1 in Iboko; 1 in Wangata)
May 30, 2018	25	**VSV-ZEBOV vaccine:** 99 people were vaccinated (18 in Mbandaka ; 54 in Bikoro; 27 in Iboko). To date, a total of 561 people have been vaccinated (444 in Mbandaka; 74 in Bikoro; 43 in Iboko). **Monitoring report:** • Deaths: 25 (16 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 4 (3 in Bikoro; 1 in Wangata) • Confirmed cases: 36 (10 in Bikoro; 22 in Iboko; 4 in Wangata) • Followed contact cases: 508 (119 in Bikoro; 324 in Iboko; 65 in Wangata) ; this represents 68% contact trace coverage rate of known contacts. • Total notified cases: 53 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
May 31, 2018	26	**PREDICT Laboratory:** Today sequence information was obtained from one of the INRB confirmed cases from Bikoro health zone (*see 25 May 2018 log-entry, above*). Initial genomic analysis is consistent with the detection of Ebola virus (species: *Zaïre ebolavirus*). Further genomic characterization of this PREDICT lab protocol generated sequence fragment is pending.

		VSV-ZEBOV vaccine: 121 people were vaccinated (53 in Mbandaka ; 40 in Bikoro; 28 in Iboko). To date, a total of 682 people have been vaccinated (497 in Mbandaka; 114 in Bikoro; 71 in Iboko). **Monitoring report:** • Deaths: 25 (17 in Bikoro; 5 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 0 • Confirmed cases: 37 (10 in Bikoro; 23 in Iboko; 4 in Wangata) • Followed contact cases: 506 (169 in Bikoro; 199 in Iboko; 138 in Wangata) ; this represents 57% contact trace coverage rate of known contacts. • Total notified cases: 50 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 1, 2018	27	**VSV-ZEBOV vaccine:** 126 people were vaccinated (30 in Mbandaka ; 56 in Bikoro; 40 in Iboko). To date, a total of 809 people have been vaccinated. *Surveillance at Ports of Entry (PoE):* Health Control is assuring surveillance at PoE in Bikoro, Mbandaka, and Kinshasa. Health screenings included 293 travelers in Bikoro, 669 in Mbandaka, and 386 in Kinshasa. Two alerts (individuals who were suspected of EVB) were reported in Ingende, traveling from Mbandaka, and investigation of those alerts is in progress. **Monitoring report:** • Deaths: 25 (17 in Bikoro; 5 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 5 (3 in Bikoro; 2 in Wangata) • Confirmed cases: 37 (10 in Bikoro; 23 in Iboko; 4 in Wangata) • Followed contact cases: 528 (169 in Bikoro; 223 in Iboko; 136 in Wangata) ; this represents 60% contact trace coverage rate of known contacts. Total notified cases: 55 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 2, 2018	28	**VSV-ZEBOV vaccine:** 38 people were vaccinated in Mbandaka and 29 in Iboko. To date, a total of 902 people have been vaccinated (567 in Mbandaka; 169 in Bikoro; 166 in Iboko).

		Case investigation update: There is currently an attempt to investigate suspected cases in the family of a deceased nurse in Itipo, whose death was likely due to having managed 20 confirmed Ebola cases. The attempt was met with strong resistance and refusal from family members, and negotiations are in progress. (Itipo is a health district within the health zone of Iboko.) **Monitoring report:** • Deaths: 25 (17 in Bikoro; 5 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 7 (2 in Bikoro; 3 in Iboko; 2 in Wangata) • Confirmed cases: 37 (10 in Bikoro; 23 in Iboko; 4 in Wangata) • Followed contact cases: 556 (152 in Bikoro; 260 in Iboko; 144 in Wangata) ; this represents 60% contact trace coverage rate of known contacts. Total notified cases: 57 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 3, 2018	29	**VSV-ZEBOV vaccine:** 147 people were vaccinated (50 in Bikoro; 97 in Iboko). To date, a total of 1,112 people have been vaccinated (567 in Mbandaka; 269 in Bikoro; 276 in Iboko). Please note that the vaccination target has been reached in Mbandaka. 2870 vaccine doses are still available at Mbandaka. **Case investigation update:** Samples from one of two alert cases in Ingende (Please see June 1 report) tested negative for Ebola. Kiri team investigators (Please see May 28 report) noted that the contacts cases followed have reached the 18th day of monitoring (incubation period for EVD is 2 to 21 days). Thus far, no particular clinical signs have been observed. **Monitoring report:** • Deaths: 25 (17 in Bikoro; 5 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 3 (in Iboko) • Confirmed cases: 37 (10 in Bikoro; 23 in Iboko; 4 in Wangata) • Followed contact cases: 442 (129 in Bikoro; 176 in Iboko; 137 in Wangata) ; this represents 47% contact trace coverage rate of known contacts. Total notified cases: 53 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative

		individuals.
June 4, 2018	30	*VSV-ZEBOV vaccine:* 87 people were vaccinated (10 in Mbandaka; 30 in Bikoro; 47 in Iboko). To date, a total of 1,199 people have been vaccinated (577 in Mbandaka; 299 in Bikoro; 323 in Iboko). Please note that ten ring contacts (contact of case contacts) who were linked to a case contact from Bikoro were vaccinated in Mbandaka. Two recovered patients were released from the Ebola treatment center of Likati. **Monitoring report:** • Deaths: 25 (17 in Bikoro; 5 in Iboko ; 3 in Wangata) • Probable cases: 13 (11 in Bikoro; 2 in Iboko) • Suspected cases: 6 (5 in Bikoro; 1 in Wangata) • Confirmed cases: 37 (10 in Bikoro; 23 in Iboko; 4 in Wangata) • Followed contact cases: 490 (116 in Bikoro; 237 in Iboko; 137 in Wangata) ; this represents 52% contact trace coverage rate of known contacts. Total notified cases: 56 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 5, 2018	31	**VSV-ZEBOV vaccine**: 145 people were vaccinated (20 in Mbandaka; 27 in Bikoro; 98 in Iboko). To date, a total of 1,369 people have been vaccinated (597 in Mbandaka; 299 in Bikoro; 473 in Iboko). Please note that in Mbandaka, contacts who were vaccinated were identified according to relationships with a contact case from Bikoro. **Case Investigation update**: Four recovered patients were released from the Ebola treatment center of Bikoro. **Monitoring report:** • Deaths: 27 (18 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 14 (11 in Bikoro; 3 in Iboko) • Suspected cases: 7 (4 in Bikoro; 3 in Iboko) • Confirmed cases: 37 (10 in Bikoro; 23 in Iboko; 4 in Wangata) • Followed contact cases: 529 (140 in Bikoro; 280 in Iboko; 109 in Wangata) ; this represents 56% contact trace coverage rate of known contacts. Total notified cases: 58 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 6, 2018	32	**VSV-ZEBOV vaccine**: 183 people were vaccinated (25 in Mbandaka; 46 in

		Bikoro; 82 in Iboko; 30 in Ingende). To date, a total of 1,579 people have been vaccinated (622 in Mbandaka; 372 in Bikoro; 555 in Iboko; 30 in Ingende). **Case Investigation update**: 21 patients are hospitalized in the respective Ebola treatment centers : 5 in Mbandaka; 2 in Moheli; 8 in Ikoko Impenge; 4 in Itipo; 2 in Iboko. **Monitoring report:** • Deaths: 27 (18 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 14 (11 in Bikoro; 3 in Iboko) • Suspected cases: 9 (2 in Bikoro; 6 in Iboko; 1 in Wangata) • Confirmed cases: 37 (10 in Bikoro; 23 in Iboko; 4 in Wangata) • Followed contact cases: 546 (97 in Bikoro; 312 in Iboko; 137 in Wangata) ; this represents 87% contact trace coverage rate of known contacts. Total notified cases: 60 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals. **NB:** All recent confirmed cases are old contacts followed through case investigation. Since May 31, the number of confirmed cases has remained stable at 37, which may indicate that the outbreak seems to be under control, according to discussions at the MOH.
June 7, 2018	33	**VSV-ZEBOV vaccine**: 247 people were vaccinated (51 in Mbandaka; 32 in Bikoro; 164 in Iboko). To date, the MOH reports a total of 1,796 people having been vaccinated (673 in Mbandaka; 398 in Bikoro; 725 in Iboko; 30 in Ingende). (Please note that the total should be 1826.) **Case Investigation update**: 5 patients are hospitalized in the respective Ebola treatment centers : 1 in Bikoro; 4 in Itipo . One recovered patient was released from the Ebola treatment center of Bikoro. **Monitoring report:** • Deaths: 27 (18 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 14 (11 in Bikoro; 3 in Iboko) • Suspected cases: 10 (2 in Bikoro; 5 in Iboko; 3 in Wangata) • Confirmed cases: 38 (10 in Bikoro; 24 in Iboko; 4 in Wangata) • Followed contact cases: 564 (116 in Bikoro; 378 in Iboko; 70 in Wangata) ; this represents 91% contact trace coverage rate of known contacts.

		Total notified cases: 62 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 8, 2018	34	**VSV-ZEBOV vaccine**: 238 people were vaccinated (25 in Mbandaka; 100 in Bikoro; 113 in Iboko). To date, the MOH reports a total of 2,034 people having been vaccinated (698 in Mbandaka; 498 in Bikoro; 838 in Iboko; 30 in Ingende). (Please note that the total should be 2,064.) **Case Investigation update**: 12 patients are hospitalized in the respective Ebola treatment centers : 3 in Mbandaka; 5 in Bikoro centre; 1 in Moheli; 2 in Ikoko Impinge (health area in Bikoro); 1 in Itipo (health area in Iboko). **Sequence analysis:** PREDICT has completed analysis of the outbreak sample on which we were requested by INRB to run PREDICT protocols. This is a known Ebolavirus (*Zaire ebolavirus*). A small fragment of the RNA genome sequence is 99% homogenous with the Kikwit strain found previously in the DRC. **Monitoring report:** • Deaths: 27 (18 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 14 (11 in Bikoro; 3 in Iboko) • Suspected cases: 7 (1 in Bikoro; 6 in Iboko) • Confirmed cases: 38 (10 in Bikoro; 24 in Iboko; 4 in Wangata) • Followed contact cases: 515 (71 in Bikoro; 369 in Iboko; 75 in Wangata) ; this represents 68% contact trace coverage rate of known contacts. Total notified cases: 59 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 9, 2018	35	**VSV-ZEBOV vaccine**: 81 people were vaccinated (15 in Mbandaka; 66 in Iboko). To date, the MOH reports a total of 2,145 people having been vaccinated (713 in Mbandaka; 498 in Bikoro; 904 in Iboko; 30 in Ingende). **Case Investigation update**: 16 patients are hospitalized in the respective Ebola treatment centers : 4 in Bikoro; 1 in Moheli; 2 in Ikoko Impinge (Bikoro health area); 9 in Itipo (Iboko health area). *Please note that there were 8 new cases admitted and 4 non-cases released. This brings the number of hospitalized to 16.*

		Monitoring report: • Deaths: 27 (18 in Bikoro; 6 in Iboko ; 3 in Wangata) • Probable cases: 14 (11 in Bikoro; 3 in Iboko) • Suspected cases: 7 (4 in Bikoro; 3 in Iboko) • Confirmed cases: 38 (10 in Bikoro; 24 in Iboko; 4 in Wangata) • Followed contact cases: 543 (43 in Bikoro; 421 in Iboko; 79 in Wangata) ; this represents 68% contact trace coverage rate of known contacts. Total notified cases: 59 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.
June 10, 2018	36	**VSV-ZEBOV vaccine**: 76 people were vaccinated (76 in Iboko). To date, the MOH reports a total of 2,221 people having been vaccinated (713 in Mbandaka; 498 in Bikoro; 980 in Iboko; 30 in Ingende). **Case Investigation update**: 17 patients are hospitalized in the respective Ebola treatment centers : 6 in Bikoro; 2 in Ikoko Impenge (Bikoro health area); 9 in Itipo (Iboko health area). *Please note that there were 4 new cases admitted, 1 death and 2 non-cases released. This brings the number of hospitalized to 17.* **Monitoring report:** • Deaths: 28 (18 in Bikoro; 7 in Iboko ; 3 in Wangata) • Probable cases: 14 (11 in Bikoro; 3 in Iboko) • Suspected cases: 14 (1 in Bikoro; 12 in Iboko; 1 in Wangata) • Confirmed cases: 38 (10 in Bikoro; 24 in Iboko; 4 in Wangata) • Followed contact cases: 533 (10 in Bikoro; 447 in Iboko; 76 in Wangata) ; this represents 84% contact trace coverage rate of known contacts. Total notified cases: 66 in 4 health zones (Bikoro, Iboko, Wangata and Ingende); this count does not include the laboratory-negative individuals.

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Sent: Mon, 11 Jun 2018 11:17:56 +0000
Subject: [predict] Y4Q2 and SAR 2018
PREDICT-2 Jordan Report Y4Q2 (1).pdf
Jordan report P2 SAR 2018.pdf

Dear respected Partners,

Please find enclosed PREDICT-2 Jordan report Y4Q2 (Jan-March) as well as the Semi Annual Report (SAR) -2018 for Jordan (two pages). For the Full Semi Annual Report (SAR) -2018 for PREDICT-2 for all countries please down load from the following website as the file is huge.

http://www.vetmed.ucdavis.edu/ohi/local_resources/pdfs/SAR%202018%20FINAL-compressed.pdf

Best Regards,

Ehab

Ehab Abu-Basha, DVM, MSc., Ph.D
PREDICT-2 Country Coordinator
[redacted]

May 27, 2018

Dear Colleagues

The PREDICT project, part of USAID's Emerging Pandemic Threats program (EPT - https://www.usaid.gov/ept2), is developing a global early warning system to detect, track, and predict the emergence of new zoonotic pathogens from wildlife that could pose a threat to human health. For more information on the PREDICT project, please visit our website (http://predict.global) or download our information sheet (http://flyer.predict.global).

In Jordan, PREDICT is implemented by EcoHealth Alliance and the Faculty of Veterinary Medicine, Jordan University of Science and Technology

Below is a summary of PREDICT achievements and progress from January-March, 2018 in Jordan, along with a brief update on upcoming plans for the period of April-June, 2018.

Please direct all correspondence to the PREDICT Jordan Country Coordinator and Global Point of Contact:

Dr. Ehab Abu-Basha
PREDICT Jordan Country Coordinator
Faculty of Veterinary Medicine, Jordan University of Science and Technology
Email: abubasha@just.edu.jo
Address: P.O. Box 3030, Irbid 22110, Jordan
Phone: +962 7 9939 9128

Dr. William Karesh
PREDICT Jordan Global Point of Contact
Executive Vice President, EcoHealth Alliance
Email: Karesh@ecohealthalliance.org
Address: 460 West 34th St, 1701, NY, NY 10001, USA
Phone: +1 212-380-4463

PREDICT Jordan Summary of Activities & Progress January-March, 2018

- PREDICT-2 Country Coordinator, Prof. Ehab Abu-Basha, continuously updated PREDICT-2 project liaisons at USAID/Jordan Mission with PREDICT-2 activity and events. Myasa Al-Khateeb, Management Specialist at the USAID Mission office in Amman, was briefed about PREDICT team accomplishments between January and March 2018. The need to upgrade veterinary and laboratory services in Southern Jordan was discussed and planned for this year and next, based on field trip visits to five different laboratories in five cities (Karak, At Tafilah, Ash Shawbak, Maan and Aqapa) in South Jordan.

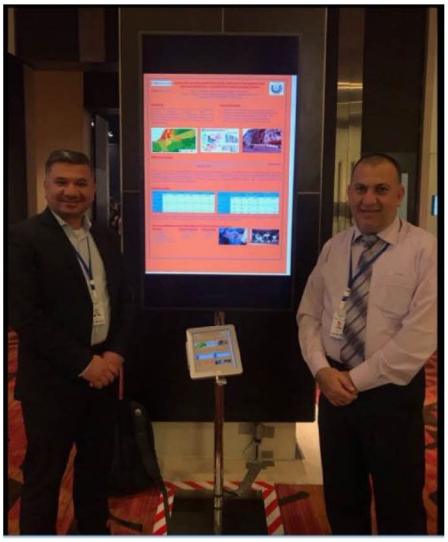
- PREDICT-2 focal point partners from USAID, Ministry of Health (MOH), Ministry of Environment (MOE), Ministry of Agriculture, World Health Organization (WHO), Food and Agriculture Organization (FAO), Royal Scientific Society (RRS) and the Hashemite Fund for Development of Jordan Badia met twice between January and March (January 25th at the Badia Fund and March 28th at the MOH). All activities of PREDICT-2 Jordan were presented and the One Health approach was discussed. Progress on the national action plan was briefed from PREDICT-2 Jordan's WHO partner.

- Prof. Ehab Abu-Basha and Prof. Borhan Al-Zogoual participated in the PREDICT All-Country Meeting in Brussels, Belgium, January 9-11th, 2018. This meeting was attended by over 100 participants including representatives from all 30 PREDICT countries, in addition to guests from the European Union, Food and Agriculture Organization of the United Nations (FAO) and USAID. It was amazing to hear from each partner and to meet with them individually. We learned about challenges facing the PREDICT project and the One Health approach during panel discussions. A poster competition was held for all PREDICT-2 countries.

The PREDICT team and partners from USAID and the Food and Agriculture Organization of the United Nations at the PREDICT 2018 All-country meeting in Brussels, Belgium. Photo: PREDICT.

- The Prince Mahidol Award Foundation, the World Health Organization, the World Bank, the United Nations Development Program, the Joint United Nations Program on HIV/AIDS, the International Organization for Migration, the Global Fund to Fight AIDS, Tuberculosis and Malaria, the U.S. Agency for International Development, the National Institute of Health, the Japan International Cooperation Agency, The Rockefeller Foundation, the China Medical Board, the Chatham House, and the Bill & Melinda Gates Foundation jointly co-hosted the Prince Mahidol Award Conference 2018, themed: "Making the World Safe from the Threats of Emerging Infectious Diseases." The conference took place from January 29th through February 3rd, 2018, in Bangkok, Thailand. **On behalf of EcoHealth Alliance and the United States Agency for International Development (USAID), PREDICT and USAID presented a poster titled:**

"SOCIAL AND CULTURAL DIFFICULTIES FACING "ONE HEALTH" IMPLEMENTATION: MERS-COV EXPEREINCE - A SUCCESS STORY FROM SOUTHERN JORDAN. Ehab Abu-Basha, Zuhair Bani Ismail, Maysa Al-Khateeb



Poster presented at Prince Mahidol Award Conference, 29 January - 3 February 2018 in Bangkok, Thailand.

- Prof. Ehab Abu-Basha nominated two graduate students (Ola and Ghadeer) for part-time work with PREDICT-2 Jordan in the Virology Laboratory. The two graduate students will be part of the International Visitor Leadership Program (IVLP) for the year 2019. In support of the Department's strategic focus on ensuring the health and economic prosperity of the United States and the world, this project brings together public health specialists to examine and strengthen their networks while building capacity in early-warning systems. Six out of every ten infectious diseases in humans are spread from animals. The Zoonotic Diseases Action Package (ZDAP), part of the Global Health Security Agenda (GHSA) launched in 2014, aims to minimize the emergence and spread of these diseases. Additionally, many high-impact infectious diseases are water-related or

vector-borne. A key practice for addressing these threats is to develop an integrated information system (IIS) to predict outbreaks of greatest public health concern and to strengthen human, animal, and environmental surveillance. Participants will observe how the One Health approach is being implemented in the United States and how an integrated information system (IIS) can be used to collect, combine, and disseminate data from earth observation, local environmental sensing, public health, and social science sources.

Hani Talafha, animal Field Coordinator, was selected for the International Visitor Leadership Program (IVLP) in 2018. Zaidoun Hijazeen was selected in 2017. We were proud to have Hani and Zaidoun in the program, and we also hope that both Ola and Ghadeer will be selected.

- PREDICT-2 Jordan arranged a field trip to a bat cave in Ajloun on the 11th of February. Participants included the USAID Mission Director (Nancy Eslick), USAID's Deputy Director of Population and Family Health Office (Andrea Halverson), Maysa Al-Khateeb and Ruba Kalouti.

Photo from the field trip, taken by PREDICT-2 Jordan.

- The Minister of Health wrote a letter to the Director of Health in several directorates to facilitate human surveillance work for the PREDICT-2 Jordan human surveillance team. Special thanks to the focal point at the Ministry of Health, Dr. Sultan Al-Qasrawi, for his continuous support.

Capacity Building

- PREDICT-2 Jordan and the USAID-Amman office is continuing to determine the needs of veterinary and laboratory services in Southern Jordan. Two laboratories were selected for upgrades (one in Karak and one in Ma'an) and will be equipped with select items to enhance diagnostic capability.

Surveillance, Field activities and Laboratory Diagnostic activity

- Bat and human samples are continuing to be tested using PREDICT protocols; conventional PCR for Paramyxoviruses, Coronaviruses, Filoviruses, and Influenza viruses. Tests are performed at the Jordan University of Science and Technology's Molecular Virology Laboratory and the Health Center Diagnostic Laboratory. Laboratory teams finished testing 260 human samples (oropharyngeal) for Coronaviruses (protocols Quan and Watanabe), Influenza, Paramayxovirus and Filovirus during the period of January-March, 2018. Bat samples (83 rectal and 83 oral) were examined for all the above viral families. All positive samples were sent for sequencing. Cloning was performed on purified PCR products in order to get accurate sequencing results. TA cloning is used to ligate the PCR product into pCR4 TOPO cloning vector, and then complete transformation into competent *E.coli* cells. Two-hundred and twenty-eight samples were sequenced during this three-month period.

- Field teams for both human and bats started sample collection for the winter season. Between January and March 2018, the human team collected 440 human samples from Amman (n=100), Zarqa (n=100), Al-Ramtha (n=130), Ajloun (n=110). During the same period, the field team for bats captured 186 bats from Ajloun (n=142) and Amman-Wadi Alseer (n=64).

PREDICT-2 Jordan Plans: April-June, 2018

- Conventional PCR for Paramyxoviruses, Coronaviruses, Filoviruses, and Influenza viruses for the remaining bat and human samples.

- PREDICT-2 Jordan team will continue to collect human and bat samples for the second season of Year 4.

- PREDICT-2 Country Coordinator will follow-up on the capacity building for Veterinary Laboratories in South Jordan.

- On April 9th, 2018, PREDICT-2 will arrange for USAID Amman staff to take a field trip to South Jordan and visit two laboratories in Karak and Ma'an (potential labs for diagnostic capacity). They will also visit a camel farm in the South of Jordan.

JORDAN

USAID | PREDICT
FROM THE AMERICAN PEOPLE

Global Health Security Agenda

WORKFORCE DEVELOPMENT

12	2	16
STAFF	GOVERNMENT	OTHER

21 MALE | 9 FEMALE

ONE HEALTH SURVEILLANCE

566

191

1,252 INDIVIDUALS
8,695 SPECIMENS

1

LAB STRENGTHENING

5,540 TESTS

JORDAN UNIVERSITY OF SCIENCE AND TECHNOLOGY (JUST)

TRAINING → LIMITED TESTING → TESTING ALL TARGET VIRAL FAMILIES

IMPACT

30 trained in One Health skills

1,252 individuals sampled
(439 humans and 813 animals)

5,540 tests for 5 viral families

3 viruses detected

VIRAL FINDINGS

1
NEW VIRUSES

2
KNOWN VIRUSES

www.predict.global

PREDICT-2

FACES OF
PREDICT

EHAB ABU-BASHA, DVM

Professor Ehab Abu-Basha joined the PREDICT team in 2016 as the Jordan Country Coordinator while serving as Dean of the Faculty of Veterinary Medicine at Jordan University of Science and Technology. As the Country Coordinator, he is responsible for training, mentoring, and supervising the PREDICT Jordan team. The project in Jordan is centered around the camel value chain because Jordan is part of the epidemiological zone for Middle East Respiratory Syndrome Coronavirus (MERS-CoV), which is believed to be transmitted from camels to humans.

Since joining the project, Ehab has elevated the role and importance of PREDICT at local, national, and international levels. He coordinates sampling trips with local leadership and communities, liaises closely with the USAID/Jordan Mission office, and represents PREDICT Jordan at international meetings. His leadership in PREDICT helped bring in additional funding from the USAID/Jordan Mission for the project, which helps fund sampling and testing activities as well as One Health capacity-building initiatives in Southern Jordan. He also worked with USAID/Jordan to implement a national One Health platform in Jordan that brings together focal points from Ministry of Health, Ministry of Agriculture, Ministry of Environment, World Health Organization (WHO), and other key partners on a regular basis to discuss PREDICT activities and One Health concerns. In September 2017, Ehab briefed colleagues from around the world on PREDICT Jordan activities at the Food and Agriculture Organization of the United Nations (FAO) – World Organisation for Animal Health (OIE) – WHO Global Technical Meeting for MERS-CoV at WHO headquarters in Geneva, Switzerland.

"PREDICT has provided me with an opportunity to become deeply involved in zoonotic disease research and health capacity building in Jordan. Our contributions to the PREDICT project will have a lasting impact on One Health implementation in Jordan."
– Dr. Ehab Abu-Basha

From: Andrew Clements <aclements@usaid.gov>
Sent: Wed, 27 Jun 2018 05:09:52 -0700
To: predict@ucdavis.edu
Cc: predictmgt@usaid.gov
Subject: [predict] Year 5 GHSA work plan guidance
Attachment
PREDICT MT Call (6.26.18)_final.docx

Following up on yesterday's call. For the year 5 work plans, use the same template and JEE 1.0 indicators as last year. Because you need to start now in order to meet the submission deadline, I think it's better to not delay while waiting for the 1.0 vs 2.0 issue to be decided especially since it will not affect any/many countries. If there is push back from the GHSA group, I will hold firm that they did not provide information on any changes in a timely manner so we're under no obligation to re-do 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

Begin forwarded message:

From: David J Wolking <djwolking@ucdavis.edu>
Date: June 26, 2018 at 1:50:45 AM GMT+2
To: "Clements, Andrew (GH/HIDN)" <AClements@usaid.gov>, Alisa Pereira Emerging Threats Division <apereira@usaid.gov>, Cassandra Louis Duthil <clouisduthil@usaid.gov>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Leilani Franciso <francisco@ecohealthalliance.org>, Lindsay Parish <lparish@usaid.gov>, Peter Daszak <daszak@ecohealthalliance.org>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, William Karesh <karesh@ecohealthalliance.org>, Karen Saylors <ksaylors@metabiota.com>, Amalhin Shek <ashek@usaid.gov>, "Cara J. Chrisman" <cchrisman@usaid.gov>, PREDICTMGT <predictmgt@usaid.gov>
Cc: Brooke Genovese <bgenovese@ucdavis.edu>, Molly Turner <turner@ecohealthalliance.org>, Amanda Andre <amanda.andre@ecohealthalliance.org>, Ava Sullivan <sullivan@ecohealthalliance.org>, "predict@ucdavis.edu" <predict@ucdavis.edu>, Catherine Machalaba <Machalaba@ecohealthalliance.org>, Evelyn Luciano <luciano@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>
Subject: PREDICT Management Team Call - Tuesday June 26, 2018 @ 10AM Pacific/1PM Eastern

Hi there,
Attached and below is our agenda for tomorrow's PREDICT Management Team call.

Talk soon,

David

PREDICT Management Call Agenda
Tuesday, June 26, 2018
10:00-11:00AM PST/1:00-2:00pm EST
REDACTED, Access code REDACTED
International Dial-in number: 310-765-4820 (toll charges apply)

USAID Updates

1. **Administrative items**

- Switching calls from conference line to Zoom?
- Confirming GHSA workplan approach
- USAID brown-bags
- EBO-Sursy meeting update
- End of project meeting in Year 5?

2. **EHP country round-up on bat book and outreach approach**

3. **Mission communications & country roundup**

4. **EPT partner collaboration/coordination updates (Billy)**

5. **Outbreak updates**

6. **Publication, media, and conference updates**
   - Evans et al 2018, Suspected Exposure to Filoviruses Among People Contacting Wildlife in Southwestern Uganda, *Journal of Infectious Diseases*
   - Read out from One Health Congress Saskatoon (June 22-25, 2018)
   - AVMA meeting in Denver (July 13, 2018)
   - International Conference on Emerging Infectious Diseases (ICEID) in Atlanta (August 26–29, 2018)
   - International Meeting on Emerging Diseases and Surveillance (IMED) 2018 in Vienna, Austria (November 9-12, 2018)
   - WDA Australasia meeting (Oct-November 2018)
   - International Symposium of Veterinary Epidemiology and Economics (ISVEE) Thailand (November 12-16, 2018).
   - Global Health Security 2019, Sydney (June 18-20, 2019)

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   - Global Health Security 2019, Sydney (June 18-20, 2019)

From: "Falgunee K. Parekh" <fparekh@metabiota.com>
Sent: Fri, 31 Aug 2018 12:11:50 -0400
Subject: Re: TZ grants - checking in
To: David Wolking <djwolking@ucdavis.edu>
Cc: "Hite, Karen" <khite@metabiota.com>, Elizabeth VanWormer <liz.vanwormer@unl.edu>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, Brian Bird <bhbird@ucdavis.edu>, "Prof. Woutrina Smith" <wasmith@ucdavis.edu>, Elizabeth Leasure <ealeasure@ucdavis.edu>
VISHA (TZ-6)_Final_Revised_Report_submitted (8.30.18).docx

Dear David, Jonna, Woutrina, Liz and Brian,
Thank you for sending the final report for VISHA. I added the Metabiota information on Table 1 and you can see that change in the attached (I was unable to edit it in Box). I have submitted everything to DTRA and am awaiting confirmation of receipt.

I would also like to let you know that my last day at Metabiota will be September 4. I have enjoyed working with all of you over the past 4 years and appreciate the interesting opportunity to learn about One Health epidemiology efforts in Tanzania. I hope that we can continue to keep in touch. My personal contact information is below, and of course I am always available on Skype. Thanks again and hope to hear from all of you.

Email: REDACTED
Phone:

Warmest Regards,
Falgunee

Falgunee K. Parekh, MPH, PhD
Senior Scientist, Clinical Research and Epidemiology
Metabiota, Inc.
Tel: 301.676.1919 | Email: fparekh@metabiota | skype: REDACTED
metabiota.com

On Thu, Aug 30, 2018 at 4:28 PM David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi Falgu,
> I've uploaded the VISHA report to the shared Box folder (the same folder where the PDF appendices were shared earlier). Here's the link for quick reference: https://ucdavis.box.com/v/visha-report

The only potential changes needed from my perspective are incorporating the Metabiota team in Table 1 and potentially adjusting the abstract if there is a word limit. I combed through all my messages, Mary's report guidance, and the contracts but could not find any info on abstract style. Please let us know if you need support with that piece.

Thanks and happy to address any questions,

David

On Wed, Aug 29, 2018 at 1:01 PM David J Wolking <djwolking@ucdavis.edu> wrote:

> Hey Falgu,
> Just a quick update, Liz had her baby boy REDACTED yesterday, both are doing great and recovering. Jonna and I are working to finalize the VISHA report and get it to you ASAP. Elizabeth Leasure (copied here) closed the VISHA account and the final financial report went out from our Sponsored Programs office to Metabiota today.

We'll be uploading the final report Word.doc to the same Box folder that the appendices are currently in.

Let us know if you have any questions,

David

On Thu, Aug 9, 2018 at 10:48 AM Falgunee K. Parekh <fparekh@metabiota.com> wrote:

> Thanks. I am starting to review all the materials, so great to have these. Thanks.
> Falgunee

Falgunee K. Parekh, MPH, PhD
Senior Scientist, Clinical Research and Epidemiology
Metabiota, Inc.
Tel: 301.676.1919 | Email: fparekh@metabiota | skype: REDACTED
metabiota.com

On Thu, Aug 9, 2018 at 12:44 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi Falgu,
> Just wanted you to know that we have also finalized the appendices for the VISHA final report and uploaded them to the Box folder. You can find them under the "VISHA Final Report (August 2018)" subfolder at this link: https://ucdavis.box.com/v/dtra-tanzania

We worked together to ensure all of the items requested by the DTRA team are captured here including the study SOPs, training record and evaluations, meeting agendas, outreach materials, posters, and presentations.

Best,

David

On Tue, Jul 31, 2018 at 9:58 AM Falgunee K. Parekh <fparekh@metabiota.com> wrote:

> Thanks Liz!

Falgunee K. Parekh, MPH, PhD
Senior Scientist, Clinical Research and Epidemiology
Metabiota, Inc.
Tel: 301.676.1919 | Email: fparekh@metabiota | skype: REDACTED
metabiota.com

On Tue, Jul 31, 2018 at 11:48 AM, Elizabeth VanWormer <liz.vanwormer@unl.edu> wrote:

> Hi Falgu,

We haven't added a new version to the Box folder as we wanted you to be able to read the original Table 1 and the sections where no edits were requested as soon as you were ready. We're in the midst of revisions on a new version, which will contain updates to all of the sections where Mary suggested edits or additions. However, for the earlier list that I sent you, the text hasn't changed from the April 20th version. Hope that helps! Please feel free to let me know if you have any other questions.

Have a great day,

Liz

From: Falgunee K. Parekh <fparekh@metabiota.com>
Sent: Tuesday, July 31, 2018 8:45:00 AM
To: Elizabeth VanWormer
Cc: Jonna Mazet; David Wolking; Brian Bird; Prof. Woutrina Smith; Hite, Karen
Subject: Re: TZ grants - checking in

Hi Liz and David,
For the VISHA report, is there a more updated version in Box besides the one dated April 20, 2018. I only see the April 20 version when I open the Box folder. Please let me know. Thanks.

Falgunee

Falgunee K. Parekh, MPH, PhD
Senior Scientist, Clinical Research and Epidemiology
Metabiota, Inc.
Tel: 301.676.1919 | Email: fparekh@metabiota | skype: REDACTED
metabiota.com

On Mon, Jul 23, 2018 at 2:36 PM, Elizabeth VanWormer <liz.vanwormer@unl.edu> wrote:

Hi Falgu,

Wonderful! I will keep you updated as we have more sections completed. I was still able to download the final report draft from the Box folder, but feel free to let us know if you have any challenges accessing it and David or I can refresh. Thanks for adding to the table for the MB oversight portion.

Have a great day,

Liz

From: Falgunee K. Parekh <fparekh@metabiota.com>
Sent: Monday, July 23, 2018 12:54:38 PM
To: Elizabeth VanWormer
Cc: Jonna Mazet; David Wolking; Brian Bird; Prof. Woutrina Smith; Hite, Karen
Subject: Re: TZ grants - checking in

HI Liz,

Thanks for the update. I'm happy to begin reviewing the sections for which there are no changes requested. Are they still in the Box folder? With regard to the table we can add in Metabiota portion for program oversight. Thanks again for the update and I will begin reviewing those sections this week. As you have other sections ready, please let me know and I will begin reviewing. Thanks.

Falgunee

Falgunee K. Parekh, MPH, PhD
Senior Scientist, Clinical Research and Epidemiology
Metabiota, Inc.
Tel: 301.676.1919 | Email: fparekh@metabiota | skype: REDACTED
metabiota.com

On Fri, Jul 20, 2018 at 9:53 AM, Elizabeth VanWormer <liz.vanwormer@unl.edu> wrote:

Hi Falgu,

I hope all is going well on the east coast! As Jonna mentioned, we are hard at work and on track for VISHA final report revisions. During our last group call, you suggested that it would be easier for you to review sections as they are completed. Although many sections are concurrently undergoing editing, there were several where Mary did not request any changes. I've included a list of those below in case you would like to start your review process with those sections (as they appear in the draft final report).

Mary also included the following comment on Table 1: "*Based on this table, Metabiota is not associated with the project, when it is, in fact, the prime contractor. Recommend updating to include Metabiota role, assuming Metabiota was involved in the management and oversight of the project as described in the SOW*". We didn't write out roles for Metabiota in the table in the draft report as we thought you would have a better perspective on the most appropriate descriptions per the contract with DTRA. Would you be able to add text for MB roles to include an updated table in the revised report?

Introduction

- No changes requested

CLINIC AND FIELD SITE CHARACTERIZATION (TASK 5)

- No changes requested

HUMAN SAMPLE ARCHIVE ASSESSMENT (TASK 6)

- No changes requested

HUMAN SURVEILLANCE (TASK 7)

- No changes requested

WILDLIFE (BAT AND NON-HUMAN PRIMATE) SURVEILLANCE (TASK 8)

- No changes requested

References
- No changes requested

Appendix A – Research permits
- No changes requested

Thanks and have a wonderful day and weekend,

Liz

From: [redacted] > on behalf of Jonna Mazet <jkmazet@ucdavis.edu>
Sent: Thursday, July 12, 2018 2:40:33 PM
To: Falgunee K. Parekh
Cc: David Wolking; Brian Bird; Prof. Woutrina Smith; Elizabeth VanWormer; Hite, Karen
Subject: Re: TZ grants - checking in

All on track for VISHA,
Jonna

On Thu, Jul 12, 2018 at 6:41 AM, Falgunee K. Parekh <fparekh@metabiota.com> wrote:

> Hi All,
> I just wanted to check in and see how everything is coming along with the final report for VISHA and the remaining work for R&B. Please let me know if you have any questions or concerns. Thanks.

Falgunee
Falgunee K. Parekh, MPH, PhD
Senior Scientist, Clinical Research and Epidemiology
Metabiota, Inc.
Tel: 301.676.1919 | Email: fparekh@metabiota | skype: REDACTED
metabiota.com

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: AOTR/Grant Manager Andrew Clements <aclements@usaid.gov>
Sent: 10/28/2018 3:56:33 AM
Subject: Re: PPE in DRC

Thanks,
J

On Sat, Oct 27, 2018 at 5:54 AM Andrew Clements <aclements@usaid.gov> wrote:
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: Andrew Clements <aclements@usaid.gov>
Date: October 27, 2018 at 1:53:32 PM GMT+1
To: jnumbi@usaid.gov, bhaberer@usaid.gov, Christopher Barrett <cbarrett@usaid.gov>, mmobula@usaid.gov
Cc: Angela Wang <awang@usaid.gov>, Dennis Carroll <dcarroll@usaid.gov>
Subject: PPE in DRC

Hi all,

PREDICT is still getting requests from INRB for PPE. Given that WHO has a stockpile and that PPE has been sent to DRC multiple times since the outbreak started, I'm not inclined to approve PREDICT providing any more (above the small amount they provided at the beginning of the outbreak).

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

From: Andrew Clements <aclements@usaid.gov>
To: Karen Saylors <ksaylors@metabiota.com>
CC: Jonna Mazet <jkmazet@ucdavis.edu>;Brian Bird <bhbird@ucdavis.edu>;PREDICTMGT <predictmgt@usaid.gov>
Sent: 10/29/2018 7:55:02 AM
Subject: Re: PPE in DRC

Hi Karen,

Sorry, must've missed this request. Do you have any more information on why this support is needed?

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: 1-571-345-4253
E-mail: aclements@usaid.gov

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

On Mon, Oct 29, 2018 at 3:42 PM Karen Saylors <ksaylors@metabiota.com> wrote:
Thanks Andrew for the clarification on the PPE. We will let INRB know that they need to request PPE directly from WHO from here on out.

One further question please regarding INRB's request a couple of weeks ago asking PREDICT to pay the cost of sending INRB lab technicians to the outbreak site for 3 weeks. I assume this is not within our purview, but we have not given INRB any response and they keep asking our team about it.

I know there was a recommendation to refer requests to the DART/OFDA focal point and we will continue to attempt to facilitate that introduction, but just hoping to close that loop directly with INRB.

Thanks very much,
Karen

On Oct 27, 2018, at 5:54 AM, Andrew Clements <aclements@usaid.gov> wrote:

FYI

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
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Begin forwarded message:

From: Andrew Clements <aclements@usaid.gov>
Date: October 27, 2018 at 1:53:32 PM GMT+1
To: jnumbi@usaid.gov, bhaberer@usaid.gov, Christopher Barrett <cbarrett@usaid.gov>, mmobula@usaid.gov

Cc: Angela Wang <awang@usaid.gov>, Dennis Carroll <dcarroll@usaid.gov>
Subject: PPE in DRC

Hi all,

PREDICT is still getting requests from INRB for PPE. Given that WHO has a stockpile and that PPE has been sent to DRC multiple times since the outbreak started, I'm not inclined to approve PREDICT providing any more (above the small amount they provided at the beginning of the outbreak).

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

From: Andrew Clements <aclements@usaid.gov>
Sent: Mon, 29 Oct 2018 10:04:04 -0700
Subject: Re: Ebola North Kivu DRC GoDRC requests
To: Brian Bird <bhbird@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Karen Saylors <ksaylors@metabiota.com>, [redacted], PREDICTMGT <predictmgt@usaid.gov>

Thanks, Brian and Karen.
I do remember this request. Since this is an internal DRC staffing issue, I think it's best to not use limited Predict funds for this.

I will let the Mission and OFDA know in case they want to fund it directly.

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 Oct 29, 2018, at 6:23 PM, Brian Bird <bhbird@ucdavis.edu> wrote:

> Hi Andrew,
>
> Following on from Karen's email just now… here's the request letter and email that I sent on once we had the official request letter and budgets etc.
>
> -b
>
> ---
>
> **From:** Brian Bird <bhbird@ucdavis.edu>
> **Date:** Tuesday, October 16, 2018 at 2:51 PM
> **To:** Andrew Clements <aclements@usaid.gov>
> **Cc:** [redacted], Jonna Mazet <jkmazet@ucdavis.edu>
> **Subject:** Ebola North Kivu DRC GoDRC requests
>
> Hi Andrew,
>
> As the outbreak continues to progress due to the tough security situation, we've received a request from INRB to support the deployment of 6 laboratory staff to the affected areas from Kinshasa for 21 days. These would not be PREDICT staff, and would have no relation to the PREDICT project per se. The proposed costs are quite high ($26,100 USD), and are well outside any readily available funds on hand to support such activities. I've attached the request letter and basic budget that we received from INRB here for your review. Personally, I don't see how this request falls within our PREDICT "outbreak framework", but perhaps you see differently?
>
> Also, today Karen fielded a call from USAID in DRC (Jean Felly) for 100 sets of PPE that the team turned over for use to INRB. Karen had travelled with additional 100 PPEs on her trip there, and the team donated them. It seems that the supplies of PPE on the ground are in very short supply? I understand that USAID had already given funds to WHO for large-scale PPE procurement, so I'm not sure what the logistical hang-up is that prevented those PPE from being available, but we did donate a small amount that was on hand following that direct request, apologies for not clearing that with you first.
>
> I've asked Karen to help understand why it is that PREDICT is getting asked for these items and this support rather than them tapping into the WHO supply chain etc. When I hear back I'll pass that information on to you.
>
> Let us know your thoughts on the staff support request, and how you want us to handle any additional PPE requests

that may come our way.

-b

Brian H. Bird DVM, MSPH, PhD
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

<Lettre Metabiota BeniOctobre2018[2].pdf>

<Budget_MVETERRAIN_INRB[2].xlsx>

From: Karen Saylors <ksaylors@metabiota.com>
Sent: Mon, 29 Oct 2018 10:11:21 -0700
Subject: Re: Ebola North Kivu DRC GoDRC requests
To: Andrew Clements <aclements@usaid.gov>
Cc: Brian Bird <bhbird@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, [redacted], PREDICTMGT <predictmgt@usaid.gov>

Thanks for the clarification Andrew.
I'll let INRB know to circle back with DART/OFDA and the Mission directly.

cheers,
Karen

On Mon, Oct 29, 2018 at 10:04 AM Andrew Clements <aclements@usaid.gov> wrote:

> Thanks, Brian and Karen.
> I do remember this request. Since this is an internal DRC staffing issue, I think it's best to not use limited Predict funds for this.

I will let the Mission and OFDA know in case they want to fund it directly.

Andrew

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Let us know your thoughts on the staff support request, and how you want us to handle any additional PPE requests that may come our way.

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Brian H. Bird DVM, MSPH, PhD

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

<Lettre Metabiota BeniOctobre2018[2].pdf>

<Budget_MVETERRAIN_INRB[2].xlsx>

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Sent: 11/7/2018 6:50:56 AM
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.

Improving effectiveness of early-warning human surveillance for Ebola outbreaks in DR Congo[1]

Problem: further shortening the time of initial detecting and reporting for Ebola outbreaks is limited by the lack of vigilance and understanding of spillover risk.

Proposed solution: improve effectiveness of early-warning human surveillance for Ebola outbreaks by focusing it on geographic areas and animal-human interfaces that have evidence of previous spillover of Ebola viruses to people.

Proposed work: (1) gather existing serosurvey data from human populations in DR Congo and (2) produce additional evidence on past and present exposure of people to Ebola viruses using existing samples.

Proposed activities:

1. *Consensus meeting*. Meet with in-country and international partners to brief them on the project and begin identifying previous serosurveys conducted and collections of human sera that could be tested for evidence of previous exposure to Ebola virus.
2. *Review and prioritize*. Conduct a desk review of all Ebola serosurveys conducted to date in DR Congo and compile a list of all banked samples (with metadata) from DR Congo that could be tested for presence of Ebola antibodies (separated by individual Ebola species). Prioritize existing serum samples (e.g. based on where there are gaps in data in terms of geography) for testing and make recommendations for where new samples should be collected to fill gaps in geographic locations and/or specific animal-human interfaces.
3. *Test*. Conduct additional serosurveys on prioritized banked samples.
4. *Report out*. Compile existing and new serosurvey results and conduct a final briefing for in-country and international partners on spillover risk at specific geographic locations and interfaces. Present recommendations for any adjustments to early-warning human surveillance for Ebola.

Estimated timeline: 18 months

Activity	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Consensus meeting																		
Review/prioritize																		
Test																		
Report out																		

Estimated cost:

Consensus meeting:	$ 20,000
Desk review/prioritization:	$ 20,000
Testing:	$240,000
Report out:	$ 20,000
Total	**$300,000**

[1] Study proposed for DR Congo since it has reported 10 Ebola outbreaks between 1976 and 2018. Gathering similar evidence from other countries such as Gabon (4 outbreaks), Republic of Congo (4 outbreaks), South Sudan (3 outbreaks), and Uganda (5 outbreaks) would provide these countries with information valuable for improving their early warning surveillance for Ebola outbreaks.

From: Jon Epstein <epstein@ecohealthalliance.org>
Sent: Wed, 14 Nov 2018 11:40:32 -0500
To: Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>
Cc: Ava Sullivan <sullivan@ecohealthalliance.org>, Evelyn Luciano <luciano@ecohealthalliance.org>, Molly Turner <turner@ecohealthalliance.org>, Predict inbox <predict@ucdavis.edu>
Subject: [predict] Re: Bangladesh: GHSA Workplan (PREDICT 2)

Corina,
We've completed the parts of the spreadsheet where Ariella asked for input.
We'll send this directly to her and copy you, PREDICT and Andrew.

Cheers,
Jon

On Tue, Nov 13, 2018 at 3:32 PM Corina Grigorescu Monagin <cgmonagin@ucdavis.edu> wrote:

HI Ava,

Checking in to see how this is progressing.

Regards,

corina

From: Ava Sullivan <sullivan@ecohealthalliance.org>
Date: Friday, November 9, 2018 at 4:25 AM
To: Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>, Molly Turner <turner@ecohealthalliance.org>, Jon Epstein <epstein@ecohealthalliance.org>, predict Sympa List <predict@ucdavis.edu>
Subject: Re: Bangladesh: GHSA Workplan (PREDICT 2)

Hi Corina,

Thanks for passing this on. I will make sure we address the comments and send a version back to you to send on to Andrew.

Thanks!

Ava

On Nov 8, 2018, at 5:58 PM, Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU> wrote:

Hi there,

Not sure who exactly this should go to but can you please review the below request from the Bangladesh Mission? They would like to see clarifications on the GHSA workplan. Please send to me as soon as possible – this fell through the cracks on our end so I'd like to give Andrew a response fairly quickly.

Thanks and let me know if you have any questions.

Regards,

Corina

---------- Forwarded message ---------
From: **Andrew Clements** <aclements@usaid.gov>
Date: Mon, Oct 22, 2018 at 4:11 AM
Subject: Fwd: Bangladesh: GHSA Workplan (PREDICT 2)
To: David J Wolking <djwolking@ucdavis.edu>
Cc: <predictmgt@usaid.gov>, Angela Wang <awang@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>

Hi David,

Can you or Arif provide the additional information requested?

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: 1-571-345-4253
E-mail: aclements@usaid.gov

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

---------- Forwarded message ---------
From: **Ariella Camera** <acamera@usaid.gov>
Date: Mon, Oct 22, 2018 at 12:19 PM
Subject: Bangladesh: GHSA Workplan (PREDICT 2)
To: Andrew Clements <aclements@usaid.gov>
Cc: Angela Wang <awang@usaid.gov>

Hi Andrew,

I need some additional support in finalizing the GHSA workplan with the PREDICT 2 activities for Bangladesh. I used what they submitted from the workplan but need additional clarification for both tabs (highlighted in yellow).

I was hoping this is something the AOR could help me with or check to see if PREDICT 2 could provide this information.

Any assistance would be much appreciated.

Thank you,

Ariella Camera

Deputy Director

Health Systems Strengthening Pillar

Office of Population, Health, Nutrition, and Education

USAID/Bangladesh

Tel: REDACTED

Cell: REDACTED

Email: acamera@usaid.gov

**Bangladesh is 10 hours ahead of Washington, D.C., and +6 GMT. Our work week is Sunday through Thursday.*

<Bangladesh - FY19 Interagency Workplan with instructions_AC.xlsx>

--

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)
REDACTED (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: Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
To: Jon Epstein <epstein@ecohealthalliance.org>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, David John Wolking <djwolking@ucdavis.edu>
Subject: Re: Action Required: Information on Bangladesh and Liberia
Sent: Tue, 27 Nov 2018 17:21:17 +0000

Hi Jon,

Thanks so much for the fast response. I'm available after 12 PST, just let me know a good time and I can call you.

C

From: Jon Epstein <epstein@ecohealthalliance.org>
Date: Tuesday, November 27, 2018 at 9:19 AM
To: Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, David Wolking <djwolking@ucdavis.edu>
Subject: Re: Action Required: Information on Bangladesh and Liberia

Hi Corina,
That sounds great. I think we could identify someone in both countries. It would be good to discuss this in more detail so I can understand the timing and specific objectives for the training. I'm available to speak by phone this afternoon, if that works for you.

In both Bangladesh and Liberia, via our country coordinators, PREDICT is very well positioned influence govt. on further inclusion of wildlife in One Health activities. In these two countries in particular, we've been strong advocates for the inclusion of wildlife departments and personnel.

In Bangladesh, wildlife is included in their national One Health strategy. The wildlife department (Forest Department) is a signatory along with IEDCR and the Department of Livestock Services. More workforce development is needed in terms of biological surveillance, but officers have participated in field activities with the PREDICT team and we've done training over the course of the project. PREDICT has had direct influence in the inclusion of wildlife in the national system, and our country coordinator, Ariful Islam has been at the table in government One Health meetings from the beginning.

In Liberia, PNR helped establish the official One Health platform, and PREDICT has been involved as well via regular participation in govt. run OH meetings and through our work with MOH. But the wildlife department (FDA) has new leadership that just began with the new government, and I'll have to ask Jim

about to what level they're engaged in govt. OH activities. Jim would be an ideal person to continue advocating for wildlife inclusion at the federal level. He is resident there, and has established a reputation as a local One Health professional among government colleagues. He also has a working relationship with the FDA as well as MOH and MOA through our PREDICT activities.

Cheers,
Jon

On Tue, Nov 27, 2018 at 11:58 AM Corina Grigorescu Monagin <cgmonagin@ucdavis.edu> wrote:

Hi Jon,

I've been tasked by Jonna to collect information on the possibility for extending limited activities in some of our countries. I'm reaching out to you as country lead in Bangladesh and Liberia. The limited activities that are being considered center on increasing capacity to analyze country data and incorporating wildlife into national planning and response strategies. I've listed several questions below that I would very much appreciate your input on. I'm happy to discuss by phone as well if you need more information. **I apologize but I need your responses fairly rapidly (Wednesday end of day would be great).**

- Can you identify an individual in-country that can be targeted for training in statistical analysis for risk assessments? This individual would need to be rapidly trained and then able to conduct the analysis themselves. This person should be on a career track to influence national government policy.
- What is the landscape in terms of wildlife inclusion in the national system and One Health platforms? Do you think PREDICT would have success encouraging increased incorporation of wildlife in the national system and are we well placed to do so? Could you identify someone in-country to lead this activity?

Thank you so much and please feel free to reach out to me if you need further info.

See you on Thursday!
Corina

--
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)
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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: Andrew Clements <aclements@usaid.gov>
Sent: Tue, 4 Dec 2018 12:15:03 -0800
Subject: Re: PREDICT-2 October 2018 Ebola Financial Report
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: Alisa Pereira <apereira@usaid.gov>, Amalhin Shek <ashek@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, David John Wolking <djwolking@ucdavis.edu>, predict Sympa List <predict@ucdavis.edu>, Hannah R Chale <hrchale@ucdavis.edu>

Thanks!
Great to see you as well.

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 4, 2018, at 7:16 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Andrew. Please find attached the Ebola Financial Report for October 2018. If you have any questions, please let me know. It was great to see you in New York!
>
> Thanks!
> Liz
>
> *Elizabeth Leasure*
> *Financial Operations Manager*
> *One Health Institute*
> REDACTED *(cell)*
> *530-754-9034 (office)*
> *Skype: ealeasure*
>
> <PREDICT Ebola Financial Report_Oct 2018_final.pdf>

Sent: Wed, 19 Dec 2018 09:45:28 -0800
Subject: Fwd: Invitation to One Health Emergency Meeting
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: "AOTR/Grant Manager Andrew Clements" <AClements@usaid.gov>, Alisa Pereira <apereira@usaid.gov>
Cc: Predict inbox <predict@ucdavis.edu>
Invitation Letter- One Health Emergency Meeting.pdf

Dear Andrew & Alisa,
See attachment & below, but super positively and optimistically surprised by the tone and content of this invite.
Have a good day,
Jonna

---------- Forwarded message ---------
From: **Brian Bird** <bhbird@ucdavis.edu>
Date: Wed, Dec 19, 2018 at 7:59 AM
Subject: Fwd: Invitation to One Health Emergency Meeting
To: Bridgette Phebean Smith <brpsmith@ucdavis.edu>, Brooke Genovese <bgenovese@ucdavis.edu>, David J Wolking <djwolking@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, Tracey Goldstein <tgoldstein@ucdavis.edu>, predict <predict@ucdavis.edu>

Well... if this invitation document isn't an endorsement of One Health by the GoSL (with our help) I'm not sure what that would look like. :)

There is an International Partners briefing today in about 30 mins. We did this too before for Bombali the day prior to the national announcement. This time, that's less important I think since most everyone is already on the inside of this one.

Finalized documents and things should be coming by mid-day today for sharing up into USAID and with our Liberia and Guinea folks as needed.

B

---------- Forwarded message ---------
From: **Bangura James J** <REDACTED>
Date: Wed, Dec 19, 2018 at 7:50 AM
Subject: Fwd: Invitation to One Health Emergency Meeting
To: Brian Bird <bhbird@ucdavis.edu>, Mercy Mwaura <REDACTED>

FYA

---------- Forwarded message ---------
From: **Patrick Lansana** <REDACTED>
Date: Wed, Dec 19, 2018 at 3:26 PM
Subject: Invitation to One Health Emergency Meeting
To: <REDACTED>, Francis Moses <REDACTED>, Augustine Jimissa <REDACTED>, Gerald Younge <REDACTED>, Samuel Massaquoi <REDACTED>, Francis Smart <REDACTED>, DMO Pujehun <REDACTED>, Prince Masuba <REDACTED>, Ronald Carshon-Marsh <REDACTED>, mohamedavandy <REDACTED>, James Squire <REDACTED>, desmond kangbai <REDACTED>, <REDACTED>, Sylvia Fasuluku <REDACTED>, Kwame Oniel <REDACTED>, Donald Grant <REDACTED>, James B Jongopie <REDACTED>, Mariama J.S. Murray <REDACTED>, <REDACTED>, Brima Osaio Kamara <REDACTED>, Musa D Sheriff <REDACTED>, AMARA STEVENS NGEGBAI <REDACTED>, <REDACTED>

[redacted], Monica Dea <mdea@usaid.gov>, Amara LENO [redacted], William Bangura [redacted], Haja Lydia Sesay [redacted], alusine kamara [redacted], Charles Keimbe [redacted], Doris Harding [redacted], Isatta Wurie [redacted], Onome Thomas AbiriPBSL [redacted], Ansumana Sillah [redacted], Sinneh Mansaray [redacted], Tseggai, Tesfai (TCE) [redacted], Robert [redacted], Wilson Gachari [redacted], [redacted], Claudette [redacted], BAGONZAJames [redacted], MelvinkuliConteh <melvinkuliconteh Brima Samai [redacted], Dorothy Peprah (dpeprah@usaid.gov) <dpeprah@usaid.gov> [redacted], Bangura James J [redacted], Melvinkuli Conteh [redacted]

Dear All,
The MoHS Directorate of Health Security and Emergency is inviting you to attend a One Health Emergency meeting.

Date : Tomorrow 20th December, 2018
Venue: Kona Lodge
Time: 10:00 a.m

Looking forward to your usual cooperation

This messages is sent on behalf Dr. Mohamed A. Vandi, Director Health Security and Emergencies,MoHS.

Best wishes,

Patrick Lansana
Information Officer & Media Analyst
Ministry of Health and Sanitation - GoSL
Directorate of Health Security and Emergencies (DHSE)
Public Health National Emergency Operation Center
Communication Department
Ema
Mob [redacted]
Alt:
--
Brian Bird, UC Davis, sent from mobile device

GOVERNMENT OF SIERRA LEONE

MINISTRY OF HEALTH AND SANITATION

DIRECTORATE OF HEALTH SECURITY AND EMERGENCIES

EOC COCKERIL WILKINSON ROAD, FREETOWN

Date: 19th December ,2018

Dear Sir,

Subject: Invitation to a One Health Emergency Meeting

Based on lesson learnt during the EVD outbreak, Sierra Leone embraced the One Health Concept as being the most suitable approach to prepare and respond to outbreaks zoonotic diseases and other emerging Pandemic threat diseases. Significant strides have been made with establishment of a One Health Platform and a One Health Secretariat.

The government, through the Directorate of Health Security and Emergencies and the One Health Secretariat kindly request you to attend this event in recognition of your strategic importance for sustaining One Health activities in Sierra Leone.
Thanking you in anticipation of your continued support towards the health sector.

Date: Thursday 20th December 2018

Venue: Kona Lodge

Time: 10:00 a.m.

Yours sincerely,

DIRECTORATE OF HEALTH SECURITY

19/12/18

Mohamed A. Vandi
DIRECTOR HEALTH SECURITY AND EMERGENCIES

Cc: **Dr Amara Jambai- Chief Medical Officer**

Dr Thomas T. Samba – Deputy Chief Medical Officer

From: Andrew Clements <aclements@usaid.gov>
Sent: Wed, 19 Dec 2018 10:51:14 -0800
Subject: Re: Invitation to One Health Emergency Meeting
To: Jonna Mazet <jkmazet@ucdavis.edu>
Cc: Alisa Pereira <apereira@usaid.gov>, Predict inbox <predict@ucdavis.edu>

Very nice!

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 19, 2018, at 6:45 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> Dear Andrew & Alisa,
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Date: Wed, Dec 19, 2018 at 7:50 AM
Subject: Fwd: Invitation to One Health Emergency Meeting
To: Brian Bird <bhbird@ucdavis.edu>, Mercy Mwaura <REDACTED

FYA

---------- Forwarded message ---------

From: **Patrick Lansana** <[redacted]>
Date: Wed, Dec 19, 2018 at 3:26 PM
Subject: Invitation to One Health Emergency Meeting
To: [redacted], Francis Moses <[redacted]>, Augustine Jimissa <[redacted]>, Gerald Younge [redacted], Samuel Massaquoi [redacted], Francis Smart [redacted], DMO Pujehun [redacted], Prince Masuba [redacted], Ronald Carshon-Marsh [redacted], James Squire [redacted], desmond kangbai [redacted], Sylvia Fasuluku [redacted], Kwame Oniel [redacted], Donald Grant [redacted], James B Jongopie [redacted], Mariama J.S. Murray [redacted], Brima Osaio Kamara [redacted], Musa D Sheriff [redacted], AMARA STEVENS NGEGBAI [redacted], [redacted], Monica Dea <mdea@usaid.gov>, Amara LENO [redacted], William Bangura [redacted], Haja Lydia Sesay [redacted], alusine kamara [redacted], Charles Keimbe [redacted], Doris Harding [redacted], Onome Thomas AbiriPBSL [redacted], Ansumana Sillah [redacted], Sinneh Mansaray [redacted], Tseggai, Tesfai (TCE) [redacted], Robert [redacted], Wilson Gachari [redacted], Claudette [redacted] BAGONZAJames [redacted], MelvinkuliConteh <melvinkuliconteh,Brima Samai [redacted], Dorothy Peprah (dpeprah@usaid.gov) <dpeprah@usaid.gov>, [redacted], [redacted] Bangura James J [redacted], Melvinkuli Conteh [redacted]

Dear All,
The MoHS Directorate of Health Security and Emergency is inviting you to attend a One Health Emergency meeting.

Date : Tomorrow 20th December, 2018
Venue: Kona Lodge
Time: 10:00 a.m

Looking forward to your usual cooperation

This messages is sent on behalf Dr. Mohamed A. Vandi, Director Health Security and Emergencies,MoHS.

Best wishes,

Patrick Lansana
Information Officer & Media Analyst
Ministry of Health and Sanitation - GoSL
Directorate of Health Security and Emergencies (DHSE)
Public Health National Emergency Operation Center
Communication Department
Email: [redacted]
Mobile: [redacted]
Alt: [redacted]
--
Brian Bird, UC Davis, sent from mobile device

<Invitation Letter- One Health Emergency Meeting.pdf>

From: Brian Bird <bhbird@ucdavis.edu>
Sent: Fri, 8 Feb 2019 05:50:08 -0500
To: Andrew Tobiason <atobiason@usaid.gov>
Cc: David J Wolking <djwolking@ucdavis.edu>, Jon Epstein <epstein@ecohealthalliance.org>, predict <predict@ucdavis.edu>
Subject: [predict] Re: Ebola Host Project presentation

Hi Andy,

Thanks for listening in, and I hope the talk was informative and fun. I agree I t would be wonderful to get more use of the "bat book" across projects and sectors.

I've cc'd David Wolking of our global operations team here for his awareness and assistance with followup if needed.

Happy to chat more about the book, and I'd be very interested to hear more about what is happening on the conservation side of things from you perspective.

All the best,

-Brian

On Thu, Feb 7, 2019 at 5:37 PM Jon Epstein <epstein@ecohealthalliance.org> wrote:

> Andy,
> That's fantastic, we'd be happy to share this resource and talk to you about other opportunities to make use of PREDICT products. I think you mentioned already having downloaded the book from UCD? if not, it's available through the PREDICT website at UC Davis. In any case, let's find a time to discuss some of these ideas sooner.

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) REDACTED
@epsteinjon

On Thu, Feb 7, 2019, 4:52 PM Andrew Tobiason <atobiason@usaid.gov> wrote:

> Hi Brian and Jonathan,
>
> I just joined your presentation remotely, asked the question about sharing your comms materials with conservation partners in the region. USAID's FIFES partnership with ACDI-VOCA, supporting community forest management in the Nimba area, is one obvious project. Our partners in Central Africas (such as familiar WCS and others like African Parks Network) might also take advantage of things like "Living Safely with Bats" if it were narrated in Lingala, Swahili, etc. And also coordinate on any relevant animal sampling they do. Could all be considered part of the "sustainability" plan for PREDICT, i.e. continuing awareness, readiness and (to a lesser degree) surveillance.
>
> Thanks for sharing the results of this cool work, please let me know if you'd like to discuss using USAID's conservation partnerships to extend the PREDICT2 legacy.
>
> Andy

Andrew Tobiason
Biodiversity Conservation Advisor
USAID | E3 Bureau | Office of Forestry and Biodiversity
atobiason@usaid.gov | +1 (202) 712-0035 | usaid.gov/biodiversity
Room 7.011, 1717 Pennsylvania Ave NW, Washington, DC 20523

Conservation is not rocket science - it's harder! Tools and evidence are available:
USAID's Conservation Effectiveness, Integration and Legality Resources

--

Brian Bird, UC Davis, sent from mobile device

From: Amalhin Shek <ashek@usaid.gov>
Sent: Fri, 8 Feb 2019 13:16:21 -0500
To: David J Wolking <djwolking@ucdavis.edu>
Cc: PREDICTMGT <predictmgt@usaid.gov>, "Clements, Andrew (GH/HIDN)" <AClements@usaid.gov>, Alisa Pereira Emerging Threats Division <apereira@usaid.gov>, "predict@ucdavis.edu" <predict@ucdavis.edu>, "Cara J. Chrisman" <cchrisman@usaid.gov>
Subject: [predict] Re: Ebola Host Project presentation

Wonderful!

Thanks so much, David. I think one of the subteams here had a call with Andy's FAB folks earlier this week, so please let us know if any additional follow up is needed.

Best,

Amalhin Shek | Budget & Communications Analyst
Bureau for Global Health, Office of Infectious Disease, Emerging Threats Division
Phone: 571-551-7102(o) REDACTED (c) | CP3 8092
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USAID-HECFAA, VP of Community Engagement

USAID **Contractor**
GHSI-III - Social Solutions International, Inc.

On Fri, Feb 8, 2019 at 12:36 PM David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi Andrew and Alisa,
> Just sharing this thread from Andrew Tobiason who listened to the EHP talk this week in DC. I'll be sure to keep you in the loop going forward as it would be great to see some of our resources compliment the work of other bureaus and projects.

David

---------- Forwarded message ---------
From: **Brian Bird** <bhbird@ucdavis.edu>
Date: Fri, Feb 8, 2019 at 2:50 AM
Subject: Re: Ebola Host Project presentation
To: Andrew Tobiason <atobiason@usaid.gov>
Cc: David J Wolking <djwolking@ucdavis.edu>, Jon Epstein <epstein@ecohealthalliance.org>, predict <predict@ucdavis.edu>

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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) REDACTED
@epsteinjon

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Thanks for sharing the results of this cool work, please let me know if you'd like to discuss using USAID's conservation partnerships to extend the PREDICT2 legacy.

Andy

Andrew Tobiason
Biodiversity Conservation Advisor
USAID | E3 Bureau | Office of Forestry and Biodiversity
atobiason@usaid.gov | +1 (202) 712-0035 | usaid.gov/biodiversity
Room 7.011, 1717 Pennsylvania Ave NW, Washington, DC 20523

Conservation is not rocket science - it's harder! Tools and evidence are available:
USAID's Conservation Effectiveness, Integration and Legality Resources

--
Brian Bird, UC Davis, sent from mobile device

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Dennis Carroll <dcarroll@usaid.gov>, Ben Oppenheim <boppenheim@metabiota.com>
Cc: Cara Chrisman <cchrisman@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, [redacted], "Dean.Jamison@ucsf.edu" <Dean.Jamison@ucsf.edu>, Dean Jamison <djamison@uw.edu>, Eddy Rubin <[redacted], Carlos Zambrana-Torrelio <zambrana@ecohealthalliance.org>, Nita Madhav <nmadhav@metabiota.com>, "Yasha Feferholtz" <feferholtz@ecohealthalliance.org>, Karen Saylors <ksaylors@metabiota.com>, Samtha Maher <maher@ecohealthalliance.org>
Subject: RE: Agenda for the meeting on March 13th
Sent: Tue, 12 Mar 2019 15:28:40 +0000

Samantha – please book one of our conference lines for the day and send the number and passcode to Dennis.

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: Dennis Carroll [mailto:dcarroll@usaid.gov]
Sent: Tuesday, March 12, 2019 12:41 AM
To: Ben Oppenheim
Cc: Cara Chrisman; Jonna Mazet; Eri Togami; Dean.Jamison@ucsf.edu; Peter Daszak; Dean Jamison; Eddy Rubin; Carlos Zambrana-Torrelio; Nita Madhav; Yasha Feferholtz; Karen Saylors; Samtha Maher
Subject: Re: Agenda for the meeting on March 13th

Ben, is there a call in number that would allow me to join from Rome?

Thanks

dennis

Dr Dennis Carroll
Director
Emerging Threats
Global Health
USAID
301-646-6235
On Mar 8, 2019, at 6:42 PM, Ben Oppenheim <boppenheim@metabiota.com> wrote:

> Dear all,
>
> Please find a revised agenda attached here.

Two changes to note:

- We would start with the EHA ROI at 11am, welcoming anyone who can start early. I've allotted 75 minutes to the first session, so we have time for a brief intro before getting into the discussion. Then at 12:15 (allowing Jonna and Cara a little wiggle room), we move into lunch and the GVP overview.
- It has also been pointed out that we have no breaks in the schedule, so a brief 15 minute break is now also included. This gives us 1:30-4pm for the BCA discussion, which is the original time we had allotted.

Kindly let me know if you have any additional considerations or concerns.
Once the agenda is finalized, we can alert the advisors and distribute the reading materials. Again, we request your input here on any additional papers or background materials that ought to be disseminated

all the best,
Ben

On Fri, Mar 8, 2019 at 8:37 AM Ben Oppenheim <boppenheim@metabiota.com> wrote:
Dear Jonna and Cara,
Thank you very much for alerting us.
Jonna, your suggestion sounds great: let's start at 11 with Yasha and Carlos' analysis, then at noon an informal lunch and discussion of GVP's goals and design. Then on to the BCA.

All: please let me know if you have any further considerations, and I'll circulate an updated schedule later today.

all the best,
Ben

On Fri, Mar 8, 2019 at 5:29 AM Cara Chrisman <cchrisman@usaid.gov> wrote:
Hi All,

I'm a similar boat as Jonna, in a meeting before this one that goes until 12pm.

Best,
Cara

Sent from my iPhone
On Mar 7, 2019, at 11:51 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> I'm afraid that I have another meeting until noon, but I can try to join as early as possible. If you are starting earlier than planned, perhaps you can start with Yasha and Carlos, as I'm more likely to be in synch with their materials. If reverting back to the agenda developed by the organizers, see you at noon.
> Sorry that I can't likely join early,
> Jonna
>
> On Thu, Mar 7, 2019 at 5:15 PM Ben Oppenheim <boppenheim@metabiota.com> wrote:
> Dear Jonna, [redacted] Peter, and Sam,
>
> There are a few different email threads going regarding the agenda for our upcoming advisory panel workshop, and so I've consolidated the various comments and inputs here (including prior edits by Jonna and [redacted] thank you both very much).
>
> We very much welcome Peter's suggestion to focus some of the workshop on Carlos and

Yasha's work on GVP's ROI. The agenda was already rather packed, so we've proposed starting earlier at 11am to ensure we have enough time to properly cover all of the content (note: we will of course need to alert the external advisors, so they can plan accordingly). We've also been corresponding with Yasha about finding time for a more intensive discussion on EHA's ROI work later in the week.

There are 4 sessions, each devoted primarily to stimulating conversation and harvesting feedback from the group:
1. Presentation of GVP's aims and design parameters, to ensure that the external advisors are up to speed on the project
2. Review of EHA analytical work on GVP's ROI: methodology, findings, lessons learned
3. Review of BCA proposed methodology: modeling GVP's impacts via exceedance probability functions and economic impact estimation
4. Open questions, closing reflections, next steps

We've included a list of participants and institutions, along with scientific papers that we'd like to disseminate (particularly to the externals) before the meeting. Please review, and let us know if there are names we are missing and/or additional papers that ought to be included here.

all the best,
Ben

On Tue, Mar 5, 2019 at 8:50 PM REDACTED > wrote:

Hi Peter,

Thank you for checking in about the status of the meeting. The meeting will still take place as planned, and Ben is currently finalizing the agenda. I have copied him in this chain so that he can reflect your suggestions to the draft agenda. I am looking forward to seeing everyone next week.
Best,
REDACTED

From: Peter Daszak [mailto:daszak@ecohealthalliance.org]
Sent: Tuesday, March 05, 2019 2:37 PM
To: REDACTED >; Jonna Mazet <jkmazet@ucdavis.edu>; Carlos Zambrana-Torrelio <zambrana@ecohealthalliance.org>; Yasha Feferholtz <feferholtz@ecohealthalliance.org>
Cc: Dean.Jamison@ucsf.edu; Cara Chrisman <cchrisman@usaid.gov>
Subject: Agenda for the meeting on March 13th
Importance: High

Dear REDACTED Jonna, Dean,

I just want to check if this meeting still on, given that Dennis will be out of the country.

If so, it would be good to nail down an agenda.

I'd like to propose that we start off the day with 1) Summary of GVP progress to date (Jonna/Peter); 2) Report from us here at EHA on the analysis for the GVP targeted sampling and the ROI analysis we completed earlier (Carlos/Yasha/Samantha). This will give a good basis from which you, Dean, can then report back on progress to date on your more detailed analysis of ROI.

After that, we can get into the details of what the next steps are for your work and future plans from our side.

Look forward to talking and hopefully seeing you here in NYC.

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

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--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

REDACTED

--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

REDACTED

--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

REDACTED
<Global Virome Advisory Panel meeting DRAFT revised 03.08.19.docx>

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:	3/24/2019 3:38:42 AM
Subject:	Re: PREDICT Group ITA: Semi-Annual Meeting (Vancouver)

Approved.

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 22, 2019, at 5:19 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Hi Andrew. Please find below a group international travel request for the PREDICT Semi-Annual meeting for your review and approval. Please let me know if you have any questions or require clarification. Thanks!

Estimated Travel Costs
See individuals listed on the attached spreadsheet

Meals & Incidentals, Lodging:
The per diem maximum established by the Department of State for Vancouver, Canada is $306 ($179 lodging, $127 M&IE).

Travel Request:
PREDICT-2 requests approval for the individuals listed in the attached spreadsheet to travel from their respective departure locations to Vancouver, Canada to participate in the PREDICT Semi-Annual Meeting to be held April 30 to May 1.

Trip purpose: Strategic planning for successful wind down and closeout of the PREDICT-2 award; meeting deliverables and planning risk communication campaigns for host country partners; final report planning.

--
Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
530-752-7526

--

From: Molly Turner <turner@ecohealthalliance.org>
Sent: Thu, 18 Apr 2019 16:05:52 -0400
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: Hannah R Chale <hrchale@ucdavis.edu>, Evelyn Luciano <luciano@ecohealthalliance.org>, predict Sympa List <predict@ucdavis.edu>
Subject: [predict] Re: Cost share certification from EHA

Thank you!!

On Thu, Apr 18, 2019 at 1:27 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Thanks! Looks good. I'll send on to Jonna for PI approval, then to Andrew.
>
> *Elizabeth Leasure*
>
> *Financial Operations Manager*
>
> *One Health Institute*
>
> REDACTED *(cell)*
>
> *530-754-9034 (office)*
>
> *Skype: ealeasure*
>
> **From:** Molly Turner <turner@ecohealthalliance.org>
> **Sent:** Thursday, April 18, 2019 9:29 AM
> **To:** Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
> **Cc:** Hannah R Chale <hrchale@UCDAVIS.EDU>; Evelyn Luciano <luciano@ecohealthalliance.org>; predict Sympa List <predict@ucdavis.edu>
> **Subject:** Re: Cost share certification from EHA
>
> Just a small change in the attached to the language for year 5 for Thailand for consistency.
>
> On Thu, Apr 18, 2019 at 12:26 PM Molly Turner <turner@ecohealthalliance.org> wrote:
>
> > You mean our overall commitment, including contributions from our partners? If so, I went ahead and did so in my last email :)
> >
> > On Thu, Apr 18, 2019 at 12:23 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:
> >
> > > Hi Molly. After giving it some thought last night, I think we should reduce the EHA portion of the revised Y5 commitment so that the net change is zero. Getting Andrew's approval for cost share revisions is more about the type of cost share being committed, not so much the exact amount (in my mind at least), so you could still certify the full revised Y5 figure for EHA personnel time plus waived IDC as long as the type of cost share is consistent with the revision that is (hopefully) approved by Andrew. I just worry that if you increase your commitment through this revision and then something falls through with your in-country partners, you'll end up in a pickle. Thoughts?

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *(cell)*

530-754-9034 (office)

Skype: ealeasure

From: Molly Turner <turner@ecohealthalliance.org>
Sent: Thursday, April 18, 2019 8:49 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Hannah R Chale <hrchale@UCDAVIS.EDU>; Evelyn Luciano <luciano@ecohealthalliance.org>; predict Sympa List <predict@ucdavis.edu>
Subject: Re: Cost share certification from EHA

Hey Liz,

I think that's right --both Chulalongkorn and Human Link were both eager to share with us the difference between the actual costs of project implementation and the amount the project is able to fund directly, and I thought it might not be a bad idea to plan to over-shoot our commitment in case something fell through. I can reduce somewhere if you like but all these amounts are currently contractually obligated, so we'll have actually "cost-shared" the higher amount.

Thanks,

Molly

On Wed, Apr 17, 2019 at 6:19 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi again. I made some minor changes to the spreadsheet to help Andrew review it as quickly as possible, and I found that the Revised Y5 amount was not pulling directly from the detailed breakdown of the requested revised Y5 cost share (cell G77). I revised this and noted that the detailed breakout of revised cost share amounts totals $1,177,304.
>
> We can submit the spreadsheet as it is attached and increase your overall commitment by $40,457, or you can revise the Year 5 revised cost share detailed section so that the total Revised Y5 figure is $306,795, which would not increase or decrease your overall commitment of $1,136,846. Please let me know how you would like to proceed.
>
> Thanks,
>
> Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *(cell)*

530-754-9034 (office)

Skype: ealeasure

From: Elizabeth Leasure
Sent: Wednesday, April 17, 2019 3:08 PM
To: Molly Turner <turner@ecohealthalliance.org>; Hannah R Chale <hrchale@ucdavis.edu>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>
Subject: RE: Cost share certification from EHA

Hi Molly. In reviewing, there were a couple questions that came up. Please see below.

- **Year 3 (Bangladesh), icddr,b:** Can you clarify if the $19K for the RT-PCR machine cost share is for the purchase of a new machine or the monetary value of the project's use of icddr,b's machine? Please also clarify how you calculated the value of the contribution to the project.
- **Multiple years, (Egypt), Human Link:** Can you please clarify how you calculated the monetary value of the equipment use and depreciation contribution to the project?
- **Multiple years, (Thailand), Chulalongkorn:** Can you please clarify how you calculated the monetary value of the equipment use contribution to the project?

Thanks,

Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *(cell)*

530-754-9034 (office)

Skype: ealeasure

From: Elizabeth Leasure
Sent: Wednesday, April 17, 2019 2:22 PM

To: Molly Turner <turner@ecohealthalliance.org>; Hannah R Chale <hrchale@ucdavis.edu>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>
Subject: RE: Cost share certification from EHA

Reviewing now…

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *(cell)*

530-754-9034 (office)

Skype: ealeasure

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Sent: Wednesday, April 17, 2019 10:53 AM
To: Hannah R Chale <hrchale@UCDAVIS.EDU>; Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>
Subject: Cost share certification from EHA

Hi ladies,

Attached, sorry for the delay. I'm sorry to nag, but any update on Andrew's approval for our revised cost share plan?

Thanks,

Molly

--

Molly Turner

PREDICT Operations Manager for EHA

EcoHealth Alliance Operations

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

1.212.380.4461 (office)

REDACTED (mobile)
www.ecohealthalliance.org

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--

Molly Turner

PREDICT Operations Manager for EHA

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Molly Turner

PREDICT Operations Manager for EHA

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Molly Turner

PREDICT Operations Manager for EHA

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Molly Turner
PREDICT Operations Manager for EHA
EcoHealth Alliance Operations

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From: Andrew Clements <aclements@usaid.gov>
Sent: Wed, 22 May 2019 10:11:48 +0200
Subject: Re: PREDICT International Travel Requests
To: Katherine Leasure <kaleasure@ucdavis.edu>
Cc: PREDICTMGT <predictmgt@usaid.gov>, Predict inbox <predict@ucdavis.edu>, Jonna Mazet <Jkmazet@ucdavis.edu>

Travel to the USA approved.

Travel to Tanzania approved subject to mission concurrence.

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/ept2

On Wed, May 22, 2019 at 1:39 AM Katherine Leasure <kaleasure@ucdavis.edu> wrote:

> Hi Andrew. I just wanted to follow-up to see if you need any further information regarding the below travel requests, as I haven't yet seen a response. Thank you!

On Thu, May 16, 2019 at 4:51 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. Aung (USA): $1500 airfare/$196 (Davis) max daily per diem
> 2. Kamau (USA): $1420 airfare/$196 (Davis) max daily per diem
> 3. Hussein (USA): $1500 airfare/$196 (Davis) max daily per diem
> 4. Mazet (Tanzania): $$8300 airfare **business class required due to* REDACTED /$309 (Dar es Salaam), $157 (Other) max daily per diems
>
> Travel Requests –
>
> 1. The Smithsonian Institution would like to request travel approval for Dr. Ohnmar Aung to travel from Yangon, Myanmar to Davis, California, USA for the period of June 3-14, 2019 to participate in the PREDICT Data Conference.
>
> **Trip Purpose:** Dr. Aung will represent the Smithsonian PREDICT-2 team at the conference. She will be attending all planned sessions for the duration of the conference.
>
> 2. The Smithsonian Institution would like to request travel approval for Mr. Joseph Kamau to travel from Nairobi, Kenya to Davis, California, USA for the period of June 4-22, 2019 to participate in the PREDICT Data Conference, and for additional serology laboratory training following the conference.
>
> **Trip Purpose:** Mr. Kamau will represent the Smithsonian PREDICT-2 team at the conference. He will be attending all planned sessions for the duration of the conference. He will also have additional serology laboratory training after the conference.
>
> 3. The Smithsonian Institution would like to request travel approval for Ms. Fatima Hussein to travel from Nairobi, Kenya to Davis, California, USA for the period of June 4-14, 2019 to participate in the PREDICT Data Conference
>
> **Trip Purpose:** Ms. Hussein will represent the Smithsonian PREDICT-2 team at the conference. She will be attending all planned sessions for the duration of the conference.
>
> 4. UC Davis would like to request travel approval for Dr. Jonna Mazet to travel from Davis, California, USA to Dar es Salaam, Tanzania from July 10-21, 2019 to meet with the PREDICT-2 Tanzania team for project oversight and successful completion of close out procedures.

Trip purpose: Dr. Mazet, Director of the PREDICT project, will travel to Dar es Salaam, Mafia Island, and Ruaha communities in Tanzania to meet with the PREDICT-2 Tanzania team and collaborate on an implementation strategy for community data dissemination. Dr. Mazet will also meet with PREDICT's implementing partners at Sokoine University of Agriculture (SUA) and other host country partners, to be determined. This trip will also serve as an opportunity for Dr. Mazet to plan and coordinate with the in-country team and partners on budgets for Year 5 closeout, as well as participate in the final capacity strengthening program for PREDICT-Tanzania and associated in-country staff scientists.

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Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
530-752-7526

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Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
530-752-7526

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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:	5/22/2019 1:32:22 AM
Subject:	Re: PREDICT International Travel Requests

ROC travel approved subject to mission concurrence.

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/ept2

On Wed, May 22, 2019 at 1:31 AM Katherine Leasure <kaleasure@ucdavis.edu> wrote:
Hi Andrew. I just wanted to follow-up to see if you received the information needed regarding the RoC travel? Please let me know if there is anything I can do to facilitate. Thanks!

On Wed, May 15, 2019 at 4:07 PM Katherine Leasure <kaleasure@ucdavis.edu> wrote:
Thanks, Andrew. It sounds like you've already reached out to EHA for more information, but please let me know if there's anything I can do to facilitate.

On Wed, May 15, 2019 at 2:21 AM Andrew Clements <aclements@usaid.gov> wrote:
CIV travel approved subject to mission concurrence.

I'm asking for additional information on ROC before approving.

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 14, 2019, at 10:05 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. Laudisoit (RoC, CIV): $120 boat crossing, $1290 airfare/$376 (Brazzaville), $344 (Abidjan) max daily per diems
2. Desmond (CIV): $500 airfare/$344 (Abidjan) max daily per diem
3. Poultolnor, Samuels, Arku, Kollie, Sackie, Harris, Larmouth, Bonason, Brown, Ross (CIV): team will drive from Monrovia to CIV, estimated cost of $600 total/$344 (Abidjan) max daily per diem
**trainee's estimate a daily per diem actual cost of $60/day while in the field*

Travel Requests –

1. EcoHealth Alliance would like to request travel approval for Dr. Anne Laudisoit to travel from Kinshasa, DRC, to Brazzaville, Republic of Congo from June 1-5, 2019 for official visits and meetings. From Brazzaville, Republic of Congo, she will travel to Abidjan, Cote d'Ivoire for from June 6-25, 2019 for meetings and trainings. **Dr. Laudisoit's origin city is Kinshasa, where she will be traveling on non-PREDICT business. From Abidjan, Cote d'Ivoire she will return to Brussels, Belgium.*

Trip purpose: RoC – As Country Liaison to RoC, Dr. Laudisoit will visit Brazzaville from June 1-5 to finalize the installation and outfitting of the PREDICT laboratory to ensure capacity for viral screening by the end of P2Y5. She will meet with the PREDICT RoC team at the Public Health Lab (LNSP) in Brazzaville. She will organize a joint meeting with the Director of Parks and Reserves, and the POC for Nagoya and CITES to arrange sample transfer from Kinshasa to Brazzaville and work on viral PREDICT results publications. CIV - As Country Liaison to CIV, Dr. Laudisoit will, with Liberia Country Coordinator Dr. Jim Desmond, conduct a joint training in wildlife surveillance sampling in the region with One Health representatives (DSV, DFRC, FAO, Zoo staff and OIPR). A team-building workshop, a theoretical training on non-invasive sampling techniques, and a practical training in Banco forest is planned between the PREDICT CIV and Liberia teams. This training is programmed in P2Y5 workplan, solicited by the Ministry of Water and Forestry (DFRC) and the Ivorian Parks and Reserves Office (OIPR). Dr. Laudisoit will be in CIV June 6-25 with the training planned for June 10-21.

2. EcoHealth Alliance would like to request travel approval for James Desmond to travel from Monrovia, Liberia to Abidjan, Cote d'Ivoire from June 7-13, 2019 to organize and conduct a joint training between the PREDICT Cote d'Ivoire team with members of the PREDICT Liberia team.

Trip Purpose: Dr. Desmond will conduct a joint training in wildlife surveillance sampling in the region. A team-building workshop, a theoretical training on non-invasive sampling techniques, and a practical training in Banco forest is planned between the PREDICT CIV and Liberia teams. The Liberia team, with their extensive experience in the field, will be able to instruct the Cote D'Ivoire team on safe bat capture and handling, sample collection and cold chain.

3. EcoHealth Alliance would like to request travel approval for **the below list of travelers*** to travel from Monrovia, Liberia to Abidjan, Cote d'Ivoire from June 9-22, 2019 to conduct a joint training between the PREDICT Cote d'Ivoire team with members of the PREDICT Liberia team.

Trip Purpose: This training is meant to be a regional capacity strengthening wildlife surveillance training between CIV and Liberia PREDICT teams. PREDICT Liberia serves as an experienced and well-trained team that can help share best practices and protocols with the newer CIV team. A team-building workshop, a theoretical training on non-invasive sampling techniques, and a practical training in Banco forest is planned between the PREDICT CIV and Liberia teams.

***PREDICT Liberia Team:** Jackson Poultolnor - Field Team lead; Sandra Samuels - Research technician; Jallah Arku – Research technician; Amos Kollie – Research technician; Melkor Sackie – Research technician; Daniel Harris – Research technician; Emmauel Larmouth – Research technician; Margret Bonason – Research technician; Joseph Brown – Driver; Albert Ross – Driver*

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Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
530-752-7526

Sent: Thu, 6 Jun 2019 09:20:59 -0700
Subject: Re: WOHC20 scientific programme committee meeting Friday June 7: meeting papers and dial-in details
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Christel Smeys [redacted]
Cc: Albert Osterhaus [redacted], John Mackenzie [redacted], Professor Martyn Jeggo [redacted], Wang Linfa [redacted], "Dr. Ottorino Cosivi" <cosivio@paho.org>, Mark Bronsvoort [redacted], MARK RWEYEMAMU <mark.rweyemamu@btinternet.com>, Marietjie Venter [redacted], Penina Munyua <ikg2@cdc.gov>, Rebecca Katz <rk952@georgetown.edu>, Larry Madoff [redacted], Bernadette Ramirez <[redacted]>, Tracey McNamara <tmcnamara@westernu.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>, Julie Fitzpatrick [redacted], Pip Beard <pip.beard@pirbright.ac.uk>, Joanne Sharp [redacted], Simon Girling [redacted], Grant Stentiford [redacted], Delia Grace <D.GRACE@cgiar.org>, [redacted], Chris Vanlangendonck [redacted]

Dear Christel, Ab, (alll),
Sorry to not be able to join the call - the timing would be 4:00am for me here in California. Looking forward to joining future calls!

Jonna

On Wed, Jun 5, 2019 at 10:55 PM Christel Smeys <[redacted]> wrote:

> Dear members of the WOHC20 scientific proramme committee
>
> On behalf of Ab Osterhaus and Anna Meredith, co-chairs of the scientific programme committee, I'm sending you the meeting papers and dial-in details for tomorrow's TC.
>
> The pdf file contains the agenda, the list of confirmed committee members and a proposal for the scientific agenda of the WOHC20.
>
> If you have any questions, don't hesitate to contact me.
>
> Kind regards
> Christel Smeys
>
> **Dail-in details:**
>
> World One Health Congress Scientific Programme Committee
> Fri, Jun 7, 2019 1:00 PM - 2:00 PM CEST
>
> Please join my meeting from your computer, tablet or smartphone.
> https://global.gotomeeting.com/[redacted]
>
> You can also dial in using your phone.
> United States: +[redacted]
>
> Access Code: [redacted]
>
> More phone numbers
> Australia: [redacted]
> Austria:
> Belgium:
> Canada:
> Denmark:
> Finland:
> France:
> Germany:
> Ireland:
> Italy:
> Netherlands:
> New Zealand:
> Norway:
> Spain:

Sweden: REDACTED
Switzerland: REDACTED
United Kingdom: REDACTED

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https://global.gotomeeting.com/install/244950365

Christel Smeys
Programme director
REDACTED
REDACTED
www.onehealthplatform.com

ONE HEALTH PLATFORM
REDACTED

Sent: Thu, 25 Jul 2019 06:58:07 -0700
Subject: Re: [Non-DoD Source] Re: Discussion with USAID - PREDICT/BTRP Transition Update
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Andrew Clements <aclements@usaid.gov>

Thanks
J

On Wed, Jul 24, 2019 at 12:07 PM Andrew Clements <aclements@usaid.gov> wrote:

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: "Brooks, Lance R CIV DTRA COOP THRT REDUCT (US)" <lance.r.brooks6.civ@mail.mil>
Date: July 24, 2019 at 8:44:25 AM EDT
To: Andrew Clements <aclements@usaid.gov>, "Stokes, Martha M CIV (USA)" <martha.m.stokes.civ@mail.mil>
Cc: "Hughes, Timothy Patrick (Tim) CIV DTRA COOP THRT REDUCT (USA)" <timothy.p.hughes3.civ@mail.mil>, "Avison, Rebecca E CTR DTRA COOP THRT REDUCT (US)" <rebecca.e.avison.ctr@mail.mil>, Katie Leahy <katie.leahy@globalsyseng.com>, Cara Chrisman <cchrisman@usaid.gov>, "Padmaja Shetty" <pshetty@usaid.gov>, Alisa Pereira <apereira@usaid.gov>, "Carroll, Dennis(GH/HIDN)" <DCarroll@usaid.gov>
Subject: RE: [Non-DoD Source] Re: Discussion with USAID - PREDICT/BTRP Transition Update

Hi Andrew,

Appreciate the follow up. We will do as outlined below in regards to contacting Jonna and working with her on any specific collaborations.

Thank you,
Lance

Lance R. Brooks

Chief, BT

Cooperative Threat Reduction

Office: 571-616-5980

Mobile: REDACTED

From: Andrew Clements <aclements@usaid.gov>
Sent: Tuesday, July 23, 2019 4:21 PM
To: Brooks, Lance R CIV DTRA COOP THRT REDUCT (US) <lance.r.brooks6.civ@mail.mil>; Stokes, Martha M CIV (USA) <martha.m.stokes.civ@mail.mil>
Cc: Hughes, Timothy Patrick (Tim) CIV DTRA COOP THRT REDUCT (USA) <timothy.p.hughes3.civ@mail.mil>; Avison, Rebecca E CTR DTRA COOP THRT REDUCT (US) <rebecca.e.avison.ctr@mail.mil>; Katie Leahy <katie.leahy@globalsyseng.com>; Cara Chrisman <cchrisman@usaid.gov>; Padmaja Shetty <pshetty@usaid.gov>; Alisa Pereira <apereira@usaid.gov>; Carroll, Dennis(GH/HIDN) <DCarroll@usaid.gov>
Subject: [Non-DoD Source] Re: Discussion with USAID - PREDICT/BTRP Transition Update

---

Hi Lance and Marty,

I'm following up on our call yesterday regarding Predict and its sample collections.

We spoke with Jonna et al. today and she confirmed that they are on track in all 28 countries to either have all of their sample collections safely stored in place or transferred to a secure location by the time the project ends (likely Dec 2019, although this has not yet been finalized). As a result, there is no need for assistance related to securing/transferring/destroying the Predict sample collections in these countries.

If DTRA and its in-country partners are interested in conducting research using the samples collected under Predict, I encourage you to contact Jonna to discuss further. It would be helpful to be specific as specific as possible about which countries and which types of samples would be of interest.

Please let me know if you have any questions.

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: 1-571-345-4253
E-mail: aclements@usaid.gov < Caution-mailto:aclements@usaid.gov >

On Mon, Jul 22, 2019 at 12:40 AM Hughes, Timothy Patrick (Tim) CIV DTRA COOP THRT REDUCT (USA) <timothy.p.hughes3.civ@mail.mil < Caution-mailto:timothy.p.hughes3.civ@mail.mil > > wrote:

Teleconference with USAID, building block of last email sent with additional information from each team as applicable.

Agenda:

Introductions

Update on email previously sent

Update on new information

Future coordination

Questions / closing

Previous Email Sent:

We think you should be aware that communicating PREDICT integration is progressing within BTRP, although not without some questions and follow-up discussions. Our integration communication team has been on a steady messaging campaign with relevant country, region, and science leads that this is not a continuation of PREDICT. In fact, we have created a new project name within the program, SECuRE (Safeguard, Secure, and Consolidate towards Research Engagements) to help with messaging the effort's objectives of support to threat reduction mission areas. We have also created the attached operational flow diagram, which shows the short, medium, and long-term goals for the effort.

The biggest challenge for BTRP is balancing program objectives against PREDICT implementer concerns. The majority of the sites are places where BTRP has long-established relationships and active research projects, so while the program acknowledges that the PREDICT implementers may not want any direct contact with site coordinators without pre-coordination, we need to collectively recognize that it may not be realistic given that these researchers are networked within an active rumor mill.

Please find our comments for SEA below. We will supply similar information for Africa labs within the week.

Cambodia: Institute Pasteur du Cambodie (IPC)

>>BTRP Response: We conducted a workshop with IPC last week on surveillance in Live Animal Markets and are in the process of establishing an institutional relationship to support country and science engagement efforts; The PREDICT site coordinator was on travel; however, we will look to leverage existing relationships with the Virology Unit there to develop a relationship

Indonesia: Primate Research Center, Bogor Agricultural University

>>BTRP Response: the terms of the BTRP engagement are restricted to TNI (Indonesian Army) by the Health Working within the Embassy – we are forbidden to engage with any other sectors

Lao PDR: National Animal Health Laboratory (NAHL) & National Center for Laboratory and Epidemiology (NCLE)

>>BTRP Response: BTRP is working to develop three research projects with NAHL and implementing Pathogen Asset Control System for inventory control and monitoring

Malaysia: PERHILITAN National Wildlife Forensic Laboratory & Sabah Wildlife Division Wildlife Health, Genetic and Forensic laboratory (WHGFL)

>>BTRP Response: BTRP has an active research project, partnership with PREDICT PI (Hughes), and we are addressing structural problems at Sabah

Thailand: WHO-CC, Chulalongkorm University & National Institute of Animal Health Laboratory (NIAH)

>>BTRP Response: BTRP has active research projects with Chula; Pathogen Asset Control System for inventory control and monitoring at both facilities; ongoing partnership PREDICT PI (Chu)

Viet Nam: Regional Animal Health Office No. 6 (RAHO6) & National Institute of Hygiene and Epidemiology (NIHE)

>>BTRP Response: BTRP has active research projects; Pathogen Asset Control System for inventory control and monitoring at both facilities; ongoing partnership with PREDICT PI (Ha); under contract to conduct facility upgrades at NIHE for PREDICT samples at NIHE

From: Andrew Clements <aclements@usaid.gov>
Sent: Tue, 17 Sep 2019 21:25:48 -0700
Subject: Re: Lancet Global Health: Do we need a Global Virome Project?
To: Ronald Waldman <ronwaldman@email.gwu.edu>
Cc: rechalar@usaid.gov, Jonna Mazet <jkmazet@ucdavis.edu>, Tim Meinke <tmeinke@usaid.gov>, lkramer@usaid.gov

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 Sep 18, 2019, at 11:36 AM, Ronald Waldman <ronwaldman@email.gwu.edu> wrote:

FYI

Sent from my iPhone

Begin forwarded message:

From: "Folkers, Greg (NIH/NIAID) [E]" <gfolkers@niaid.nih.gov>
Date: September 18, 2019 at 04:27:51 GMT+7
To: Undisclosed recipients:;
Subject: Lancet Global Health: Do we need a Global Virome Project?

<image001.png>
Volume 7, Issue 10, October 2019, Pages e1314-e1316
<image002.gif>

Comment

Do we need a Global Virome Project?

Author links open overlay panelOlgaJonas[ab]RichardSeifman[ab]
https://doi.org/10.1016/S2214-109X(19)30335-3Get rights and content

There is debate in the scientific community about whether the animal-human infectious disease nexus warrants substantially more funding, science effort, and global policy discussion. One promising idea is to develop a global atlas of pathogens that are, as yet, unknown but might threaten humanity already or are likely to evolve into clear threats. Such an atlas would be a foundational necessity for anticipating and reducing the threats, but it would also be ambitious and costly, even if it was restricted initially to viruses, as in the proposed Global Virome Project.[1] Michael Osterholm, the director of the University of Minnesota's Center for Infectious Diseases Research and Policy, is a noted doubter. “I wouldn't sit here and say, ‘Such studies shouldn't be done,’ but I still fail to see at this point how it's going to better prepare the human race for the next infectious disease that jumps from animals to humans,” Osterholm said, wondering whether we could even hear the signal through the static that so much data would create.[2]

Others look to many past and present spillovers of pathogens from animals to humans and see a pattern. In some cases, inadequate preparedness and vigilance have led to humans being sentinels for animal diseases. In other cases, the pathogens might not cause disease symptoms in animals but an absence of basic data on the reservoir results in delayed diagnosis and preventable morbidity and mortality in humans. Spillovers where scarcity of data caused deadly and costly delays in diagnosis and response to human illness include novel strains of influenza, Ebola virus, Marburg virus, Dengue virus,

AIDS, and tuberculosis between pastoralists and their livestock in Ethiopia.[3] According to the World Organisation for Animal Health, 60% of pathogens capable of causing symptoms in, and even killing, humans originate in animals.[4] The spillover of Middle East respiratory syndrome coronavirus from camels in Saudi Arabia in 2013 was exported halfway across the world, causing an outbreak in humans and a severe, though thankfully temporary, shock to the economy of South Korea in 2015. Severe acute respiratory syndrome from civets in China spread to infect people in over 30 countries in 2003. Other infectious zoonotic pathogens, such as malaria, rabies, Zika, or Lyme disease, transmit in human populations, although not directly through human-to-human contact.

Viruses and other microbes are phenomenally successful. They are the oldest form of life on Earth and together comprise 60% of the Earth's living matter. Most are beneficial or cause no great harm to humans and their livestock, but some are a formidable and constant challenge to humanity. In their June 2019 consensus statement,[5] leading microbiologists reviewed the implications of climate change for microorganisms and what is known about microbial effects on climate change. They issued a stark warning about the consequences of inadequate microbial research, arguing that our knowledge about viruses and other microbes is surprisingly and dangerously scant. Since 2009, the US Agency for International Development has supported the PREDICT project in 35 countries and US research institutions to provide proof of concept that collecting samples from host species can lead to important scientific findings.[6] The Prince Mahidol Awards Conference in 2018 in Bangkok, Thailand, highlighted the importance of the topic: "Global trends indicate that new microbial threats will continue to emerge at an accelerating rate, driven by our growing population, expanded travel and trade networks, and human encroachment into wildlife habitat. Most emerging viruses are zoonotic, that is, transferred between vertebrates and humans…Estimations show that there are more than 1·5 million mammalian and waterfowl viruses, spanning across 25 viral families. Compared with the more than 260 viruses known in humans, the unknown viruses represent 99·9% of potential zoonoses. These viruses usually remain undetected until they cause disease in humans."[7]

Much like map-making for newly-discovered continents, the Global Virome Project would be a pathway to improve capacity to detect, diagnose, and discover viruses that potentially pose threats to human populations, particularly in low-income and middle-income countries. Between 631 000 and 827 000 unknown viruses might be zoonotic and thus have the potential to infect humans after spillover from host animal populations. The big idea is to gradually build a global atlas of most of the planet's naturally occurring potentially zoonotic viruses by systematically creating the missing maps. Broadening the knowledge base on viral sequences, geographical ranges, and host distributions would provide vital intelligence about humanity's formidable microbial enemy. The three specific benefits that the project would provide are early warning of future threats, data to improve prevention and reduction of these threats, and inputs for advance preparation of responses for unexpected outbreaks of unknown diseases.

Major global actors are starting to engage. "China will help lead a project to identify unknown viruses from wildlife to better prepare humans for major epidemics—if not global pandemics…The Global Virome Project will start in China and Thailand with field work to collect samples from wild animals and analyze the viruses detected", said Gao Fu, the head of the Chinese Centre for Disease Control and Prevention.[8] Cost estimates for the Global Virome Project range from an initial $1·2 billion to $3·4 billion over a 10-year period.[9] The projected cost is modest when it is put in perspective, in at least four regards.

First, even a single regional disease outbreak, especially one that crosses borders, can result in considerable human illness and death and cost tens of billions in productivity, trade, economic growth, and social welfare. For example, the economic, health, and social costs of the 2014–15 Ebola outbreak in west Africa are estimated to be over $53 billion.[10] The economic cost of pandemics of novel influenza (or other readily transmissible viral diseases) has been conservatively estimated as $80 billion annually when averaged over a century.[11] Investments to reduce these risks yield high economic benefits. An expenditure of $400 million a year on the Global Virome Project—which is at the higher end of the Global Virome Project cost range—would be equivalent to just 0·5% of the ongoing annual economic risk of $80 billion from pandemic influenza (and other readily transmissible viral diseases) and thus be justified as a prudential measure. The Global Virome Project would complement ongoing efforts, such as the Coalition for Epidemic Preparedness Innovations, the International Vaccines Task Force, and the surveillance and preparedness capacity-building projects in the REDISSE programme financed by the World Bank.

Second, analyses of viral risks would increasingly become possible as data collection proceeds; such analyses would be important inputs to the newly created Global Preparedness Monitoring Board, which

assesses efforts to reduce pandemic risks.
Third, the viral atlas might yield large co-benefits since concentrated research in one area often leads to unforeseen benefits elsewhere; for example, in the mapping of the human genome and the development of the internet.
Fourth, the Global Virome Project would create an international partnership that cuts across political adversaries for a common cause—China and the USA are two key actors in preventing infectious disease outbreaks and the mutual gains for them and the rest of the world are substantial.
Both the supporters of the Global Virome Project and its skeptics need to be heard. An objective, apolitical assessment would be helpful in deciding whether spending up to $3·4 billion over the next decade is likely to produce scientific knowledge whose benefits are greater than the costs. If the conclusion of such an assessment is that filling in some of the missing knowledge about viruses has significant merit, then the second step would be to set out how, where, and when to take it forward, and how to arrange adequate and sustained financing. Side discussions at venues such as the G20 or the UN General Assembly, could be opportunities for policy makers to set out implementation arrangements. They will need to draw on the advice of knowledgeable experts, including animal and human health researchers from low-income and middle-income countries, biomedical industry interests, economists, financial analysts, and big data expertise. How about it?
We declare no competing interests.

References

1

D Carroll, P Daszak, ND Wolfe, *et al.***The Global Virome Project**
Science, 359 (2018), pp. 872-874
View Record in ScopusGoogle Scholar

2

H Branswell**There are more than 1 million viruses that we know absolutely nothing about**
https://theweek.com/articles/667704/there-are-more-than-1-million-viruses-that-know-absolutely-nothing-about (Dec 27, 2016), Accessed 25th Jun 2019
Google Scholar

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B Gumi, E Schnelling, S Berg, *et al.***Zoonotic transmission of tuberculosis between pastoralists and their livestock in south-east Ethiopia**
Ecohealth, 9 (2012), pp. 139-149
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4

World Organisation for Animal Health**Animal health: a multifaceted challenge**
https://www.oie.int/fileadmin/Home/eng/Media_Center/docs/pdf/Key_Documents/ANIMAL-HEALTH-EN-FINAL.pdf (August, 2015), Accessed 25th Jun 2019
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5

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Nature Rev Microbiol, 17 (2019), pp. 569-586
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6

USAID**Reducing panedemic risk, promoting global health**
https://www.usaid.gov/sites/default/files/documents/1864/predict-global-flyer-508.pdf, Accessed 25th Jun 2019
Google Scholar

7

D Carroll, B Watson, REDACTED *et al.***Building a global atlas of zoonotic viruses**
Bull World Health Organ, 96 (2018), pp. 292-294
View Record in ScopusGoogle Scholar

8

X Wang, S Jua**China to help ID unknown lethal viruses**
https://www.chinadaily.com.cn/a/201805/22/WS5b035506a3103f6866ee9b83.html (May 22, 2018), Accessed 25th Jun 2019
Google Scholar

9

H Branswell**Finding the world's unknown viruses—before they find us**
https://www.statnews.com/2016/12/13/world-viruses-global-virome-project/ (Dec 13, 2016), Accessed 25th Jun 2019
Google Scholar

10

C Huber, L Finelli, W Stevens**The economic and social burden of the 2014 Ebola outbreak in west Africa**
J Infect Dis, 218 (2018), pp. S698-S704
View Record in ScopusGoogle Scholar

11

VY Fan, DT Jamison, LH Summers**Pandemic risk: how large are the expected loses?**
https://www.who.int/bulletin/volumes/96/2/17-199588/en/, Accessed 25th Jun 2019
Google Scholar

View Abstract

Sent: Thu, 19 Sep 2019 13:09:40 +0200
Subject: Thanks & Lancet Global Health: Do we need a Global Virome Project?
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Ronald Waldman <ronwaldman@email.gwu.edu>, Tim Meinke <tmeinke@usaid.gov>, Ricardo Echalar <rechalar@usaid.gov>, "Kramer, Lisa" <lkramer@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>, John Mackenzie [redacted], Amalhin Shek <ashek@usaid.gov>, Subhash Morzaria [redacted], "Claes, Filip (AGAH)" [redacted], [redacted]
Cc: Andrew Clements <aclements@usaid.gov>, Lonnie King [redacted], jmhughe <jmhughe@emory.edu>, Billy Karesh <karesh@ecohealthalliance.org>, Dennis Carroll [redacted], Alisa Pereira <apereira@usaid.gov>

Yes, saw *The Lancet* piece -- thanks for sharing, Ron!
Pretty amazing, unsolicited endorsement of GVP. It is a nice capstone to our time in Bali. To see that the efforts we have all made for Predict's success are stimulating ongoing sparks for even small world changes is very encouraging.

While I have you, I would like to express my sincere appreciation to all of you for your long-standing commitments and hard work to steer the activities and resulting successes of the Predict aims and teams. Some of you helped to make the project possible from the beginning & had the vision and fortitude to see it through from start to finish. Others made sacrifices and contributed sweat equity on a regular basis to make sure we stayed on track. And all of you provided thoughtful input and guidance to make the project work. I hope, like me, that your expectations have been and will continue to be exceeded by our amazing team and their products. They are the future of preparedness and risk reduction and you all helped significantly to make that happen.

I can't thank you enough,
Jonna

On Sep 18, 2019, at 11:36 AM, Ronald Waldman <ronwaldman@email.gwu.edu> wrote:

FYI

Sent from my iPhone

Begin forwarded message:

From: "Folkers, Greg (NIH/NIAID) [E]" <gfolkers@niaid.nih.gov>
Date: September 18, 2019 at 04:27:51 GMT+7
To: Undisclosed recipients:;
Subject: Lancet Global Health: Do we need a Global Virome Project?

<image001.png>

Volume 7, Issue 10, October 2019, Pages e1314-e1316

<image002.gif>

Comment

Do we need a Global Virome Project?

Author links open overlay panelOlgaJonas[ab]RichardSeifman[ab]

https://doi.org/10.1016/S2214-109X(19)30335-3Get rights and content

There is debate in the scientific community about whether the animal-human infectious disease nexus warrants substantially more funding, science effort, and global policy discussion. One promising idea is to develop a global atlas of pathogens that are, as yet, unknown but might threaten humanity already or are likely to evolve into clear threats. Such an atlas would be a foundational necessity for anticipating and reducing the threats, but it would also be ambitious and costly, even if it was restricted initially to viruses, as in the proposed Global Virome Project.[1] Michael Osterholm, the director of the University of Minnesota's Center for Infectious Diseases Research and Policy, is a noted doubter. "I wouldn't sit here and say, 'Such studies shouldn't be done,' but I still fail to see at this point how it's going to better prepare the human race for the next infectious disease that jumps from animals to humans," Osterholm said, wondering whether we could even hear the signal through the static that so much data would create.[2]

Others look to many past and present spillovers of pathogens from animals to humans and see a pattern. In some cases, inadequate preparedness and vigilance have led to humans being sentinels for animal diseases. In other cases, the pathogens might not cause disease symptoms in animals but an absence of basic data on the reservoir results in delayed diagnosis and preventable morbidity and mortality in humans. Spillovers where scarcity of data caused deadly and costly delays in diagnosis and response to human illness include novel strains of influenza, Ebola virus, Marburg virus, Dengue virus, AIDS, and tuberculosis between pastoralists and their livestock in Ethiopia.[3] According to the World Organisation for Animal Health, 60% of pathogens capable of causing symptoms in, and even killing, humans originate in animals.[4] The spillover of Middle East respiratory syndrome coronavirus from camels in Saudi Arabia in 2013 was exported halfway across the world, causing an outbreak in humans and a severe, though thankfully temporary, shock to the economy of South Korea in 2015. Severe acute respiratory syndrome from civets in China spread to infect people in over 30 countries in 2003. Other infectious zoonotic pathogens, such as malaria, rabies, Zika, or Lyme disease, transmit in human populations, although not directly through human-to-human contact.

Viruses and other microbes are phenomenally successful. They are the oldest form of life on Earth and together comprise 60% of the Earth's living matter. Most are beneficial or cause no great harm to humans and their livestock, but some are a formidable and constant challenge to humanity. In their June 2019 consensus statement,[5] leading microbiologists reviewed the implications of climate change for microorganisms and what is known about microbial effects on climate change. They issued a stark warning about the consequences of inadequate microbial research, arguing that our knowledge about viruses and other microbes is surprisingly and dangerously scant. Since 2009, the US Agency for International Development has supported the PREDICT project in 35 countries and US research institutions to provide proof of concept that collecting samples from host species can lead to important scientific findings.[6] The Prince Mahidol Awards Conference in 2018 in Bangkok, Thailand, highlighted the importance of the topic: "Global trends indicate that new microbial threats will continue to emerge at an accelerating rate, driven by our growing population, expanded travel and trade networks, and human encroachment into wildlife habitat. Most emerging viruses are zoonotic, that is, transferred between vertebrates and humans…Estimations show that there are more than 1·5 million mammalian and waterfowl viruses, spanning across 25 viral families. Compared with the more than 260 viruses known in humans, the unknown viruses represent 99·9% of potential zoonoses. These viruses usually remain undetected until they cause disease in humans."[7]

Much like map-making for newly-discovered continents, the Global Virome Project would be a pathway to improve capacity to detect, diagnose, and discover viruses that potentially pose threats to human populations, particularly in low-income and middle-income countries. Between 631 000 and 827 000 unknown viruses might be zoonotic and thus have the potential to infect humans after spillover from host animal populations. The big idea is to gradually build a global atlas of most of the planet's naturally occurring potentially zoonotic viruses by systematically creating the missing maps. Broadening the knowledge base on viral sequences, geographical ranges, and host distributions would provide vital intelligence about humanity's formidable microbial enemy. The three specific benefits that the project would provide are early warning of

future threats, data to improve prevention and reduction of these threats, and inputs for advance preparation of responses for unexpected outbreaks of unknown diseases.

Major global actors are starting to engage. “China will help lead a project to identify unknown viruses from wildlife to better prepare humans for major epidemics—if not global pandemics…The Global Virome Project will start in China and Thailand with field work to collect samples from wild animals and analyze the viruses detected”, said Gao Fu, the head of the Chinese Centre for Disease Control and Prevention.[8] Cost estimates for the Global Virome Project range from an initial $1·2 billion to $3·4 billion over a 10-year period.[9] The projected cost is modest when it is put in perspective, in at least four regards.

First, even a single regional disease outbreak, especially one that crosses borders, can result in considerable human illness and death and cost tens of billions in productivity, trade, economic growth, and social welfare. For example, the economic, health, and social costs of the 2014–15 Ebola outbreak in west Africa are estimated to be over $53 billion.[10] The economic cost of pandemics of novel influenza (or other readily transmissible viral diseases) has been conservatively estimated as $80 billion annually when averaged over a century.[11] Investments to reduce these risks yield high economic benefits. An expenditure of $400 million a year on the Global Virome Project—which is at the higher end of the Global Virome Project cost range—would be equivalent to just 0·5% of the ongoing annual economic risk of $80 billion from pandemic influenza (and other readily transmissible viral diseases) and thus be justified as a prudential measure. The Global Virome Project would complement ongoing efforts, such as the Coalition for Epidemic Preparedness Innovations, the International Vaccines Task Force, and the surveillance and preparedness capacity-building projects in the REDISSE programme financed by the World Bank.

Second, analyses of viral risks would increasingly become possible as data collection proceeds; such analyses would be important inputs to the newly created Global Preparedness Monitoring Board, which assesses efforts to reduce pandemic risks.

Third, the viral atlas might yield large co-benefits since concentrated research in one area often leads to unforeseen benefits elsewhere; for example, in the mapping of the human genome and the development of the internet.

Fourth, the Global Virome Project would create an international partnership that cuts across political adversaries for a common cause—China and the USA are two key actors in preventing infectious disease outbreaks and the mutual gains for them and the rest of the world are substantial.

Both the supporters of the Global Virome Project and its skeptics need to be heard. An objective, apolitical assessment would be helpful in deciding whether spending up to $3·4 billion over the next decade is likely to produce scientific knowledge whose benefits are greater than the costs. If the conclusion of such an assessment is that filling in some of the missing knowledge about viruses has significant merit, then the second step would be to set out how, where, and when to take it forward, and how to arrange adequate and sustained financing. Side discussions at venues such as the G20 or the UN General Assembly, could be opportunities for policy makers to set out implementation arrangements. They will need to draw on the advice of knowledgeable experts, including animal and human health researchers from low-income and middle-income countries, biomedical industry interests, economists, financial analysts, and big data expertise. How about it?

We declare no competing interests.

References

1

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View Record in ScopusGoogle Scholar

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USAID**Reducing panedemic risk, promoting global health**

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Google Scholar

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D Carroll, B Watson, REDACTED, *et al.***Building a global atlas of zoonotic viruses**

Bull World Health Organ, 96 (2018), pp. 292-294

View Record in ScopusGoogle Scholar

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X Wang, S Jua**China to help ID unknown lethal viruses**

https://www.chinadaily.com.cn/a/201805/22/WS5b035506a3103f6866ee9b83.html (May 22, 2018), Accessed 25th Jun 2019

Google Scholar

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H Branswell**Finding the world's unknown viruses—before they find us**

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Google Scholar

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J Infect Dis, 218 (2018), pp. S698-S704

View Record in ScopusGoogle Scholar

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Google Scholar

View Abstract

Sent: Wed, 06 Nov 2019 14:28:54 +0000
Subject: GVP call Tomorrow
From: cchrisman@usaid.gov
To: chmura@ecohealthalliance.org, [redacted] maher@ecohealthalliance.org, [redacted] erubin@metabiota.com, cchrisman@usaid.gov, daszak@ecohealthalliance.org, [redacted], nwolfe@metabiota.com

Hi All,

Just a quick reminder that we have our regularly scheduled GVP call tomorrow (Thursday). Please let me know if you have any additional agenda items, beyond those listed below. Look forward to speaking with you all then!

Best.
Cara

Agenda:
- Retreat debrief
- 501c3 updates
- BoD Meeting
- Core Team Logistics (check in on timing/frequency)
- External engagement
- AOB

GVP call
When Thu Nov 7, 2019 1pm – 2pm Eastern Time - New York

Where call in line [redacted], passcode [redacted]

Who
- [redacted] - organizer
- Aleksei Chmura
- maher@ecohealthalliance.org
- cchrisman@usaid.gov
- [redacted]
- nwolfe@metabiota.com
- Peter Daszak
- [redacted]
- erubin@metabiota.com

call in line [redacted], passcode [redacted]

From:	Andrew Clements <aclements@usaid.gov>
To:	David J Wolking <djwolking@ucdavis.edu>
CC:	Cara J. Chrisman <cchrisman@usaid.gov>;Cassandra Louis Duthil <clouisduthil@usaid.gov>;Amalhin Shek <ashek@usaid.gov>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent:	2/18/2020 11:10:02 PM
Subject:	[predict] Re: Feedback needed: March 17-19th plans

Thanks, David. Will be review and get back to you.

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 18, 2020, at 11:19 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi Andrew,

We're planning on doing a Hill briefing the afternoon of March 18th or 19th but need some feedback soon so we can begin coordinating with congressional offices and staff.

Also on our Executive Board call today we came to the consensus that USG personnel probably only have the appetite for one or even a half day of the data meeting/workshop, so it might work best to do a summary/presentations and Q&A/discussion on the short day and the deeper dive with those that really want to get in the weeds the longer day (PREDICT, FAO, WHO, and select USG personnel). Maybe a half day on the 18th full day on the 19th would work well?

If you let us know what USAID thinks would work best, we'll keep moving forward with plans...

Best,

David

From:	David J Wolking <djwolking@ucdavis.edu>
To:	Peter Daszak <daszak@ecohealthalliance.org>;Kevin Olival <olival@ecohealthalliance.org>
CC:	Johnson Christine Kreuder (ckjohnson@ucdavis.edu) <ckjohnson@ucdavis.edu>;Jonna Mazet (jkmazet@ucdavis.edu) <jkmazet@ucdavis.edu>;Alison Andre <andre@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>
Sent:	7/27/2020 9:26:42 AM
Subject:	Re: First shot at M&A final report section - my edits still to do

Hey Peter,

Just checking in on this report. Did you have a chance to work through it? We're still aiming to a draft to Andrew this week as part of the 5 year CoAg report.

Thanks,

David

On Wed, Jul 22, 2020 at 8:22 AM Peter Daszak <daszak@ecohealthalliance.org> wrote:

Look forward to talking today. Here's a first draft from Kevin. I'll be editing this over next 2 days, so you will have a revised draft by COB Friday.

Apologies for the rough nature of it and for delays..

Cheers,

Peter

Peter Daszak

President

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Website: www.ecohealthalliance.org

Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

--
David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

From: Jon Epstein <epstein@ecohealthalliance.org>
Sent: Mon, 17 Aug 2020 16:46:41 -0400
To: Oladele Ogunseitan <oladele.ogunseitan@uci.edu>, Ava Sullivan <sullivan@ecohealthalliance.org>
Cc: Tracey Goldstein <tgoldstein@ucdavis.edu>, Woutrina A Smith <wasmith@ucdavis.edu>, onehealthnextgen Sympa List <onehealthnextgen@ucdavis.edu>
Subject: [onehealthnextgen] Re: SEAOHUN OHWA Steering Committee

Ava,
Thank you, I agree it looks good. A question for Dele:

As part of item 1, would you be willing to give a brief orientation to the steering committee to the curated list of OH content? I was hoping we'd be able to send it to them in advance, but at this point it probably would make more sense to show it to them, then perhaps we could ask each country rep to review their country's list over the next week and email recommendations for ready-to-go course content that addresses the core competencies and that we could use as examples on the website.

This would also help us identify gaps where we might need to create new content.

What do you think?

Cheers,
Jon

On Mon, Aug 17, 2020 at 4:08 PM Oladele Ogunseitan <oladele.ogunseitan@uci.edu> wrote:

> Many thanks, Ava.
> I agree fully, and the agenda looks good to me. We should also include an item #5: "Other topics" to provide an opportunity for the SEAOHUN members to propose topics that they may want to discuss, but that we have not brought up.
>
> The eventual goal is to have the SEAOHUN members drive the process with our guidance. At the beginning, it is of curse important for us to provide guideposts as presented in the agenda that you outline.
>
> If there are other ways to get the SEAOHUN members to speak more at the meetings, everyone, please feel free to share ideas.
>
> Best wishes.
>
> - Dclc
>
> Dele Ogunseitan
> University of California Presidential Chair
> Professor of Population Health & Disease Prevention
> Irvine CA 92697
>
> www.linkedin.com/in/deleogunseitan
> https://zoom.us/my/deleogunseitan
>
> On Aug 17, 2020, at 12:59 PM, Ava Sullivan <sullivan@ecohealthalliance.org> wrote:
>
> Hi Jon and Dele,
> I am hoping to send out the invitation ASAP. Does this following agenda sound good to you? I think the best way to have a productive steering committee meeting is to have clear objectives for the time we have together. Please let me know what I should remove/add in service to that goal.
>
> Proposed agenda:
> 1) Walk group through beta website, One Health Modules section
> a) Discussion points: What are key elements? Proposed timeline, how to collect/populate Module content
> 2) Each Country briefly discuss assets and gaps/opportunities for the Academy offerings, informed by curation docs
> 3) Present revised mission/vision statement with time for instant final live edits on GoogleDocs
> 4) From last week's agenda which we didn't get to: update from meeting with ASEAN Centre for Biodiversity &

partnership idea (Jon)

Ava Sullivan
Project Manager and Research Assistant

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EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

On Aug 11, 2020, at 4:44 PM, Ava Sullivan <sullivan@ecohealthalliance.org> wrote:

Hi Jon,
Dele and I chatted after the Academy website meeting on Friday, where we discussed sharing the individual documents directly with the respective members (i.e, Malaysia won't receive access to Indonesia's). We also discussed the limitations of assigning members to recommend courses, as it is unlikely that each member will have the full picture of course availability. These documents have potential courses listed, but it is unlikely each steering committee member will be able to speak to what is listed. We also discussed sharing the beta version of the website. I think seeing the website spurs vision and excitement. However, it is important to describe the specific feedback we want, so we don't end up eliciting too much feedback that won't be incorporated.

I agree with you that the meeting would benefit from a clear goal and method forward to achieve tangible results between now and the next meeting. My proposal is the following:

1) Share the curation document with each individual steering member, and ask them to come ready to present on assets/gaps/opportunities for the Academy (**Dele/Jon, please let me know if there are more specific assignments we want them to prepare)**
2) Walk the steering committee through the One Health modules on the new website (screen share) to show structure. Structured feedback on this: What are key elements, what to add, proposed timeline, how to collect/populate...
3) Edit the mission/vision with (small) updates from last week's conversation and share a new version on Google Docs for instant feedback during next weeks' meeting. Show on website where this will show up.

Here is the agenda from last time:
Also, and agenda item we didn't get to from last week

5. update from meeting with ASEAN Centre for Biodiversity & partnership idea (Jon)

Ava Sullivan
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On Aug 11, 2020, at 3:58 PM, Jon Epstein <epstein@ecohealthalliance.org> wrote:

Dele and Ava,
Should we assign members to provide recommendations for specific courses that cover the core competencies?
I'm trying to find a way to engage them and give them ownership of content, and at the same time more the ball forward in terms of getting real content onto the website.
Should I send this link to the curation document?

Your thoughts?

-Jon

On Fri, Aug 7, 2020 at 1:53 PM Oladele Ogunseitan <oladele.ogunseitan@uci.edu> wrote:

> Greetings, Jon and Ava.
> Here is the link to the google-drive folders for the training curation documents for SAEOHUN countries, including the draft reports:
>
> REDACTED
>
> As we discussed, the SOHWA steering committee members should be familiar with the status of implementation, institutionalization, and accreditation of One Health training activities in their respective OHUNs.
>
> The next meeting of the steering committee will hopefully include a review of the current website structure and contents, and the curation project should help the OHUNs identify opportunities for the Academy:
>
> http://devclients.wpengine.com/
>
> Thanks again for your work on this committee!
>
> Enjoy the weekend.
>
> - Dele
>
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> Professor of Population Health & Disease Prevention
> Irvine CA 92697
>
> www.linkedin.com/in/deleogunseitan
> https://zoom.us/my/deleogunseitan

--
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From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Alisa Pereira <apereira@usaid.gov>
BCC: Elizabeth Leasure <ealeasure@ucdavis.edu>
Sent: 1/17/2017 5:51:15 PM
Subject: Fwd: Ebola host study funding

Found it -- we did have a written exchange. Please see all the way down through this chain, as well as the attachment.
All coming out consistently with what we've spent so far. Only big development since this exchange and the preparation of the attachment is that we will be extending beyond the two-year timeframe originally proposed for reasons you already know.
We'll proceed as discussed, but let us know if there is more that could/should be done with this information,
Jonna

---------- Forwarded message ----------
From: **Jonna Mazet** <jkmazet@ucdavis.edu>
Date: Mon, Apr 4, 2016 at 4:25 PM
Subject: Re: Ebola host study funding
To: Andrew Clements <aclements@usaid.gov>
Cc: Alisa Pereira <apereira@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>

Here's the most recent EHP description with my budget explanation at the very end.
Have a nice night,
Jonna

On Tue, Mar 1, 2016 at 1:59 PM, Andrew Clements <aclements@usaid.gov> wrote:
yes. will pass this information along.

On Tue, Mar 1, 2016 at 10:52 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Yes, so we have a year worth of funding for EHP and then we'll need to make tough decisions about stopping work in those countries (or stop work in other countries to accommodate that work) if the rest of the funding doesn't come through.
Also has ceiling implications in the long run.
Thanks,
J

On Tue, Mar 1, 2016 at 1:22 PM, Andrew Clements <aclements@usaid.gov> wrote:
Yes, if you go with 15+/5.7.

On Tue, Mar 1, 2016 at 10:15 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Works out for one year, only though, right?
J

On Tue, Mar 1, 2016 at 12:31 PM, Andrew Clements <aclements@usaid.gov> wrote:
Thanks. I didn't remember the budget figures per country, but it's clear the math does come close to working out without the extra funding for the host study.

On Mar 1, 2016, at 8:38 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Hi there,
Yes, sorry forgot about that one when we were chatting.

The EHP was estimated by us $15+M by us, and then submitted for $11+M. We have approximately $5.7M in our current three years of budgets for these operations (budgeted originally at the regular Predict scale & scope @ 1.9M/ year for all three countries; excludes the distributed staff costs that are assigned to the countries). So if we operate at the planned scale & scope, we will run out of money in approximately 1 year (have on the order of one year of the $15M anticipated expense in hand, if we spend all three years of our funding for the three countries as soon as fully operational). That means that we will either need to stop after one year or need to use funds from other countries to achieve the sample and testing targets for the EHP if no further money comes as planned/requested. Of course, these numbers also assume that we won't be initiating any regular Predict activities in these countries. If we intend to start that implementation, we will have to use some of the originally-budget $5.7M for that.
Probably clear as mud, so let me know if you'd like to discuss.
Have a good night,
Jonna

On Tue, Mar 1, 2016 at 10:10 AM, Andrew Clements <aclements@usaid.gov> wrote:
Hi Jonna,

Following up in the EHS, you mentioned that funds will go quickly when this project gets going.

Since you got 3 years of funding up front for the three countries, is your concern about the possibility of not getting reimbursed that (1) you won't have enough to do the EHS or (2) that without reimbursement there will not much left to do capacity building which the countries desperately need?

Thanks!

1-571-345-4253
aclements@usaid.gov

--

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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

PREVENTING THE NEXT EBOLA EPIDEMIC:
IDENTIFYING THE ANIMAL RESERVOIR(S) AND NOVEL HOSTS FOR EBOLA VIRUS IN WEST AFRICA

Introduction: After more than 28,000 cases and 11,000 deaths, the largest Ebola virus epidemic ever recorded has been nearly brought under control in West Africa. The global goal of zero new human cases and a cessation of human-to-human transmission has proved elusive with periodic small flare-ups of cases in Sierra Leone and Liberia. Despite the tremendous progress in controlling the outbreak, the fact Ebola emerged to affect humans in West Africa in late 2013 suggests Ebola virus may have become endemic in the region, potentially by circulation among animal populations. Without the identification of these possible animal sources and prevention programs to block transmission from animals to people, it is likely that future "spillover" of ebolaviruses from animals into humans will continue to occur. As we have seen over the years in Central and Eastern Africa where filovirus outbreaks have repeatedly occurred, effective control of these rare "spillover" events is possible and can even be limited to a small number of human cases. The challenge in controlling future Ebola virus outbreaks in West Africa, however, will be dependent on how widely disbursed the virus is across the region and which animal populations may be involved as reservoirs. In Central Africa, a number of different species of bats are proposed as the principle reservoir hosts for the virus. Similarly, in West Africa, the current epidemic is thought to have been triggered by a "spillover" event from an infected bat. Given the wide exposure other animal populations may have had across West Africa to the virus, largely through direct or indirect contact with Ebola-infected humans, there is the risk that the host range of the virus has expanded to now include domestic animals, such as dogs and cats, goats and pigs, as well as other wildlife, in addition to bats.

Despite several high quality studies in specific geographic areas over the last 2 decades, a comprehensive, long-term, simultaneous, multi-country coordinated investigation into Ebola including a wide taxonomic range of potential virus hosts has never been conducted. The purpose of this project is to determine how widely distributed the virus may be among animal populations, and how this host distribution will affect the risks of future outbreaks. This comprehensive, multi-year effort is designed to identify a range of possible animal hosts for all filoviruses that could serve as a source of human infections, as well as the behaviors and conditions associated with increased likelihood of another outbreak[1] – information that is key to reducing the risk of future outbreaks.

USAID's existing partnerships with experts in disease surveillance, modeling, risk mapping, and management of livestock and wildlife populations provides a unique opportunity to identify these potential animal reservoir(s). A coordinated and longitudinal approach is essential to help ensure success, given the ecological and species diversity involved and the potential seasonal characteristics of the virus' transmission dynamics. In USAID's consultation with NIH, CDC, and DOD, this approach to intensive surveillance was identified as a gap in activity. In particular,

[1]As concluded at the Ebola Risk Mapping Symposium hosted by USAID on May 11, 2015, that included representatives from the U.S. Centers for Disease Control and Prevention, the Center for International Forestry Research, EcoHealth Alliance, the Global Environment Facility, the University of California-Davis, the U.S. Agency for International Development, the U.S. Department of Defense, the U.S. Fish and Wildlife Service, and the US Forest Service.

this project will be coordinated with the U.S. CDC Viral Special Pathogens Branch team that is working with partners in Sierra Leone, as well as with ministries and other investigators working toward the same goal in the three most affected countries.

This surveillance project greatly enhances existing plans by expanding both the geographic range and diversity of species examined, and provides for a sufficient timeframe to examine seasonality. This work also brings in leading U.S. and international expertise from USAID, UC Davis, EcoHealth Alliance, Metabiota, and FAO. Additionally, a diverse range of partners are being identified in Sierra Leone, Guinea, and Liberia to implement the project.

Background and Problem Description: Ebola virus (*Zaire ebolavirus*) is suspected to be present in animal populations in West Africa, and whether future spillover events are rapidly contained or cause protracted epidemics depends on a number of factors, including the strength of infectious disease surveillance and response capacity within the region, an understanding of which animals are natural reservoirs and potential intermediate hosts for the virus so that preventive measures can be put in place. Because people in West Africa (and elsewhere) have routine contact with multiple types of animals including wildlife, livestock, and companion animals (e.g. cats, dogs) – identifying which of these animals may act as transmission hosts for the Ebola virus is critical for developing and targeting prevention measures to reduce the risk of Ebola virus spillover from animals to people.

This project is focused on three critical factors:

1. Geographic distribution. The unprecedented geographic spread of the virus among human populations across multiple countries in West Africa raises the prospect that the Ebola virus could have "spilled back" from people into previously unaffected animal populations—wildlife, companion animals and livestock—resulting in a broader geographic distribution of the virus. As a result, efforts to monitor the virus and risk factors for transmission will need to be more expansive than traditional research investigations in order to fully understand the extent of the potential risk.

2. Seasonality. Increasing evidence shows that many zoonotic viruses such as avian influenza, Marburg virus, and MERS coronavirus appear to have increased transmission during specific times of the year when there is heightened shedding in animal hosts, optimal environmental conditions, and/or human behaviors facilitating contact. As a result, the viruses cannot always be detected throughout the year. To date, "one-off" efforts to detect the Ebola virus in animals have not been successful, suggesting that this virus may also have a seasonal pattern. To address this gap in key knowledge, a "longitudinal surveillance" effort lasting at least two years will be needed to routinely collect samples from all targeted animals. The first year of surveillance will be to detect viral shedding and a second year is needed to validate seasonal patterns and identify risk factors associated with animal-human contact at these times of year. This information is critical for targeting prevention and control measures temporally and geographically and to specific populations to prevent the future spillover of the virus from animals that can lead to subsequent spread within human populations. This prevention approach has helped to successfully mitigate avian influenza and other emerging diseases.

3. Distribution among host species. In other parts of the world, filoviruses are known to naturally infect wildlife (bats, non-human primates) and domestic pigs (specifically, *Reston ebolavirus*). In order to more fully understand the range of animals possibly infected by the Ebola virus in West Africa, it will be necessary to collect samples from a variety of wildlife and domestic animal populations across the region over the course of two years. Importantly, the scale of the most recent epidemic has potentially led to higher rates of exposure to the virus by novel animal species as a result of poor sanitary conditions and open defecation or vomiting by infected individuals. In theory, this repeated exposure could have resulted in novel host/reservoir dynamics which may have a substantial impact on future outbreaks and risk mitigation strategies.

Proposed approach: This project will be looking at four domestic species and three broad wildlife taxa (dogs, cats, domestic pigs, goats, rodents, non-human primates, and bats) across the three countries and will sample approximately 54,000 animals over the two-year period, a scale that is unprecedented. Analyses of available data on all ebolaviruses and host ecology conducted by PREDICT-2 are being used to optimize sampling design targeting species, geographic and temporal distribution.

Using existing partnerships with experts in disease surveillance, modeling, and management of livestock and wildlife populations, the project partners will implement activities to identify the animal host(s) of ebolaviruses and risk factors associated with spillover from these animals to people by tapping into existing mechanisms and relationships that have been the backbone of USAID's Emerging Pandemic Threats (EPT) portfolio. NIH, CDC, and DTRA have signaled interest in aligning key parts of their resources to work with this effort. Further, discussions will be held with international organizations such as WHO, donor organizations, host-governments, and non-governmental organizations to ensure complementarity with other on-going efforts and avoid duplication before finalizing the proposed activities for these partners.

Diagnostic plan:

Specimens will be collected from approximately 54,000 animals for testing by conventional and next generation methods. The most commonly used ebolavirus diagnostic tests for acute phase infection utilize molecular methods (reverse transcriptase polymerase chain reaction, RT-PCR) that detect a fragment of the viral genome. Duplicate biological specimens for testing will be collected into either Trizol (inactivated specimen for RT-PCR), and viral transport media (for potential virus isolation), and frozen at -80°C until analysis. Highly specific real-time quantitative assays (qRT-PCR) are also available for Ebola virus testing, and will be used, in conjunction with the broad consensus based PREDICT Filovirus family conventional PCR protocols. These two approaches will be used in tandem to test samples for evidence of acute infection by both novel and known filoviruses. All amplification products from specimens that test positive by these molecular diagnostic methods will be subsequently sequenced for identity confirmation. Following confirmation, high throughput sequencing will be employed to attempt to obtain complete genome(s) sequence for comparison and characterization. To detect evidence of previous ebolavirus infection, serum for serological assays will be collected and aliquoted in 0.5ml volumes and stored frozen at -80°C until analysis. Serological assays to detect anti-ebolavirus IgM and/or IgG antibodies will be developed and optimized for multiple host species (platforms likely to be employed include ELISA and/or Luciferase immunoprecipitation (LIPS) systems).

Expected results:

- The biological and ecological data generated will be combined to produce a comprehensive zoonotic Ebola virus risk map for the three countries in West Africa based on potential animal host(s) of ebolaviruses, environmental conditions, and geographic areas associated with high-risk of spillover from animal host(s) to people that can be generalized more broadly throughout the region.
- These data will be used for policy dialogue with countries and economic unions in West Africa, as well as international donor organizations, to help improve monitoring for Ebola virus and to focus risk-mitigation strategies.
- In-country capacities in West Africa for surveillance, laboratory detection, and mapping of Ebola virus risk will be strengthened. While designed specifically for Ebola virus, these skill sets could be later applied to other pathogens increasing overall Global Health Security capacity.

Budget Requirements:

- In order to achieve sampling & testing for a sample size of 54,000 animals, we will require the $11.916M (requested for EHP) + $5.7M (the field budgets originally allocated to support the PREDICT-2 strategy, as we understood that all activities would be redirected to EHP) = $17.616 if we deplete all GHSA funds to get the project done (implemented over PREDICT operational years 2-4).
- We have however planned to complete the project over two fully active calendar years starting approximately now, so we should realize some savings in the last year of GHSA funding (estimated at $1M).
- If we add normal PREDICT activities to EHP activities and estimate the budget based on previous allocations, including field and testing costs for wildlife and people, funds needed above the $17.616M should be approximately $3.8M for PREDICT operational years 3&4 combined (note that global and in-country salaries of individuals who have been budgeted in EHP are not included because these costs have already been accommodated in EHP allocation for the countries).
- We have not been advised of any GHSA funding for PREDICT operational year 5, so we would ramp down all activities in that year to allowing only for completion of testing and analyses. If we have a budget savings as mentioned in second bullet, we could potentially apply that to continue activities at a very minimal level.

From:	Jonna Mazet <jkmazet@ucdavis.edu>
To:	Elizabeth S Chase <eschase@ucdavis.edu>;Alisa Pereira <apereira@usaid.gov>
CC:	Cassandra Louis Duthil (clouisduthil@usaid.gov) <clouisduthil@usaid.gov>; (dcarroll@usaid.gov) <dcarroll@usaid.gov>
Sent:	3/3/2017 8:33:03 AM
Subject:	Re: Call to discuss future of surveillance with change to FAO scope

Oops-- I think we might have a miscommunication on our end.
Liz, the meeting I was wanting clarity on for time with Dennis was suggested by Alisa, separate from the meeting with Richard.
Looping Alisa into the chain. I'm guessing that if this meeting is happening, it will occur before I go over to Crystal City for the noon meeting.
Thanks for info in advance,
Jonna

On Fri, Mar 3, 2017 at 8:09 AM, Elizabeth S Chase <eschase@ucdavis.edu> wrote:

Good Morning,

Jonna's schedule for March 7 has changed. She is meeting with Richard Green at 12:00pm EST in Crystal City. Is Dennis planning to join given the new time/location?

Thanks, Liz

Liz Chase

Executive Assistant to Dr. Jonna Mazet

One Health Institute

University of California, Davis

530-752-3630

eschase@ucdavis.edu

From: Eddy Rubin <erubin@metabiota.com>
To: Jonna Mazet <jkmazet@ucdavis.edu>
Cc: Peter Daszak <daszak@ecohealthalliance.org>, Nathan Wolfe <nwolfe@metabiota.com>, Cara Chrisman <cchrisman@usaid.gov>, Dennis Carroll <dcarroll@usaid.gov>, Taylor Elnicki <telnicki@metabiota.com>
Subject: Re: Another follow up from today's phone call re CUGH (Eddy, especially)
Sent: Mon, 3 Apr 2017 05:41:44 +0000
GVPCUGH..Eddy.pptx

Hi

I have attached some high level slides about the human genome project and GVP what you can do if you have lots of data halo... and some fluff to end with. Sorry to have missed the discussion so please don't hesitate to offer suggestions/directions/

Eddy

From: [redacted] on behalf of Jonna Mazet <jkmazet@ucdavis.edu>
Sent: Friday, March 31, 2017 8:29 AM
To: Eddy Rubin
Cc: Peter Daszak; Nathan Wolfe; Cara Chrisman; Dennis Carroll; Taylor Elnicki
Subject: Another follow up from today's phone call re CUGH (Eddy, especially)

Hi Eddy,
I hope Singapore travel is going great.
We had a productive discussion about CUGH on our regular call.
After much deliberation regarding pros and cons of order for the best effect for this audience, we settled on:

- Dennis: Setting the stage -- problem/justification, project description
- Jonna: Predict proof of concept with some recent papers/findings to ensure confidence
- Peter: Further feasibility, costing, and recent modeling team outcomes resulting in more reasonable price tag
- Eddy: Big finish with correlates to Human Genome Project and why the time is right to take a risk on this big idea

Hope this also looks good. By next Tuesday (COB), I will have a go at a reorder of the slides again and add in some Predict ones for my part. Peter will also be claiming and updating some of the slides/maps.

We all thought that you likely had more HGP slides or slides from your talk at the genomics conference that you'd like to insert for your section. Please send those along for incorporation if you have them. We mostly saw just the one in the current set, but I will look at the slide numbers you selected to see if I missed that more were on your topic.

Please advise or send on the slides from your other talk that looked great when you showed them to me a few months ago.

Travel well,
Jonna

The Global Virome Project

- The Global Virome Project (GVP) is a global venture to document and characterize within ten years virtually all of the planet's viruses in wildlife that could pose a threat to mankind
- The GVP aims to create a data rich field - enabling disruptive approaches for the development of countermeasures
- The GVP will make it possible to analyze data for entire viral families spanning tens of thousands of viruses, rather than just a few viral members
- The GVP will transform the culture – *from being Reactive (and ineffective) to one that is Proactive (and effective)*

GLOBAL VIROME PROJECT

Global Virome Project parallels the Human Genome Project

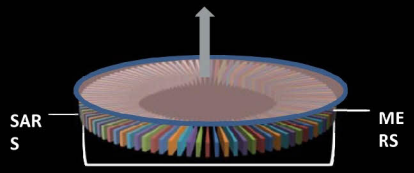
- An Audacious but doable VISIONARY PROJECT
- CLEAR METRICs and goals
- The potential to change the way we do science

The Impact– Disruptive & Transformative

Convert Virology into a data rich field:

The Next-Gen of Broad Spectrum Countermeasures

Universal Corona Virus Vaccine



Thousands of other Corona Viruses

GLOBAL VIROME PROJECT

The Impact– Disruptive & Transformative

Targeted, High Impact Risk Mitigation

Detailed characterization of virus's ecologic profile - spanning host range, geographic distribution, and epidemiology – will enable the identification of viruses that pose the greatest potential threat - and the targeting of measures to prevent spillover

Minimizing the Risk of Spillover

GLOBAL VIROME PROJECT

The Impact– Disruptive & Transformative

Encourage new technologies and build capabilities for detection and response

GLOBAL VIROME PROJECT

The Impact– Disruptive & Transformative

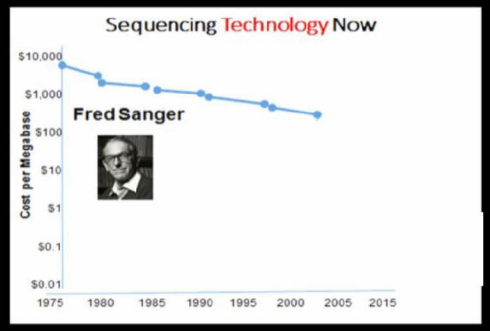
Building a Long-Term Global Surveillance Network for Emerging Viral Threats

- GVP database will serve as a critically important "snap shot in time" on viral ecology, epidemiology, and genetics
- An inherent characteristic of the most dangerous EVDs is that their host range, epidemiology, and genetic profiles evolve over time –
- GVP's surveillance and laboratory platforms have the potential to remain beyond the GVP as a long term system for monitoring evolving viral threats – ensuring early and effective deployment of biomedical and preventive countermeasures

GLOBAL VIROME PROJECT

The Impact– Disruptive & Transformative

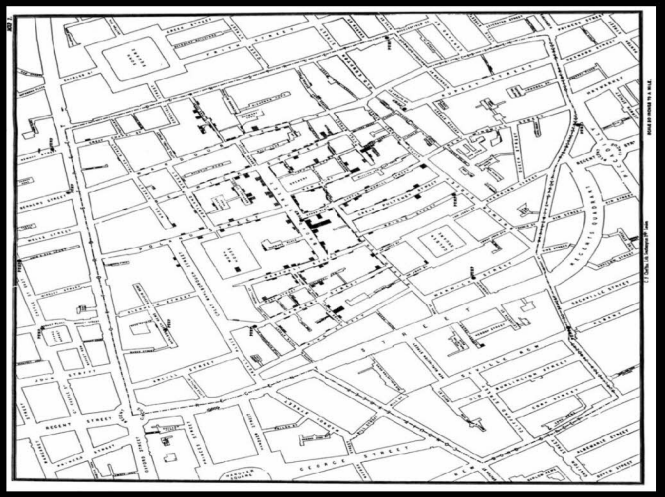
The "Halo Effect"



- As in the Human Genome Project, the GVP will dramatically accelerate the development of new diagnostic & analytic tools
- Data generated will have unanticipated impact – for example, the potential identification of unknown viral causes of chronic diseases like cancer
- GVP's surveillance and lab platforms will remain after GVP is completed as a long term system for monitoring evolving viral threats

GLOBAL VIROME PROJECT

JOHN SNOW'S GHOST MAP 1854 LONDON



HOW WOULD JOHN SNOW VIEW TODAY'S WORLD?

If you know your enemies and know yourself, you will not be imperiled in a hundred battles; ..... if you do not know your enemies nor yourself, you will be imperiled in every single battle.

Sun Tzu

The Global Virome Project
will
Make the "Enemy" We Don't Know Known

GLOBAL VIROME PROJECT

"We can't solve problems by using the same kind of thinking we used when we created them"

Albert Einstein

GLOBAL VIROME PROJECT

From: Andrew Clements <aclements@usaid.gov>
Sent: Sat, 15 Apr 2017 20:49:51 +0200
Subject: Re: PREDICT International Travel Requests
To: Katherine Leasure <kaleasure@ucdavis.edu>
Cc: PREDICTMGT <predictmgt@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>

Hi Katie,

Machalaba travel approved.

All other travel approved subject to mission concurrence.

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 15, 2017, at 12:45 AM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

> *Please find below international travel requests for your review and approval. Our apologies for the late submission for Catherine Machalaba; we were delayed resolving questions with the partner. Please let me know if you have any questions. Thanks!!*
>
> 1. Machalaba (Switzerland): $3,000 airfare/$460 (Geneva) max daily per diem
> 2. Obodai (Uganda): $1,000 airfare/$280 (Entebbe), $110 (Buhoma) max daily per diems
> 3. White, Johnson (Indonesia): $100 airfare each/$362 (Jakarta) max daily per diem
> 4. Gutierrez Jimenez (Liberia): $1,400 airfare/$295 (Monrovia) max daily per diem
> 5. Mazet (Tanzania): $7,000 airfare **business class fare required due* REDACTED /$309 (Dar es Salaam) max daily per diem
>
> Travel Requests:
>
> 1. EcoHealth Alliance would like to request travel approval for Ms. Catherine Machalaba to travel from New York City, NY, USA to Geneva, Switzerland from May 3-5, 2017 to attend the WHO-UNEP CBD Liaison Group on Health and Environment.
>
> **Trip purpose:** Ms. Machalaba will attend the WHO-UNEP CBD Liaison Group on Health and Environment at WHO headquarters. Agenda items will include best practice guidance to inform One Health toolkits for countries. While in Geneva she will also participate in a meeting with colleagues from WHO's One Health office on May 3 to discuss avenues for enhancing wildlife considerations in the WHO IHR Monitoring and Evaluation framework's Joint External Evaluation and follow-up country planning for health security.
>
> 2. UC Davis would like to request travel approval for Dr. Evangeline Obodai to travel from Accra, Ghana to Entebbe and Buhoma, Uganda from May 13-20, 2017 for human disease surveillance training.
>
> **Trip purpose:** Dr. Obodai will participate in training on PREDICT human disease surveillance protocols with the PREDICT Uganda human disease surveillance coordinator.
>
> 3. EcoHealth Alliance would like to request travel approval for Erica Johnson and Allison White to travel from Kuala Lumpur, Malaysia to Jakarta, Indonesia from May 10-12, 2017 for meetings with INDOHUN team regarding modeling collaboration.

Trip purpose: The trip will provide an opportunity for the EHA team to meet with the INDOHUN team to launch the project collaboration, including data sharing and project planning activities. **Departure from Mayalsia as travelers will be there for other IDEEAL work (separate funding source)*

4. EcoHealth Alliance would like to request travel approval for Dr. Leticia Gutiérrez Jiménez to travel from New York, NY, USA to Monrovia, Liberia from May 9-25, 2017 for rodent/bat training and field sampling in Liberia, and meetings with the PREDICT-2 Liberia team.

Trip purpose: Dr. Gutiérrez Jiménez will meet with Country Coordinator, Dr. Jim Desmond, regarding PREDICT-2 field activities. She will conduct rodent sampling training and bat sampling, and provide veterinary and ecological support to the PREDICT-2 Liberia team for implementing the new rodent sampling guidance.

5. UC Davis would like to request travel approval for Dr. Jonna Mazet to travel from Sacramento, California, USA to Dar es Salaam, Tanzania from June 2-18, 2017 for meetings with project partners, laboratory and field site visits, and training for PREDICT staff.

Trip purpose: Dr. Mazet will meet with project partners at Sokoine University of Agriculture and Ifakara Health Institute. She will also visit labs and field headquarters to meet with teams and engage in further capacity building.

Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
530-752-7526
530-752-3318 FAX
kaleasure@ucdavis.edu

--

Subject: Re: Special thanks
From: rajesh bhatia <[redacted]>
Sent: Fri, 5 May 2017 13:03:42 +0530
Cc: Jon Epstein <epstein@ecohealthalliance.org>
To: Jonna Mazet <jkmazet@ucdavis.edu>

Dear Jonna

Thanks for the affectionate mail.

It was indeed our honour to be with you. I am glad that you liked our food and the Indian wine. Hope we can repeat this experience in near future.

I shall be glad to join any efforts on AMR in any country. I was in Nepal during past 10 days helping them in strengthening their labs. A few years ago, during my stint with WHO, I was able to catalyse a national network of health labs on AMR. It is still functional and generating quality data on sustainable basis.

Currently I am working with FAO and have assisted India in development of its National Action Plan on AMR which has substantial number of activities for veterinary sector for each of the six objectives of national plan.

Shall be grateful if you could connect me to PI and also share with me technical material and presentations on AMR. So nice of you.

Have a safe trip and thanks a million for being with us. Hope to see you soon.

Best wishes

Rajesh

> On 05-May-2017, at 12:12, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
>
> Dear Rajesh,
> Just a quick note to specifically thank you for the fabulous dinner and opportunity to socialize. I really enjoyed the evening and the chance to learn more about your amazing country and the cuisine, even the wine ;)
>
> I am just finishing up my meeting in New Zealand where we had a productive discussion of AMR globally and the One Health approaches that are being implemented in the UK and Canada to address gaps, as well as our project in Nepal. If you would like to be introduced to our PI and researchers on the Nepal project or to hear more about the Nepal plan, please do let me know. If you'd like, I will also send you the slides from the Canadian and EU efforts from this conference, once they become available. I was happy to plug the early successes of India in getting a national plan in place -- congratulations again on that!
>
> Good luck with everything & you have my sincere appreciation,
> Jonna

From: Andrew Clements <aclements@usaid.gov>
To: predict@ucdavis.edu <predict@ucdavis.edu>
CC: predictmgt@usaid.gov <predictmgt@usaid.gov>
Sent: 5/9/2017 6:07:05 AM
Subject: [predict] Request for pipeline information (estimate through Sep 30, 2017)

Hi all,

Good news: Congress has passed an appropriation bill for FY17 and it has been signed by the President.

To help us start the process of identifying regular (non Ebola) funding needs for Oct 2017-Sep 2018, we're asking all of our implementing partners for their estimated pipelines as of Sep 30, 2017.

Would it be possible for you to provide the Predict pipeline information by the end of this week? If not, please propose an alternative date.

Thanks!

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

Sent: Tue, 30 May 2017 17:16:47 -0700
Subject: Fwd: PMAC side meeting concept note and guiedlines
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: "predict@ucdavis.edu" <predict@ucdavis.edu>

For discussion on last EB bullet,
J

---------- Forwarded message ----------
From: **Kevin Olival, PhD** <olival@ecohealthalliance.org>
Date: Mon, May 29, 2017 at 7:30 PM
Subject: Re: PMAC side meeting concept note and guiedlines
To: "Sudarat Damrongwatanapokin D.V.M., Ph.D." <sdamrongwatanapokin@usaid.gov>
Cc: Supaporn Wacharapluesadee <REDACTED>, "Dr. Jonna Mazet" <jkmazet@ucdavis.edu>, Jonna Mazet <REDACTED>, "William B. Karesh" <karesh@ecohealthalliance.org>, Peter Daszak <daszak@ecohealthalliance.org>, Dennis Carroll <dcarroll@usaid.gov>, Evelyn Luciano <luciano@ecohealthalliance.org>

Sudarat,
Thank you for sending the PMAC side meeting guidelines and examples. I'll be sure to discuss this with the PREDICT team, and we'll coordinate our concept note submissions well in advance of the deadline (as you advised, it's first come, first serve).

It was great to see you and Dan last week, and to observe the triangulated (human) surveillance in Chonburi. As always, I was very impressed by the excellent and productive work by Supaporn and her team on Saturday!

Cheers,
Kevin

Kevin J. Olival, PhD
Associate Vice President for Research

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

1.212.380.4478 (direct)
REDACTED (mobile)
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.

On May 26, 2017, at 3:27 AM, Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov> wrote:

Dear Kevin and Supaporn,
It was very nice to meet with you today at RDMA. Regarding our discussion on PMAC side meeting, please see attachments for PMAC side meeting guidelines (2017) and 2 concept notes on AMR and One Health Education that FAO and SEAOHUN in collaboration with USAID submitted to PMAC Secretariat for PMAC 2017 side meetings. There is no associated cost for organizing the side meeting. PMAC Secretariat will provide the meeting room, lunch and 2 coffee breaks/day for all participants. The concept note for PMAC 2018 side meeting need to be submitted to PMAC secretariat before September 30, 2017.

Please do not hesitate to contact us if you have any questions or concerns. Look forward to seeing you early tomorrow morning for the field trip.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
REDACTED
E-mail: sdamrongwatanapokin@usaid.gov
Tel: REDACTED

<Guidelines for Side Meetings - PMAC2017 (1).pdf><AMR Side Meeting at PMAC 2017_Nov 30,2016.docx><PMAC2017_Side Meeting Agenda _SEAOHUN _9 Nov, 2016.docx>

From: Andrew Clements <aclements@usaid.gov>
To: Katherine Leasure <kaleasure@ucdavis.edu>
CC: PREDICTMGT <predictmgt@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Predict inbox <predict@ucdavis.edu>
Sent: 9/27/2017 2:29:45 AM
Subject: Re: PREDICT International Travel Requests

Thanks.

In the future, I only need to see the amount Predict will be spending from USAID funding. But keep track of the cost share to document collaboration with other partners.

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 25, 2017, at 11:29 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Hi Andrew,

The total cost of Billy's flight is $6,000; the cost will be shared 50-50, so the PREDICT contribution will be $3,000.

Thank you,
Katie

From: Andrew Clements [mailto:aclements@usaid.gov]
Sent: Thursday, September 21, 2017 11:03 AM
To: Katherine Leasure
Cc: PREDICTMGT; Jonna Mazet; Predict inbox
Subject: Re: PREDICT International Travel Requests

Karesh travel to Canada approved.

Li, Simon, Dawson travel approved subject to mission concurrence.

I'd like additional information on Karesh travel to Jordan. Airfare is $6,000 including the DTRA cost share? If so, please subtract the DTRA share. If $6,000 is just he USAID part of the cost share, please include additional information to justify the cost.

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 Sep 21, 2017, at 5:56 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

From: Andrew Clements <aclements@usaid.gov>
Sent: Thu, 28 Sep 2017 09:30:41 +0200
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: David John Wolking <djwolking@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, Karen L Wood <klwood@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>, Cara Chrisman <cchrisman@usaid.gov>
Subject: [predict] Re: Construction, refurbishment, rehabilitation + Uganda Ministerial

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 Sep 27, 2017, at 11:18 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Andrew. You are correct. The answer is no.
>
> Elizabeth Leasure
> One Health Institute
> University of California, Davis
> 530-754-9034 (office)
> REDACTED (cell)
>
> **From:** David J Wolking [mailto:djwolking@ucdavis.edu]
> **Sent:** Wednesday, September 27, 2017 1:56 PM
> **To:** Elizabeth Leasure
> **Subject:** Fwd: Construction, refurbishment, rehabilitation + Uganda Ministerial
>
> ---------- Forwarded message ----------
> From: **Andrew Clements** <aclements@usaid.gov>
> Date: Tue, Sep 26, 2017 at 11:52 PM
> Subject: Fwd: Construction, refurbishment, rehabilitation + Uganda Ministerial
> To: David J Wolking <djwolking@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
> Cc: Cara Chrisman <cchrisman@usaid.gov>
>
> Hi Jonna and David,
>
> We've been asked if any of our projects have done "construction, refurbishment, or rehabilitation" (see definition below) to host country facilities.
>
> I suspect the answer is 'no' for Predict but wanted to confirm with you.
>
> 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: Cara Chrisman <cchrisman@usaid.gov>
Date: September 26, 2017 at 11:09:33 PM GMT+2
To: Andrew Clements <aclements@usaid.gov>
Cc: Alisa Pereira <apereira@usaid.gov>, Shana Gillette <sgillette@usaid.gov>, Kendra Chittenden <kchittenden@usaid.gov>, Amalhin Shek <ashek@usaid.gov>
Subject: Re: Construction, refurbishment, rehabilitation + Uganda Ministerial

Actually, I'm guessing they would use some part of this ADS definition, although it's not clear to me how exactly refurbishment would be defined within this:

"Improvements, renovation, alteration and refurbishment" for purposes of this policy includes any betterment or change to an existing property to allow its continued or more efficient use within its designed purpose (renovation), or for the use of a different purpose or function (alteration). Improvements also include improvements to or upgrading of primary mechanical, electrical, or other building systems. "Improvements, renovation, alteration and refurbishment" does NOT include non-structural, cosmetic work, including painting, floor covering, wall coverings, window replacement that does not include changing the size of the window opening, replacement of plumbing or conduits that does not affect structural elements, and non-load bearing walls or fixtures (e.g., shelves, signs, lighting, etc.).

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 (USAID)

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

On Tue, Sep 26, 2017 at 5:05 PM, Cara Chrisman <cchrisman@usaid.gov> wrote:
Thanks, Andrew. I'll note that and cc you in my response.

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 (USAID)

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

On Tue, Sep 26, 2017 at 4:41 PM, Andrew Clements <aclements@usaid.gov> wrote:
I don't think they have. However, it would help to have a definition of what is meant by refurbishment.

On Tue, Sep 26, 2017 at 7:29 PM, Cara Chrisman <cchrisman@usaid.gov> wrote:
Hi Andrew & All,

Andrew, for background, in Senior Staff yesterday, they noted that during SMT there was a question around which projects may be doing construction, refurbishment, and/or rehabilitation.

From: Andrew Clements <aclements@usaid.gov>
Sent: Wed, 18 Oct 2017 13:24:41 +0200
Subject: Re: [predict] Re: Reminder: PREDICT Management Team Call - Tuesday October 17, 2017 @ 10AM PDT/1PM EDT
To: Jonna Mazet <jkmazet@ucdavis.edu>

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 Oct 18, 2017, at 2:46 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> Here is that GHSA poster, just for your reference. Numbers are just P-2.
> Jonna

On Tue, Oct 17, 2017 at 8:51 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi,
> Apologies for the delay, this message didn't leave my outgoing mail folder yesterday. Below is our agenda for today's call.

David

PREDICT Management Team Call Agenda

Tuesday, October 17, 2017

10:00-11:00AM PDT/1:00-2:00pm EDT

REDACTED **Access code** REDACTED

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

Standing items

USAID Updates

1. **Administrative items**
   a. Brussels planning update
   b. Pending subawards & ceiling raise update
   c. Request for update on Core and Ebola budget pipelines
   d. RoC budget request from Mission
   e. Core workplan feedback
2. **Sierra Leone updates and Mission communications**
   a. Data sharing
   b. Breakthrough Action meeting feedback
3. **Mission communications roundup**
4. **EPT partner collaboration/coordination updates (Billy)**

5. **Publication, media, and conference updates**
   - Uppsala Health Summit "Tackling Infectious Disease Threats" readout
   - Scowcroft Pandemic Preparedness and Global Health Innovation Forum (Oct 17, 2017)
   - AERC Congressional briefing, Washington D.C. (Oct. 24, 2017)
   - One Health Day (Nov. 3, 2017)
   - NME Ready Together Symposium on Epidemic Preparedness, Harvard University (Nov 13, 2017)
   - PREDICT participation in PMAC and GVP launch
   - CUGH Global Health Conference, New York (March 15-18, 2018)
   - One Health Congress Saskatoon (June 22-25, 2018)

On Mon, Oct 16, 2017 at 9:16 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

Hi there,
Just a reminder about our regularly scheduled PREDICT management team call tomorrow at our usual time (Tuesday October 17, 2017 @ 10AM PDT/1PM EDT). I'll follow up with an agenda soon.

David

<ghsa-poster-draft2[1].pdf>

From: "Groschup, Martin" <REDACTED>
To: "William B. Karesh" <karesh@ecohealthalliance.org>, Tracey Goldstein <tgoldstein@ucdavis.edu>
Cc: "Mettenleiter, Thomas C." <REDACTED>, Simon Anthony <anthony@ecohealthalliance.org>, Brian Bird <bhbird@ucdavis.edu>, "Predict inbox" <predict@ucdavis.edu>
Sent: Thu, 19 Oct 2017 12:28:00 +0000
Subject: [predict] Re: Filovirus testing

Dear Tracey and Billy,
many thanks for the interest you take in our work. Yes, we have had quite some progress in terms of assay development for EBOV, so that we can proceed now with animal testing. This is about what was presented in Marburg. Plans are also to infect swine in the BSL4 on the Island of Riems, but this will take a few more months more to be realized. Instead Sandra Diederich from FLI has participated in EBOLAV infection studies of swine in Winnipeg and is doing all necessary BSL4 work herself at CFIA.
We are open for a skype call on this issue, if you are interested.
Kind regards
Martin

****
Prof. Dr. Martin H. Groschup, Dir. u. Prof.
Head of the Institute of Novel and Emerging Infectious Diseases
at the Friedrich-Loeffler-Institut
Federal Research Institute for Animal Health
REDACTED
REDACTED
Phone REDACTED
FAX +
****

Hello Billy and Thomas,

Thank so much for your emails. From a presentation at the Filovirus meeting in Germany we understand that your team has also moved forward with some of the plans that were discussed on the FAO coordinated calls, which is great! In particular it sounds like your team did some pig experimental studies in part to produce positive control sera? This is one area during the FAO calls we thought we could collaborate in terms of producing positive control material that could be tested.

We too have moved forward and have been developing a peptide ELISA assay to try to distinguish between antibodies to the various ebolavirus species. We are at a point that we could really use positive sera to determine if the assay can really differentiate between the virus species and so were wondering if it would be possible to obtain some for you to assess the assay further? If you are able to spare 1 ml serum from a pig infected with EBOV that would allow us to test for antibodies to those that would be really helpful! Please let us know if you think this is something that would be possible?

Thanks so much for considering this, Tracey

On Tue, Oct 10, 2017 at 10:43 PM, Mettenleiter, Thomas C. <REDACTED> wrote:
Dear Billy,
thank you very much for your message. As we briefly discussed during our meeting here on Insel Riems, we are interested in collaborating with you on these issues.
Martin is on duty travel today but I am sure he will contact you as well. Let's keep in touch about this!
All the best,
Thomas

Prof. Dr. Dr. h.c. Thomas C. Mettenleiter
Präsident

REDACTED

Von: William B. Karesh [mailto:karesh@ecohealthalliance.org]
Gesendet: Dienstag, 10. Oktober 2017 18:35
An: Groschup, Martin; Tracey Goldstein; Simon Anthony; Brian Bird; REDACTED
Cc: Predict inbox
Betreff: Filovirus testing

Dear Drs. Mettenleiter and Groschup,

Please allow me to introduce you to my PREDICT colleagues - Dr. Tracey Goldstein, Dr. Simon Anthony, and Dr. Brian Bird. Tracey and Simon are the co-lead on the PREDICT lab testing platforms and Brian coordinates our Ebola efforts in West Africa.

about a year and a half ago, FAO was asked by USAID to coordinate some efforts on filovirus / EHV testing among a numbe of partners and FLI was included in this group. Since then, USAID asked FAO to shift focus, but we in PREDICT are still pursuing and variety of test protocols.

I discussed my recent visit to FLI and Tracey mentioned that we are still interested in some comparison testing, particularly (but not limited to) the serology side and wondered if you and your staff at FLI would be interested in pursuing a few collaborative avenues.

Please let us know if this sounds interesting.

All the Best,

Billy

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

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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

--
Tracey Goldstein, PhD
One Health Institute
School of Veterinary Medicine
University of California
Davis, CA 95616
Phone: (530) 752-0412
Fax: (530) 752-3318
E-mail: tgoldstein@ucdavis.edu

From: William B. Karesh <karesh@ecohealthalliance.org>
To: PREDICT-outbreak <predict-outbreak@ucdavis.edu>
Sent: 10/19/2017 8:28:04 AM
Subject: [predict] [predict-outbreak] Marburg - Uganda

UVRI reported two human cases of Marburg yesterday.

BK

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

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:	1/5/2018 9:21:19 AM
Subject:	Re: Change to Approved Group ITA - Brussels Attendees

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 Jan 5, 2018, at 5:51 PM, Katherine Leasure <kaleasure@ucdavis.edu> wrote:

Hi Andrew. Please find below a change to the group ITA submitted for travel to Brussels for the All-Country Meeting in January 2018. The total approved number of participants will remain the same. Please let me know if you have any questions. Thanks!

PARTICIPANT CHANGES:

NEW	REPLACING	DEPARTURE LOCATION	AIRFARE COST
Mat Lebreton	Joseph Diffo	Yaounde, Cameroon	$2,000

Katherine Leasure
HR/Payroll/Financial Assistant
One Health Institute
University of California, Davis
530-752-7526
530-752-3318 FAX
kaleasure@ucdavis.edu

--

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Leilani Francisco <francisco@ecohealthalliance.org>
CC: David J Wolking <djwolking@ucdavis.edu>;Brian Bird <bhbird@ucdavis.edu>;Brooke Genovese <bgenovese@ucdavis.edu>;Karen Saylors <ksaylors@metabiota.com>;Jon Epstein <epstein@ecohealthalliance.org>;Tracey Goldstein <tgoldstein@ucdavis.edu>;Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>;Emily Hagan <hagan@ecohealthalliance.org>;Jaber Belkhiria <jabelkhiria@ucdavis.edu>
Sent: 5/15/2018 7:58:28 AM
Subject: More comments from Guinea (& Tanzania) on the bat book

Hi Bat Book Team,
I had a chance to go through our bat book with the Guinea team on this trip. First & foremost they are very thankful to have such a great resource. They think the messaging and the pictures are extremely good. Following the Sierra Leone team's lead, they will likely try delivering in a couple of community engagement meetings to give us more feedback. They said that they are asked all of the questions that are answered by the book routinely & that it would be nice to have a resource and to educate communities all at once, rather than over & over again one-on-one, as they do now. They said that they will only try the book after the behavior team has done their surveys, as a conclusion to leaving the village. Let me know if you have any concerns about that.

Some initial feedback:

- Most excited about the steel wool idea & helping people to have some ways to keep bats out of the home.
- They were asking why there is nothing in the book about hunting & specifically said that they are discouraging bat hunting & would like that included in the book.
- Can we have different versions with and without the anti-hunting and cooking messages if you have concerns about including that for palatability in other communities?
- I explained our concerns about viable options and compliance with the initial messaging & they told me that they are already spending a lot of time explaining about not buying and eating bat meat because that encourages hunters to be exposed, who can later bring disease to the whole community, even if eating well-cooked or smoked meat. They are very sensitized to the issue that the Ebloa outbreak started with just one exposure and then spread human-to-human.
- We all had the concern that when we tell the people to seek medical attention after a bite or scratch that the clinic staff won't know what to do when the injured person shows up. They said that they will invite the clinic staff to the community meeting, but that they anticipate questions from them about how to treat the patients. What shall we do about that? Should we consider a companion poster or something to leave behind at the clinic in the future?

In addition, Brian, David & I have also just been in Tanzania for multiple projects, including DTRA-funded work. As we discussed and was approved by USAID, the team & DTRA CBEP reps would love to have the bat book messaging used in their communities, as results are being provided with full credit to Predict & USAID. The DTRA funds could also be used to translate into Swahili if desirable. I believe David was looking into printing a version flip chart size to see how it would work in that format for community meetings, again rather than one-on-one.

Neither team had any concerns about the pictures or cultural representations depicted.

Excited to be piloting such a great resource,
Jonna

On Mon, Apr 30, 2018 at 11:08 AM, Brian Bird <bhbird@ucdavis.edu> wrote:

Hi folks,

I had the team go through solicit some informal feedback about what folks in the community are actually seeing on each page as a quick spot check on clarity.

Here are summary comments. I think for most of the images were on track, but there are a few that we'll need to explain a bit more with the words that are used, and in the long run, we should probably look at some edits to the graphics for a clearer representation of our intent (especially regarding the time secs vs. mins, little bats, use or not of eye protection).

The team started giving only the first half of the book (personal safety) on day 1, and the second half (house safety) approach this past week at it was well received. Seemed to hit better the balance of time available to community members and their interest-level.

Comments below are taken directly from their report. It's helpful to have a copy of the book open as you review them.

***CHALLENGES**: Some of the challenges faced in the field were as follows,*

- *The team had to wait for many participants to come from their fishing to administered questionnaires.*
- *There is no specific time to administered questionnaires; one should go strictly by the time of the participant.*
- *Concerning the bat book, they community was demanding that we should have posters to leave with them*

***RECOMMENDATION**:*

- *One must be ready to abide with the time and program of the study participant*
- *You must be ready at all time to answer question concerning your project.*
- *We should be going there to sensitize the entire community not only the participants*
- *The participants were very appreciative of the bat book as this was there first time of hearing what we were telling then about the bat.*

Some responses of the bat book from people by page

Page 1: the see bat eating fruits and dropping some of the fruits, there is a big and small tree.

Page 2: I see bat on flower, bat eat flowers.

Page 3: the bat and flowers were clearly identify but the insect were missed, some called then little bats

Page 4: the man with catapult, and picking up bat and cooking

Page 5: see hand touching a bat with blood and one without blood.

Page 6: see bat, drum and plate. The cover drum and plate nothing from the bat entered it but the uncovered one bat dropping is entered

Page 7: I see the bat eating fruit and a woman and got eating fruit, what the bat is eating human and animals eat too.

Page 8: I see a hand in glove/ plastic picking up a bat, a bat in the shovel and putting it in the fire and burning it or digging a hole and put it.

Page 9: I see a woman washing her hand with soap

Page 10: I see a woman watching or picking the fruits, something from the bat drop on her face and she is washing her face for 5 seconds

Page 11: one should wash hands for 5 seconds when you play with bats.

Page 12: somebody gets biting by bat and she ran to the hospital or nurse.

Page 13: I see a fruit tree, a man, woman and her kid with fowl and house

Page 15: I see a window with net and roof also with net

Page 16: I see bats hangs up the roof, toileting on the open food and the door is open, there are marks on the wall.

Page 17: I see a man covering his nose and a woman covering her nose too, the man doesn't wear glasses while the woman and others do. The woman is sweeping, and she has gloves on

Page 18: house, bat inside and outside; the door is open food is also open

Page 20: House without bats, woman with kid, food covered on the table and net on the window, door is close. The house is seal everywhere.

Each of the pages were explain to them, and at the end of the bat book questions like "how does urinate, remove feces etc.? because many of them believe that bat don't have anus and that the urinate and defecate through their mouth. But we explain to them that bat has anus and even sex organs that which can distinguish a male from a female bat.

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

Sent: Thu, 24 May 2018 10:59:06 -0700
Subject: Re: FAO WEBINAR:: Ebola and animals/Ebola et les animaux : Our knowledge to date and how AH can support the PH emergency - Tuesday 29 May 2018 at 14.30h Rome time
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: PREDICT-oubreak <predict-outbreak@ucdavis.edu>
Cc: Brooke Genovese <bgenovese@ucdavis.edu>

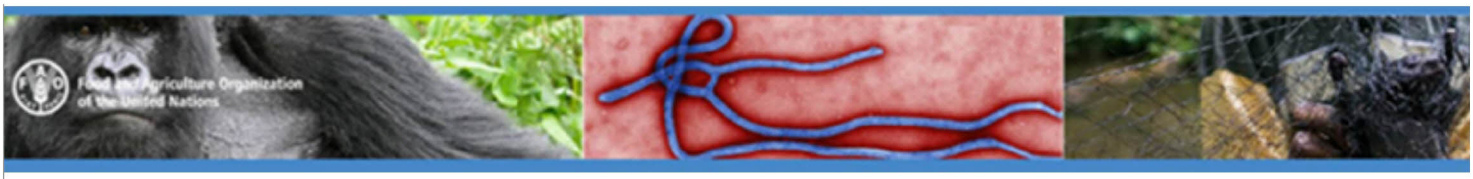
We should have somebody on this one to make sure we're all on the same page.
Any volunteers?
J

On Thu, May 24, 2018 at 8:09 AM, William B. Karesh <karesh@ecohealthalliance.org> wrote:

FYI

Begin forwarded message:

From: "VonDobschuetz, Sophie (AGAH)" <REDACTED>
Subject: WEBINAR:: Ebola and animals/Ebola et les animaux : Our knowledge to date and how AH can support the PH emergency - Tuesday 29 May 2018 at 14.30h Rome time
Date: May 24, 2018 at 6:39:31 AM EDT
To: "VonDobschuetz, Sophie (AGAH)" <REDACTED>
Cc: "Lubroth, Juan (AGAH)" <REDACTED>, "Elldrissi, Ahmed (SP5)" <REDACTED>, "Kaizman, Eran (AGAH)" <REDACTED>, "Myers, Lee (AGAH)" <REDACTED>, "Roche, Xavier, (TCE)" <REDACTED>, "Pittiglio, Claudia (AGAH)" <REDACTED>, "Ingabire, Clarisse (AGAH)" <REDACTED>, "Alviti, Alessandra" <REDACTED>, "Rumich, Nadia (AGAH)" <REDACTED>, "Sumption, Keith (AGAH)" <REDACTED>, "Biaou, Cyprien (FAOSFC)" <REDACTED>, "Kone, Philippe (FAOCD)" <REDACTED>, "NdengeHello, Marthe (FAOCD)" <REDACTED>, "BonkelaIsaNkoy, Vincent (FAOCD)" <REDACTED>, "Bebay, Charles (FAOCG)" <REDACTED>, "Soumare, Baba (FAORAF)" <REDACTED>, "Makonnen, Yilma (FAOKE)" <REDACTED>, "Gonde, Abdoulaye (FAORAF)" <REDACTED>, "SaidouniOulebsir, Asma (FAORAF)" <REDACTED>, "Newman, Scott (FAORAF)" <REDACTED>, "Bedane, Berhanu (FAOSFS)" <REDACTED>



Ebola and animals *- Ebola et les animaux*

Our knowledge to date and how AH can support the PH emergency

Les connaissances à ce jour et comment la Santé Animale peut soutenir l'urgence de Santé Publique

****WEBINAR****

Tuesday, 29 May 2018 – 14.30h Rome time
The webinar will be held in English. However, French translation of the slides will be provided.

Le webinar se tiendra en anglais. Une version française des diapositives sera fournie.

link to webinar

Prompted by the ongoing Zaire Ebola Virus (EBOV) outbreak in humans in the Democratic Republic of the Congo, the Food and Ag Organization (FAO) is updating its qualitative assessment on the risks of human exposure to EBOV from contact with wild or domestic ar their products, originally published in January 2015. We present findings from animal field surveillance and laboratory infection distribution of potential reservoir hosts (i.e. different fruit bat species) and risk modelling approaches as well as the current status of dia available for testing of animal samples (serology and virology). As an EBOV outbreak is primarily a public health (PH) emergency once h human infection occurs, we will discuss how best the animal health (AH) sector can support the PH emergency response and where we s role in a One Health coordination mechanism.

Suite à l'apparition du foyer à virus Ebola Zaïre (EBOV) en République Démocratique du Congo, l'Organisation pour l'alimentation et l'agr (FAO) a décidé de mettre à jour l'analyse de risque qualitative sur les risques d'exposition de l'homme au EBOV par contact avec les an sauvages ou domestiques ou leurs produits qui avait été initialement publié en Janvier 2015. Nous présentons ici les résultats de surveill le terrain et d'études de laboratoires, de la distribution des hôtes réservoirs potentiels et les approches de modélisation du risque ainsi l diagnostiques actuels disponibles pour les dépistages sérologique et virologique des échantillons animaux. Etant donné qu'un foyer EB avant tout une urgence de santé publique (PH) lorsque l'infection d'humain à humain se produit, nous discuterons les approches du se santé animale (AH) afin de soutenir de façon optimale l'intervention d'urgence de la santé publique et aussi où nous voyons le rôle de la sein du mécanisme de coordination One Health (i.e. « Une Santé »).

29 May 2018 at 14.30h
Local time in Rome, please check here for your timezones

Since the number of participants is restricted, we would like to ask you for your kind collaboration to please organize, wherever possible access to the webinar by office location through just one single log-in.
A recording of this webinar and French translation will be made available.

To join the webinar please click the following link, from 10 minutes prior to the start:
http://fao.adobeconnect.com/ebola_epidemiology/

When prompted, please select **"Enter as guest"** and type your **name and country** in the box provided.

You will need earphones or speakers connected to your computer and reasonable internet bandwidth. Please note that it is also possil connect on a smartphone or tablet device. In this case you will be prompted to download an app when you visit the above link.

To check that your computer is set up to connect to the webinar, please click connection test.

Please check the time in your zone: http://www.timeanddate.com/worldclock/

Please note that if you are not able to join the webinar live, a **recording will be made available later**.

Thank you to the EuFMD for its technical support.

Sophie von Dobschuetz, DVM, PhD, MSc
Veterinary Epidemiologist
Animal Health Service – FAO
Rome, Italy
Tel: REDACTED
EMPRES-i: http://empres-i.fao.org/

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>;djwolking@ucdavis.edu <djwolking@ucdavis.edu>;ealeasure@ucdavis.edu <ealeasure@ucdavis.edu>
CC: predictmgt@usaid.gov <predictmgt@usaid.gov>
Sent: 11/8/2018 10:43:17 PM
Subject: Predict-2 remaining ceiling

Total ceiling: $138,400,000
Obligated (As of Sept 30, 2018): $ 114,250,000
Ceiling Remaining: $24,150,000

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Ben Oppenheim <boppenheim@metabiota.com>, Cara Chrisman <cchrisman@usaid.gov>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, [redacted], "Dean.Jamison@ucsf.edu" <Dean.Jamison@ucsf.edu>, Dean Jamison <djamison@uw.edu>, Eddy Rubin <[redacted]>, "Carlos Zambrana-Torrelio" <zambrana@ecohealthalliance.org>, Nita Madhav <nmadhav@metabiota.com>, Yasha Feferholtz <feferholtz@ecohealthalliance.org>, Karen Saylors <ksaylors@metabiota.com>, Samtha Maher <maher@ecohealthalliance.org>, "dcarroll@usaid.gov" <dcarroll@usaid.gov>
Subject: RE: Agenda for the meeting on March 13th
Sent: Tue, 12 Mar 2019 11:21:37 +0000

Hi Ben,

I don't see the point of going through the EHA RoI work if it's before everyone arrives, so we'll just kick off at 12pm as planned, and I'll squeeze in a bit of info on the work we've done on targeting and the ROI as part of the update on the current status of the GVP.

Samantha will revise the agenda and send it round.

Cheers,

Peter

Peter Daszak
President

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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: Ben Oppenheim [mailto:boppenheim@metabiota.com]
Sent: Friday, March 8, 2019 12:43 PM
To: Cara Chrisman
Cc: Jonna Mazet; [redacted] Dean.Jamison@ucsf.edu; Peter Daszak; Dean Jamison; Eddy Rubin; Carlos Zambrana-Torrelio; Nita Madhav; Yasha Feferholtz; Karen Saylors; Samtha Maher; dcarroll@usaid.gov
Subject: Re: Agenda for the meeting on March 13th

Dear all,

Please find a revised agenda attached here.

Two changes to note:

- We would start with the EHA ROI at 11am, welcoming anyone who can start early. I've allotted 75 minutes to the first session, so we have time for a brief intro before getting into the discussion. Then at 12:15 (allowing Jonna and Cara a little wiggle room), we move into lunch and the GVP overview.
- It has also been pointed out that we have no breaks in the schedule, so a brief 15 minute break is now also included. This gives us 1:30-4pm for the BCA discussion, which is the original time we had allotted.

Kindly let me know if you have any additional considerations or concerns.
Once the agenda is finalized, we can alert the advisors and distribute the reading materials. Again, we request your input here on any additional papers or background materials that ought to be disseminated

all the best,
Ben

On Fri, Mar 8, 2019 at 8:37 AM Ben Oppenheim <boppenheim@metabiota.com> wrote:
Dear Jonna and Cara,
Thank you very much for alerting us.
Jonna, your suggestion sounds great: let's start at 11 with Yasha and Carlos' analysis, then at noon an informal lunch and discussion of GVP's goals and design. Then on to the BCA.

All: please let me know if you have any further considerations, and I'll circulate an updated schedule later today.

all the best,
Ben

On Fri, Mar 8, 2019 at 5:29 AM Cara Chrisman <cchrisman@usaid.gov> wrote:
Hi All,

I'm a similar boat as Jonna, in a meeting before this one that goes until 12pm.

Best,
Cara

Sent from my iPhone
On Mar 7, 2019, at 11:51 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> I'm afraid that I have another meeting until noon, but I can try to join as early as possible. If you are starting earlier than planned, perhaps you can start with Yasha and Carlos, as I'm more likely to be in synch with their materials. If reverting back to the agenda developed by the organizers, see you at noon.
> Sorry that I can't likely join early,
> Jonna
>
> On Thu, Mar 7, 2019 at 5:15 PM Ben Oppenheim <boppenheim@metabiota.com> wrote:
> Dear Jonna, [redacted] Peter, and Sam,
>
> There are a few different email threads going regarding the agenda for our upcoming advisory panel workshop, and so I've consolidated the various comments and inputs here (including prior edits by Jonna and [redacted]–thank you both very much).
>
> We very much welcome Peter's suggestion to focus some of the workshop on Carlos and Yasha's work on GVP's ROI. The agenda was already rather packed, so we've proposed starting earlier at 11am to ensure we have enough time to properly cover all of the content (note: we will of course need to alert the external advisors, so they can plan accordingly). We've also been corresponding with Yasha about finding time for a more intensive discussion on EHA's ROI work later in the week.
>
> There are 4 sessions, each devoted primarily to stimulating conversation and harvesting feedback from the group:
> 1. Presentation of GVP's aims and design parameters, to ensure that the external advisors are up to speed on the project
> 2. Review of EHA analytical work on GVP's ROI: methodology, findings, lessons learned

3. Review of BCA proposed methodology: modeling GVP's impacts via exceedance probability functions and economic impact estimation
4. Open questions, closing reflections, next steps

We've included a list of participants and institutions, along with scientific papers that we'd like to disseminate (particularly to the externals) before the meeting. Please review, and let us know if there are names we are missing and/or additional papers that ought to be included here.

all the best,
Ben

On Tue, Mar 5, 2019 at 8:50 PM REDACTED > wrote:

Hi Peter,

Thank you for checking in about the status of the meeting. The meeting will still take place as planned, and Ben is currently finalizing the agenda. I have copied him in this chain so that he can reflect your suggestions to the draft agenda. I am looking forward to seeing everyone next week.
Best,
REDACTED

From: Peter Daszak [mailto:daszak@ecohealthalliance.org]
Sent: Tuesday, March 05, 2019 2:37 PM
To: REDACTED; Jonna Mazet <jkmazet@ucdavis.edu>; Carlos Zambrana-Torrelio <zambrana@ecohealthalliance.org>; Yasha Feferholtz <feferholtz@ecohealthalliance.org>
Cc: Dean.Jamison@ucsf.edu; Cara Chrisman <cchrisman@usaid.gov>
Subject: Agenda for the meeting on March 13th
Importance: High

Dear REDACTED Jonna, Dean,

I just want to check if this meeting still on, given that Dennis will be out of the country.

If so, it would be good to nail down an agenda.

I'd like to propose that we start off the day with 1) Summary of GVP progress to date (Jonna/Peter); 2) Report from us here at EHA on the analysis for the GVP targeted sampling and the ROI analysis we completed earlier (Carlos/Yasha/Samantha). This will give a good basis from which you, Dean, can then report back on progress to date on your more detailed analysis of ROI.

After that, we can get into the details of what the next steps are for your work and future plans from our side.

Look forward to talking and hopefully seeing you here in NYC.

Cheers,

Peter

Peter Daszak
President

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Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

REDACTED

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Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

REDACTED

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Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

REDACTED

From: Molly Turner <turner@ecohealthalliance.org>
Sent: Thu, 18 Apr 2019 12:26:02 -0400
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: Hannah R Chale <hrchale@ucdavis.edu>, Evelyn Luciano <luciano@ecohealthalliance.org>, predict Sympa List <predict@ucdavis.edu>
Subject: [predict] Re: Cost share certification from EHA

You mean our overall commitment, including contributions from our partners? If so, I went ahead and did so in my last email :)

On Thu, Apr 18, 2019 at 12:23 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Molly. After giving it some thought last night, I think we should reduce the EHA portion of the revised Y5 commitment so that the net change is zero. Getting Andrew's approval for cost share revisions is more about the type of cost share being committed, not so much the exact amount (in my mind at least), so you could still certify the full revised Y5 figure for EHA personnel time plus waived IDC as long as the type of cost share is consistent with the revision that is (hopefully) approved by Andrew. I just worry that if you increase your commitment through this revision and then something falls through with your in-country partners, you'll end up in a pickle. Thoughts?
>
> *Elizabeth Leasure*
>
> *Financial Operations Manager*
>
> *One Health Institute*
>
> REDACTED *(cell)*
>
> *530-754-9034 (office)*
>
> *Skype: ealeasure*
>
> **From:** Molly Turner <turner@ecohealthalliance.org>
> **Sent:** Thursday, April 18, 2019 8:49 AM
> **To:** Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
> **Cc:** Hannah R Chale <hrchale@UCDAVIS.EDU>; Evelyn Luciano <luciano@ecohealthalliance.org>; predict Sympa List <predict@ucdavis.edu>
> **Subject:** Re: Cost share certification from EHA
>
> Hey Liz,
>
> I think that's right --both Chulalongkorn and Human Link were both eager to share with us the difference between the actual costs of project implementation and the amount the project is able to fund directly, and I thought it might not be a bad idea to plan to over-shoot our commitment in case something fell through. I can reduce somewhere if you like but all these amounts are currently contractually obligated, so we'll have actually "cost-shared" the higher amount.
>
> Thanks,
>
> Molly

On Wed, Apr 17, 2019 at 6:19 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

Hi again. I made some minor changes to the spreadsheet to help Andrew review it as quickly as possible, and I found that the Revised Y5 amount was not pulling directly from the detailed breakdown of the requested revised Y5 cost share (cell G77). I revised this and noted that the detailed breakout of revised cost share amounts totals $1,177,304.

We can submit the spreadsheet as it is attached and increase your overall commitment by $40,457, or you can revise the Year 5 revised cost share detailed section so that the total Revised Y5 figure is $306,795, which would not increase or decrease your overall commitment of $1,136,846. Please let me know how you would like to proceed.

Thanks,

Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *(cell)*

530-754-9034 (office)

Skype: ealeasure

From: Elizabeth Leasure
Sent: Wednesday, April 17, 2019 3:08 PM
To: Molly Turner <turner@ecohealthalliance.org>; Hannah R Chale <hrchale@ucdavis.edu>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>
Subject: RE: Cost share certification from EHA

Hi Molly. In reviewing, there were a couple questions that came up. Please see below.

- **Year 3 (Bangladesh), icddr,b:** Can you clarify if the $19K for the RT-PCR machine cost share is for the purchase of a new machine or the monetary value of the project's use of icddr,b's machine? Please also clarify how you calculated the value of the contribution to the project.
- **Multiple years, (Egypt), Human Link:** Can you please clarify how you calculated the monetary value of the equipment use and depreciation contribution to the project?
- **Multiple years, (Thailand), Chulalongkorn:** Can you please clarify how you calculated the monetary value of the equipment use contribution to the project?

Thanks,

Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *(cell)*

530-754-9034 (office)

Skype: ealeasure

From: Elizabeth Leasure
Sent: Wednesday, April 17, 2019 2:22 PM
To: Molly Turner <turner@ecohealthalliance.org>; Hannah R Chale <hrchale@ucdavis.edu>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>
Subject: RE: Cost share certification from EHA

Reviewing now…

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *(cell)*

530-754-9034 (office)

Skype: ealeasure

From: Molly Turner <turner@ecohealthalliance.org>
Sent: Wednesday, April 17, 2019 10:53 AM
To: Hannah R Chale <hrchale@UCDAVIS.EDU>; Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>
Subject: Cost share certification from EHA

Hi ladies,

Attached, sorry for the delay. I'm sorry to nag, but any update on Andrew's approval for our revised cost share plan?

Thanks,

Molly

--

Molly Turner

PREDICT Operations Manager for EHA

EcoHealth Alliance Operations

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--

Molly Turner

PREDICT Operations Manager for EHA

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--
Molly Turner
PREDICT Operations Manager for EHA
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From: Ben Oppenheim <boppenheim@metabiota.com>
Sent: Thu, 25 Jul 2019 17:50:31 -0700
Subject: Re: Gavin has now said yes...
To: Dean Jamison <REDACTED
Cc: Nita Madhav <nmadhav@metabiota.com>, "Dr. Stefano Bertozzi" <sbertozzi@berkeley.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, Gavin Yamey <gavin.yamey@duke.edu>
Building_a_global_atlas_of_zoonotic_viruses.pdf
Science GVP Supplementary 2018-Carroll-SM.pdf
Holmes, Rambaut Andersen.pdf
Science GVP 2018.pdf
2018-04-16-edi-economic-case-for-the-GVP.pdf

That's wonderful news, and Gavin, welcome aboard!
Attached, you will find several papers, including:

- the "pitch" for the GVP, which appeared in science, along with its technical appendix
- A brief economic analysis of the impacts of GVP (our approach here is quite different but useful to see what they're doing)
- an important critique of GVP's design and aims by Holmes et al.

and of course happy to share more background material, including our workplan, if you would find that useful

all the best,
Ben

On Thu, Jul 25, 2019 at 12:17 PM Dean Jamison <REDACTED> wrote:

> …to joining the BCA Advisory Committee, although he will be unable to join us in Berkeley in August. He will plan to join us for AC3 in NY in October or November as we begin the transition from developing our analysis to inserting it into policy discourse.
>
> Gavin, as you know, has worked for many years on analysis of the R&D pipeline and on new directions for development assistance for health. And he and I have collaborated closely for many years with Larry Summers as (the writing) members of the Commission for Investing in Health. I'm absolutely delighted that Gavin can join us even fairly late in the process.
>
> GAVIN — there are two of the 4 or 5 papers that will emerge from this project that may particularly interest you. One concerns cross country spillovers of emergent viral infections and implications for DAH. I think a phone call with several of us, particularly Ben and Nita, may be useful for all of us. Stef is looking at (possible) implications of GVP for accelerating the product development pipeline, and again a phone call might be useful for us all.
>
> BEN — I wonder if you could please send Gavin a few key background items? The short Science article is I think particularly important as is our slide deck. And maybe you could circulate to all of us the list of AC members (after adding Gavin's name!).
>
> Best
>
> Dean

--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

REDACTED

Building a global atlas of zoonotic viruses

Dennis Carroll,[a] Brooke Watson,[b] REDACTED [c] Peter Daszak,[b] Jonna AK Mazet,[c] Cara J Chrisman,[a] Edward M Rubin,[d] Nathan Wolfe,[d] Carlos M Morel,[e] George F Gao,[f] Gian Luca Burci,[g] Keiji Fukuda,[h] Prasert Auewarakul[j] & Oyewale Tomori[k]

At the Prince Mahidol Awards Conference on 30 January 2018 in Bangkok, Thailand, policy- and decision-makers, experts, researchers, donors and private sector representatives from across the globe came together to introduce and explore the dynamics of the Global Virome Project. The project is an innovative 10-year proposed partnership to develop a global atlas of most of the planet's naturally occurring potentially zoonotic viruses. The project aims to transform the study of emerging diseases by building an unprecedented database of viruses in their ecological contexts. This foundation of information on viral sequences, geographic ranges and host distributions will be used to drive the development of prevention efforts against future threats. This international alliance will connect the next generation of scientists, build capacity at hotspots of viral emergence and promote equitable access to data and strategies to prevent epidemics.

Despite the human and economic impact of viral epidemics, the world is not well enough prepared for the next emerging viral outbreak. Global trends indicate that new microbial threats will continue to emerge at an accelerating rate, driven by our growing population, expanded travel and trade networks, and human encroachment into wildlife habitat.[1] Most emerging viruses are zoonotic, that is, transferred between vertebrates and humans.[2] Nearly all zoonoses originate in mammalian or avian hosts;[3–5] for example, type 1 human immunodeficiency virus (HIV-1) originated in chimpanzees and Ebola virus in bats.[6] Estimations show that there are more than 1.6 million mammalian and waterfowl viruses, spanning 25 viral families known to cause human infections.[4] Compared to just over 260 viruses known in humans,[7] the unknown viruses represent 99.9% of potential zoonoses. These viruses usually remain undetected until they cause disease in humans.

Discovering and characterizing viruses in wildlife reservoirs is economically and technologically challenging. However, recent initiatives, including the PREDICT project of the United States Agency for International Development's Emerging Pandemic Threats programme, have shown that systematic viral discovery, even in countries with limited laboratory infrastructure, is feasible.[8,9] Previous studies have identified mammalian species,[10] geographic regions[11] and zoonotic viral transmission pathways[12,13] with increased risk of zoonotic disease emergence. These data enable targeting of viral discovery in wildlife to expand our knowledge of likely zoonotic agents with a high potential for spillover to people. The PREDICT project has already discovered over 1000 viruses, including novel Severe Acute Respiratory Syndrome (SARS)-like coronaviruses that can infect human cells.[14]

The Global Virome Project seeks to significantly expand the scale of targeted viral discovery over a decade-long sampling and laboratory testing period.[4] An international consortium of leading disease ecologists, public health practitioners, veterinarians, epidemiologists, biologists and laboratory scientists designed the project.[4] The project's working groups of ecologists, epidemiological modellers and field biologists will select sampling sites and species that harbour the greatest number of unknown zoonoses,[7] and researchers will systematically collect and characterize viruses and their associated metadata in these areas. Protocols for the project's implementation, including training, sampling, specimen handling, laboratory testing, reporting and data management are being developed by the PREDICT project, which has been operating for eight years in over 35 countries.[8,9] The Global Virome Project will operate as a federation of national and regional projects led by in-country researchers, who are in turn connected to a global hub that provides standardized protocols and monitors progress.

The Global Virome Project seeks to identify the majority of unknown viral diversity, catalogue the ecological conditions at sampling sites, and collect metadata that can be used to analyse the risk of viral spillover into humans. These data will be housed in an open-access database available to the global health community. Such a data set can be used to develop, train and test machine learning algorithms to identify patterns among viruses, classify traits that are more common in zoonoses than in other viruses, and predict which viruses have an increased risk of emerging in humans.

[a] Pandemic Influenza and other Emerging Threats Unit, Bureau for Global Health, United States Agency for International Development, Washington DC, United States of America (USA).
[b] EcoHealth Alliance, New York, USA.
[c] One Health Institute, School of Veterinary Medicine, University of California, Davis, California, USA.
[d] Metabiota, San Francisco, California, USA.
[e] Center for Technological Development in Health, Oswaldo Cruz Foundation, Rio de Janeiro, Brazil.
[f] Institute of Microbiology, Chinese Academy of Sciences, Beijing, China.
[g] International Law Department, Graduate Institute of International and Development Studies, Geneva, Switzerland.
[h] School of Public Health, Hong Kong University, Hong Kong, China.
[j] Department of Microbiology, Faculty of Medicine, Siriraj Hospital, Mahidol University, Bangkok, Thailand.
[k] Nigerian Academy of Science, University of Lagos, Lagos, Nigeria.
Correspondence to REDACTED (email: REDACTED
(*Submitted: 20 October 2017 – Revised version received: 4 December 2017 – Accepted: 7 February 2018 – Published online: 5 March 2018*)

To ensure equitable sharing of benefits from this project, a working group for ethical, legal and social implications has been an integral part of the Global Virome Project since its inception. All research conducted as a part of the Global Virome Project will hold to ethical standards that ensure sharing, including authorship and intellectual property. Central to the ethos of the Global Virome Project is the commitment to building scientific and response capacity in the areas that need it most.

Building capacity

Novel viruses usually emerge in regions where dense human populations and biodiversity intersect.[11] However, these areas often have limited laboratory, surveillance and health system infrastructure, which delays detecting emerging pathogens and preventing their potential to become pandemic.[15] Thus, to be effective, pandemic prevention should take place at the source of viral spillover events, before they spread regionally.[16] The Global Virome Project seeks to make data on novel potential zoonotic viruses available to public health agencies that face undiagnosed illness in humans and animals. The project has the potential to benefit human and animal health through broad measures, such as: (i) using polymerase chain reaction assays for an expanded diversity of potentially zoonotic viral families to shorten the time between outbreak detection and pathogen identification; (ii) strengthening global epidemic preparedness through investment and training in epidemiological surveillance, field biology, laboratory techniques and biosafety; (iii) identifying high-risk pathogens in wildlife populations that have high contact with people (for example hunted species and peridomestic species); (iv) establishing sample biobanks, making data and samples available for public health risk assessments and mitigation as well as more detailed pathogen studies; and (v) identifying intervention strategies for human behaviours that increase the risk of novel viral spillover.

Enhancing our understanding

The Global Virome Project will catalyse new approaches to identify the viruses that represent the greatest threat to human or animal health. The project will use artificial intelligence across the largest viral data set ever assembled, similar to machine learning techniques that are used in genomics to identify gene function, expression and disease biomarkers.[17] The project will use a risk assessment framework that includes data on viral phylogeny, host traits and ecological conditions where the virus exists, as well as a series of viral characteristics known to be associated with spillover, to triage viruses for further characterization.[4] The scale of the project's viral testing will also enable piloting and enhancing novel testing platforms technologies, such as virome capture and sequencing.[18]

The project is ambitious but feasible, enabled by technological developments that allow for rapid and affordable genetic and viral sequencing. The project is time-bound and limited in scope and has tangible progress metrics. In the past, the Human Genome Project, another ambitious science project, sequenced and mapped the human genome, starting with a focus on the genes with the greatest relevance to people. The ultimate success of the Human Genome Project is in the medical advances made after the project's conclusion. Similarly, the Global Virome Project aims to focus testing on the minimum number of mammalian and waterfowl samples that have the greatest potential of harbouring viruses with zoonotic potential. The exclusion of invertebrates, plants, fish and other hosts from the project's core focus is a deliberate intent to address zoonotic disease. The legacy of the Global Virome Project will probably consist of the countermeasures, diagnostics, vaccines, policies and systems that it enables. Thus, this project has the potential to achieve for pandemics and large-scale epidemics what the Human Genome Project is just beginning to do for personalized medicine.[19]

Novel countermeasures

The development of countermeasures to viral threats requires significant time and investment, and it is unlikely that these would be developed during the initial Global Virome Project phases. The recently launched Coalition for Epidemic Preparedness Innovations represents a critical step to address known viral threats, such as the Middle East respiratory syndrome coronavirus, Lassa fever and Nipah virus, for which vaccine or countermeasure development is challenging.[20] The Global Virome Project aims to complement the coalitions' innovations by characterizing the size, structure and composition of the pool of unknown viruses related to the viral targets on which the coalition is focused. For example, if a candidate vaccine against Middle East respiratory syndrome could be tested against hundreds of near relatives of that same syndrome, vaccines that have broader prevention capacity could be selected and rolled out to provide better protection against future emergence of this syndrome. This approach could enhance biotechnological efforts to move from single-virus countermeasures to ones that target a whole family of viruses.[21]

Project investment

In a single outbreak in one year, the Severe Acute Respiratory Syndrome virus wiped between 10 and 50 billion United States dollars (US$) of value from Asian stock markets due to disrupted trade and commerce.[22,23] Influenza pandemics are estimated to cause an average of US$ 570 billion in economic damages per year to the global economy,[24] and these costs will rise as our economies expand and become more interconnected. The Global Virome Project will cost US$ 1.2 billion, which is less than 0.2% of this estimated loss[4] and less than the estimated US$ 2.2 billion loss in gross domestic product due to forgone economic growth in Guinea, Liberia, Sierra Leone in 2015 alone during the 2013–2016 Ebola virus disease outbreak.[25] Much like the Global Fund, Gavi, the Vaccine Alliance and other international public health initiatives, the Global Virome Project will likely rely on a broad mix of funding streams from governments, development agencies, research agencies, private foundations and industries. Considering the increasing inevitability of pandemics and their substantial economic impact, the next generation of scientists and field workers trained through this project will have the capacity to monitor viral evolution throughout the coming years. Furthermore, the project's open database will catalyse technological advances in risk assessment, diagnostics and countermeasures. ■

Competing interests: None declared.

References

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of the convention — CCAMLR must be more precautionary and adaptive. This may mean that quotas are reduced, or that allocations are more temporally and spatially explicit. If the threat of overfishing is deemed readily apparent, or if the level of uncertainty is too high, then CCAMLR may need to temporarily close regions of the Southern Ocean to fishing.

Develop more-robust research and monitoring programmes. The Scientific Committee on Antarctic Research (SCAR) should first compile the available information and ongoing research regarding the effects of climate change and fish populations in Southern Ocean ecosystems. The committee undertook these analyses for krill, before establishing the CCAMLR convention. SCAR should then work with CCAMLR scientists, independent experts and non-governmental organizations to identify crucial questions, and what is required to answer them. CCAMLR needs to be more transparent and to invite SCAR and other independent experts into its scientific working groups, from which they are currently excluded.

Governments that are part of CCAMLR will need to fund the research and monitoring efforts, which must be independent of the fishing industry. The Palmer LTER programme shows that the techniques are available, but investment is needed to expand the scientific reach.

CCAMLR states have acted quickly in the past, but change is accelerating in the Southern Ocean. Countries must rise swiftly to this challenge. ■ SEE INSIGHT P.199

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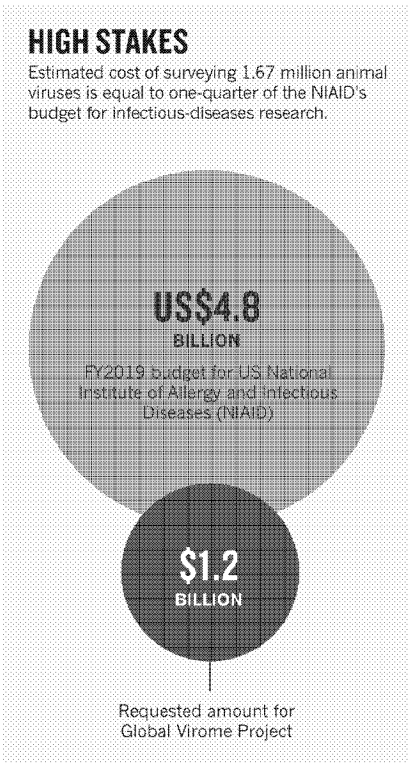
Pandemics: spend on surveillance, not prediction

Trust is undermined when scientists make overblown promises about disease prevention, warn **Edward C. Holmes, Andrew Rambaut** and **Kristian G. Andersen.**

The resurgence of Ebola virus in the Democratic Republic of the Congo this May is a stark reminder that no amount of DNA sequencing can tell us when or where the next virus outbreak will appear. More genome sequence data were obtained for the 2013–16 Ebola epidemic than for any other single disease outbreak. Still, health workers in Mbandaka, the country's northwestern provincial capital, are scrambling to contain a growing number of cases.

Over the past 15 years or so, outbreaks caused by viruses such as Ebola, SARS and Zika have cost governments billions of US dollars. Combined with a perception among scientists, health workers and citizens that responses to outbreaks have been inadequate, this has fuelled what seems like a compelling idea. Namely, that if researchers can identify the next pandemic virus before the first case appears, communities could drastically improve strategies for control, and even stop a virus from taking hold[1,2]. Indeed, since 2009, the US Agency for International Development has spent US$170 million on evaluating the "feasibility of preemptively mitigating pandemic threats"[1].



Various experts have flagged up problems with this approach (including the three of us)[3,4]. Nonetheless, an ambitious biodiversity-based approach to outbreak prediction — the Global Virome Project — was announced in February this year, with its proponents soliciting $1.2 billion in funding from around the world (see 'High stakes'). They estimate that other mammals and birds contain 1.67 million unknown viruses from the families of viruses that are most likely to jump to humans, and will use the funding to conduct a genomic survey of these unknown viruses, with the aim of predicting which might infect people[1].

Broad genomic surveys of animal viruses will almost certainly advance our understanding of virus diversity and evolution. In our view, they will be of little practical value when it comes to understanding and mitigating the emergence of disease.

We urge those working on infectious disease to focus funds and efforts on a much simpler and more cost-effective way to mitigate outbreaks — proactive, real-time surveillance of human populations.

The public has increasingly questioned the scientific credibility of researchers working on outbreaks. In the 2013–16 Ebola epidemic, for instance, the international response was repeatedly criticized for being too slow. And during the 2009 H1N1 influenza epidemic, people asked whether the severity of the virus had been overblown, and if the stockpiling of pharmaceuticals was even necessary[5]. Making promises about disease prevention

JUNIOR KANNAH/AFP/GETTY

A health official checks for Ebola symptoms by taking the temperature of passengers arriving at Mbandaka Airport in the Democratic Republic of the Congo.

and control that cannot be kept will only further undermine trust.

FORECASTING FALLACY

Supporters of outbreak prediction maintain that if biologists genetically characterize all of the viruses circulating in animal populations (especially in groups such as bats and rodents that have previously acted as reservoirs for emerging viruses), they can determine which ones are likely to emerge next, and ultimately prevent them from doing so. With enough data, coupled with artificial intelligence and machine learning, they argue, the process could be similar to predicting the weather[6].

Reams of data are available to train models to predict the weather. By contrast, it is exceedingly rare for viruses to emerge and cause outbreaks. Around 250 human viruses have been described, and only a small subset of these have caused major epidemics this century.

Advocates of prediction also argue that it will be possible to anticipate how likely a virus is to emerge in people on the basis of its sequence, and by using knowledge of how it interacts with cells (obtained, for instance, by studying the virus in human cell cultures).

This is misguided. Determining which of more than 1.6 million animal viruses are capable of replicating in humans and transmitting between them would require many decades' worth of laboratory work in cell cultures and animals. Even if researchers managed to link each virus genome sequence to substantial experimental data, all sorts of other factors determine whether a virus jumps species and emerges in a human population, such as the distribution and density of animal hosts. Influenza viruses have circulated in horses since the 1950s and in dogs since the early 2000s, for instance[7]. These viruses have not emerged in human populations, and perhaps never will — for unknown reasons.

> *"The challenge is to link genomic, clinical and epidemiological data within days of an outbreak being detected."*

In short, there aren't enough data on virus outbreaks for researchers to be able to accurately predict the next outbreak strain. Nor is there a good enough understanding of what drives viruses to jump hosts, making it difficult to construct predictive models.

Biodiversity-based prediction also ignores the fact that viruses are not fixed entities. New variants of RNA viruses appear every day. This speedy evolution means that surveys would need to be done continuously to be informative. The cost would dwarf the proposed $1.2-billion budget for one-time sequencing.

Even if it were possible to identify which viruses are likely to emerge in humans, thousands of candidates could end up being identified, each with a low probability of causing an outbreak. What should be done in that case? Costs would skyrocket if vaccines and therapeutics were proposed for even a handful of these.

SCREEN AND SEQUENCE

Currently, the most effective and realistic way to fight outbreaks is to monitor human populations in the countries and locations that are most vulnerable to infectious disease. This can be done by local clinicians, health workers in non-governmental organizations such as Médecins Sans Frontières (MSF; also known as Doctors Without Borders), and global institutions such as the World Health Organization (WHO).

We advocate the detailed screening of people who are exhibiting symptoms that cannot easily be diagnosed. Such tests should use the latest sequencing

technologies to characterize all the pathogens that have infected an individual — the human 'infectome'[8]. To track previous infections, investigators should also assess each person's immune response, by analysing components of their blood using broad-scale serology[9].

Emerging diseases are commonly associated with population expansions — when people encroach on habitats occupied by animals — as well as with environmental disturbances and climate change. Deforestation, for instance, can promote human interactions with animals that carry new threats, and can increase encounters with new vector species such as ticks and mosquitoes[10]. Animal die-offs, for example that of bar-headed geese (*Anser indicus*) at Lake Qinghai in China in 2005 (which was caused by the H5N1 influenza virus), can also flag problem regions or emerging pathogens. Surveillance efforts should therefore focus on communities that live and work in such environments.

Identifying which pathogen is causing an outbreak is no longer the bottleneck it once was. It took researchers two years to determine HIV as the cause of AIDS in the early 1980s using microscopy and other techniques. By contrast, in 2012 it took only weeks for investigators using genomic technologies to discover the coronavirus that caused Middle East respiratory syndrome (MERS).

Rapid identification of viruses can be achieved only if such technologies — and the people trained to use them — are globally available, including in resource-limited regions where the risk of outbreaks might be higher. Thankfully, relevant capacity-building programmes are now beginning to be established, such as the Human Heredity and Health in Africa (H3Africa) Initiative, run by the UK Wellcome Trust and the US National Institutes of Health[11].

Once an emerging outbreak virus has been identified, it needs to be analysed quickly to establish what type it is; which molecular mechanisms (such as receptor type) enable it to jump between individuals; how it spreads through human populations; and how it affects those infected. In other words, at least four kinds of analysis are needed: genomic, virological, epidemiological and clinical. And the data must be passed to key stakeholders, from researchers and health workers on the ground to international agencies such as the WHO and the MSF. Data must be kept as free of restrictions as possible, within the constraints of protections of patient privacy and other ethical issues.

This will best be achieved through an established global network of highly trained local researchers, such as the WHO Global Outbreak Alert and Response Network (GOARN). Real-time tools for reconstructing and tracking outbreaks at the genomic level, such as portable sequencing devices, are improving fast[8]. Information gathered during recent outbreaks has quickly had tangible impacts on public-health decisions, largely owing to data generation and analysis by many research teams within days of people being infected[12].

KENNY KATOMBE/REUTERS

People in Mbandaka are taking extra precautionary measures to stop the spread of Ebola virus.

For instance, in the 2013–16 Ebola epidemic, genome sequencing of the virus proved that a person could sexually transmit the disease more than a year after becoming infected. This prompted the WHO to increase its recommended number of tests for persistent infection in survivors of the disease.

"There is a growing move towards real-time, open-access data and analysis."

Ultimately, the challenge is to link genomic, clinical and epidemiological data within days of an outbreak being detected, including information about how people in an affected community are interacting. Such an open, collaborative approach to tackling the emergence of infectious disease is now possible. This is partly thanks to technology, but is mainly due to a shift in perception about the importance of this approach. At least in genomic epidemiology, there is a growing move towards real-time, open-access data and analysis, aided by the use of preprint servers and wikis such as Virological (http://virological.org). This type of collaborative effort can complement the work of agencies including the WHO and the MSF, which focus predominantly on providing information, isolating those who have been infected, and so on.

So far, researchers have sampled little of the viral universe. Surveys of animals will undoubtedly result in the discovery of many thousands of new viruses. These data will benefit studies of diversity and evolution, and could tell us whether and why some pathogens might jump species boundaries more frequently than others. But, given the rarity of outbreaks and the complexity of host–pathogen interactions, it is arrogant to imagine that we could use such surveys to predict and mitigate the emergence of disease.

New viruses will continue to emerge unexpectedly. There is a lot we can and must do to be better prepared. ■

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EMERGING DISEASE **INSIGHTS**

Research from the PREDICT Modeling & Analytics team

Global Costs of Emerging Infectious Diseases: an Economic Case for the Global Virome Project

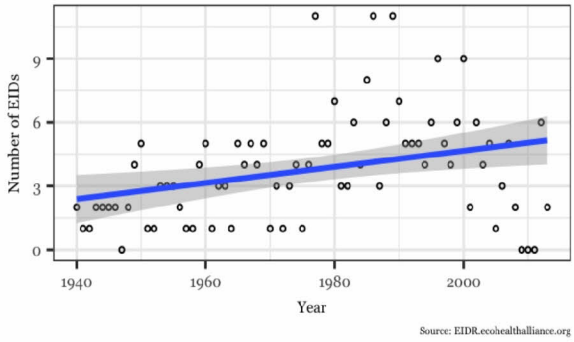
A single emerging infectious disease epidemic such as the SARS pandemic in 2003 can cost the global economy an estimated $30-50 billion, but investments in prevention and research are often insufficient. To make the economic case for investing in large-scale research, surveillance, and prevention programs, it is important to model and quantify the future economic impacts of Emerging Infectious Diseases (EIDs) and pandemics.

The Global Virome Project (GVP) is a proposed 10-year global effort to discover the majority of viruses with likely zoonotic potential residing in mammals and waterfowl. This project could reduce the burden of emerging infectious diseases by creating a viral sequence and metadata atlas that will support risk assessments, development of mitigation plans, and lower response times. The data generated by the GVP is also likely to speed technological advancements and provide a starting point for diagnostic and therapeutic discovery and development. Based on current projected lab and field costs, the GVP is estimated to be achievable for $1.2 billion or $120M annually over the next ten years. Given our estimations of EID frequency, mortality rates, and impacts on the global economy, we project the costs of all potential zoonotic emerging disease events over the next 30 years and calculate projected Return on Investment (ROI).

COSTS OF EMERGING INFECTIOUS DISEASES

The incidence of emerging infectious disease events is on the rise (1). A majority of these diseases, including SARS, MERS, Avian Influenza, and Ebola, are zoonoses caused by spillover from animal into human populations. To project future annual rates of zoonotic EID events, we calculate the average frequency and variance of EID events per year and the rate of change over time (2). We built a model to estimate the mortality, morbidity, and economic shocks per event, based on case fatality data from the Emerging Infectious Diseases Repository (EIDR).

Figure 1: Annual frequency of Emerging Infectious Diseases from 1940 to 2013.



ESTIMATING GLOBAL DAMAGES FROM EID EVENTS

Global damages, or economic costs, from emerging infectious diseases (EID) depend on the annual number of EID events and the average cost of each event. Damages of one event are the sum costs from mortality $M(t)$, morbidity $A(t)$, and economic shocks $G(t)$. To find the total present value of global damages $PVGD$, we use a standard five percent rate (δ=0.05) to discount future savings to their current value.

$$PVGD = \int_{t=0}^{t=30} (M(t) + A(t) + G(t))\, e^{-\delta t}$$

We use conventional methods to calculate the value of a statistical life and the value of one day

April 16, 2018

For details on methods or analysis contact: PREDICTmodeling@ecohealthalliance.org

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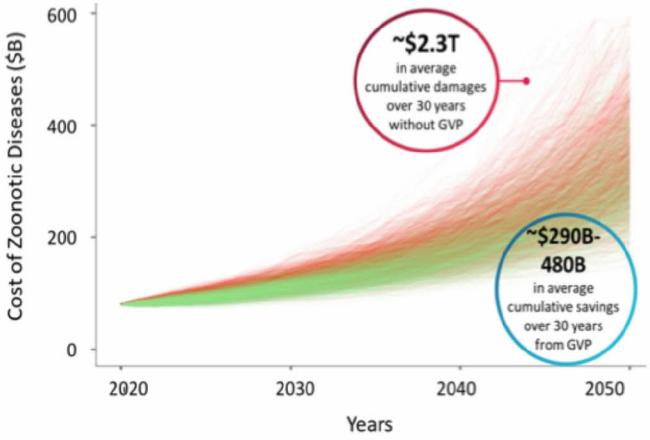
of work lost (3). In our model, economic shocks are proportional to the mortality of the event. We parameterized our model using the forecasted number of annual EID events, the historical global GDP growth rate of 2.4%, and the 2015 global GDP of $73.4 trillion. **Averaged over 5000 simulations, we find the discounted cost of emerging infectious diseases to be US$2.3 trillion over the next 30 years.**

COSTS AND ROI OF A GLOBAL VIROME PROJECT

To determine how much it would cost to discover all viral diversity in mammals, mark-recapture ecological techniques were used to estimate the sampling effort required to discover all viruses present in one species (4). We estimate that there are 1,669,106 (se 697,623 - 2,640,590) undiscovered viruses likely to reside in mammal and water bird hosts (2). However, only 32.2-45.0% (493,856-689,285) of these are likely to be zoonotic, and the ones that are more costly to find are less likely to spillover. Assuming that all mammal species would have equivalent lab and field costs, discovering 71% of all mammalian viruses and water bird influenzas would cost $1.2 billion, or an average of $120 million per year over 10 years.

Having a baseline of identified viral sequences would lead to earlier detection and quicker response times, lowering both epidemic frequency and impact. These improvements would not have an immediate impact, but benefits would accumulate throughout and beyond the lifespan of the GVP. For our calculations, we assume that these benefits collectively lead to an average of 10% in savings from damages in all events in the next 30 years ($290-480 billion). As such, a $1.2 billion Global Virome Project would return over $200 dollars in savings for each dollar invested.

Figure 2. Forecasted economic damages from EIDs over the next 30 years.



Red line shows damage growth under business-as-usual, green line shows reduced growth if the GVP causes a 10% reduction in damages.

Even if the GVP only reduces the likelihood and impact of EIDs by 10%, this project would generate large returns on investment due to the high and rising costs of pandemics. The premature loss of lives and economic shocks account for the largest proportion of economic damages from EID events. A $120 million annual budget for a 10-year Global Virome Project is an investment that could produce exceptionally high returns.

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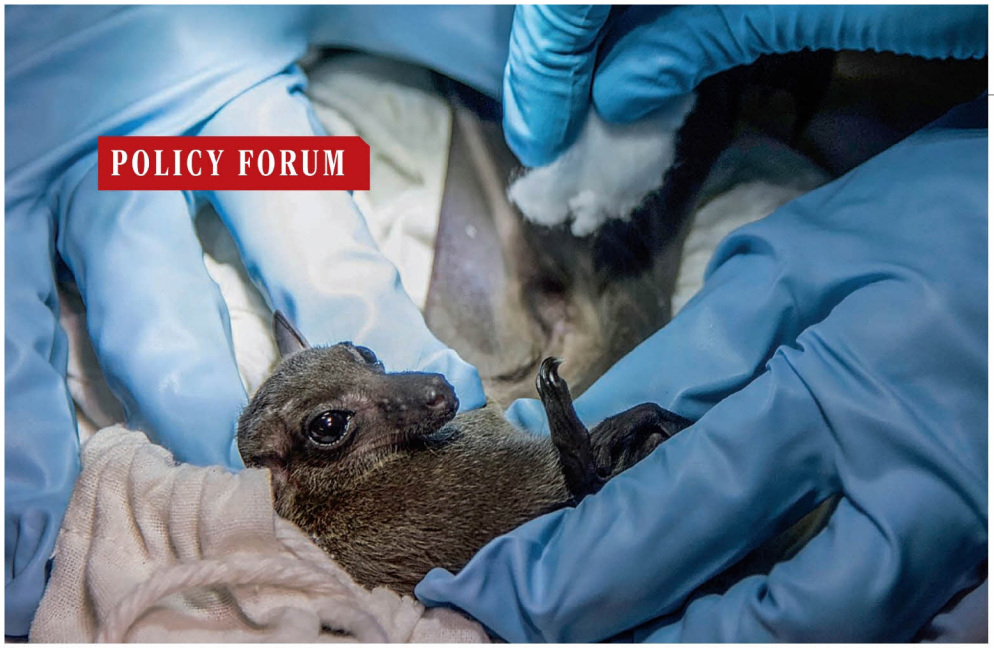

POLICY FORUM

Scientists prepare to collect a blood sample from a *Rousettus sp.* fruit bat in Thailand to test for novel viruses. The Global Virome Project aims to identify and characterize the majority of currently unknown viruses in key wildlife groups, including rodents, nonhuman primates, and bats.

INFECTIOUS DISEASES

The Global Virome Project

Expanded viral discovery can improve mitigation

By **Dennis Carroll, Peter Daszak, Nathan D. Wolfe, George F. Gao, Carlos M. Morel, Subhash Morzaria, Ariel Pablos-Méndez, Oyewale Tomori, Jonna A. K. Mazet**

Outbreaks of novel and deadly viruses highlight global vulnerability to emerging diseases, with many having massive health and economic impacts. Our adaptive toolkit—based largely on vaccines and therapeutics—is often ineffective because countermeasure development can be outpaced by the speed of novel viral emergence and spread. Following each outbreak, the public health community bemoans a lack of prescience, but after decades of reacting to each event with little focus on mitigation, we remain only marginally better protected against the next epidemic. Our ability to mitigate disease emergence is undermined by our poor understanding of the diversity and ecology of viral threats, and of the drivers of their emergence. We describe a Global Virome Project (GVP) aimed to launch in 2018 that will help identify the bulk of this viral threat and provide timely data for public health interventions against future pandemics.

Nearly all recent pandemics have a viral etiology with animal origins, and with their intrinsic capacity for interspecies transmission, viral zoonoses are prime candidates for causing the next great pandemic (*1*, *2*). However, if these viruses are our enemy, we do not yet know our enemy very well. Around 263 viruses from 25 viral families are known to infect humans (*3*) (see the figure), and given the rate of discovery following identification of the first human virus (yellow fever virus in 1901), it is likely many more will emerge in the future (*4*). We estimate, from analysis of recent viral discovery data (*5*), that ~1.67 million yet-to-be-discovered viral species from key zoonotic viral families exist in mammal and bird hosts—the most important reservoirs for viral zoonoses (supplementary text).

By analyzing all known viral-host relationships (*3, 6*), the history of viral zoonoses (*7*), and patterns of viral emergence (*1*), we can reasonably expect that between 631,000 and 827,000 of these unknown viruses have zoonotic potential (supplementary text). We have no readily available technological countermeasures to these as-yet-undiscovered viruses. Furthermore, the rate of zoonotic viral spillover into people is accelerating, mirroring the expansion of our global footprint and travel networks (*1, 8*), leading to a nonlinear rise in pandemic risk and an exponential growth in their economic impacts (*8*).

PROMISING PILOT, CHALLENGING SCALE

Since 2009, the U.S. Agency for International Development (USAID) has conducted a large-scale pilot project, spanning more than 35 countries over 8 years at a cost of around $170 million, to evaluate the feasibility of preemptively mitigating pandemic threats. Other previous studies had begun to conduct targeted viral discovery in wildlife (*9*), and develop mitigation strategies for the emergence of avian flu, for example. However, the USAID Emerging Pandemic Threats (EPT) PREDICT project is the first global-scale coordinated program designed to conduct viral discovery in wildlife reservoir hosts, and characterize ecological and socioeconomic factors that drive their risk of spillover, to mitigate their emergence in people (*10*).

Working with local partners and governments, wildlife and domestic animals and at-risk human populations in geographic hotspots of disease emergence (*1*) are sampled, and viral discovery conducted. A strategy to identify which novel viruses are most at risk of spillover has been developed (*11*), and further work is conducted on these to characterize them prior to, or in the early stages of, spillover. Metadata on the ecology of wildlife–livestock–human transmission interfaces, and on human behavioral patterns in communities, are concurrently analyzed so that strategies to reduce spillover can be developed (supplementary text). To date, EPT PREDICT has discovered more than 1000 viruses from viral families that contain zoonoses, including viruses involved in recent outbreaks (*12*), and others of ongoing public health concern (*13*). The focus of EPT PREDICT on capacity building, infrastructure support, training, and epidemiological analysis differs substantially from the GVP's emphasis on large-scale sampling and viral discovery. However, to discover the bulk of the projected remaining 1.67 million unknown viruses in animal reservoirs and characterize the majority of 631,000 to 827,000 viruses of highest zoonotic potential requires overcoming some challenges of scale.

The first challenge is cost. To estimate this, we analyzed data on field sampling and laboratory expenditures for viral discovery from (*5*, *10*), and estimates of unknown viral diversity in mammalian and avian hosts (supplementary text). 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 (supplementary text). However, previous work shows that viral discovery rates are vastly higher in the early stages of a sampling program, and that discovering the last few, rare, viruses is extremely costly and time-consuming owing to the number of samples required to find

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them (*5*) (supplementary text). We used data on rates of viral discovery (*5*) to estimate that the substantial majority of the viral diversity from our target zoonotic reservoirs could be discovered, characterized, and assessed for viral ecology within a 10-year time frame for ~$1.2 billion (16% of total costs for 71% of the virome, considering some fixed costs) (fig. S1). Those viruses remaining undiscovered will, by the nature of sampling bias toward more common host species, represent the rarest viruses with least opportunity for spillover, and therefore reduced public health risk. Their discovery would require exponentially greater sampling effort and funding that could be better spent on countermeasures for the more likely threats (supplementary text).

Stakeholders from Asia, Africa, the Americas, and Europe, spanning industry, academia, intergovernmental agencies, nongovernmental organizations (NGOs), and the private sector, began meeting in 2016 to design a framework for the governance, management, technical operation, and scope of the GVP. Key efforts include developing finance streams; establishing a transparent, equitable implementation strategy; designing data- and sample-sharing protocols; developing laboratory and metadata platforms; targeting of host taxa and sampling sites; analyzing return on investment; forming collaborative field and laboratory networks; developing risk characterization frameworks for viruses discovered; designing a strategy to assess and mitigate risk behaviors that facilitate viral emergence; and planning in-country capacity building for sustainable threat mitigation. Funding has been identified to support an initial administrative hub, and fieldwork is planned to begin in the first two countries, China and Thailand, during 2018.

With outputs intended to serve the global public good, the GVP is 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 Nagoya Protocol to the Convention on Biological Diversity and the Pandemic Influenza Preparedness Framework, negotiated by the World Health Organization (WHO). The international collaborative nature and global ownership of the project should help leverage funding from diverse international donors, including government agencies focused on national virome projects or on international development projects in other countries, and private-sector philanthropic donors focused on technology and big science.

The diversity of tasks required to conduct the GVP should reduce the potential for it to divert funds from current public health programs. For example, discrete work streams on targeted sampling of wildlife, on bioinformatics, and on behavioral risk analysis fall within the focus of current scientific research programs in a range of donor agencies. Governments and 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, and technological platforms). In addition, leaders in China and a number of countries have begun developing national virome projects as part of the GVP, leveraging current research funding to include GVP sites.

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 need to be enhanced and expanded within standardized sampling and testing frameworks. Existing networks of field biologists from environment ministries, academic institutions, and conservation and health NGOs may assist in surveillance. National science and technology agencies, regional One Health platforms, transboundary disease surveillance networks, Institut Pasteur laboratories, WHO, United Nations Food and Agricultural Organization, and the World Organization for Animal Health collaborating, and reference centers and viral discovery laboratories, including USAID EPT PREDICT, are currently involved in planning these activities around a decade-long sampling and testing time frame. A monitoring and evaluation strategy is being developed based on analysis of viral discovery rates against predicted viral diversity, to identify when to halt surveillance and testing as the GVP progresses. Stakeholders will also tackle the challenge of how to decide when enough potentially dangerous viruses have been discovered in a host species or region to call for action to reduce underlying drivers of emergence (e.g., hunting and trading of a wildlife reservoir).

> ***"...the GVP goals...improve capacity to detect, diagnose, and discover viruses in vulnerable populations..."***

Laboratory platforms developed by USAID EPT PREDICT have proven capacity to identify novel viruses and are relatively inexpensive and reliable, being based on polymerase chain reaction using degenerate primers that target a range of viral families of known zoonotic potential. However, scaling up to a full global virome project will require discovery of three orders of magnitude more viruses in a similar time frame. Technological solutions will be needed to increase the speed and efficiency, and reduce the cost, of sequence generation. These will likely include next-generation sequencing and other unbiased approaches to identify evolutionarily distinct viral clades.

A key challenge is how to assess the potential for novel viruses to infect people or become pandemic (*14*). The EPT PREDICT project (*11*) and others (*2*, *6*) have developed preliminary 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 triage novel viruses for further characterization to assess their zoonotic capacity (supplementary text). In vitro receptor binding analyses coupled with in vivo models have proven useful in this capacity for some viral families [e.g., coronaviruses (*13*)]. Although this is not yet feasible for all potentially zoonotic viral clades, applying these techniques to a larger viral data set as the GVP progresses will allow validation of risk frameworks and may increase our capacity to predict zoonotic potential. However, advancing these goals will require new collaboration among lab virologists, epidemiologists, and modelers, innovative approaches to field-testing the boundaries of virus-host relationships, and support across agencies that often fund separate virology, public health, evolutionary biology, and biodiversity modeling initiatives.

INVESTMENTS, RETURNS

The cost of the GVP represents a sizable investment and, even if a large number of potential zoonoses are discovered, only a minority is likely to have the potential to cause large-scale outbreaks and mortality in people (*1*, *2*, *7*). However, given the high cost of single epidemic events, data produced by the GVP may provide substantial return on investment by enhancing diagnostic capacity in the early stages of a new disease outbreak or by rapidly identifying spillover hosts, for example. Recent analysis of the exponentially rising economic damages from increasing rates of zoonotic disease emergence suggests that strategies to mitigate pandemics would provide a 10:1 return on investment (*1*, *8*). Even small reductions in the estimated costs of a future influenza pandemic (hundreds of billions of dollars) or of the previous SARS (severe acute respiratory syndrome) epidemic ($10 billion to $30 billion) could be substantial. The goal of the GVP is to improve efficiency in the face of these increasing viral

spillover rates by enhancing (not replacing) current pandemic surveillance, prevention, and control strategies. If we were to invest only in surveillance for known pathogens (our current business-as-usual strategy), our calculations suggest we would protect ourselves against less than 0.1% of those viruses that could conceivably infect people, even using the lower bounds of our uncertainty for our viral estimates (i.e., 263 viruses known from humans out of 263,824 unknown potential zoonoses; supplementary text).

The potential benefits of the GVP may be enhanced to maximize public health benefits (supplementary text) by (i) optimizing sampling to target species most likely to harbor "missing zoonoses" (*6*), or to target emerging disease hotspot regions most likely to propagate major disease outbreaks (*1*); (ii) using human and livestock syndromic surveillance to identify regions for wildlife sampling proximal to repeated outbreaks of severe influenza-like-illnesses, fevers of unknown origin, encephalitides, livestock "abortion storms," and other potential emerging disease events; (iii) initially targeting RNA viruses, which caused 94% of the zoonoses documented from 1990 to 2010; and (iv) fostering economies of scale and adoption of technological innovation as the GVP ramps up. This includes 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 decrease as technology is enhanced, much as the development of next-generation sequencing reduced genetic sequencing costs by up to four orders of magnitude in a decade.

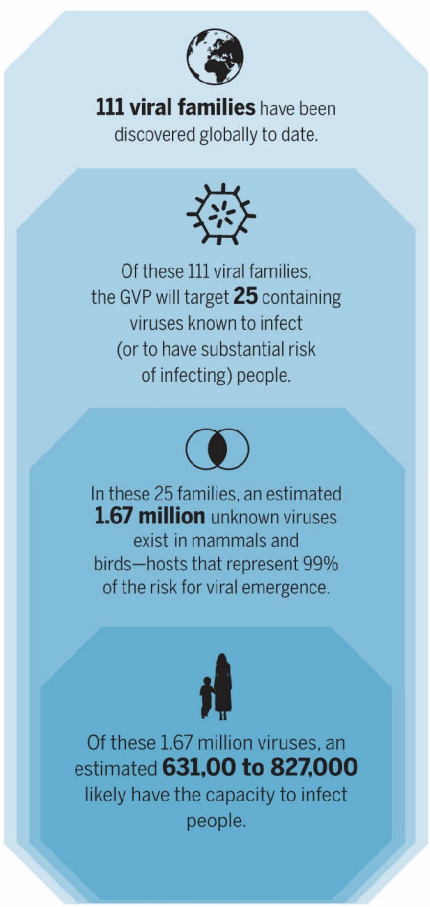
The accelerated pace of viral discovery under the GVP will make the virological, phylogenetic, and modeling approaches used in pandemic preparedness more data-rich, and likely more effective. For example, having the sequence data for thousands, rather than a few, viruses from a single family could extend vaccine, therapeutic, or drug development to a wider range of targets, leading to broad-spectrum vaccines and other countermeasures. Identification of novel viruses may be useful to programs like the Coalition for Epidemic Preparedness Innovations (CEPI) in assessing the breadth of action of candidate vaccines and therapeutics, and in expanding their efficacy. More broad-scale prevention approaches could provide immediate return on investment prior to vaccine and countermeasure development, which would require substantial investment and time. For example, metadata on viral reservoir host identity, geography, seasonality, proximity to people, and drivers of emergence will refine our mechanistic understanding of spillover and enhance published models of emerging infectious diseases risk (*1, 6*). Identification of novel viruses in hunted, traded, or farmed wildlife species could be used to enhance biosecurity in markets and farming systems, reducing public health risk, increasing food security, and assisting in conservation of hunted species. The presence of hosts harboring high-risk novel viruses in proximity to human populations may allow targeted follow-up to examine evidence of spillover and design intervention strategies (supplementary text). Ultimately, the benefits of the GVP may include enhancing our understanding of viral biology, such as drivers of competition or cooperation among viruses within hosts, genomic underpinnings of host-virus coevolution, processes underlying deep evolution of viral clades, and the identification of novel viral groups (*15*).

The regions targeted by the GVP are largely highly biodiverse, rapidly developing countries in the tropics, which often have low capacity to deal with public health crises (*1*). The expanded laboratory capacity, field sampling, and data generation intrinsic to the GVP goals will therefore improve capacity to detect, diagnose, and discover viruses in vulnerable populations within regions most critical to preventing future pandemics. This enhanced capacity may also help improve diagnosis and control for endemic diseases, as well as the portion of the virome that remains undiscovered.

The HIuman Genome Project in the 1980s catalyzed technological innovation that dramatically shortened the time and cost for its completion, and ushered in the era of personalized genomics and precision medicine. The GVP will likely accelerate development of pathogen discovery technology, diagnostic tests, and science-based mitigation strategies, which may also provide unexpected benefits. Like the Human Genome Project, the GVP will provide a wealth of publicly accessible data, potentially leading to discoveries that are hard to anticipate, perhaps viruses that cause cancers and chronic physiological, mental health, or behavioral disorders. It will provide orders-of-magnitude more information about future threats to global health and biosecurity, improve our ability to identify vulnerable populations, and enable us to more precisely target mitigation and control measures to foster an era of global pandemic prevention. ■

GVP targeting strategy

The project will capitalize on economies of scale in viral testing, systematically sampling mammals and birds to identify currently unknown, potentially zoonotic viruses that they carry.



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SUPPLEMENTARY MATERIALS

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The Global Virome Project

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Supplementary Materials for

The Global Virome Project

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Supplementary Text

The steps taken to estimate the global number of mammalian and avian viruses are detailed below. Data and code necessary to reproduce the analysis are available at **http://www.github.com/ecohealthalliance/GVP_Science**.

Estimating viral diversity in wildlife hosts of zoonotic relevance

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 *(7, 16)*. 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 (*1*), 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 that are transmitted by them at some stage in their emergence. In many biological studies, estimates of diversity include the number of species or other taxonomic units in a region (the species richness), as well as the variability within species, among species, and across landscapes, i.e. the degree of difference among organisms (*17*). For the purposes of this paper, we follow previous work (*5, 16*) and use 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. Estimates of 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 contain zoonoses (*5*). Estimates of viral diversity for the rhesus macaque *Macaca mulatta* targeted 21 viral families by PCR, as well as high-throughput sequencing (HTS) (*16*). For each host species, we obtained raw test data from (*5, 16*) ((https://github.com/ecohealthalliance/GVP_Science/blob/master/data/macaque_data.xlsx), (https://github.com/ecohealthalliance/GVP_Science/blob/master/data/pteropus_data.csv)) 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 (Code available at https://github.com/ecohealthalliance/GVP_Science/blob/master/R/pteropus_validation_anthony_2013.R and https://github.com/ecohealthalliance/GVP_Science/blob/master/R/macaque_validation_anthony_2015.R, respectively). 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 Picobirnoviruses 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 the Global Virome Project (GVP), the mean is a more useful metric so that costs are not underestimated. The likely variability in viral diversity among mammalian species and viral families highlights the need for a strategy to monitor sampling and test results in real time to guide per-species sampling as the GVP proceeds (see below).

To decide which viral families to include in GVP testing protocols, we used the stringent database from (*6*) that requires PCR evidence of viral sharing among humans and other animals, and is derived from (*3*). All 21 viral families targeted in (*5, 16*) contain known zoonoses, based on PCR reports in the database from (*6*), but neither study covered the Hepeviridae, which also contains zoonoses, so this was included. 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 viral emergence from either known or unknown viral *Arterivirus* species, given close evolutionary relationships between humans and other primates. The Bornaviridae was not included because the evidence for its zoonotic origin is unclear, and most reports of animal

infections are from livestock, not wildlife (*18, 19*). The Hepadnaviridae was included because there is PCR and *in vitro* infection evidence of viral origin in wildlife species that are known high zoonotic risk reservoirs, suggesting high likelihood of related novel viruses capable of spilling over into people (*20*). We therefore multiply the per-viral family mean of 11.58 species by 25 (see specific viral families listed below) to give an estimate of the total viral diversity within all 25 viral families that have high zoonotic potential as 289.5 (se 121.0 - 458.0) for each mammalian host species. Given that there are 5,291 known mammal species (*21*) (excluding marine mammals which have limited contact with humans relative to terrestrial and volant mammals) we estimate global mammalian viral richness in our 25 target viral families at 1,531,745 (se 640,211 - 2,423,278). In addition, influenza viruses derived from mammals 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 of the 11,862 known bird species bird species (*22*). This gives an estimated avian influenza viral richness of 137,362.96 (se 57,412 - 217,312), and a total global richness of viral species from families with high zoonotic potential of around 1,669,106 (se 697,623 - 2,640,590).

The viral families to be targeted by the GVP include 16 families of RNA viruses known to infect people: Arenaviridae, Astroviridae, Bunyaviridae, Caliciviridae, Coronaviridae, Filoviridae, Flaviviridae, Hepeviridae, Orthomyxoviridae, Paramyxoviridae, Picobirnaviridae, Picornaviridae, Reoviridae, Retroviridae, Rhabdoviridae, and Togaviridae; an additional RNA viral family (Arteriviridae) that infects non-human primates will be included, as explained above; and an additional 8 families of DNA viruses which contain known zoonoses (Adenoviridae, Anelloviridae, Hepadnaviridae, Herpesviridae, Papillomaviridae, Parvoviridae, Polyomaviridae, Poxviridae), bringing the total to 25 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 diversity may not remain static over the period of the GVP. However, the large standard error around the GVP estimates of viral diversity suggests that they err on the side of over-estimation of viral diversity by using the mean per-family value. Therefore, the evolution of novel viral lineages during the GVP is unlikely to significantly alter total diversity discovered. Furthermore, the work on which these estimates are based used a conservative approach to the definition of a viral species, and this has been followed in the current calculations (*5, 16*). It is also likely that viral evolution is more constrained in reservoir hosts (the subject of the GVP sampling and testing) than in spillover hosts (e.g. humans, the subject of many studies of RNA viral evolution, e.g. (*23*), 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 (*5, 16*), 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 testing 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 (*5, 16*) 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 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 could be altered accordingly to maximize discovery, by expanding, reducing or halting sampling and testing.

Estimating the number of potentially zoonotic unknown 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 (*3, 6*) on the host species range for all known mammalian viruses and the proportion of those viruses that can infect humans. We found that, of 580 known mammalian viruses in the 25 viral families targeted by the GVP, 261 (45.0%) infect humans (2 other viruses are not within these families: the unassigned Hepatitis delta virus, and Borna disease virus-1; bringing the total known human viruses from (*3, 6*) to 263). (https://github.com/ecohealthalliance/HP3/blob/master/data/viruses.csv) As evidence for a mammalian viral species' capacity to infect people, we used data from the less stringent database in (*6*), which includes those with either PCR or serology evidence of infection. This reduces the likelihood of underestimating zoonotic potential, and reflects the large number of studies of spillover potential that use serological surveys of exposed people. We did not include Hepatitis delta virus, in our calculations because this is considered an RNA viroid, requires hepatitis B virus (HBV) as a 'helper virus' for its replication and transmission, and is only known in nature from HBV-infected humans (*24-26*). Furthermore, it has not been categorized into a viral family by the ICTV. Of the 580 known mammalian viruses in the 25 viral families targeted by the GVP, 74 are thought to be exclusively human and 187 are zoonotic (32.2% of the known mammalian viruses in the targeted families). Considering evidence that most exclusively human viruses appear to have originated in animals (*7*), we assume that between 493,856 (se 206,412 - 781,298) (32.2%) and 689,285 (se 288,095 - 1,090,475) (45.0%) of the total unknown mammalian viruses have potential to infect humans. Because influenza viruses have exceptional capacity for genetic recombination, we made the conservative assumption that all strains of influenza virus in birds are likely capable of zoonotic transmission. Our best estimate of the total number of potential zoonoses globally is therefore between 631,218 (se 263,824 – 998,610) and 826,647 (se 345,507 - 1,307,787). It is possible that as-yet-undiscovered viruses harbor a lower proportion with zoonotic potential than those already known, given our long history of interaction with wildlife on

the planet, and our likely skewed surveillance of hosts known to harbor zoonoses (*6*). 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 all emerging pathogens (*1, 8*). This suggests that any reduced potential for zoonotic emergence in the undiscovered pool may be far less important in driving risk than the very large number of pathogens to which humans have not yet been significantly exposed, or the exponentially increasing drivers of high-risk contact with wildlife that leads to disease emergence (*1, 27*). Furthermore, the identification of a pathogen as zoonotic requires that it infects people and is then clinically observed. Capacity to conduct disease detection and viral discovery in people, livestock and wildlife is likely lowest in countries with the highest mammalian biodiversity (and therefore viral diversity), so that many viruses may remain undiscovered, even if they have already emerged repeatedly into human populations in these regions. This hypothesis is supported by the apparent repeated spillover of HIV-1 progenitors prior to its emergence (*28*), and PCR evidence of simian foamy virus infections in three bushmeat hunters in Cameroon in a survey of 1099 individuals, ten of which had serological evidence of exposure (*29*). In addition, analysis of ICTV data and the literature (*6*) suggests that prior surveillance studies have not skewed to hosts with higher proportions of zoonoses due to research focused on identifying reservoirs of zoonotic pathogens. For example, this work shows that bats have a statistically significant higher proportion of zoonoses than any other mammalian order, even though bat viruses are not historically well-studied relative to other mammalian host groups (*21*). 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 ease of capture, and therefore have focused more on diurnal terrestrial species (e.g. rodents, primates) 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 >220,000 viruses of zoonotic potential. Given the high, and growing, public health impact and economic costs of EID outbreaks (*8*), 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 work conducted by the 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 (*1*). Target mammalian species primarily would be 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 (*30*). For avian influenza viruses, the GVP could reasonably target only water birds (Anatidae, Laridae, Charadriiformes and others, with a global species richness of 871) which harbor a wide diversity of known zoonotic avian influenzas, and include species that are closely related to widely-domesticated species, and that are hunted extensively (*22*). 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 coronavirus and camels). The GVP could sample a small number of livestock and poultry species (n=10) in regions that are known emerging disease hotspots (*1, 27*). 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.

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 EPT/PREDICT project, which has a goal of conducting zoonotic viral discovery in wildlife to identify potentially zoonotic pathogens and build capacity to reduce the risk of pandemics (*10, 11*). This project has been operating in over 25 developing countries, in emerging disease hotspots, for just over 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 (*5, 16*). The cost of estimating the viral diversity of *P. giganteus*, collecting metadata, conducting risk assessment and partially characterizing some of the viruses discovered 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. giganteus* work multiplied by the number of extant terrestrial and volant mammals) for 100% of the estimated unknown 1,531,745 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 relatively unaffected 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 to conduct limited domestic animal sampling (n=50, as described in the SM, above). This would bring the total costs of the GVP to $7.454 billion, which, if annualized over a decade would cost around $745 million per year to discover virtually 100% of the viral zoonotic threats to our species.
(https://github.com/ecohealthalliance/GVP_Science/blob/master/data/GVP_costs_from_anthony2013.xlsx)

However, because the viral discovery curves reported in (*5, 16*) are asymptotic, marginal returns (i.e. rates of new virus discovery) diminish rapidly as the number of samples collected increases. Using the discovery rates and total costs from (*5*), and assuming a linear relationship between samples collected, we examined the relationship between total project costs and the percentage of the undiscovered global virome found. (Fig. S1). 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), 85% of targeted viral diversity would be discovered with only 23% of the costs ($1.69 billion), and 71% diversity with only 16% of the costs ($1.2 billion, considering some fixed costs). 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 Fig. S1, 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 $1.2 billion could discover a substantial majority (71%) of unknown viral diversity in non-marine mammals and of the zoonotic influenza risk from water birds, with some limited domestic animal sampling. GVP costs likely would 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 the project, because

the bulk of the costs are in the collection of field samples rather than sequencing a larger number of PCR products.

Further strategic targeting to increase return-on-investment

Further targeting strategies are proposed in the main text to increase return-on-investment from the GVP, and deliver public health value as rapidly as possible: *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 than others 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, or their 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 (*31*), and are more closely related phylogenetically (*32, 33*) are more likely to harbor viruses with the potential to be zoonotic. Analysis of data on all mammalian host-virus relationships in (*3*), after controlling for reporting effort, demonstrates that both the total number of viruses that infect a given species, and the proportion likely to be zoonotic are predictable (*6*). The proportion of viral species that are zoonotic in mammalian 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 to the maximum known for any wild mammal, it is possible to identify geographic regions with the largest estimated number of 'missing viruses' and proportion of 'missing zoonoses' (*6*). Prioritizing sampling of these species and regions would therefore provide the highest rate of zoonotic viral discovery for the GVP. *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 (*1*). 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 (*27*). 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 the highest relative propensity to emerge, other traits being equal. *3) Syndromic surveillance at wildlife-livestock-human interfaces.* 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 encephalitis and other discrete syndromes with potential infectious etiology from the literature and from internet-based reporting. During the late 1990s,

analyses of these reports for South Asia suggested that some outbreaks may 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 (*34*). Syndromic surveillance allowed identification *post hoc*, of the causative agent of outbreaks in South Asia (*35, 36*). Similarly, syndromic surveillance of livestock has been used to identify diseases of significance to livestock production or public health (*37-40*). 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 have caused 94% of the zoonoses documented from 1990 to 2010, 28 times higher than the proportion of RNA viruses detected among all vertebrate viruses (*30*). 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 that issues of 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 viruses identified from wildlife species, or 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 (*41-43*). At a national scale, the presence of biodiversity hotspots across country boundaries could lead to repetitive sampling over two adjacent countries if targeting is based on country-by-country analyses. A regional (multinational) 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 remit may increase efficiency and reduce costs of laboratory capacity building. Similarly, regional 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 decade-long timescale of the GVP may allow for technological innovation to significantly reduce testing and bioinformatics costs and therefore to increase efficiencies. As an extreme example, the cost of sequencing a human genome fell from $100,000,000 to around $10,000 in 10 years (2002-2012), i.e. 4 orders of magnitude, exceeding projected increased efficiency by Moore's Law (*44*). Technological advances continue in biased and unbiased viral discovery technology (*45*), and are likely to increase testing efficiency and reduce costs (*46*).

Potential direct benefits of the GVP to reducing risk of zoonotic viral emergence

The GVP's goal of identifying the bulk of currently-unknown viruses with zoonotic potential from wildlife reservoirs will have substantial potential for preventing and controlling zoonotic viral emergence in the future. 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 (*47-49*). 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 strains and to develop vaccines for them in advance of their emergence. However, their efficacy appears to be variable (*50*), and vaccine development to the recently emerging H1N1 pandemic strain lagged its global spread, albeit that speed of production was greatly enhanced (*51, 52*).

Despite the challenges of countermeasure development, there are a number of ways that the GVP could rapidly and feasibly improve efforts to pre-empt zoonotic viral emergence, more rapidly diagnose cases, and intervene earlier in outbreaks: *1) Greater diversity of viral reagents for countermeasure development.* Having the sequence data for 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 (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 (*13, 53*). However, both a vaccine and monoclonal therapy that reduces SARS-CoV infection in this model failed to neutralize and protect from infection with the SL-CoV chimera *(54)*. 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) Capacity building.* To facilitate the scaling up of current surveillance and viral discovery programs, the GVP would necessarily require 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 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 (*55*). 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; *3) Enhancing rapid diagnosis during outbreaks.* The identification of relatives of known zoonotic viruses in new regions may enhance the speed and 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 (*56-58*). This group of viruses can now be included in investigation of future outbreaks of Nipah- or Hendra-like disease in livestock in the region. *4) Designing risk mitigation policies.* 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. Sequence data from new relatives of known agents can be used to increase the breadth of coverage of PCR-based diagnostic tests. Ecological and human behavioral data collected in the GVP will help refine our mechanistic understanding of spillover, and can be used to develop novel interventions. 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 (*13, 54, 59*). Ecological data collected during site evaluation prior to wildlife sampling, and human behavioral data collected routinely in the USAID EPT/PREDICT project identified human communities with significant exposure to bats from these caves. Targeting these communities for serological surveillance to SARS-like coronaviruses may help identify early evidence of spillover prior to full-scale emergence. Identification of potential zoonoses in hunted, traded and consumed wildlife 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 reduce the risk of spillover. These mitigation strategies may also help prevent spillover of yet-to-be identified viruses within the same risk pathway or interface. The GVP metadata will also allow refinement of predictive models of zoonotic disease emergence, and viral host ranges (*1, 6, 11, 27*). 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. *5) Strategies to triage potentially pandemic viruses for enhanced characterization and risk mitigation policies.* It would not be feasible to design and target control and intervention programs against all novel viruses identified by the GVP, and strategies to distinguish which novel viruses have true pandemic potential are rudimentary at present (*14*). 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 is enhanced by a great deal of data on influenza viruses recently and currently circulating in people. To begin 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 geographic range, abundance and proximity to people; viral prevalence in host; location of host in an EID hotspot) (*11*). Some of these approaches have been shown to predict zoonotic potential from large databases of virus-host relationships (*6, 30*). 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 (*11, 55*). This approach was used successfully to further characterize the spike proteins of SARS-like coronaviruses discovered in this project, assess their capacity to bind to human cells, and conduct behavioral and serological surveys to assess the potential that spillover has occurred into the human population (*54, 59*). We propose that if this triage approach is used in the GVP, it will not only provide a preliminary framework for risk assessment, but will ultimately involve orders magnitude more data on viral sequence, geographic and host distribution, human behavioral and ecological risk and other parameters. This significant scaling up of available data will underpin a strategy to produce more realistic projections of zoonotic and pandemic potential.

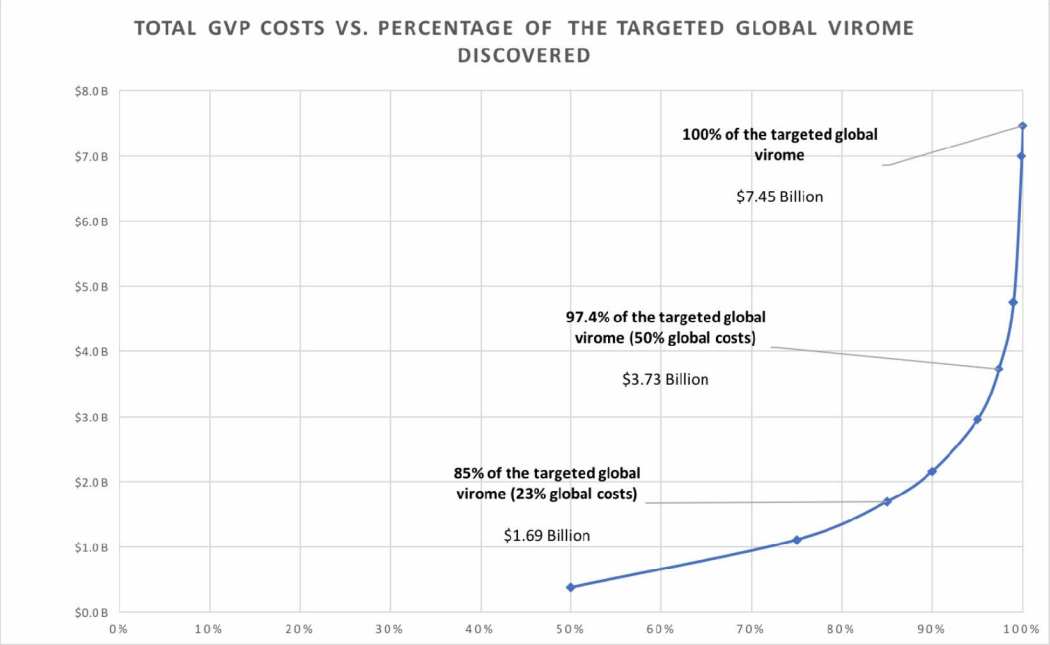

Fig. S1. Cost estimates of the GVP compared to the percentage of the targeted global virome discovered. The targeted global virome includes sampling from all 5,291 terrestrial mammal species and testing for 25 viral families of zoonotic potential, 871 species of water birds tested for influenza viruses, and limited (n=50) sampling of domestic animals and testing for 25 viral families.

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Human-animal interactions and bat coronavirus spillover potential among rural residents in Southern China

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ABSTRACT

Human interaction with animals has been implicated as a primary risk factor for several high impact zoonoses, including many bat-origin viral diseases. However the animal-to-human spillover events that lead to emerging diseases are rarely observed or clinically examined, and the link between specific interactions and spillover risk is poorly understood. To investigate this phenomenon, we conducted biological-behavioral surveillance among rural residents in Yunnan, Guangxi, and Guangdong districts of Southern China, where we have identified a number of SARS-related coronaviruses in bats. Serum samples were tested for four bat-borne coronaviruses using newly developed enzyme-linked immunosorbent assays (ELISA). Survey data were used to characterize associations between human-animal contact and bat coronavirus spillover risk. A total of 1,596 residents were enrolled in the study from 2015 to 2017. Nine participants (0.6%) tested positive for bat coronaviruses. 265 (17%) participants reported severe acute respiratory infections (SARI) and/or influenza-like illness (ILI) symptoms in the past year, which were associated with poultry, carnivore, rodent/shrew, or bat contact, with variability by family income and district of residence. This study provides serological evidence of bat coronavirus spillover in rural communities in Southern China. The low seroprevalence observed in this study suggests that bat coronavirus spillover is a rare event. Nonetheless, this study highlights associations between human-animal interaction and zoonotic spillover risk. These findings can be used to support targeted biological behavioral surveillance in high-risk geographic areas in order to reduce the risk of zoonotic disease emergence.

1. Introduction

In the highly biodiverse southern region of China, interactions among humans, wildlife, and livestock are likely to be common, and are hypothesized to be a risk factor in the emergence of zoonotic infectious diseases [1–3]. Human-animal interactions may pose a particular public health threat in rural communities where frequent contact with animals occurs and where disease prevention measures are likely less well-developed [4]. Although human-animal interactions are thought to be associated with zoonotic disease emergence, few studies have addressed the nature of specific interactions that occur between animals (particularly wild animals) and humans that lead to pathogen spillover.

Bats (order Chiroptera) are reservoirs of a large number of zoonotic viruses, including coronaviruses (CoVs) that have caused disease outbreaks in human and livestock populations [5–13]: Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), the causative agent of the SARS outbreak affecting 32 countries in 2002-3, infecting 8,096 people and causing 774 deaths [14]; Middle East Respiratory Syndrome coronavirus (MERS-CoV), which has caused 823 deaths from 2,374 human cases in 27 countries by the end of February 2019, and is thought to have originally spilled over from bats into camels, in which is it now endemic [15–18]; and Severe acute diarrhea syndrome coronavirus (SADS-CoV) which emerged in the pig population of Southern China and caused the deaths of more than 20,000 piglets in 2017 and 2018 [5].

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HIGHLIGHTS

Scientific question

What are the behavioral risks in human-animal interactions that could lead to the emergence of bat coronaviruses in human population.

Evidence before this study

Bat borne coronaviruses have caused several emerging infectious disease outbreaks of global significance, including SARS. Novel SARS-related coronaviruses have been discovered in bat populations in Southern China, some of which have the capacity to infect human cells. Human-animal interactions are thought to be critical for the emergence of bat coronaviruses, however the specific interactions linked to animal-to-human spillover remain unknown.

New findings

This study found serological evidence for bat-borne coronavirus transmission to people. Direct contact with bats was not identified as a risk factor. However, self-reported severe acute respiratory infection (SARI) and/or influenza-like illness (ILI) was linked to human interaction with other wildlife and livestock, suggesting that there may be other zoonotic exposures leading to clinical illness in these populations.

Significance of the study

Findings from this study suggested that an integrated biological and behavioral surveillance in healthy community settings can help identify potential zoonotic disease spillover events or target surveillance to at-risk populations. This approach represents a potential early-warning system that could be used under non-outbreak conditions to identify potential zoonotic emerging diseases prior to largescale outbreaks.

A large diversity of coronaviruses, including SARS-related Coronaviruses (SARSr-CoVs), has been discovered in bats, and phylogenetic and pathogenesis studies of these suggest a high capacity for transmission across species barriers [9,11,13,18–22]. However, few studies have analyzed bat-to-human spillover events in non-outbreak conditions, likely due to the rarity of these events and difficulties in identifying at-risk populations or target geographies. Additionally, the symptoms of novel bat coronavirus infection in the human population may not be clinically recognized at the time of emergence as a result of a lack of adequate surveillance or confusion with other diseases. This represents a significant biosafety risk considering the large and increasing number of coronaviruses discovered in bats [23,24] and the wide distribution of bat populations in rural regions such as Southern China [25].

In this paper we report on a study designed to characterize the bat coronavirus spillover potential associated with presumed high-risk human behavior in rural communities of Southern China [26]. We collected data during a community serological and behavioral survey to understand the driving factors of bat coronavirus spillover, providing evidence for developing community-based strategies in preventing zoonotic disease emergence.

2. Materials and methods

2.1. Study location and target population

We conducted a cross-sectional study in the districts of Yunnan, Guangxi, and Guangdong, China, which are known for their high levels of wildlife biodiversity, active wildlife trade activity, and historic zoonotic disease emergence events [3,5,10,14,22,24,27]. Eight study sites were selected in areas where we have previously reported diverse coronaviruses in bat populations [24] roosting close (within 5 km) to human dwellings. The study targeted human populations that are highly exposed to bats and other wildlife, including people who visit or work around bat caves, work in local live animal markets, raise animals, or are involved in wildlife trade (e.g., wild animal harvest, trade, transportation, and preparation), as identified by previous exploratory ethnographic interviews.

2.2. Recruitment and sampling

Prior to the recruitment and sampling, project staff who received human subject research training visited each participating site to introduce the project to the local community, assisted by officials from provincial and city-level Centers for Disease Control and Prevention. To generate interest and develop recruitment strategies, project staff held meetings with village committees to discuss topics relevant to their daily contact with animals and any health issues in the community that were particularly concerning for them. With permissions from local authorities, community leaders conducted house visits and broadcast announcements a week before data collection took place to inform community residents about the study and its recruitment plan. All information was communicated in local dialects using easily understandable language to convey the study purpose, eligibility and inclusion guidelines, potential risks and benefits of participation, and the time and locations at which the study would take place.

We aimed to obtain a minimum sample size of 400 participants from each of the three districts (Yunnan, Guangxi, and Guangdong), for a total sample size of over 1,200 participants. A snowball sampling method was used because the population size at selected sites and the people who were highly exposed to wild animals were difficult to elucidate [28]. During each house visit, we requested information about potential eligible participants from the residents' networks, and we then followed their referrals to recruit from the community. Only one person per household was recruited to participate in this study, and no participants were recruited from clinics or healthcare settings. We made every effort to include participants across a range of demographic indices including gender, age, and socioeconomic status, as well as to ensure that any contribution was voluntary and involved minimal risk to the participants.

2.3. Data collection and management

Following the completion of the informed consent process, a standardized Mandarin questionnaire was administered by study staff speaking in local dialects. The interview was conducted in a private environment where confidentiality was maintained, and interviewers and participants were paired by sex. Children aged 10 to 18 years were interviewed with the permission and in the presence of a parent or guardian.

The questionnaire included five sections consisting of demographics, living circumstances and livelihood, travel, types of contact with animals, and unusual illness symptoms in the past 12 months. The survey assessed symptoms including fever with cough and shortness of breath or difficulty breathing (severe acute respiratory infection [SARI] symptoms) and fever with muscle aches, cough, or sore throat (influenza-like illness [ILI] symptoms) (Appendices). SARI and ILI symptoms were included in the survey in anticipation of potentially low coronavirus sero-positivity rates. These symptoms are commonly used as metrics in emerging infectious respiratory disease surveillance and are known to be associated with coronavirus infections (e.g., MERS-CoV, SARS-CoV) [29]. Therefore, SARI and ILI symptom histories can be analyzed in addition to serological testing to maximize our understanding of bat coronavirus spillover risk.

After the questionnaire interview, participants were asked to provide a blood sample (2.5-5 mL stored in a serum-separating tube) and an oropharyngeal swab (stored in a cryotube with viral transport medium). Samples were collected by study staff from local clinics. All samples were stored in liquid nitrogen immediately after collection and transferred to an ultralow (-80°C) freezer within 48 h.

A unique alphanumeric identification code was assigned to each questionnaire and biological specimen collected from each participant. No personal identifying information was collected. Only authorized study personnel who received human subject research training were allowed access to the questionnaire and biological data.

2.4. Serological testing

Serum samples collected from study participants were analyzed using newly developed IgG enzyme-linked immunosorbent assays (ELISA) based on selected nucleocapsid proteins (NP) expressed and purified in *E. coli* for four specific coronaviruses: SARSr-CoV (DQ071615, Bat SARS coronavirus Rp3, NP), HKU10-CoV (sample 3740, NP), HKU9-CoV (MG762674, BatCoV_HKU9-2202, NP), and MERS-CoV (JX869059, Human betacoronavirus 2c EMC/2012, NP). Micro-titer plates were coated with recombinant and purified NP (100ng/well); samples were tested at 1:20 dilution; and an anti-Human IgG-HRP conjugated monoclonal antibody (Kyab Biotech Co., Ltd, Wuhan, China) was used as the secondary antibody with different dilution ratios for different coronaviruses. 100 serum samples collected from healthy people in Wuhan were tested using this ELISA kit to set up the cutoff value, and positive test results were determined by the cut-off value in each run for each of the four coronaviruses, as the product of the mean of all serum samples' optical density (OD) values plus three standard deviations, and confirmed by Western blot test [30].

2.5. Questionnaire data analysis

Questionnaire data were entered into an Excel database with quality control for data cleaning and validation. The glmnet package in R version 3.6.0 was used to fit a least absolute shrinkage and selection operator (LASSO) regression to characterize associations between animal contact and SARI and/or ILI symptoms in the preceding 12 months [31,32]. The bat coronavirus serology testing outcome was not analyzed in the LASSO due to low rates of sero-positivity.

The LASSO regression is an adaptation of the generalized linear model (GLM) and was selected because it is effective at minimizing prediction error for datasets with many predictor variables. The model identifies subsets of predictors that are associated with the outcome of interest by applying a shrinkage operation to regression coefficients and shrinking some coefficients to exactly 0. The LASSO is often utilized for its variable selection capabilities for sparse datasets including surveys and questionnaires. Demographic variables (age, gender, province, and income) were included in the model as independent and interaction terms in order to account for potential confounding. Because the LASSO does not generate confidence intervals, we repeated the model using bootstrapping instead to calculate bootstrap support, i.e., the proportion of times a predictor variable is selected in the model [33–36].

Chi-Square and fisher exact tests were also conducted to explore associations between potential risk factors in local demographics, behaviors, attitudes (independent variables) and bat CoV serological evidence (dependent variables), with effect size examined. However, due to the low positivity rate (9/1,497), the results were not robust and are not reported in this paper.

3. Results

From October 2015 to July 2017, a total of 1,596 residents from eight sites in Yunnan (n = 761), Guangxi (n = 412), and Guangdong (n = 423) provinces were enrolled in this study. Of these, 1,585 participants completed the questionnaires and 11 participants withdrew from the questionnaire interview due to scheduling reasons. After the interviews, 1,497 participants provided biological samples for lab analysis.

3.1. Demographics

More female (62%) than male (38%) community members participated in this study. Most participants were adults over 45 years old (69%) and had been living in the community for more than 5 years (97%) with their family members (95%). A majority (86%) relied on a comparatively low family annual per capita income less than 10,000 RMB which is below the national mean for per capita disposable income of rural households from 2015 to 2017 (11,422 - 13,432 RMB) [37]. Most participants (98%) had not received a college education and were making a living in crop production (76%). 9% of participants frequently traveled outside the county as migrant laborers. Some participants were working in sectors where frequent human-animal contact occurs, such as the animal production business (1.7%), wild animal trade (0.5%), slaughterhouses or abattoirs (0.5%), protected nature reserve rangers (0.4%) or in wildlife restaurants (0.3%). It was common for participants to have multiple part-time jobs as income sources (Table 1)

3.2. Animal contact and exposure to bat coronaviruses

Serological testing of serum samples from 1,497 local residents revealed that 9 individuals (0.6%) in four study sites were positive for bat

Table 1
Demographics of study participants.

Variable		Total	
		N	Valid %
Gender (n = 1,574)	Female	968	61.5
	Male	605	38.4
	Other	1	0.1
Age (n = 1,582)	Under 18 years	71	4.5
	18 to 44 years	420	26.5
	45 to 64 years	780	49.3
	Age 65 or older	311	19.7
Province (n = 1,585)	Guang Dong	420	26.5
	Guang Xi	412	26.0
	Yun Nan	753	47.5
Residence time (n = 1,568)	< 1 month	4	0.3
	1 month – 1 year	12	0.8
	1 year – 5 years	26	1.7
	> 5 years	1,526	97.3
Family annual PCI (n = 1,565)	<1000 yuan	271	17.3
	1001-10000 yuan	1067	68.2
	>10000 yuan	227	14.5
Livelihood since last year	Extraction of minerals, gas, oil, timber (n = 1,566)	5	0.3
	Crop production (n = 1,569)	1,196	76.2
	Wildlife restaurant business (n = 1,564)	5	0.3
	Wild/exotic animal trade/market business (n = 1,566)	8	0.5
	Rancher/farmer animal production business (n = 1,566)	27	1.7
	Meat processing, slaughterhouse, abattoir (n = 1,567)	8	0.5
	Zoo/sanctuary animal health care (n = 1,565)	1	0.1
	Protected area worker (n = 1,567)	7	0.4
	Hunter/trapper/fisher (n = 1,565)	3	0.2
	Forager/gatherer/non-timber forest product collector (n = 1,566)	4	0.3
	Migrant laborer (n = 1,567)	144	9.2
	Nurse, doctor, healer, community health worker (n = 1567)	7	0.4
	Construction (n = 1,564)	41	2.6
	Other (n = 1,568)	293	18.7
Education (n = 1,570)	None	428	27.3
	Primary School	632	40.3
	Secondary school/Polytechnic school	479	30.5
	College/university/professional	31	2.0
Live with family (n = 1,564)	No	73	4.7
	Yes	1491	95.3

Notes: Total counts differ due to missing responses.

coronaviruses, indicating exposure at some point in their life to bat-borne SARSr-CoVs (n = 7, Yunnan), HKU10-CoV (n = 2, Guangxi), or other coronaviruses that are phylogenetically closely related to these. All individuals who tested positive (male = 6, female = 3) were over 45 years old, and most (n = 8) were making a living from crop production. None of those participants reported any symptoms in the 12 months preceding the interview.

Due to the low rate of sero-positivity, we did not obtain robust results from the statistical comparisons of animal-contact behavior by coronavirus outcome. Figure 1 shows animal contact rates in the previous 12 months among the survey population (n = 1,585) and among seropositive individuals (n = 9). Participants reported common contact with poultry and rodents/shrews, and most animal contact occurred in domestic settings through animal raising or food preparation activities.

3.3. Self-report SARI/ILI symptoms and animal contact

Among the 1,585 participants who responded, 265 (17%) reported experiencing SARI (n = 73) and/or ILI (n = 227) symptoms in the last year. The LASSO regression showed that eating raw or undercooked carnivores in the preceding 12 months was the most salient predictor of self-reported SARI and/or ILI symptoms over the same time period (odds ratio [OR] = 1.6; bootstrap support = 0.67). Additional salient predictors were slaughtering poultry as a resident of Guangxi province (OR = 1.4; support = 0.68), having an income below 10,000 RMB as a resident of Guangxi province (OR = 1.3; support = 0.84), domestic contact with bats (OR = 1.3; support = 0.63) and domestic contact with rodents or shrews as a resident of Guangdong province (OR = 1.2; support = 0.63) (Figure 2).

Some demographic variables were associated with self-reported SARI and/or ILI symptoms as either independent or interactive terms. For example, respondents aged 41 to 60 and residents of Yunnan province were less likely to report symptoms. Slaughtering poultry was positively associated with the outcome only in Guangxi residents, whereas the association was negative in Guangdong residents. Family income also showed interactions, with family income less than 10,000 RMB being positively associated with the outcome in respondents who raised poultry but negatively associated in respondents who cooked or handled poultry. Gender was not found to be salient in either direction.

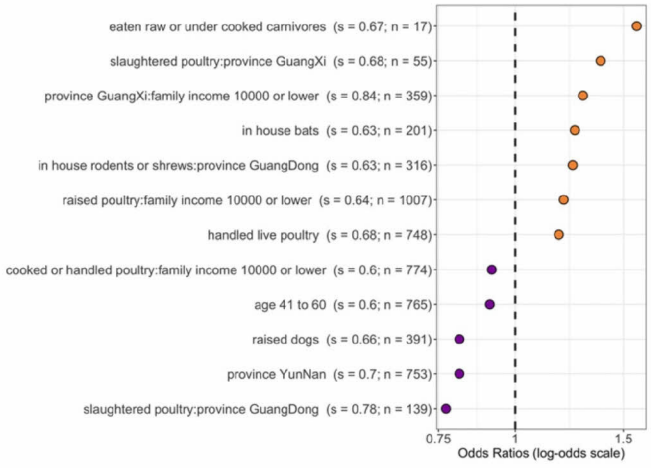

Figure 2. Most salient predictors of self-reported ILI and/or SARI symptoms in the last year (s = bootstrap support; n = count positive out of 1,585 respondents). Bootstrap support values ≥ 0.6 are demonstrated here, meaning they were identified as associated with the outcome for 60% or more of the bootstrap iterations. Odds ratios >1 (orange) are positively associated with the outcome, and odds ratios <1 (purple) are negatively associated with the outcome.

3.4. Attitudes towards zoonotic diseases emergence

When asked about animals and disease transmission, more than half of the study participants believed that animals could spread disease (n = 871, 56%) and were worried about disease emergence from animals at wet markets (n = 810, 52%). Of those worried about disease emergence, 46% (n = 370) purchased animals from wet markets in the past 12 months. Among all participants who purchased animals from wet markets in the past 12 months (n = 502, 32%), some (n = 194, 39%) took protection measures or strategies such as washing hands, purchasing live animals less often (n = 153, 30%), or purchasing meat at supermarkets instead of live animal markets (n = 148, 29%). Very few participants considered wearing a mask (n = 7, 1%) or gloves (n = 7, 1%) while visiting the markets.

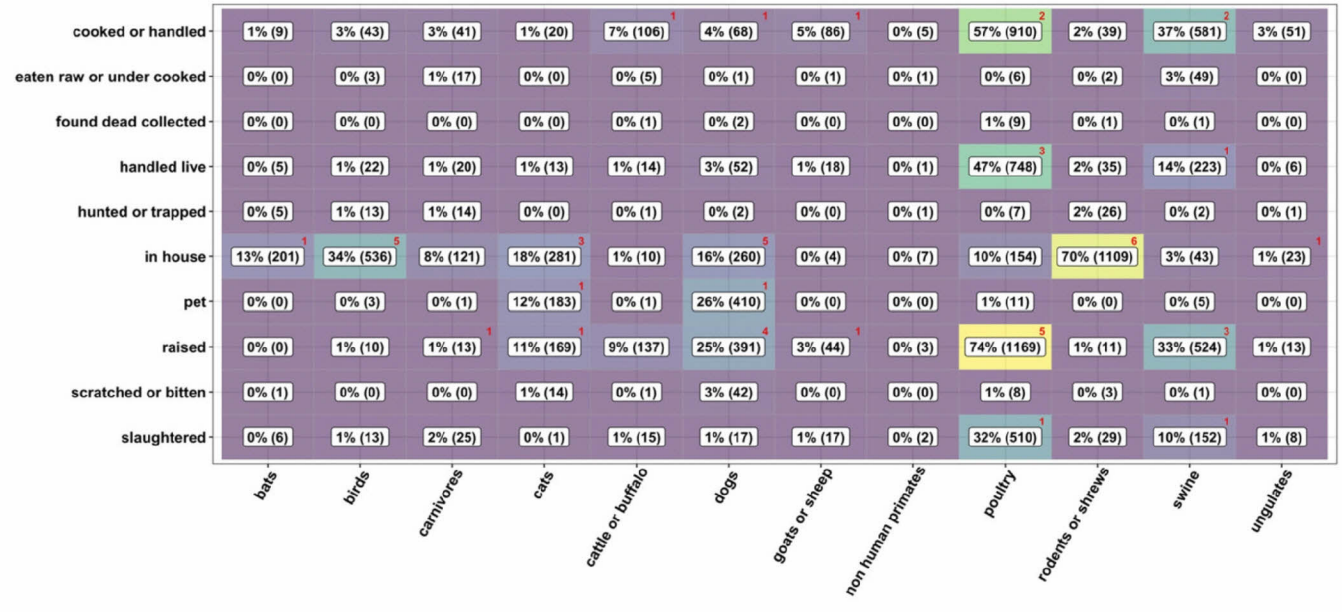

Figure 1. Animal contact by taxa and activities. Values and shading represent the survey population; red numbers in the upper-right corners of the cells indicate the number of seropositive individuals with the given contact.

4. Discussion

We used a novel human surveillance approach to integrate serological and behavioral data to characterize associations between human-animal contact and zoonotic disease spillover risk in Southern China. This study provides the first serological evidence of bat-borne SARSr-CoVs and HKU10-CoV transmission to people and highlights potential spillover pathways through animal contact. Given the high diversity and recombination rate of bat coronaviruses, and close relationship of SARSr-CoVs to SARS-CoV, it is possible that exposure to these coronaviruses may lead to disease emergence in human populations. Continuous surveillance of both human and bat populations, as well as further pathogenesis studies of these viruses, are important to determine the extent of the disease risk.

Contact with animals was prevalent among the survey population. Raising poultry and having rodents/shrews in the house were the most common types of contact. Correspondingly, contact with poultry and rodents/shrews, as well as with carnivores, was identified in the LASSO regression as being associated with self-reported ILI and/or SARI symptoms, with results varying by income and province. It's important to note that the questionnaire used broad classification of the type of animals for these exposures due to the presumed variability in respondent's capacity to identify species or genera of wildlife. It is likely that the most significant exposure we identified (to carnivores) reflects animals as diverse as civets, porcupines, ferret badgers and taxas that respondents recognized as non-rodent and non-shrew. This study also assessed health risks from human interaction activities for each study participant in the survey based on their travel history and the health history of people who they lived with. The goal was to minimize the possibility that illness was caused by human-to-human transmission of pathogens causing ILI and/or SARI symptoms. We did not find evidence supporting a direct relationship between bat contact and bat coronavirus sero-positivity in the human population. However, there is frequent contact with domestic animals in these communities and it is known that other bat-borne viruses have been transmitted to humans via livestock (e.g. henipavirses and filoviruses) [38–41]. It is possible that these findings reflect other indirect exposures to bat CoVs, and future surveillance may benefit from including a wide range of livestock and peridomestic animals in viral and serological studies to identify potential spillover pathways [42–45].

While it is known that bias can occur in self-reported illness data, this approach has been widely used in previous disease surveillance and risk factor studies [46–49]. It is useful as an early warning system to assess broad categories of factors within high-risk communities in a non-outbreak condition. This is particularly important in rural regions, where people have high levels of contact with domestic and wild animals but may not seek diagnosis or treatment in a timely fashion, slowing early detection and response.

While the majority of survey respondents believed that animals could spread disease and were worried about disease emergence from animals at wet markets, many did not take measures to protect themselves from exposure. Further work on what drives these local attitudes to risk may help in developing risk-mitigation behavior change programs. A number of affordable and readily adaptable measures could be targeted to these at-risk populations, including the use of gloves and masks while killing or butchering animals, and handwashing.

The low levels of sero-positivity found in the study could reflect a number of factors: 1) the rarity of spillover and bat-to-human transmission, as has been reported for other virus-host systems [50–54]; 2) the use of a snowball technique for sample selection that could have biased the population sampled; 3) the limited diversity of CoVs that this study tested for; 4) the possibility that these infections cause high mortality rates and therefore the number of survivors and number of seropositive people is low, although this seems unlikely because the mortality rate from SARS was >10% during an outbreak that included hospital exposure and therefore likely high infectious doses [55,56]; and 5) that antibodies to these viruses wane rapidly in humans. The latter hypothesis is supported by findings that antibodies to SARS decline rapidly (2–3 years) after illness [57]. Expanding this approach to a larger population, using a longitudinal (repeated sampling) approach, and targeting people who are in the higher-risk categories identified here may provide a larger number of sero-positives and more critical information on the driving factors of viral spillover. However, despite the small sample sizes, this study suggests that there are a substantial number of people in rural Southern China who are exposed to bat-borne viruses, and that exposure likely occurs through the daily or normal practices of rural communities, rather than specific high-risk behaviours (e.g. wild animal hunting). Considering the proven potential of some SARSr-CoVs currently circulating in bats in southern China, to infect human cells, cause clinical signs in humanized mouse models, and lead to infections that cannot be treated with monoclonal therapies effective against SARS-CoV [58–60], this represents a clear and present danger to our biosafety and public health. Further studies to determine the relationship between SARSr-CoV and HKU10-CoV exposure and illness in people may help elucidate this risk and provide critical mitigation strategies.

Ethics statement

This study was approved by Wuhan University School of Health Sciences Medical Ethics Committee; Institutional Review Board Administration of University of California, Davis (No. 804522-6); and Hummingbird IRB (No. 2014-23).

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Conflict of interest statement

The authors declare that there are no conflicts of interest.

Author contributions

All authors read and approved the final manuscript. PD, ZS, MM, EH, SL, HY, and AC designed the study, developed the research tools, and obtained ethical approval; SL, HY, HH, and GZ implemented the field data collection; WZ and NW conducted the serological testing; HL, CZ, EM, EH, and NR contributed to the data management, analysis, and writing; and PT, MF, and PD edited and approved the final version.

Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.bsheal.2019.10.004.

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LETTER

Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China

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Dear Editor,

Severe acute respiratory syndrome coronavirus (SARS-CoV) is the causative agent of the 2002–2003 SARS pandemic, which resulted in more than 8000 human infections worldwide and an approximately 10% fatality rate (Ksiazek et al. 2003; Peiris et al. 2004). The virus infects both upper airway and alveolar epithelial cells, resulting in mild to severe lung injury in humans (Peiris et al. 2003).

During the SARS outbreak investigation, epidemiological evidence of a zoonotic origin of SARS-CoV was identified (Xu et al. 2004). Isolation of SARS-related coronavirus (SARSr-CoVs) from masked palm civets and the detection of SARS-CoV infection in humans working at wet markets where civets were sold suggested that masked palm civets could serve as a source of human infection (Guan et al. 2003). Subsequent work identified genetically diverse SARSr-CoVs in Chinese horseshoe bats (*Rhinolophus sinicus*) in a county of Yunnan Province, China and provided strong evidence that bats are the natural reservoir of SARS-CoV (Ge et al. 2013; Li et al. 2005; Yang et al. 2016). Since then, diverse SARS-related coronaviruses (SARSr-CoVs) have been detected and reported in bats in different regions globally (Hu et al. 2015). Importantly, SARSr-CoVs that use the SARS-CoV receptor, angiotensin converting enzyme 2 (ACE2) have been isolated (Ge et al. 2013). These results indicate that some SARSr-CoVs may have high potential to infect human cells, without the necessity for an intermediate host. However, to date, no evidence of direct transmission of SARSr-CoVs from bats to people has been reported.

In this study, we performed serological surveillance on people who live in close proximity to caves where bats that carry diverse SARSr-CoVs roost. In October 2015, we collected serum samples from 218 residents in four villages in Jinning County, Yunnan province, China (Fig. 1A), located 1.1–6.0 km from two caves (Yanzi and Shitou). We have been conducting longitudinal molecular surveillance of bats for CoVs in these caves since 2011 and have found that they are inhabited by large numbers of bats including *Rhinolophus* spp., a major reservoir of SARSr-CoVs. This region was not involved in the 2002–2003 SARS outbreaks and none of the subjects exhibited any evident respiratory illness during sampling. Among those sampled, 139 are female and 79 male, and the median age is 48 (range 12–80). Occupational data were obtained for 208 (95.4%) participants: 85.3% farmers and 8.7% students. Most (81.2%) kept or owned livestock or pets, and the majority (97.2%) had a history of exposure to or contact with livestock or wild animals. Importantly, 20 (9.1%) participants witnessed bats flying close to their houses, and one had handled a bat corpse. As a control, we also collected 240 serum samples from random blood donors in 2015 in

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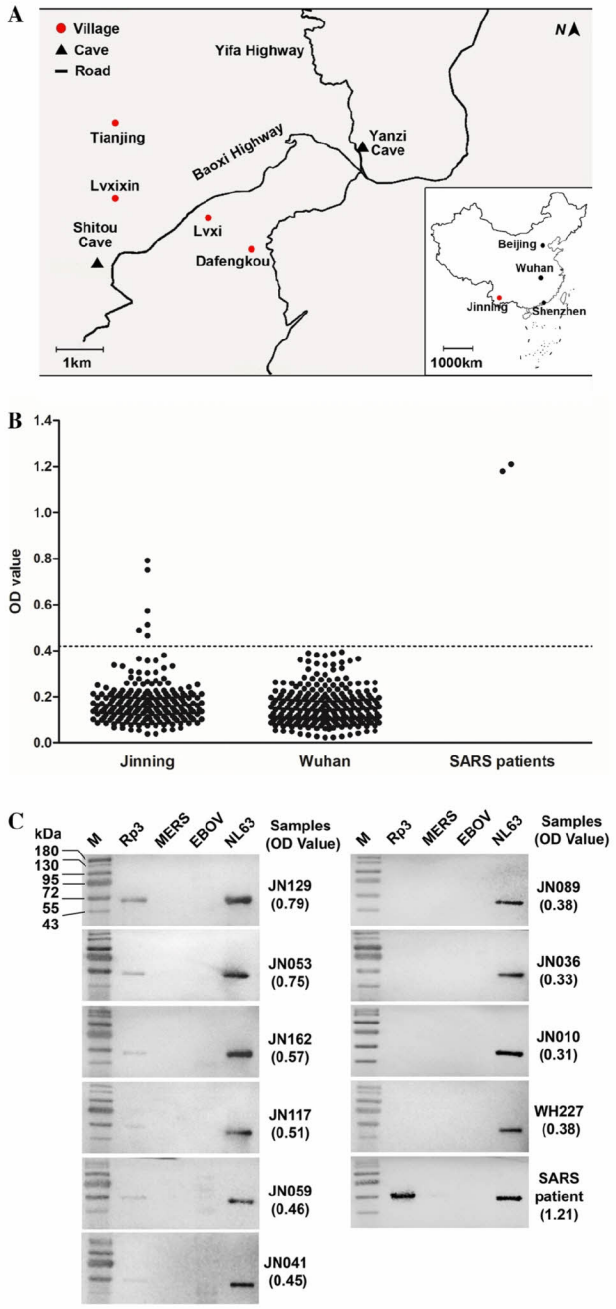

Fig. 1 SARSr-CoV serosurveillance. (**A**) Map of Xiyang town, Jinning County, Yunnan Province, China. Shown here is the location of the 4 villages (Tianjing, Dafengkou, Lvxi, Lvxixin) around 2 bat caves (Yanzi Cave and Shitou Cave) chosen for this study. The map of China is also shown in the inset indicating the location of Wuhan, where the negative control sera were collected, in relation to Jinning, Shenzhen and the capital Beijing. Serological reactivity of serum samples with recombinant SARSr-CoV NP protein. **B** ELISA test. The dotted line represents the cutoff of the test. **C** Western blot analysis. Numbers on the left are molecular masses in kDa.

Wuhan, Hubei Province more than 1000 km away from Jinning (Fig. 1A) and where inhabitants have a much lower likelihood of contact with bats due to its urban setting. None of the donors had knowledge of prior SARS infection or known contact with SARS patients.

His-tagged nucleocapsid protein (NP) of the following viruses were expressed and purified in *E. coli* for this study: SARSr-CoV Rp3; human coronaviruses (HCoVs) HKU1, OC43, 229E, NL63; Middle East Respiratory Syndrome Coronavirus (MERS-CoV); and Ebola virus (EBOV). In addition, the receptor binding domains (RBD) of the spike protein (S) from SARS-CoV, bat SARSr-CoVs Rp3, WIV1, and SHC014 were produced in mammalian cells (Ge et al. 2013; Yang et al. 2016).

Polyclonal antibodies against each of the six NPs were prepared in rabbits as previously published (He et al. 2006). Cross-activity was evaluated with ELISA and Western blot (Supplementary Figures S1, S2). No significant cross-activity was detected among NPs and their corresponding antibodies for Rp3, MERS-CoV, NL63, or 229E. Cross-reaction was detected between OC43 and HKU1 as reported previously (Lehmann et al. 2008).

The Rp3 NP was chosen to develop a SARSr-CoV specific ELISA for serosurveillance. Micro-titer plates were coated with 100 ng/well of recombinant Rp3 NP and incubated with human sera in duplicates at a dilution of 1:20, followed by detection with HRP labeled goat anti-human IgG antibodies (Proteintech, Wuhan, China) at a dilution of 1:20,000. The 240 random serum samples collected in Wuhan and two SARS positive samples from Zhujiang Hospital, Southern Medical University (kindly provided by Prof. Xiaoyan Che)[1] were used to set a cutoff value. We used the mean OD value of the 240 samples plus three standard deviations to set the cutoff value at 0.41. A total of six positive samples were detected by ELISA (Fig. 1B). The specificity of these positive samples was confirmed by Western blot with recombinant Rp3 NP (Fig. 1C) together with NP of NL63, MERS-CoV and EBOV. The degree of reactivity in Western blot correlated well with the ELISA OD readings, providing further confidence in the ELISA screening method. None of the sera reacted with NPs of either MERS-CoV or EBOV. On the other hand, all 10 human sera (9 from Jinning and 1 from Wuhan), regardless of their Rp3 NP reactivity, reacted strongly with the NL63 NP as expected due to high prevalence of NL63 infection in humans worldwide (Abdul-Rasool and Fielding 2010).

We conducted a virus neutralization test for the six positive samples targeting two SARSr-CoVs, WIV1 and WIV16 (Ge et al. 2013; Yang et al. 2016). None of them were able to neutralize either virus. These sera also failed to react by Western blot with any of the recombinant RBD proteins from SARS-CoV or the three bat SARSr-CoVs Rp3, WIV1, and SHC014. We also performed viral nucleic

[1] Prof. Xiaoyan Che—deceased

acid detection in oral and fecal swabs and blood cells, and none of these were positive.

The demography and travel histories of the six positive individuals (four male, two female) are as follows. Two males (JN162, 45 years old, JN129, 51 years old) are from the Dafengkou village; two males (JN117, 49 years old, JN059, 57 years old) from Lvxi village; and two females (JN053, JN041, both 55 years old), from Tianjing village. In the 12 months prior to the sampling date, JN041 was the only individual who travelled outside of Yunnan, to Shenzhen, a city 1400 km away from her home village (Fig. 1A). JN053 and JN059 had travelled to another county 1.4 km away from their village. JN162 had travelled to Kunming, the capital of Yunnan, 63 km away. JN129 and JN117 had never left the village. It is worth noting that all of them had observed bats flying in their villages.

Our study provides the first serological evidence of likely human infection by bat SARSr-CoVs or, potentially, related viruses. The lack of prior exposure to SARS patients by the people surveyed, their lack of prior travel to areas heavily affected by SARS during the outbreak, and the rapid decline of detectable antibodies to SARS-CoV in recovered patients within 2–3 years after infection strongly suggests that positive serology obtained in this study is not due to prior infection with SARS-CoV (Wu et al. 2007). The 2.7% seropositivity for the high risk group of residents living in close proximity to bat colonies suggests that spillover is a relatively rare event, however this depends on how long antibodies persist in people, since other individuals may have been exposed and antibodies waned. During questioning, none of the 6 seropositive subjects could recall any clinical symptoms in the past 12 months, suggesting that their bat SARSr-CoV infection either occurred before the time of sampling, or that infections were subclinical or caused only mild symptoms. Our previous work based on cellular and humanized mouse infection studies suggest that these viruses are less virulent than SARS-CoV (Ge et al. 2013; Menachery et al. 2016; Yang et al. 2016). Masked palm civets appeared to play a role as intermediate hosts of SARS-CoV in the 2002–2003 outbreak (Guan et al. 2003). However, considering that these individuals have a high chance of direct exposure to bat secretion in their villages, this study further supports the notion that some bat SARSr-CoVs are able to directly infect humans without intermediate hosts, as suggested by receptor entry and animal infection studies (Menachery et al. 2016).

The failure of these NP ELISA positive sera to either neutralize live virus or react with RBD proteins in Western blot could be explained by at least two hypotheses. First, the immune response to the bat SARSr-CoV S protein may be weaker than that to the NP protein or may wane more rapidly, especially in subclinical infections, resulting in antibody levels is too low to be detected by our assays. Secondly, other bat SARSr-CoV variants may be circulating in bats in these villages that have highly divergent S proteins and have not yet been detected in our surveillance studies.

Coronaviruses are known to have a high mutation rate during replication and are prone to recombination if different viruses infect the same individual (Knipe et al. 2013). From our previous studies of bat SARSr-CoVs in the two caves near these villages, we have found genetically highly diverse bat SARSr-CoVs and evidence of frequent coinfection of two or more different SARSr-CoVs in the same bat (Ge et al. 2013). Our current study suggests that our surveillance is not exhaustive, as one would have expected, and that further, more extensive surveillance in this region is warranted. It might also be prudent to combine serological surveillance with molecular surveillance of bats in future, despite the technological challenges that this represents.

Acknowledgements This study was jointly funded by the National Natural Science Foundation of China Grant (81290341) to ZLS; the National Institute of Allergy and Infectious Diseases of the National Institutes of Health (Award Number R01AI110964) to PD and ZLS, United States Agency for International Development (USAID) Emerging Pandemic Threats PREDICT project Grant (Cooperative Agreement No. AID-OAA-A-14-00102) to PD; and Singapore NRF-CRP Grant (NRF2012NRF-CRP001–056) and CD-PHRG Grant (CDPHRG/0006/2014) to LFW.

Compliance with Ethical Standards

Conflict of interest The authors declare that they have no conflict of interest.

Animal and Human Rights This study was approved by the Wuhan Institute of Virology Institutional Review Board (China) and by Hummingbird IRB (USA).

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From: Andrew Clements <aclements@usaid.gov>
To: David J Wolking <djwolking@ucdavis.edu>
CC: Cara J. Chrisman <cchrisman@usaid.gov>;Cassandra Louis Duthil <clouisduthil@usaid.gov>;Amalhin Shek <ashek@usaid.gov>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 2/24/2020 12:26:00 PM
Subject: [predict] Re: Feedback needed: March 17-19th plans

Hi David,

Go ahead and set the Hill briefing for whenever is best (either 18th AM or 19th PM). We'll work around that. If no preference, then have the Hill briefing on 18th AM and we'll have the data meeting on 18th PM and 19th all day.

Andrew

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

On Tue, Feb 18, 2020 at 11:19 PM David J Wolking <djwolking@ucdavis.edu> wrote:
Hi Andrew,

We're planning on doing a Hill briefing the afternoon of March 18th or 19th but need some feedback soon so we can begin coordinating with congressional offices and staff.

Also on our Executive Board call today we came to the consensus that USG personnel probably only have the appetite for one or even a half day of the data meeting/workshop, so it might work best to do a summary/presentations and Q&A/discussion on the short day and the deeper dive with those that really want to get in the weeds the longer day (PREDICT, FAO, WHO, and select USG personnel). Maybe a half day on the 18th full day on the 19th would work well?

If you let us know what USAID thinks would work best, we'll keep moving forward with plans...

Best,

David

From: Andrew Clements <aclements@usaid.gov>
Sent: Thu, 12 Mar 2020 14:53:29 -0700
Subject: Re: Slide deck for March 17th
To: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, djwolking@ucdavis.edu

Thanks, Chris. I took most of the others off this reply.
The format looks good (with one exception—see below). We do need to leave a little time for others to provide information on what they are doing. How long do you think the Predict presentations will be?

Can you explain the Myanmar-focused presentation? I assume it's to give balance (for SI), but considering we're cutting back the time available for the whole meeting, it seems harder to justify a country-specific presentation when we want this to be about what was learned across countries.

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On Mar 12, 2020, at 4:10 AM, Christine Kreuder Johnson <ckjohnson@ucdavis.edu> wrote:

> Andrew et al,
> How's this for an outline for the PREDICT aspects of March 18/19th meetings?
> We can use our same slide content and format as we've been planning.
> Day 1 SESSION 1: Review of data related to spillover, amplification and spread of emerging zoonotic viruses
> *Surveillance (CKJ), virus discoveries (SA/TG), surveillance in Myanmar (SM)*
> Day 1 SESSION 2: Review of risk profiles and trends related to spillover, amplification, and spread of emerging zoonotic viruses
> *Modeling & analytics insights (PD), behavior and community engagement (KS), capacity and pandemic preparedness (JM)*
> Day 2 SESSION 3: Review of tools and strategies related to spillover, amplification, and spread of emerging zoonotic viruses
> *Public data site (DW/CKJ), Virus detection tools (TG/SA), outbreak response (BB), policy, partnerships and health security (BK)*
> Pls share thoughts and ideas, thank you/ckj
>
> ---
>
> **From:** Jonna Mazet <jkmazet@ucdavis.edu>
> **Date:** Wednesday, March 11, 2020 at 3:23 PM
> **To:** Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>
> **Cc:** Tracey Goldstein <tgoldstein@ucdavis.edu>, Simon Anthony <sja2127@columbia.edu>, Peter Daszak <daszak@ecohealthalliance.org>, William Karesh <karesh@ecohealthalliance.org>, "Murray, Suzan" <MurrayS@si.edu>, Karen Saylors [REDACTED], Andrew Clements <AClements@usaid.gov>, David John Wolking <djwolking@ucdavis.edu>
> **Subject:** Re: Slide deck for March 17th
>
> Just checking if we are changing format, schedule, or amount of time allotted for each of us for the USAID briefing, given the change to remote and possibly time determined by USAID?
> Thanks in advance for preparation of slides,
> Jonna
>
> On Wed, Mar 4, 2020 at 8:34 PM Christine Kreuder Johnson <ckjohnson@ucdavis.edu> wrote:

Hello - USAID slides here adapted for us to use for the briefing, and a box folder to help us coordinate our content. https://ucdavis.app.box.com/folder/105783605026.
Pls upload your section by Friday the 13th and I will format these all together.
Let me know if I can do anything else to help us organize.
Here's to hoping our pandemic threats briefing isn't cancelled by a pandemic.
/ckj

From: David J Wolking <djwolking@ucdavis.edu>
Date: Wednesday, March 4, 2020 at 11:06 AM
To: Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, Tracey Goldstein <tgoldstein@ucdavis.edu>, Simon Anthony <sja2127@columbia.edu>, Peter Daszak <daszak@ecohealthalliance.org>, William Karesh <karesh@ecohealthalliance.org>, "Murray, Suzan" <MurrayS@si.edu>, Karen Saylors [REDACTED], Jonna Mazet <jkmazet@ucdavis.edu>, Andrew Clements <AClements@usaid.gov>
Subject: Review: Draft program for March 17th

Dear honorable speakers!

Eunah drafted a short program for the March 17th event at the NMAI (the 2-4PM event not the earlier USAID briefing). I'm attaching it here for quick feedback, especially for review of talk titles and photos. Let us know if you want any changes or have suggestions and I'll work with Chris and Eunah to modify/update as needed.

Just FYI - we're also developing a 4 pager with more "meat" that will have achievements, impact, and recommendations so the attached program is not intended to serve that purpose. We'll print about 300 of these programs (one for each seat in the theater).

Thanks and let me know if you have any questions...

David

From:	William B. Karesh <karesh@ecohealthalliance.org>
To:	Andrew Clements <aclements@usaid.gov>
CC:	Chris Johnson <ckjohnson@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;David Wolking <djwolking@ucdavis.edu>;predictmgt@usaid.gov" <predictmgt@usaid.gov>
Sent:	4/13/2020 12:04:48 PM
Subject:	Re: COVID-19 lab support to Jordan?

Dr. Ehab is planning to be on the next call being organized for requests. They have been a bit out of the loop since we closed the project last September but we have been pitching new project ideas to get the tea up an running again this year. He put together a nice concept note for a project in Jordan for CoV surveillance that he is sending to the Mission. I reviewed it last week, but I do not know if he has sent it to the Mission yet.

BK

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EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Apr 13, 2020, at 2:57 PM, Andrew Clements <aclements@usaid.gov> wrote:

Have you been in contact with Jordan about COVID-19 lab support? Are they in need? Do you have plans to possibly provide support?

The mission is asking about mechanisms for lab support.

Andrew P. Clements, Ph.D.
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From: Dennis Carroll <[redacted]
Sent: Mon, 11 May 2020 14:29:02 -0400
Subject: Re: a PREDICT, GVP derived structural biology proposal in response to DOE request for COVID-19 ideas
To: "Becker, Michael" <mbecker@anl.gov>
Cc: Eddy Rubin <[redacted] Erica Ollmann Saphire <erica@lji.org>, Jonna Mazet <jkmazet@ucdavis.edu>, R Holland Cheng <rhch@ucdavis.edu>

Michael, would you be available at 4:00 Wednesday? I am copying Eddy and Jonna to confirm their availability as well

thanks

On Fri, May 8, 2020 at 2:35 PM Becker, Michael <mbecker@anl.gov> wrote:

Hi Dennis,

Thank you very much for your encouraging reply!

Yes, I could talk anytime on Mon., Wed., or Fri. afternoon of next week. My cell is [redacted] and my home is [redacted] [redacted] If you prefer that I call you, please let me know the # and time.

When I e-mailed you, I thought to include everyone on the GVP leadership list, including Eddy, but I couldn't find everyone's email address, and thought it best not to overdo it until leadership here had a sense of what might develop.

Erica Ollman Saphire (https://www.lji.org/faculty-research/labs/saphire/#overview) has also expressed interest, indicating that she could support with Xray, cryoEM, cryoET and antibody discovery, which is fantastic. You may know that in addition to her very impressive work on Ebola, Lassa, and other filoviruses, she is currently involved in efforts on COVID-19.

Meanwhile, Holland Cheng (https://www.pioms.org/), and I have been communicating further on developing plans, including near-term aims on COVID-19, and efforts that could dovetail into a larger strategic plan. For insight, I am attaching a one-page LDRD pre-proposal (internal ANL grant pre-proposal) that I submitted here at ANL on Monday, and a very rough outline of a 'white paper' for a 'One Health Structural Biology Center' concept with some ideas for vetting and improvement. Apologies for the roughness.

Finally, I managed to find the viral genome sequences from PREDICT, via the very nice Healthmap. I know that PREDICT has been extended 6 months, but I am wondering if there will be a program that will collect new viruses and generate new sequences going forward, such as a USAID 'Spillover' program or an effort by the GVP?

I look forward to your reply and to talking with you next week.

Thank you for your interest!

Michael

From: Dennis Carroll <[redacted]
Sent: Thursday, May 7, 2020 3:31 PM
To: Becker, Michael <mbecker@anl.gov>; Eddy Rubin <[redacted]>; Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: a PREDICT, GVP derived structural biology proposal in response to DOE request for COVID-19 ideas

Michael, apologies for the tardy reply. Your proposal is really interesting and we would welcome a chance to discuss more with you. I am copying Eddy Rubin on this email. He is a previous Director of the Joint Genome Institute, a DOE supported lab. Eddy is now a key player on the Global Virome Project. Are there times next week when you might be available for a call - preferably in the afternoon?

Looking forward to hearing from you

dennis

On Wed, Apr 29, 2020 at 9:11 PM Becker, Michael <mbecker@anl.gov> wrote:

> Dear Colleagues,
>
> The DOE Director of the Office of Science, Chris Fall, recently circulated a letter requesting strategic ideas for how the DOE and National Laboratories might help with the COVID-19 crisis. Please see attached. Some examples given therein may be applicable to the current situation, whereas others are more forward looking.
>
> Taking note of the groundbreaking efforts of PREDICT and of the Global Virome Project, it occurred to me that by using materials and results from such programs as input, systematic efforts with structure-based design could potentially help provide improved diagnostics, and leads for pan-vaccine, and pan-therapeutics to help avert future pandemics. DOE is very good at helping to support structural biology. A single-slide flow chart, a single-page structural biology center concept, and a draft letter to Chris Fall are attached. Improvements are welcome. I called the concept "PREVENT", but it it might be better to use "One Health" or "GVP" in the name.
>
> I sincerely hope that each of you might be interested to help improve, and support the concept. But many of you may be way too busy with the crisis right now. I am aiming to submit the concept to Stephen Streiffer, who is the Associate Laboratory Director for Photon Sciences here at Argonne National Laboratory on about Mon., May 4th, which is necessary prior to submitting it to Chris Fall. If any of you would be willing to help improve the ideas and lend your names to the letter, that could greatly increase the chances of it possibly leading to an actionable project.
>
> Very sorry if this is naive or redundant. Thank you very much for your consideration, and best wishes!
>
> Michael Becker, Ph.D.
> GM/CA@APS (https://www.gmca.aps.anl.gov/)
> Argonne National Laboratory

--
Dr Dennis Carroll
President, Global Virome Project
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, Bangkok, Thailand

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From: "Lichtveld, Maureen Y" <mlichtve@tulane.edu>
To: "Goodtree, Hannah" <HGoodtree@nas.edu>, 'Amy Pruden' <apruden@vt.edu>, "'Barton Behravesh, Casey (CDC/OID/NCEZID)'" <dlx9@cdc.gov>, "'daszak@ecohealthalliance.org'" <daszak@ecohealthalliance.org>, David Rizzo <dmrizzo@ucdavis.edu>, [redacted], [redacted], "'Hermsen, Elizabeth D'" <elizabeth.hermsen@merck.com>, "'Hughes, James M'" <jmhughe@emory.edu>, John Parrish-Sprowl <johparri@iupui.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, "'kevin.anderson@dhs.gov'" <kevin.anderson@dhs.gov>, "'mary_wilson@harvard.edu'" <'mary_wilson@harvard.edu'>, "'mewilson@hsph.harvard.edu'" <mewilson@hsph.harvard.edu>, "'Miller, Sally'" <miller.769@osu.edu>, "'MUMFORD, Elizabeth'" [redacted] "'Rushton, Jonathan'" <[redacted]
Cc: "Pavlin, Julie" <JPavlin@nas.edu>, "Buckley, Gillian" <GBuckley@nas.edu>, "'andre@ecohealthalliance.org'" <andre@ecohealthalliance.org>, "Neville, Geraldine L" <gneville@tulane.edu>, 'Mary Radford' <maradford@ucdavis.edu>
Subject: in case you haven't seen this--RE: OHAC Call #23 Doodle Poll
Sent: Fri, 10 Jul 2020 15:39:22 +0000

https://www.unenvironment.org/resources/report/preventing-future-zoonotic-disease-outbreaks-protecting-environment-animals-and

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From: Goodtree, Hannah <HGoodtree@nas.edu>
Sent: Tuesday, July 7, 2020 9:25 AM
To: 'Amy Pruden' <apruden@vt.edu>; 'Barton Behravesh, Casey (CDC/OID/NCEZID)' <dlx9@cdc.gov>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; David Rizzo <dmrizzo@ucdavis.edu>; [redacted] <[redacted]>; 'Hermsen, Elizabeth D' <elizabeth.hermsen@merck.com>; 'Hughes, James M' <jmhughe@emory.edu>; John Parrish-Sprowl <johparri@iupui.edu>; Jonna Mazet <jkmazet@ucdavis.edu>; 'kevin.anderson@dhs.gov' <kevin.anderson@dhs.gov>; 'mary_wilson@harvard.edu'; 'mewilson@hsph.harvard.edu' <mewilson@hsph.harvard.edu>; 'Miller, Sally' <miller.769@osu.edu>; Lichtveld, Maureen Y <mlichtve@tulane.edu>; 'MUMFORD, Elizabeth' <[redacted]>; 'Rushton, Jonathan' <[redacted]
Cc: Pavlin, Julie <JPavlin@nas.edu>; Buckley, Gillian <GBuckley@nas.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; Neville, Geraldine L <gneville@tulane.edu>; 'Mary Radford' <maradford@ucdavis.edu>
Subject: OHAC Call #23 Doodle Poll

I hope you're all well and enjoyed the holiday weekend.

Please review and complete the doodle poll for our next call, which will take place the week after the Forum's virtual workshop on The Critical Public Health Value of Vaccines – Tackling Issues of Access and Hesitancy (calendar invite to be sent shortly). **Please complete this poll by COB 7/14.**

Thank you and I look forward to seeing you all (virtually) at our next meeting,
Hannah

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From: Dennis Carroll <[redacted]>
Sent: Thu, 3 Sep 2020 08:34:46 -0400
Subject: Re: GVP letter of agreement for KAA initiative
To: [redacted]>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, Samantha Maher <maher@ecohealthalliance.org>

[redacted] thanks for pushing these actions along. I don't believe a LOA requires legal input, but I will defer to Peter on that

d

On Wed, Sep 2, 2020 at 12:23 PM [redacted]> wrote:

Hi Peter / Dennis,

Jonna and I just spoke the Earth Biogenome Project and they would very much like to have GVP be part of their initiative and we think this would be a worthwhile relationship to pursue. As such they would like

GVP to sign their MOU and letter of intent (see attached). This approach would be the same as the Trinity Challenge whereby GVP becomes a partner of another initiative. EBP are having a meeting with their partners and potential funders including the Wellcome

Trust in early October and would like to announce the partnership with GVP at the forum.

Given the Trinity Challenge launch will be on September 14th where we will announce GVP's partnership with them, it would be good to drive the momentum and reinvigorate interest in GVP by also announcing

partnership with EBP as well as the KAA mentioned in my previous email (I've reattached a draft LOA).

Do you know if we are able to sign an LOA / MOA with these groups? Do you need to ask the lawyers? We could discuss further in the next board meeting but it would be useful to move forward before then, given

the short timeline.

Many thanks,

[redacted]

From: [redacted]

Date: Tuesday, August 25, 2020 at 11:33 AM

To: Peter Daszak <daszak@ecohealthalliance.org>

Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Dennis Carroll <[redacted]>, Samantha Maher <maher@ecohealthalliance.org>

Subject: GVP letter of agreement for KAA initiative

Hi Peter,

I hope you are well. I have attached a draft letter of agreement proposed between the Global Virome Project and the KAA initiative. Do you think the you or the lawyers would be able to look over

the LOA in terms of legalities for the 501c3?

We would like to pursue a similar letter of agreement with the Earth Biogenome Project/iBiol, so it would be a useful template for the

future. As these are established groups (KAA and EBP), GVP

would be forming relationships in the same way as we are linking with the Trinity challenge.

Cheers,

--
Dr Dennis Carroll
President, Global Virome Project
Inline image

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, Bangkok, Thailand

mobile: REDACTED
email: REDACTED