From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 27 Apr 2020 09:42:27 -0600
To: LaTrielle, Sara
Cc: Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: Re: RML update to DARPA

Would bullet points work? If so

- Modeling of surface and fluid environmental stability of SARS-CoV-2 in human respiratory tract fluids
- Modeling of surface and aerosol environmental stability of SARS-CoV-2 under conditions mimicking winter, summer and indoors
- SARS-CoV-2, decontamination of PPE, including re-use of N95s (under review EID)
- Rhesus macaque animal model development (accepted Nature)
- Analyses of SARS-CoV-2 spike using pseudotype systems
- Vaccine development (ChadOx1 COVID19), currently in phase 1 clinical trials
- Antiviral development (remdesivir) against SARS-CoV-2 (submitted)
- Small animal model development (hamsters and mice)
- SARS-CoV-2 surveillance in Republic of the Congo and Ghana (part of WHO framework)
- Vaccine development J&J (Adenovirus) and Curevac (mRNA vaccine)

Published:

- Letko M, Marzi A, **Munster V**. Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses. Nat Microbiol. 2020.
- **Munster VJ**, Koopmans M, van Doremalen N, van Riel D, de Wit E. A Novel Coronavirus Emerging in China - Key Questions for Impact Assessment. N Engl J Med. 2020;382(8):692-4.
- van Doremalen N, Bushmaker T, Morris DH, Holbrook MG, Gamble A, Williamson BN, Tamin A, Harcourt JL, Thornburg NJ, Gerber SI, Lloyd-Smith JO, de Wit E, **Munster VJ**. Aerosol and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1. N Engl J Med. 2020.
- Judson SD, Neeltje van Doremalen, **Munster VJ** Stability and Viability of SARS-CoV-2, reply of the authors. NEJM 2020
- **Vincent J. Munster**, Friederike Feldmann, Brandi N. Williamson, Neeltje van Doremalen, Lizzette Pérez-Pérez, Jonathan Schulz, Kimberly Meade-White, Atsushi Okumura, Julie Callison, Beniah Brumbaugh, Victoria A. Avanzato, Rebecca Rosenke, Patrick W. Hanley, Greg Saturday, Dana Scott, Elizabeth R. Fischer, Emmie de Wit. Respiratory disease and virus shedding in rhesus macaques inoculated with SARS-CoV-2. Nature accepted.

From: "LaTrielle, Sara" <[redacted] (b) (6)
Date: Monday, April 27, 2020 at 9:21 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6) "Plowright, Raina"
<[redacted] (b) (6)
Subject: RML update to DARPA

Vincent and Kwe,

Can you provide a brief update in regards to your COVID19 work in the last few weeks? I get some of RML updates via UCLA- but it would be great to get a few sentences each Monday that we can submit- per DARPA's request for weekly (but very brief) updates. Does this work for your team?

Best,

Sara LaTrielle

Program Manager
PREEMPT Project
Montana State University

(b) (6)

From: Letko, Michael (NIH/NIAID) [F]
Sent: Fri, 24 Apr 2020 23:18:09 +0000
To: Schountz, Tony
Cc: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: SARS2 spike entry with Artibeus ACE2

If you want the data, let me know. I can even provide you some western blots.

-michael

Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
[redacted] (b) (6)

On Apr 24, 2020, at 4:49 PM, Schountz,Tony <[redacted] (b) (6) wrote:

Hi Michael, thanks much for the figure. That is very, very cool! Congrats on the findings.

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Apr 24, 2020, at 4:07 PM, Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6)
wrote:

Hi Tony,

I want to thank you again for providing us with the Artibues cells we used in our paper!

Attached is some data that Vincent told me you may find interesting. I have recently tested our pseudotype system with *Artibeus jamaicensis* ACE2 and see clear entry with SARS2 and significantly less entry with SARS1. I have repeated this experiment a few times and with different DNA clones of Artibeus ACE2, and these results seem consistent. M

<image.jpg>

Am always eager to discuss data if you're interested.

Hope all is well.

Regards,
-michael

—

Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 24 Apr 2020 08:21:07 -0600
To: Laing, Eric
Cc: Broder, Chris (USU-DoD); De wit, Emmie (NIH/NIAID) [E]
Subject: Re: SARS-CoV-2

We don't

you mean using these finger prick devices to determine suitability for your luminex?

We could, but would need to put an dedendum in asap, to collect some blood using these devices. We have some vaccinated NHP sitting, so that might be an option (but would need these devices asap).

Btw, let me know if you have a bead panel ready to rumble, more than eager to set-it up over here and have Steph run our Congo (and Jordan and Oz) bat samples on them. We are getting some human samples in as well and are part of the WHO solidarity II program (with sites in Congo and Ghana) for human serosurveillance.

Cheers,

Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

From: Eric Laing <(b) (6)
Date: Friday, April 24, 2020 at 8:13 AM
To: "(b) (6) <(b) (6)
Cc: "Broder, Chris (USU-DoD)" <(b) (6) Emmie De wit
<(b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie and Vincent,

Are you collecting any NHP dpi blood with Mitra devices? I'm wondering if there's a way to pilot extraction and antibody testing with control animal samples before receiving human samples.

Eric

On Mon, Apr 20, 2020 at 2:03 PM Laing, Eric <(b) (6) wrote:
Emmie, that just blew my mind. Can you imagine the conspiracy theories that would pop up from that?

Vincent, yes, we are supporting a serology arm of an IDCRP study and will start screening acute/convalescent sera from military treatment facilities that should be arriving shortly. Based on sample size, Chris reached out a biotech to help us acquire enough transient expressed S proteins.

Chris is going to pitch a larger CoV S trimer panel for immediate use and then downstream surveillance. Our wish list has SARS-1, SARS-2, 4 HCoVs, MERS, bat SARS-2-like ZXC21, HKU9 and bat MERS-like PDF-2180 (pipistrelles seq from Simon's paper). We have WIV16 S on our wish list, but I'm wondering now if it's too similar to SARS-CoV to be very interesting. We already have Rs4874 in our expression system which is in that WIV16 clade of SARS-CoV bat progenitors. Any others you think we are missing? We also have RaTG13 in our system, but I think ZXC21 will be more interesting.

- Eric

Eric D. Laing, Ph.D.
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lab: [redacted] (b) (6)

[redacted] (b) (6)

On Mon, Apr 20, 2020 at 10:24 AM Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6)
wrote:
Pretty cool,

Can't wait to throw some of our Congo bat sera on this panel! Are you trying to transfer to human serology as well?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Emmie De wit <[redacted] (b) (6)
Date: Monday, April 20, 2020 at 7:50 AM
To: Eric Laing <[redacted] (b) (6) "[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Williamson, Brandi (NIH/NIAID) [E]" <[redacted] (b) (6) "Shupert, W. Lesley (NIH/NIAID) [E]" <[redacted] (b) (6) "Broder, Chris (USU-DoD)" <[redacted] (b) (6)
Subject: RE: SARS-CoV-2

Hi Eric,
This looks pretty good. 1ml of serum really isn't a problem. Do you want 1 ml for all 4 NHPs?
I'll try to get it out this week. Can you email me the shipping address again? Finding anything in my inbox has become impossible somehow (e.g. by emails about crop-dusting the planet with negative EM stain so that we can detect the virus with a microscope from space-no I did not make this up).
Emmie

From: Laing, Eric <[redacted] (b) (6)
Sent: Monday, April 20, 2020 4:47 AM
To: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Cc: De wit, Emmie (NIH/NIAID) [E] <[redacted] (b) (6) Williamson, Brandi (NIH/NIAID) [E] <[redacted] (b) (6) Shupert, W. Lesley (NIH/NIAID) [E] <[redacted] (b) (6) Broder, Chris (USU-DoD) <[redacted] (b) (6)
Subject: Re: SARS-CoV-2

Data slides attached.

Eric D. Laing, Ph.D.
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lab: [redacted] (b) (6)

[redacted] (b) (6)

On Sun, Apr 19, 2020 at 8:49 PM Laing, Eric < (b) (6) wrote:
Hi Emmie and Vincent,

My laptop's battery that had the data I was working on just died and the charger is in our nursery room so I'll send over two figures tomorrow morning. The figures show specificity of SARS-CoV-2 (+)ve sera for SARS-CoV-2 S (trimer), that anti-SARS-CoV-2 sera IgG reacts strongly with S trimer and that the SARS-CoV-2 S trimer is more specific than S1 subunit monomer or RBD peptide antigens when differentiating SARS-CoV-2 and SARS-CoV-1 in an antigen-based immunoassay. We ran a 4-fold dilution starting at 1:4 and detected sera titers at 1:4,096 (21 dpi).

Emmie's questions
1) How much serum would you need? We received a lot of requests for convalescent serum so deposited a large volume in BEI. We kept some back, but I would have to check how much. My estimate is that we should have another 10ml for you (this would be pooled from 4 rhesus), not sure if that would get you anywhere near what you need. We haven't taken any additional animals out past day 7.
1mL would work. But more discussion will be necessary to decide if this is a worthy route.

2) Andrea Marzi here at RML is working on a replication competent VSV-not sure if it has a reporter.
Ok, I don't know Andrea, but Steph introduced me in a previous email regarding VSV-LLOV GP.

Vincent's question
Is that even possible given different IgG subclasses, epitopes and affinities? Wouldn't you rather correlate it back to a standardized titer as you would do with ELISA?
Do you think if we report sera titers from Luminex immunoassay that would be sufficient for research studies and quantification with a 'standard' (IgG concentration) would be unnecessary? I think we should compare our Luminex titer results with an ELISA starting at non-saturating dilutions to see if the Luminex optics are more sensitive. If we use a protein G column we should grab all IgG FC so I don't think we'd be limited by subclasses, etc...

Regarding a cut-off, where would you draw the line: 3xFold or MEAN+3*STDEV above, normal NHP/human sera? It should be straightforward for prospective studies monitoring seroconversion 4-fold increase between time point collections.

- Eric

Eric D. Laing, Ph.D.
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lab: [redacted] (b) (6)

[redacted] (b) (6)

On Sun, Apr 19, 2020 at 11:05 AM Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6) wrote:
Hi Eric,

Is that even possible given different IgG subclasses, epitopes and affinities? Wouldn't you rather correlate it back to a standardized titer as you would do with ELISA?

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Emmie De wit < [redacted] (b) (6)
Date: Sunday, April 19, 2020 at 8:17 AM
To: Eric Laing < [redacted] (b) (6)
Cc: "Williamson, Brandi (NIH/NIAID) [E]" < [redacted] (b) (6) "Shupert, W. Lesley (NIH/NIAID) [E]" < [redacted] (b) (6) "Broder, Chris (USU-DoD)" < [redacted] (b) (6) " [redacted] (b) (6) < [redacted] (b) (6)
Subject: RE: SARS-CoV-2

Hi Eric,
1) How much serum would you need? We received a lot of requests for convalescent serum so deposited a large volume in BEI. We kept some back, but I would have to check how much. My estimate is that we should have another 10ml for you (this would be pooled from 4 rhesus), not sure if that would get you anywhere near what you need. We haven't taken any additional animals out past day 7.
2) Andrea Marzi here at RML is working on a replication competent VSV-not sure if it has a reporter.
Emmie

From: Laing, Eric < [redacted] (b) (6)
Sent: Saturday, April 18, 2020 1:38 PM
To: De wit, Emmie (NIH/NIAID) [E] < [redacted] (b) (6)
Cc: Williamson, Brandi (NIH/NIAID) [E] < [redacted] (b) (6) Shupert, W. Lesley (NIH/NIAID) [E] < [redacted] (b) (6) Broder, Chris (USU-DoD) < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie,

Our lab piloted a SARS-CoV-2 spike glycoprotein antigen-based multiplex immunoassay (MIA) yesterday and I'm wrapping a repeat today. Data looks pretty solid with the four 21 dpi NHP sera you sent. I designed the pilot around the 21 dpi sera since we had the most volume and could start with an initial 1:4 dilution and get an idea of MFI for piloting human screening. Next step is to get a couple more antigens into the assay that are still in prep and then screen with the complete NHP dpi set at a single dilution.

2 questions before I head home.
1) How can we move from a qualitative fluorescence value to a quantitative assay? With our henipavirus sG polyclonal rabbit antisera, we have purified IgG and spiked that back into pre-bleed sera to make a quantitative IgG concentration/MFI value. What's the volume of terminal bleed sera and is something we can try to do with the NHP sera?

2) Replication-competent VSV_SARS-CoV-2_S reporter viruses. Who has em and who wants to share? Figured I'd ask before ordering a full-length S gene and rescuing it here. Our main research studies are supporting acute sera samples coming in from military treatment facilities, but having that SNT data will go a long way to understanding the binding assay data in the context of nAbs and protection.

Our S-based MIA pilot currently includes SARS-CoV-2 S tri, S1 monomer, RBD; SARS-CoV-1 S tri, S1 monomer. We put some of the bat SARS-related CoV S expression on hold while working on beta/alphaHCoV S1 monomer expression. It does look like the trimer is more immunogenic, but differentiation between SARS-CoV-2 and SARS-CoV-1 S tri is really clean and specific.

I'll finish data processing tomorrow and send some figures for your review and comment.

If you also want to chat about streamlining serology so we can pair up or run in parallel, and make a solid cross-agency collaboration, I'm down.

- Eric

Eric D. Laing, Ph.D.
Research Assistant Professor
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[redacted] (b) (6)

On Thu, Mar 19, 2020 at 9:51 PM De wit, Emmie (NIH/NIAID) [E] <(b) (6) wrote:
Hi Eric,
You're the first one to ask, so we can share all timepoints for all macaques with you. In our IgG S ELISA, 1 animal is positive by 7 dpi, the others by 10dpi. We will plan to ship on Monday.
I have also been hoarding AGM NiV sera from surviving AGMs (from remdesivir treatment studies), so at some point when we can start thinking of things non-CoV we can irradiate some of that if you need some.
Emmie

From: Laing, Eric <(b) (6)
Sent: Thursday, March 19, 2020 7:44 PM
To: De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Cc: Williamson, Brandi (NIH/NIAID) [E] <(b) (6) Shupert, W. Lesley (NIH/NIAID) [E] <(b) (6) Broder, Chris (USU-DoD) <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie,

That's good news, we are open for now but the situation may change. Chris was going to draft another assurance letter if necessary.

We're working on transiently expressing S-2P trimers and S1 monomers for SARS-2, the other human CoVs, a couple bat SARSr-CoV-1/2 and were going to start testing cross-reactivity in the multiplex. S-2P take longer to express in stable cell lines and purify so we wanted to test MERS S-2P vs S1 reactivity with the MERS+/- camel sera from you. One goal of the antigen-based multiplex will be to describe the IgM/IgG immunological response to SARS-CoV-2. I would definitely like to have samples within the IgM window. If you have enough to share all the time points from all 4 animals we can run the experiments with our multiplex panel when complete and share results with you all. Tell me what time points you can spare and we can work with that from our end. We definitely need 0 dpi and/or if you have a pooled NHP (-) we would use that. We've nearly exhausted out NiV(-) AGM stocks.

/R
- Eric

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
cell: (b) (6)
office: (b) (6)
lab: (b) (6)

(b) (6)

On Thu, Mar 19, 2020 at 4:47 PM De wit, Emmie (NIH/NIAID) [E] < (b) (6) wrote:
Hi Eric,
I heard we have all the paperwork complete, so we will ship on Monday (I hope you are still open!).
Besides 21 dpi for which we have plenty, which timepoints would you like a small volume of serum for:
0, 1, 3, 5, 7, 10, 12, 14 dpi. And would you like serum from all 4 animals at each timepoint or just one?
Emmie

From: Laing, Eric < (b) (6)
Sent: Friday, March 13, 2020 11:07 AM
To: De wit, Emmie (NIH/NIAID) [E] < (b) (6)
Cc: Shupert, W. Lesley (NIH/NIAID) [E] (b) (6) Broder, Chris (USU-DoD)
< (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie,

No worries, will the attached letter work?

- Eric

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
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office: (b) (6)
lab: (b) (6)

(b) (6)

On Fri, Mar 13, 2020 at 12:57 PM De wit, Emmie (NIH/NIAID) [E] < (b) (6) wrote:
Hi Eric,
Sorry, I got a bit busy and this disappeared off my radar for a few days. We can certainly spare a few microliters of serum for a couple of time points. We will need a letter from your biosafety office that you are allowed to receive this material, since it came out of BSL4 (gamma irradiated). Les Shupert (copied here) can send you an example of such a letter that you can adapt.
Emmie

From: Laing, Eric < (b) (6)
Sent: Monday, March 9, 2020 12:57 PM

To: De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Cc: Broder, Chris (USU-DoD) <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6)
Subject: Re: SARS-CoV-2

For the multiplex assay could get away with 4.5 uL but 10 uL would be a safe bet if you can spare. Maybe if you have something in the 5-10 uL range?

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
4301 Jones Bridge Road
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lab: (b) (6)

(b) (6)

On Mon, Mar 9, 2020 at 2:37 PM De wit, Emmie (NIH/NIAID) [E] <(b) (6) wrote:
We have quite a few timepoints between 0 and 21 dpi, but volumes are limited for times other than 21 dpi. How much would you need?
Let me see about the letter, I'll get back to you on that.
Emmie

From: Laing, Eric <(b) (6)
Sent: Monday, March 9, 2020 9:50 AM
To: De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Cc: Broder, Chris (USU-DoD) <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie,

Thank you, yes those would be useful. Have you collected any samples in the IgM window?

I just sent over a reassurance letter from our Biosafety Officer to Kay regarding receipt for fruit bat, VSV-challenged sera samples from Steph/Vincent. Let me know if I should collect another letter or if that one will be applicable for this as well.

- Eric

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
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lab: (b) (6)

(b) (6)

On Sat, Mar 7, 2020 at 3:12 PM De wit, Emmie (NIH/NIAID) [E] < (b) (6) wrote:
Hi Eric,
We have sera from 4 rhesus macaques collected at 21 dpi. All react in S1 ELISA, but we haven't done neuts yet (day 21 was yesterday). I can send you an aliquot of all 4 if that would be useful.
I am hoping to get the sera irradiated out early next week, so we should be able to ship soon. This would require some paperwork since the sera are coming out of BSL4, so I'll be in touch again when I know when we will be ready to ship.
Emmie

From: Laing, Eric < (b) (6)
Sent: Saturday, March 7, 2020 10:43 AM
To: Broder, Chris (USU-DoD) < (b) (6)
Cc: De wit, Emmie (NIH/NIAID) [E] < (b) (6) Munster, Vincent (NIH/NIAID) [E]
< (b) (6)
Subject: Re: SARS-CoV-2

Hi Vincent and Emmie,

We have cell lines expressing prefusion S-2P trimers for SARS, MERS, HKU1 and still cooking SARS-2. Cell lines are not yet stable, but we can work off of transient expression for a quick turnaround. Also working on transient S1 monomer expression, which doesn't require as laborious purification.

Any control sera will go a long way to demonstrate antisera reactivity in a multiplex. We were going to chase MERS first with the camel sera you provided. But can add SARS-2 NHP+ sera when possible.

Eric

On Fri, Mar 6, 2020 at 7:20 PM Broder, Christopher < (b) (6) wrote:
hey Vincent / Emmie

Many thanks again. Eric cc'd here. Yes. we would be excited to get your monkey sera!!
Eric is leading an S spike expansion on the bioplex

thanks so much, i have sent along your contact info to Trent.

all best
Chris

On Fri, Mar 6, 2020 at 6:42 PM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
No problem, if there are testing requests we send him to the larger NIAID workgroup on this,

Btw 1 will have NHP sera for you if you want it for the Luminex. Will still need to be irradiated etc, but would give you guys a headstart.

Btw 2 planning to apply for coronavirus serology grants? More than happy to provide LOS for NIH/NSF grants,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Broder, Christopher" <(b) (6)
Date: Friday, March 6, 2020 at 3:04 PM
To: "(b) (6) <(b) (6)
Cc: Emmie De wit <(b) (6)
Subject: Re: SARS-CoV-2

Thanks much Vincent / Emmie

Can I forward your email contact to him ? He may reach out.

it is::
Prof. Trent Munro
Director National Biologics Facility
Program Director Rapid Response Vaccine Pipeline
Australian Institute for Bioengineering and Nanotechnology
The University of Queensland
Brisbane Qld 4072 Australia
O: (b) (6)
M: (b) (6)
E: (b) (6)

On Fri, Mar 6, 2020 at 9:08 AM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Yes, we have established rhesus as a very suitable model (lot of URT and LRT shedding),

Probably will take us ~ 2 more weeks to get all the data analyzed,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Broder, Christopher" <(b) (6)
Date: Friday, March 6, 2020 at 5:58 AM
To: Emmie De wit <(b) (6) "(b) (6)
<(b) (6)
Subject: SARS-CoV-2

Hey guys

are doing NHPs SARS-CoV-2 ? planning to? a model?
Contacts in Queensland are reaching out. Not sure
what for, but I told them I would touch base with you

Chris

--
Christopher C. Broder, Ph.D.
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TEL: (b) (6)
FAX: 301-295-3773

Lucille Washington
Administrative Officer
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Eric D. Laing, Ph.D.
Research Assistant Professor
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cell: (b) (6)
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lab: (b) (6)

(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 23 Apr 2020 13:04:46 -0600
To: Plowright, Raina; (b) (6)
Subject: Re: Important- MSU press release

Go ahead, no problem

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <(b) (6)
Date: Thursday, April 23, 2020 at 12:56 PM
To: (b) (6) '(b) (6)
<(b) (6)
Subject: Re: Important- MSU press release

It's a news piece on what the lab is doing on COVID and mostly about how the students doing their blog for the local community. MSU news service – so really big time ☺ I'm sure it will get taken up by the NYT!!!

From: (b) (6)
Date: Thursday, April 23, 2020 at 12:51 PM
To: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Cc: Raina Plowright <(b) (6)
Subject: Important- MSU press release

Vincent,
Can I ask Ken Pekoc if Raina can put a thing in a press release about me working on COVID for her lab?

It would say " One graduate student, (b) (6), is working at RML doing COVID work including studies of aerosol transmission, preventative measures, and viral stability of SARS-CoV-2" She would site out NEJM paper.

(b) (6)

From: Schountz,Tony
Sent: Thu, 23 Apr 2020 15:59:18 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Artibeus sera

Vinnie, did Kwe transfect BHK21 with Aj Ace2? Or some other?
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Apr 21, 2020, at 2:19 PM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Yes, the ACE2 of the Artibeus works fine,

Weird results though. Very inconclusive? Anything on serology? If you send the sera we can run them here,

Busy times big man!

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From: Tony Schountz <[redacted] (b) (6)
Date: Monday, April 20, 2020 at 3:04 PM
To: [redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Artibeus sera

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I've gotten dragged into several projects now and am trying to juggle them all at once. I feel like I'm in graduate school again!

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Cc: Tony Schountz <(b) (6) "(b) (6)
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Thanks Tony, much appreciated!

Cheers,
Steph

From: "Schountz,Tony" <(b) (6)
Date: Friday, April 17, 2020 at 6:31 AM
To: "Seifert, Stephanie (NIH/NIAID) [E]" (b) (6)
Cc: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Port, Julia (NIH/NIAID)

[F]" <[redacted] (b) (6)
Subject: Re: Artibeus sera

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3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Seifert, Stephanie (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Thursday, April 16, 2020 1:50 PM
To: Schountz,Tony <[redacted] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) Port, Julia (NIH/NIAID) [F]
<[redacted] (b) (6)
Subject: Re: Artibeus sera

Hi Tony,

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Sent via Skynet

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Vincent Munster, PhD
Chief, Virus Ecology Section
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Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 21 Apr 2020 19:18:16 -0600
To: Miles Eckley; Seifert, Stephanie (NIH/NIAID) [E]
Cc: Schountz, Tony
Subject: Re: Aj SARS-CoV-2 Sera

Thanks Miles,

cheers

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Miles Eckley <[redacted] (b) (6)
Date: Tuesday, April 21, 2020 at 2:37 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6)
Subject: Aj SARS-CoV-2 Sera

Hi Vincent,

These samples are headed your way for delivery tomorrow. A link with tracking information is below if you need it. Thanks.

[redacted] (b) (6)

Miles

From: Schountz,Tony
Sent: Tue, 21 Apr 2020 21:14:35 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Schountz, Tony
Subject: Re: Artibeus sera

Well, that's really good news. :)

Juliette set up a neutralization test today on the serum samples. We euthanized the remaining bats yesterday (day 28); 3 inoculated, 3 contact and the 3 "negative" control bats.

The sera that Miles sent you are from the 3 pilot bats, blood collected on days 14 and 24, and 3 bats from the colony as negative controls. So, a total of 9 serum samples should arrive tomorrow for Stephanie.

T.

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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 20 Apr 2020 07:52:11 -0600
To: De wit, Emmie (NIH/NIAID) [E]; Laing, Eric
Cc: Williamson, Brandi (NIH/NIAID) [E]; Shupert, W. Lesley (NIH/NIAID) [E]; Broder, Chris (USU-DoD)
Subject: Re: SARS-CoV-2

awesome

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Emmie De wit <(b) (6)
Date: Monday, April 20, 2020 at 7:50 AM
To: Eric Laing <(b) (6) "(b) (6) <(b) (6)
Cc: "Williamson, Brandi (NIH/NIAID) [E]" <(b) (6) "Shupert, W. Lesley (NIH/NIAID) [E]" <(b) (6) "Broder, Chris (USU-DoD)" <(b) (6)
Subject: RE: SARS-CoV-2

Hi Eric,
This looks pretty good. 1ml of serum really isn't a problem. Do you want 1 ml for all 4 NHPs?
I'll try to get it out this week. Can you email me the shipping address again? Finding anything in my inbox has become impossible somehow (e.g. by emails about crop-dusting the planet with negative EM stain so that we can detect the virus with a microscope from space-no I did not make this up).
Emmie

From: Laing, Eric <(b) (6)
Sent: Monday, April 20, 2020 4:47 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: De wit, Emmie (NIH/NIAID) [E] <(b) (6) Williamson, Brandi (NIH/NIAID) [E] <(b) (6) Shupert, W. Lesley (NIH/NIAID) [E] <(b) (6) Broder, Chris (USU-DoD) <(b) (6)
Subject: Re: SARS-CoV-2

Data slides attached.

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology

Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
cell: [redacted] (b) (6)
office: [redacted] (b) (6)
lab: [redacted] (b) (6)

[redacted] (b) (6)

On Sun, Apr 19, 2020 at 8:49 PM Laing, Eric < [redacted] (b) (6) wrote:
Hi Emmie and Vincent,

My laptop's battery that had the data I was working on just died and the charger is in our nursery room so I'll send over two figures tomorrow morning. The figures show specificity of SARS-CoV-2 (+)ve sera for SARS-CoV-2 S (trimer), that anti-SARS-CoV-2 sera IgG reacts strongly with S trimer and that the SARS-CoV-2 S trimer is more specific than S1 subunit monomer or RBD peptide antigens when differentiating SARS-CoV-2 and SARS-CoV-1 in an antigen-based immunoassay. We ran a 4-fold dilution starting at 1:4 and detected sera titers at 1:4,096 (21 dpi).

Emmie's questions
1) How much serum would you need? We received a lot of requests for convalescent serum so deposited a large volume in BEI. We kept some back, but I would have to check how much. My estimate is that we should have another 10ml for you (this would be pooled from 4 rhesus), not sure if that would get you anywhere near what you need. We haven't taken any additional animals out past day 7.
1mL would work. But more discussion will be necessary to decide if this is a worthy route.

2) Andrea Marzi here at RML is working on a replication competent VSV-not sure if it has a reporter.
Ok, I don't know Andrea, but Steph introduced me in a previous email regarding VSV-LLOV GP.

Vincent's question
Is that even possible given different IgG subclasses, epitopes and affinities? Wouldn't you rather correlate it back to a standardized titer as you would do with ELISA?
Do you think if we report sera titers from Luminex immunoassay that would be sufficient for research studies and quantification with a 'standard' (IgG concentration) would be unnecessary? I think we should compare our Luminex titer results with an ELISA starting at non-saturating dilutions to see if the Luminex optics are more sensitive. If we use a protein G column we should grab all IgG FC so I don't think we'd be limited by subclasses, etc...

Regarding a cut-off, where would you draw the line: 3xFold or MEAN+3*STDEV above, normal NHP/human sera? It should be straightforward for prospective studies monitoring seroconversion 4-fold increase between time point collections.

- Eric

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Subject: Re: SARS-CoV-2

Hi Emmie,

Our lab piloted a SARS-CoV-2 spike glycoprotein antigen-based multiplex immunoassay (MIA) yesterday and I'm wrapping a repeat today. Data looks pretty solid with the four 21 dpi NHP sera you sent. I designed the pilot around the 21 dpi sera since we had the most volume and could start with an initial 1:4 dilution and get an idea of MFI for piloting human screening. Next step is to get a couple more antigens into the assay that are still in prep and then screen with the complete NHP dpi set at a single dilution.

2 questions before I head home.
1) How can we move from a qualitative fluorescence value to a quantitative assay? With our henipavirus sG polyclonal rabbit antisera, we have purified IgG and spiked that back into pre-bleed sera to make a quantitative IgG concentration/MFI value. What's the volume of terminal bleed sera and is something we can try to do with the NHP sera?

2) Replication-competent VSV_SARS-CoV-2_S reporter viruses. Who has em and who wants to share? Figured I'd ask before ordering a full-length S gene and rescuing it here. Our main research studies are supporting acute sera samples coming in from military treatment facilities, but having that SNT data will go a long way to understanding the binding assay data in the context of nAbs and protection.

Our S-based MIA pilot currently includes SARS-CoV-2 S tri, S1 monomer, RBD; SARS-CoV-1 S tri, S1 monomer. We put some of the bat SARS-related CoV S expression on hold while working on beta/alphaHCoV S1 monomer expression. It does look like the trimer is more immunogenic, but differentiation between SARS-CoV-2 and SARS-CoV-1 S tri is really clean and specific.

I'll finish data processing tomorrow and send some figures for your review and comment.

If you also want to chat about streamlining serology so we can pair up or run in parallel, and make a solid cross-agency collaboration, I'm down.

- Eric

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lab: [redacted] (b) (6)

[redacted] (b) (6)

On Thu, Mar 19, 2020 at 9:51 PM De wit, Emmie (NIH/NIAID) [E] < [redacted] (b) (6) wrote:
Hi Eric,
You're the first one to ask, so we can share all timepoints for all macaques with you. In our IgG S ELISA, 1 animal is positive by 7 dpi, the others by 10dpi. We will plan to ship on Monday.
I have also been hoarding AGM NiV sera from surviving AGMs (from remdesivir treatment studies), so at some point when we can start thinking of things non-CoV we can irradiate some of that if you need some.
Emmie

From: Laing, Eric < [redacted] (b) (6)
Sent: Thursday, March 19, 2020 7:44 PM
To: De wit, Emmie (NIH/NIAID) [E] < [redacted] (b) (6)
Cc: Williamson, Brandi (NIH/NIAID) [E] < [redacted] (b) (6) Shupert, W. Lesley (NIH/NIAID) [E] < [redacted] (b) (6) Broder, Chris (USU-DoD) < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie,

That's good news, we are open for now but the situation may change. Chris was going to draft another assurance letter if necessary.

We're working on transiently expressing S-2P trimers and S1 monomers for SARS-2, the other human CoVs, a couple bat SARSr-CoV-1/2 and were going to start testing cross-reactivity in the multiplex. S-2P take longer to express in stable cell lines and purify so we wanted to test MERS S-2P vs S1 reactivity with the MERS+/- camel sera from you. One goal of the antigen-based multiplex will be to describe the IgM/IgG immunological response to SARS-CoV-2. I would definitely like to have samples within the IgM window. If you have enough to share all the time points from all 4 animals we can run the experiments with our multiplex panel when complete and share results with you all. Tell me what time points you can spare and we can work with that from our end. We definitely need 0 dpi and/or if you have a pooled NHP (-) we would use that. We've nearly exhausted out NiV(-) AGM stocks.

/R
- Eric

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology

Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
cell: [redacted] (b) (6)
office: [redacted] (b) (6)
lab: [redacted] (b) (6)

[redacted] (b) (6)

On Thu, Mar 19, 2020 at 4:47 PM De wit, Emmie (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
Hi Eric,
I heard we have all the paperwork complete, so we will ship on Monday (I hope you are still open!). Besides 21 dpi for which we have plenty, which timepoints would you like a small volume of serum for: 0, 1, 3, 5, 7, 10, 12, 14 dpi. And would you like serum from all 4 animals at each timepoint or just one?
Emmie

From: Laing, Eric <[redacted] (b) (6)
Sent: Friday, March 13, 2020 11:07 AM
To: De wit, Emmie (NIH/NIAID) [E] <[redacted] (b) (6)
Cc: Shupert, W. Lesley (NIH/NIAID) [E] <[redacted] (b) (6) Broder, Chris (USU-DoD) <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie,

No worries, will the attached letter work?

- Eric

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
cell: [redacted] (b) (6)
office: [redacted] (b) (6)
lab: [redacted] (b) (6)

[redacted] (b) (6)

On Fri, Mar 13, 2020 at 12:57 PM De wit, Emmie (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
Hi Eric,

Sorry, I got a bit busy and this disappeared off my radar for a few days. We can certainly spare a few microliters of serum for a couple of time points. We will need a letter from your biosafety office that you are allowed to receive this material, since it came out of BSL4 (gamma irradiated). Les Shupert (copied here) can send you an example of such a letter that you can adapt.
Emmie

From: Laing, Eric <(b) (6)
Sent: Monday, March 9, 2020 12:57 PM
To: De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Cc: Broder, Chris (USU-DoD) <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6)
Subject: Re: SARS-CoV-2

For the multiplex assay could get away with 4.5 uL but 10 uL would be a safe bet if you can spare. Maybe if you have something in the 5-10 uL range?

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
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office: (b) (6)
lab: (b) (6)

(b) (6).

On Mon, Mar 9, 2020 at 2:37 PM De wit, Emmie (NIH/NIAID) [E] <(b) (6) wrote:
We have quite a few timepoints between 0 and 21 dpi, but volumes are limited for times other than 21 dpi. How much would you need?
Let me see about the letter, I'll get back to you on that.
Emmie

From: Laing, Eric <(b) (6)
Sent: Monday, March 9, 2020 9:50 AM
To: De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Cc: Broder, Chris (USU-DoD) <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6)
Subject: Re: SARS-CoV-2

Hi Emmie,

Thank you, yes those would be useful. Have you collected any samples in the IgM window?

I just sent over a reassurance letter from our Biosafety Officer to Kay regarding receipt for fruit bat, VSV-challenged sera samples from Steph/Vincent. Let me know if I should collect another letter or if that one will be applicable for this as well.

- Eric

Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
cell: [redacted] (b) (6)
office: [redacted] (b) (6)
lab: [redacted] (b) (6)

[redacted] (b) (6)

On Sat, Mar 7, 2020 at 3:12 PM De wit, Emmie (NIH/NIAID) [E] < [redacted] (b) (6) wrote:
Hi Eric,
We have sera from 4 rhesus macaques collected at 21 dpi. All react in S1 ELISA, but we haven't done neuts yet (day 21 was yesterday). I can send you an aliquot of all 4 if that would be useful.
I am hoping to get the sera irradiated out early next week, so we should be able to ship soon. This would require some paperwork since the sera are coming out of BSL4, so I'll be in touch again when I know when we will be ready to ship.
Emmie

From: Laing, Eric < [redacted] (b) (6)
Sent: Saturday, March 7, 2020 10:43 AM
To: Broder, Chris (USU-DoD) < [redacted] (b) (6)
Cc: De wit, Emmie (NIH/NIAID) [E] < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E]
< [redacted] (b) (6)
Subject: Re: SARS-CoV-2

Hi Vincent and Emmie,

We have cell lines expressing prefusion S-2P trimers for SARS, MERS, HKU1 and still cooking SARS-2. Cell lines are not yet stable, but we can work off of transient expression for a quick turnaround. Also working on transient S1 monomer expression, which doesn't require as laborious purification.

Any control sera will go a long way to demonstrate antisera reactivity in a multiplex. We were going to chase MERS first with the camel sera you provided. But can add SARS-2 NHP+ sera when possible.

Eric

On Fri, Mar 6, 2020 at 7:20 PM Broder, Christopher <[redacted] (b) (6) wrote:
hey Vincent / Emmie

Many thanks again. Eric cc'd here. Yes. we would be excited to get your monkey sera!!
Eric is leading an S spike expansion on the bioplex

thanks so much, i have sent along your contact info to Trent.

all best
Chris

On Fri, Mar 6, 2020 at 6:42 PM Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
No problem, if there are testing requests we send him to the larger NIAID workgroup on this,

Btw 1 will have NHP sera for you if you want it for the Luminex. Will still need to be irradiated etc, but would give you guys a headstart.

Btw 2 planning to apply for coronavirus serology grants? More than happy to provide LOS for NIH/NSF grants,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Broder, Christopher" <[redacted] (b) (6)
Date: Friday, March 6, 2020 at 3:04 PM
To: "[redacted] (b) (6) [redacted] (b) (6)
Cc: Emmie De wit <[redacted] (b) (6)
Subject: Re: SARS-CoV-2

Thanks much Vincent / Emmie

Can I forward your email contact to him ? He may reach out.

it is::
Prof. Trent Munro
Director National Biologics Facility
Program Director Rapid Response Vaccine Pipeline
Australian Institute for Bioengineering and Nanotechnology
The University of Queensland
Brisbane Qld 4072 Australia
O: [redacted] (b) (6)

M: [redacted] (b) (6)
E: [redacted] (b) (6)

On Fri, Mar 6, 2020 at 9:08 AM Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6) wrote:
Yes, we have established rhesus as a very suitable model (lot of URT and LRT shedding),

Probably will take us ~ 2 more weeks to get all the data analyzed,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Broder, Christopher" < [redacted] (b) (6)
Date: Friday, March 6, 2020 at 5:58 AM
To: Emmie De wit < [redacted] (b) (6) " [redacted] (b) (6)
< [redacted] (b) (6)
Subject: SARS-CoV-2

Hey guys

are doing NHPs SARS-CoV-2 ? planning to? a model?
Contacts in Queensland are reaching out. Not sure
what for, but I told them I would touch base with you

Chris

--
Christopher C. Broder, Ph.D.
Professor and Chair
Department of Microbiology and Immunology
Uniformed Services University, B4152
4301 Jones Bridge Rd, Bethesda, MD 20814-4799

USU is "America's Medical School"
Email: [redacted] (b) (6)
https://www.usuhs.edu/national/faculty/christopher-broder-phd
TEL: [redacted] (b) (6)
FAX: 301-295-3773

Lucille Washington
Administrative Officer
email - (b) (6)
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--
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--
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--
Eric D. Laing, Ph.D.
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(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 17 Apr 2020 12:00:08 -0600
To: Schountz, Tony
Cc: Seifert, Stephanie (NIH/NIAID) [E]; Port, Julia (NIH/NIAID) [F]
Subject: Re: Artibeus sera

Sounds good

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, April 17, 2020 at 11:52 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6) "Port, Julia (NIH/NIAID) [F]" <[redacted] (b) (6)
Subject: Re: Artibeus sera

I've screened a bunch from a company and there are several clones that neutralize on Vero cells. Working on the IC50s now.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Apr 17, 2020, at 11:50 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Not directly, we are currently overloaded with stuff to do. I assume you guys can do this yourself?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, April 17, 2020 at 11:38 AM
To: "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6) "[redacted] (b) (6)
<[redacted] (b) (6) "Port, Julia (NIH/NIAID) [F]" <[redacted] (b) (6)
Subject: Re: Artibeus sera

Would you be interested in testing a few human monoclonal antibodies to the spike? If so, I'll include them in the shipment.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Apr 17, 2020, at 11:17 AM, Seifert, Stephanie (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Thanks Tony, much appreciated!

Cheers,
Steph

From: "Schountz,Tony" <[redacted] (b) (6)
Date: Friday, April 17, 2020 at 6:31 AM
To: "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Cc: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6) "Port, Julia (NIH/NIAID) [F]" <[redacted] (b) (6)
Subject: Re: Artibeus sera

Hi Stephanie, we will ship a few serum samples to you on Monday.

Tony

—

Tony Schountz, PhD
Associate Professor

Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

From: Seifert, Stephanie (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, April 16, 2020 1:50 PM
To: Schountz,Tony <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Port, Julia (NIH/NIAID) [F]
<(b) (6)
Subject: Re: Artibeus sera

Hi Tony,

Even a small amount of serum would be great, I know that bat serum is precious! We're doing cross-neutralization experiments with both live SARS-CoV-1 & SARS-CoV-2 as well as pseudotyped particles with the spike glycoprotein of some of the novel sarbecoviruses that have not been isolated (e.g. RatG13).

Cheers,
Steph

Sent via Skynet

On Mar 28, 2020, at 9:16 AM, Schountz,Tony <(b) (6) wrote:

Vinnie, that should be fine depending on how much you need and how much we have. I'll have to check with Miles when he gets in on Monday to see how much he collected from each at terminal bleed.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692

(b) (6)
(b) (6)

On Mar 28, 2020, at 8:18 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Hi Tony,

Can you spare some sera from your SARS-CoV-2 seropositive Artibeus? We can do he pseudotype assay here, would like to see how this compares to your and our Elisa,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 16 Apr 2020 08:26:10 -0600
To: Letko, Michael (NIH/NIAID) [F]
Cc: Seifert, Stephanie (NIH/NIAID) [E]
Subject: Re: Referee reports from Nature Reviews Microbiology - NRMICRO-18-165V3

Perfect!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Michael Letko <[redacted] (b) (6)
Date: Thursday, April 16, 2020 at 8:24 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: Re: Referee reports from Nature Reviews Microbiology - NRMICRO-18-165V3

Yep working on it.

-michael

--
Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Section, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
[redacted] (b) (6)

On Apr 16, 2020, at 8:24 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Any updates on this one?, would be nice to get it out before all of the 1000s of other reviews will hit the pavement

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Michael Letko <[redacted] (b) (6)
Date: Thursday, March 26, 2020 at 9:45 AM
To: "[redacted] (b) (6) <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: Re: Referee reports from Nature Reviews Microbiology - NRMICRO-18-165V3

Yes this is really pretty straightforward. Should have it back to them in no time.

-michael

--
Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
[redacted] (b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Thursday, March 26, 2020 at 9:38 AM
To: "Letko, Michael (NIH/NIAID) [F]" <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: FW: Referee reports from Nature Reviews Microbiology - NRMICRO-18-165V3

We are getting there,

Haven't looked at it yet, but any update on SARS-CoV-2 might be nice (although very limited info on the interface for now)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Reply-To: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Date: Thursday, March 26, 2020 at 1:39 AM
To: '(b) (6) <(b) (6)
Subject: Referee reports from Nature Reviews Microbiology - NRMICRO-18-165V3

Dear Vincent,

Manuscript number: NRMICRO-18-165V3
Title: Bat-borne viruses: mechanisms of spillover and emergence
Author(s): Vincent Munster, Michael Letko, Stephanie Seifert, Kevin Olival, and Raina Plowright
Submission date for revisions: 23d April 2020

I now have the peer-review comments on your Review article entitled "Bat-borne viruses: mechanisms of spillover and emergence" for Nature Reviews Microbiology, which are presented in the attached Word file. The referees have raised some points that I would like you to address before we proceed. I therefore invite you to revise the manuscript and provide a formal rebuttal to all points raised by the referees. You should detail how you have addressed each comment, including your reasons for not making any of the suggested changes, by adding your comments after each point in the Word document.

I have attached the version of your article with page and line numbers to help you navigate the referees' comments and would be most grateful if you could make your changes to this document, ensuring that you use the 'track changes' function.

(b) (5)

I would like to receive your revised manuscript and rebuttal by 23d April 2020; please contact me if this deadline presents any problems.

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We hope that you will support this initiative and supply the required information. Should you have any query or comments, please do not hesitate to contact me.

To submit your revised manuscript, please click on the link below:
https://mts-nrmicro.nature.com/cgi-bin/main.plex?el=A4Z4PDX2C4TyV6I2A9ftddkDSbNEYz0xZrp8nuh6SAZ

I look forward to receiving your revised manuscript. Please don't hesitate to get in touch if you wish to discuss any of the points raised in this letter or in the referees' reports.

Best wishes and I hope all of you are alright,
Ursula

Ursula Hofer, MD PhD
Chief Editor, Nature Reviews Microbiology
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COVID 19 and impact on peer review
As a result of the significant disruption that is being caused by the COVID-19 pandemic we are very aware that many researchers will have difficulty in meeting the timelines associated with our peer review process during normal times. Please do let us know if you need additional time. Our systems will continue to remind you of the original timelines but we intend to be highly flexible at this time.

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 13 Apr 2020 09:45:09 -0600
To: Alison Peel; Plowright, Raina
Cc: [redacted] (b) (6)
Subject: Re: Updated CoV protocol

Yes free to share with them, they are still a RT-PCR (the RT stands for reverse-transcriptase which is the step needed for transcribing the RNA into cDNA). Btw, I wouldn't call this high-throughput as it involves multiple pcr steps (nested).

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 4/12/20, 8:28 PM, "Alison Peel" <[redacted] (b) (6) wrote:

> Hi Vincent,
>
> Are we able to share this protocol with our University of Sydney and CSIRO collaborators for the DARPA bat CoV screening study (Ina Smith, John-Sebastian Eden and Ed Annand?
> Are these conventional PCRs, and could the approach be described as "samples will be screened with pan-coronavirus high throughput conventional PCR"? (rather than RT-PCR)
>
> Thanks
> Ali
>
> On 27/3/20, 2:26 am, "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6) wrote:
>
>> Dear team,
>>
>> Please find our updated protocol (from Watanabe et al), for screening for coronaviruses.
>>
>> We have ensured specificity and sensitivity for this one (and will (likely) detect all coronaviruses).
>>
>> Not for use outside the PREEMP group, please refer to me if someone else would be interested.
>>
>> Cheers,
>>
>> Vincent Munster, PhD
>> Chief, Virus Ecology Section
>> Laboratory of Virology
>> Rocky Mountain Laboratories
>> NIAID/NIH
>>
>> On 3/23/20, 9:38 AM, "Plowright, Raina" <[redacted] (b) (6) wrote:
>>
>>> Very relieved to get this email.
>>> Key will be to keep [redacted] (b) (6) informed.
>>> Raina

On 3/23/20, 7:59 AM, [redacted] (b) (6) wrote:

Dear PREEMPT colleagues and friends,

I meant to send this to you all last week, but as I am sure was also the case for you, the week was overwhelmed by standard work plus having to deal with COVID-19 related changes/impacts. So I am writing now.

We hope that you, your teams, colleagues, friends and families are faring well given the new normal. DARPA recognizes that given the unprecedented nature of the COVID-19 pandemic and the current worldwide situation, it is completely expected that milestones and deliverables will be delayed in the PREEMPT program (understanding the ramp down and ramp up period needed, as well). That is expected and understandable. You will not be penalized by DARPA for not meeting deadlines as a result of the current outbreak. I suspect that there will be some no cost extensions to this program in any case. I am doing my best as PM to support your good work and build a program for the future, if possible. Clearly this outbreak has shown us that a program like PREEMPT was not only farsighted, but under-resourced. Of course, it's an atypical program at DARPA, but maybe that might change moving forward. Notwithstanding, we will do our best with current resources to meet program goals. I remain excited and hopeful by the work you are doing.

To state the obvious, your safety and that of your team is foremost, so please follow policies in your country/institutions to stay safe. The DARPA team is available and working remotely during this time so please contact us with any questions or if you need any help.

What I would like from all PIs (now to include Iowa State University- welcome, Phil) every Sunday evening or Monday, is to send me and the DARPA team (those on the Cc: line of this email) an update on how things are going with you and your subs. No specific format or length- just send something so that we are aware of status of program and staff health. Keep it simple but please send it weekly. I heard from some of you already, but you can start this as of the coming week. Shawn can weigh in if she needs anything further on a weekly basis.

Feel free to forward this email to your colleagues as you see fit.

Many thanks and warm regards,
[redacted] (b) (6)

--
[redacted] (b) (6)
Program Manager
Biological Technologies Office (BTO)
DARPA
Office: [redacted] (b) (6)
Work mobile: [redacted] (b) (6)
Personal mobile: [redacted] (b) (6)
[redacted] (b) (6)
[redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 7 Apr 2020 19:20:52 -0600
To: Laing, Eric
Cc: Broder, Chris (USU-DoD); Plowright, Raina
Subject: Re: CoV serology question

We'll obviously have all the ones in the nat micro paper, but most are Rhinolophus,

Getting some quality time in with the little one? Btw, it has been the longest stretch of me not being in Africa (or other fieldwork) since my move to the US!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Eric Laing <[redacted] (b) (6)
Date: Tuesday, April 7, 2020 at 7:16 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Broder, Chris (USU-DoD)" <[redacted] (b) (6) "Plowright, Raina"
<[redacted] (b) (6)
Subject: Re: CoV serology question

Hi, no worries. I'll think about maybe adding [redacted] (b) (6) HKU9, and hit up Simon about any other sequences.

Thanks, Vincent.

Eric

On Tue, Apr 7, 2020 at 8:57 PM Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
Hi guys,

[redacted] (b) (4)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" (b) (6)
Date: Tuesday, April 7, 2020 at 4:28 PM
To: "(b) (6) <(b) (6) Eric Laing
<(b) (6) "Broder, Chris (USU-DoD)" <(b) (6)
Subject: CoV serology question

Hi Vincent,
We are working out how to move forward with serology and Eric asked me this question (he has a lot of confidence in my understanding of virology □)!
Can you help?

> (b) (4)

Raina
--
Eric D. Laing, Ph.D.
Research Assistant Professor
Department of Microbiology and Immunology
Uniformed Services University
4301 Jones Bridge Road
Bethesda, MD 20814
cell: (b) (6)
office: (b) (6)
lab: (b) (6)

(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 6 Apr 2020 08:05:04 -0600
To: Clif McKee; Manuel Ruiz; Plowright, Raina; Kwe Claude, Yinda (NIH/NIAID) [F]; Port, Julia (NIH/NIAID) [F]
Subject: Re: CoV grant from DAPRA and invitation to contribute to a CoV-bat-review

Hi guys,

We'll have Kwe and Julia contributing to this from our end:

- How many words?
- Specific focus?
- Figures?

I think the biggest challenge will to be to keep it concise if you want to go for a larger journal (~5500 words), so it would be good if you guys put some guidelines out there for people (typically all groups will get you an over 2000 words sections),

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Sunday, April 5, 2020 at 10:22 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: Clif McKee <[redacted] (b) (6) Manuel Ruiz <[redacted] (b) (6)
Subject: CoV grant from DAPRA and invitation to contribute to a CoV-bat-review

Hi Preempt PIs,

Tomorrow, we will send a big update to the full team but I wanted to quickly mention a small project and invite you to support a review/perspective that our team is assembling.

[redacted] (b) (6) will fund our seed grant for CoV screening of Aussie and Bangladesh samples. That may seem like old news, but it was on-again/off-again and only confirmed late Friday. I've summarized the details of the grant at the bottom of this email. Please let us know if you would like to be involved.

To prepare this grant, we reviewed the bat CoV literature and found it lacking. Information relevant to bat surveillance (e.g., patterns & drivers of shedding, ecological interactions, distributions) was hard to find. For our own research needs, and to position our group for funding, **Manuel (MSU) and Clif (Hopkins) will co-lead a review/perspective on ecology/dynamics/shedding /zoonotic spillover of coronaviruses in bats**.

We invite you to contribute to this review, if you can do so quickly, before we are scooped! Our group could add intelligent discourse in this area, especially on the integrative perspective of ecology & spillover. We will aim for Nature Communications, Lancet, or similar.

If you or your postdocs/students would like to contribute, read the details below.

Best,

Raina

Invitation to contribute to CoV bat review:

We envision **a couple of well-referenced paragraphs from a few of you or your students/postdocs**. Happy to have many authors but we ask for a substantial contribution—intellectually and/or by assembling information — e.g., review of the literature in a specific area and/or insights and opinions. Probably ~ 1-3 paragraphs per area. Please nominate your postdocs/grad students where they have relevant expertise. Manuel & Clif have an outline and these are some sections and non-exhaustive ideas for contributions. When we have a co-author group, we will refine the theme of our major intellectual contribution.

Oliver, Aaron, or Tamika: population-level circulation of CoVs in bats
Ali: interaction among multiple viruses including CoVs
Tony, Aga, Dan, or Caylee: Bat-CoV immune dynamics
Vincent, Kwe, Trent or other RML folks: CoV biology
Emily: undetected CoVs in humans
Jamie, Amandine, or Dylan, Hector, David: comment on critical factors for cross-spp transmission and likely scenarios of future spillover events
Barbara: alternative hosts
Nita: distribution
CoV experiments in bats, CoV diversity (within- and between-hosts), biogeography (not much emphasis on this bc PREDICT has done a good job here)
More ideas welcome after you see the outline.

Clif and Manuel have assembled the literature in a Box drive.

Please reply to Manuel and Clif with ideas. They have an outline on a google doc and will share with all coauthors to develop a plan. We envision the first draft by end of April. We are hoping for a true team paper!

Thanks – and I'll hand this back over to Manuel and Clif!

Raina

Details of CoV grant:

- We will screen a subset of fecal samples for coronaviruses using a beta-coronavirus pan-S RT-PCR developed by Vincent. Positive samples will then be sequenced by methods TBD.
- We will do serology on ~1000 samples from each country. We have developed a collaboration with Eric Laing and Chris Broder and they will provide antigens for filoviruses, paramyxoviruses (including rubulaviruses and henipaviruses), and coronaviruses (neucleoproteins, and spike proteins).
- We will extend Bangladesh sampling by 4 months to achieve a full 12 month longitudinal dataset as fecal sampling was added in January.

We are actively looking for more funding opportunities so that we can screen samples for multiple viruses and do metabolomics and microbiome etc. One potential opportunity is via DOE funds via Oak Ridge Laboratory (through a politically connected -ex Obama White House employee now at MSU). If you have connections or experience with Oak Ridge, please let me know.

From: Schountz,Tony
Sent: Fri, 3 Apr 2020 21:24:52 +0000
To: Bimczok, Diane; Munster, Vincent (NIH/NIAID) [E]
Cc: Raina Plowright
Subject: Re: Bat organoids - COVID funding at MSU

Diane, very encouraging news. Happy to help and I'll look for your draft letter when you send it.

Tony

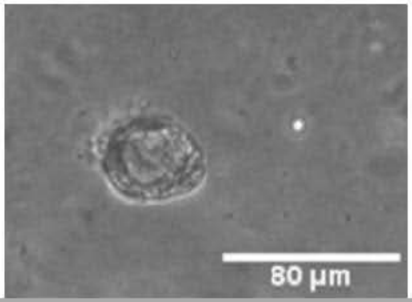
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Bimczok, Diane <[redacted] (b) (6)
Sent: Friday, April 3, 2020 3:01 PM
To: Schountz,Tony <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6)
Cc: Raina Plowright <[redacted] (b) (6)
Subject: Bat organoids - COVID funding at MSU

Dear Tony and Vincent,

As you know from Raina, a group of folks at MSU are trying to get some COVID-19 research up and running.
I am currently working on a competitive supplement application to add on to our NIH U01 on organoids-on-a-chip. We are looking to investigate the role of gastrointestinal epithelial cells in viral propagation and to compare responses of gastrointestinal epithelial cells to the coronavirus between bats and humans.

Tony, thanks for providing us with some frozen bat tissues for some pilot experiments. Marziah and Andy in my lab have already started to derive some organoid cultures , with some limited success. Please see below. The protocol still needs a lot of tweaking and optimization, but we are seeing a few organoids!



[redacted] (b) (4)

Thanks, and stay safe and healthy!

Diane

Diane Bimczok, D.V.M., Ph.D.
Assistant Professor
Department of Microbiology and Immunology
Montana State University
2155 Analysis Drive
Bozeman, MT, 50717
Phone [redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 3 Apr 2020 10:56:52 -0600
To: (b) (6)
Cc: Plowright, Raina
Subject: Re: exploring a pivot to COVID-19 work

Nope doesn't ring a bell, but a lot of collaborative work with Mark Pallanch/Sue Gerber/Tim Uyeki and the people of special path (former Stuart Nichol, now Joel Brennan and Jon Towner) and even further back with the flu people

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 4/3/20, 10:31 AM, (b) (6) wrote:

Got it. Very busy. Thanks for all that you are doing. BTW, did you ever meet or come across Ray Arthur by chance? He's a Hopkins trained virologist whom I worked for at CDC a while ago. He's still there, though probably should retire soon, he's likely in his late 70s now.

-----Original Message-----
From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Friday, April 3, 2020 11:57 AM
To: (b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: Re: exploring a pivot to COVID-19 work

Not yet,

Working on remdesivir, ChadOx (jenner), Moderna, CurVac and J&J.

And running tons of environmental stability and decon studies (re-use respirator N95s), starting-up to do small animal work (hamster and hACE2 mice) to complement our NHP work (Rhesus, GM and squirrel monkey). And working with tony Schountz of CSU with our bat work, and if successful transfer the model to RML to do some immunological comparisons between rhesus and Atribeus bats.

However, main focus is in providing information to the public health community and the development of MCMs,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 4/3/20, 9:38 AM, (b) (6) wrote:

Thanks, Vincent. Are you supporting Amy Jenkins also in DARPA BTO, by chance? I think she is working with Moderna on a mAb or other therapeutic approach. I also think I had seen this paper of yours on ACE2, great work.

Best wishes,
(b) (6)

-----Original Message-----
From: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Sent: Friday, April 3, 2020 11:33 AM
To: (b) (6); Peter A Barry < (b) (6) Plowright, Raina < (b) (6) LaTrielle, Sara < (b) (6)
Cc: (b) (6); (b) (6) ; (b) (6)
Subject: Re: exploring a pivot to COVID-19 work

Hi (b) (6)

If you need any supporting material for this outbreak to present to DARPA leadership. My lab has been working on beta-coronaviruses since 2012 and has extensive experience in natural history, ecology, (molecular) biology, pathogenesis, transmission, and countermeasure development (we are currently working on several vaccines, including the Moderna one). In addition, since you mentioned the pseudotypes take note of our recent Nature Microbiology paper, my lab was the first one who confirmed ACE2 as the receptor using pseudotypes: . Letko M, Marzi A, Munster V. Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses. Nat Microbiol. 2020.

Biography for B-corona's including SARS-CoV-2 (last 5)

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receptor, dipeptidyl peptidase 4. J Virol. 2014;88(16):9220-32 14. Munster VJ, Adney DR, van Doremalen N, Brown VR, Miazgowicz KL, Milne-Price S, Bushmaker T, Rosenke R, Scott D, Hawkinson A, de Wit E, Schountz T, Bowen RA. Replication and shedding of MERS-CoV in Jamaican fruit bats (Artibeus jamaicensis). Sci Rep. 2016;6:21878 15. Tynell J, Westenius V, Ronkko E, Munster VJ, Melen K, Osterlund P, Julkunen I. Middle East respiratory syndrome coronavirus shows poor replication but significant induction of antiviral responses in human monocyte-derived macrophages and dendritic cells. J Gen Virol. 2016;97(2):344-55.

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Munster, Friederike Feldmann, Brandi N. Williamson, Neeltje van Doremalen, Lizzette PérezPérez, Jonathan Schulz, Kimberly MeadeWhite, Atsushi Okumura, Julie Callison, Beniah Brumbaugh, Victoria A. Avanzato, Rebecca Rosenke, Patrick W. Hanley, Greg Saturday, Dana Scott, Elizabeth R. Fischer, Emmie de Wit doi: hxxps://doi.org/10.1101/2020.03.21.001628

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Kind regards,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 4/3/20, 8:41 AM, (b) (6) wrote:

Dear PREEMPT colleagues,

Given the current COVID-19 challenge, we are aware that the PREEMPT program will suffer from delays in field sampling and most experiments. Since much work has stopped, I would like to know how you can conduct work now based on any data or samples you already have collected. For example, MSU has been working on modelling for this outbreak and may be able to leverage their collected samples to look for bat coronaviruses and more.

Since PREEMPT's focus is directly relevant to the current pandemic, I am curious if we can leverage our existing analytics infrastructure and modelling efforts to respond to some outstanding questions, using data emerging from the currently available SARS2 sequences in animals and humans. I wonder if we can generalize parts of the models across different viruses. Even though none of you are working with SARS2 virus, are any of you able to work with a pseudotyped (SARS2) virus (so only BSL2 needed)? If you have any ideas, I'd love to hear about them; we may be able to find extra funds to do this. Data generated in this space could help with guidance to authorities and enhance visibility of the program with the Front Office and DARPA leadership. Other areas might include epidemiologic analysis to determine probable ways of COVID-19 human-to-human transmission. This seems not to be well understood. Could we have predicted the high transmissibility of the virus from its primary sequence in animals? (genotype to phenotype) In any case, I am/we are brainstorming. Welcome your thoughts to our DARPA team (me and those copied).

NOTE: None of this has funding implications at this point. I am trying to get additional funds for COVID-19 related work. I am hoping to be able to show the DARPA Director how PREEMPT performers pivoted during this current crisis to tackle COVID-19 and show off these data in November at our annual program review to help ensure full program continuation. And then look at a way to do a PREEMPT 2.

Thanks!
(b) (6)

--
(b) (6)
Program Manager
Biological Technologies Office (BTO)
DARPA
Office: (b) (6)
Work mobile: (b) (6)
Personal mobile: (b) (6)
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 3 Apr 2020 10:37:29 -0600
To: Plowright, Raina
Subject: Re: exploring a pivot to COVID-19 work

Yeah, thought we mark of the territory of our PREEMPT team a bit more clearly.

I agree, they should understand how challenging it is to be responsible for people on soft money and that any add on should be properly funded

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 4/3/20, 10:15 AM, "Plowright, Raina" <(b) (6) wrote:

> Awesome Vincent, thanks for jumping in!
> Not sure why (b) (6) keeps dangling carrots at us -- we presented the fecal screening then his fiscal person said there was no money and we had to use our current budget. I said no way. I'm not going to fire people to start a new project... still optimistic they will fund us but could also be deluded! (
>
> On 4/3/20, 9:56 AM, "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) wrote:
>
>> Not yet,
>>
>> Working on remdesivir, ChadOx (jenner), Moderna, CurVac and J&J.
>>
>> And running tons of environmental stability and decon studies (re-use respirator N95s), starting-up to do small animal work (hamster and hACE2 mice) to complement our NHP work (Rhesus, GM and squirrel monkey). And working with tony Schountz of CSU with our bat work, and if successful transfer the model to RMl to do some immunological comparisons between rhesus and Atribeus bats.
>>
>> However, main focus is in providing information to the public health community and the development of MCMs,
>>
>> Cheers,
>>
>> Vincent Munster, PhD
>> Chief, Virus Ecology Section
>> Laboratory of Virology
>> Rocky Mountain Laboratories
>> NIAID/NIH
>>
>> On 4/3/20, 9:38 AM, (b) (6) wrote:
>>
>>> Thanks, Vincent. Are you supporting Amy Jenkins also in DARPA BTO, by chance? I think she is working with Moderna on a mAb or other therapeutic approach. I also think I had seen this paper of yours on ACE2, great work.
>>>
>>> Best wishes,
>>> (b) (6)

-----Original Message-----
From: Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6)
Sent: Friday, April 3, 2020 11:33 AM
To: [redacted] (b) (6) Peter A Barry < [redacted] (b) (6) Plowright, Raina
< [redacted] (b) (6) LaTrielle, Sara < [redacted] (b) (6)
Cc: [redacted] (b) (6); [redacted] (b) (6)
[redacted]; [redacted] (b) (6)
Subject: Re: exploring a pivot to COVID-19 work

Hi [redacted] (b) (6)

If you need any supporting material for this outbreak to present to DARPA leadership. My lab has been working on beta-coronaviruses since 2012 and has extensive experience in natural history, ecology, (molecular) biology, pathogenesis, transmission, and countermeasure development (we are currently working on several vaccines, including the Moderna one). In addition, since you mentioned the pseudotypes take note of our recent Nature Microbiology paper, my lab was the first one who confirmed ACE2 as the receptor using pseudotypes: . Letko M, Marzi A, Munster V. Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses. Nat Microbiol. 2020.

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9. Alagaili AN, Briese T, Mishra N, Kapoor V, Sameroff SC, Burbelo PD, de Wit E, Munster VJ, Hensley LE, Zalmout IS, Kapoor A, Epstein JH, Karesh WB, Daszak P, Mohammed OB, Lipkin WI. Middle East respiratory syndrome coronavirus infection in dromedary camels in Saudi Arabia. MBio. 2014;5(2):e00884-14 10. Falzarano D, de Wit E, Feldmann F, Rasmussen AL, Okumura A, Peng X, Thomas MJ, van Doremalen N, Haddock E, Nagy L, LaCasse R, Liu T, Zhu J, McLellan JS, Scott DP, Katze MG, Feldmann H, Munster VJ. Infection with MERS-CoV causes lethal pneumonia in the common marmoset. PLoS Pathog. 2014;10(8):e1004250.

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Rebecca Rosenke, Patrick W. Hanley, Greg Saturday, Dana Scott, Elizabeth R. Fischer, Emmie de Wit doi: hxxps://doi.org/10.1101/2020.03.21.001628

35. Seth D. Judson, Neeltje van Doremalen, Emmie de Wit, Vincent J. Munster. SARS-CoV-2 Stability and Aerosol Generating Medical Procedures. NEJM in press.

Kind regards,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 4/3/20, 8:41 AM, (b) (6) wrote:

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Thanks!
(b) (6)

--
(b) (6)
Program Manager
Biological Technologies Office (BTO)
DARPA
Office: (b) (6)
Work mobile: (b) (6)
Personal mobile: (b) (6)
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 3 Apr 2020 09:33:08 -0600
To: (b) (6); Peter A Barry; Plowright, Raina; LaTrielle, Sara
Cc: (b) (6); (b) (6) (b) (6)
bto)
Subject: Re: exploring a pivot to COVID-19 work

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Rocky Mountain Laboratories
NIAID/NIH

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> Thanks!
> (b) (6)
>
> --
> (b) (6)
> Program Manager
> Biological Technologies Office (BTO)
> DARPA
> Office: (b) (6)
> Work mobile: +(b) (6)
> Personal mobile: (b) (6)
> (b) (6)
> (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 1 Apr 2020 11:48:44 -0600
To: Menk, Kay (NIH/NIAID) [E]; Shupert, W. Lesley (NIH/NIAID) [E]
Cc: Bushmaker, Trenton (NIH/NIAID) [E]; Letko, Michael (NIH/NIAID) [F]
Subject: Re: Montana State University - SARS-CoV-2 protocol request

Two virus isolates: SARS-CoV-1 and MERS-CoV

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Kay Menk <[redacted] (b) (6)
Date: Wednesday, April 1, 2020 at 10:37 AM
To: "Shupert, W. Lesley (NIH/NIAID) [E]" <[redacted] (b) (6)
"[redacted] (b) (6) <[redacted] (b) (6)
Cc: Trenton Bushmaker <[redacted] (b) (6) Michael Letko <[redacted] (b) (6)
Subject: RE: Montana State University - SARS-CoV-2 protocol request

In order for me to do the SLA I will need to have the exact materials to be shipped.

Not sure who all is in the loop on this.

Thanks.
Kay

From: Shupert, W. Lesley (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Wednesday, April 1, 2020 9:44 AM
To: Menk, Kay (NIH/NIAID) [E] <[redacted] (b) (6)
Subject: Fwd: Montana State University - SARS-CoV-2 protocol request

Miss Kay,

Not sure what we will need from MSU, just passing on info from Vincent.

Les

Begin forwarded message:

From: "Bartlett, Ryan" <[redacted] (b) (6)
Date: April 1, 2020 at 9:10:55 AM MDT

To: "Lubick, Kirk" <[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]"
<[redacted] (b) (6) "Shupert, W. Lesley (NIH/NIAID) [E]" <[redacted] (b) (6)
Cc: "Bushmaker, Trenton (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: RE: Montana State University - SARS-CoV-2 protocol request

Good morning Vincent, Les,

Can you provide details about the origin of your SARS-CoV-2 (i.e. country it was isolated)? This will likely determine if we need a CDC permit for this or not.

Thank you for your help.

Ryan Bartlett
Biosafety Officer
Office of Research Compliance
114 Hamilton Hall
[redacted] (b) (6)
[redacted] (b) (6)

From: Lubick, Kirk <[redacted] (b) (6)
Sent: Wednesday, April 1, 2020 7:53 AM
To: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) Loveday, Emma
<[redacted] (b) (6) Taylor, Matthew <[redacted] (b) (6) Shupert, W. Lesley
(NIH/NIAID) [E] <[redacted] (b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <[redacted] (b) (6) Ron Fouchier
<[redacted] (b) (6) Bartlett, Ryan <[redacted] (b) (6)
Subject: Re: Montana State University - SARS-CoV-2 protocol request

Hi Vincent, Les,

I miss the good old days of working at RML – great times! We definitely want to get both of these bugs here as soon as possible as we are ready to go. I have Cc'd Ryan Bartlett the Biosafety Officer who can work with you Les. Ryan can you get started on the CDC paper work for MERS-CoV? My understanding is it is not needed for SARS-CoV2, but I could be wrong.

Thanks for the help, we owe you big time.

Kirk

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Tuesday, March 31, 2020 at 10:50 AM
To: "Loveday, Emma" <[redacted] (b) (6) "Lubick, Kirk"
<[redacted] (b) (6) "Taylor, Matthew" <[redacted] (b) (6) "Shupert, W. Lesley (NIH/NIAID) [E]" <[redacted] (b) (6)

Cc: "Bushmaker, Trenton (NIH/NIAID) [E]" <[redacted] (b) (6) Ron Fouchier <[redacted] (b) (6)
Subject: Re: Montana State University - SARS-CoV-2 protocol request

Hi Les,

See the request for MERS-CoV and SARS-CoV-2. Can you let MSU organize the necessary paperwork needed for transfer to Bozeman (Kirk Lubick is part the email as well in his function as the head of their biosafety, that former young maverick at the Best lab).

For the MERS-CoV they will need to get permission from the original source as we are not allowed to share (Ron Fouchier [redacted] (b) (6) The MERS-CoV will need a CDC permit for transport too (but I assume the SARS-CoV-2 as well).

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Loveday, Emma" <[redacted] (b) (6)
Date: Tuesday, March 31, 2020 at 10:44 AM
To: "[redacted] (b) (6) <[redacted] (b) (6) "Lubick, Kirk" <[redacted] (b) (6) "Taylor, Matthew" <[redacted] (b) (6)
Cc: Trenton Bushmaker <[redacted] (b) (6) Jonathan Schulz <[redacted] (b) (6) Michael Letko <[redacted] (b) (6) "Brose, Megan (NIH/OD/ORS) [E]" <[redacted] (b) (6)
Subject: Re: Montana State University - SARS-CoV-2 protocol request

Hi Vincent,

Thank you so much to you and your lab for all your help so far.

We are running into trouble getting shipments from BEI to get virus delivered to MSU and we were wondering if it was possible to acquire SARS-CoV-2 and MERS directly from your lab? Can you let us know if this is possible and what we need to do, paperwork wise, to get this rolling asap?

Thank you again!

Emma Kate Loveday Ph.D.
Postdoctoral Researcher
Chang Soft Matter and Microfluidics Lab

Montana State University - Bozeman
[redacted] (b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Friday, March 20, 2020 at 12:28 PM
To: "Loveday, Emma" <[redacted] (b) (6)
Cc: Raina Plowright <[redacted] (b) (6) "Lubick, Kirk" [redacted] (b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]" <[redacted] (b) (6) "Schulz, Jonathan (NIH/NIAID) [F]" <[redacted] (b) (6) "Letko, Michael (NIH/NIAID) [F]" <[redacted] (b) (6) "Brose, Megan (NIH/OD/ORS) [E]" <[redacted] (b) (6)
Subject: Re: Montana State University - SARS-CoV-2 protocol request

Hi Emma,

Contract Trent (tissue culture & titration), Jon (qRT-PCR), Michael (Molecular Biology) for specific lab protocols

Kirk: contact Megan Brose for support on Biosafety and our BSL3/4 protocols

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Loveday, Emma" <[redacted] (b) (6)
Date: Friday, March 20, 2020 at 11:57 AM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Cc: Raina Plowright <[redacted] (b) (6) "Lubick, Kirk" <[redacted] (b) (6)
Subject: Montana State University - SARS-CoV-2 protocol request

Hi Dr. Munster,

My name is Dr. Emma Loveday and I am a postdoc at MSU (and Myndi's former mentor!) working with Raina and others to get our BSL3 up to speed to tackle some exciting SARS-CoV-2 research.

We are very quickly ramping up to get the BSL3 ready for virus work and we were hoping we could collaborate with your group in terms of accessing working SARS-CoV-2 laboratory protocols?

I have previous training from NML in Winnipeg with high path flu, but have not worked with coronaviruses before, so any information your lab is willing to share, would be very usefiul and helpful to get us off the ground here in Bozeman!

Please let me know if this is possible. We look forward to further strengthening our ties between MSU and RML!!

Talk to you soon-
Emma Kate Loveday Ph.D.
Postdoctoral Researcher
Chang Soft Matter and Microfluidics Lab
Montana State University - Bozeman
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 31 Mar 2020 12:02:33 -0600
To: Plowright, Raina; Emily Gurley
Subject: Re: Oak Ridge National Labs

Never heard off,

Cheers and good luck!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <[redacted] (b) (6)
Date: Tuesday, March 31, 2020 at 11:53 AM
To: '[redacted] (b) (6) <[redacted] (b) (6) Emily Gurley [redacted] (b) (6)
Subject: Oak Ridge National Labs

Hi V and E,

We have a new associate VP for research at MSU (who used to run a white house task force under Obama) and she has written a white paper on our work and put it out to our MT congressional delegations, asking for $5 million for a center. I included your institutions/names on the white paper—the hope is that other states would also kick in money.

She is working all her DC contacts encouraging a collaboration with Oak Ridge Labs where they have major sequencing and super-computer capacity. This is the guy at Oak Ridge…do you know him?

Dan Jacobson, Ph.D.
[redacted] (b) (6)
Chief Scientist for Computational Systems Biology
Biosciences
Oak Ridge National Laboratory

So Dan just wrote to me and said he has convinced IARPA (another government agency) to sequence our samples to generate preliminary data. I did explain to him earlier that getting samples here is complex and that we can't sequence aussie samples outside of Australia and we have lots of existing partnerships to consider when sequencing.

Emily, correct me if I'm wrong, but I don't think you have any samples here that could be sequenced? All the paramyxoviruses are being sequenced by RML and none of the fecal samples are in the USA. Do we have anything worth sequencing… I don't think we do but maybe I've forgotten about something.

Have you guys worked with Oak Ridge? They have great capabilities in the satellite/env data side of things. Could be productive as we really haven't got much to show for our environmental work on the PREEMPT team.

Raina

Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: (b) (6)
Lab website: http://bzndiseaselab.org
Phone: (b) (6)

From: Schountz,Tony
Sent: Tue, 31 Mar 2020 16:56:57 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Schountz, Tony
Subject: Re: Tissues

OK, thanks. Keep your head above water!

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
970-491-7350

> On Mar 31, 2020, at 10:56 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
>
[redacted] (b) (4)
>
> Vincent Munster, PhD
> Chief, Virus Ecology Section
> Laboratory of Virology
> Rocky Mountain Laboratories
> NIAID/NIH
>
> On 3/31/20, 10:52 AM, "Schountz,Tony" <[redacted] (b) (6) wrote:
>
[redacted] (b) (4)
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
> 3185 Rampart Road
> Fort Collins, CO 80523-1692
> [redacted] (b) (6)
> [redacted] (b) (6)
>
>

>

From: Schountz,Tony
Sent: Tue, 31 Mar 2020 16:55:04 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Schountz, Tony
Subject: Re: Tissues

You'll soon be getting an email from Jon about it!

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

> On Mar 31, 2020, at 10:52 AM, Schountz,Tony <[redacted] (b) (6) wrote:
>
[redacted] (b) (4)
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
> 3185 Rampart Road
> Fort Collins, CO 80523-1692
> [redacted] (b) (6)
> [redacted] (b) (6)
>

From:	Munster, Vincent (NIH/NIAID) [E]
Sent:	Sun, 29 Mar 2020 10:42:25 -0600
To:	Port, Julia (NIH/NIAID) [F]; Seifert, Stephanie (NIH/NIAID) [E]
Cc:	Kwe Claude, Yinda (NIH/NIAID) [F]; Letko, Michael (NIH/NIAID) [F]
Subject:	Re: Updated serology

Talk to Michael and Kwe on the AJ receptor, I think they are looking into this.

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Port, Julia (NIH/NIAID) [F]" <[redacted] (b) (6)
Date: Saturday, March 28, 2020 at 12:37 PM
To: "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Cc: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Updated serology

The question to the Ajs I would have right now is: do we have quick viral control because the receptor doesn't fit well or is the immune control that keeps it down. Or a mix. In this case comparison with a bat adapted virus would be very interesting.
When using a humanized/ batified model one needs a strongly immunocompromised background (so that there is actually increased viral replication and disease ... normally mice are used that have no immune system anymore and get irradiated. But I like that idea ..I will see if there is a way to get around the replication resistance in the mouse. And have a look what tools would actually be available for hamsters. I need to check if it is possible to immunocompromised them as needed.

I am also thinking that to investigate the adaptive response in bats... especially of B cells maybe not much replication would be needed actually...considering that Tony got titers even in this set up now. So I think that analysis of the B cell response (flow, transcriptomics, receptor sequencing etc, maybe even functional work) could be done in either Ajs or batified mice even at low virus replication. So I am super curious to see what comes out of that.
Thanks Steph!

Best,
Julia

From: "Seifert, Stephanie (NIH/NIAID) [E]"
Date: Sat, Mar 28, 2020, 10:04 AM
To: "Port, Julia (NIH/NIAID) [F]"
CC: "Munster, Vincent (NIH/NIAID) [E]"
Subject: Re: Updated serology

Would your set-up work in hamsters (e.g. batified hamsters) or would that defeat the purpose?

Sent via Skynet

On Mar 28, 2020, at 9:01 AM, Port, Julia (NIH/NIAID) [F] <(b) (6) wrote:

Thank you Vincent,

Space in the 3 would also be super helpful.

About the bat mice: I am not sure it is worth the effort without having better data on replication. For those mice to work we either need replication in the mouse tissue, which most likely will not happen, or in the bat cells. I fear that with only the bat hematopoietic system transferred that will also not be enough to support replication unless we may also get some bat lung or bat organoid transferred. If that would be an option?

Best,
Julia

From: "Munster, Vincent (NIH/NIAID) [E]"
Date: Sat, Mar 28, 2020, 8:46 AM
To: "Seifert, Stephanie (NIH/NIAID) [E]"
CC: "Port, Julia (NIH/NIAID) [F]"
Subject: Re: Updated serology

Btw, we are checking whether there will be space in ABSL3,

That might be smtg for the bats too?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Seifert, Stephanie (NIH/NIAID) [E]" <(b) (6)
Date: Saturday, March 28, 2020 at 8:40 AM
To: '(b) (6) <(b) (6)
Cc: "Port, Julia (NIH/NIAID) [F]" <(b) (6)
Subject: Re: Updated serology

Yes, sounds good. I wanted to compare to live virus neutralization as well. Has the protocol changed from the MERS neutralization assay (e.g. 100 TCID50/mL)?

To clarify, are you going to ask Tony for serum or should I?

Cheers,
Steph

Sent via Skynet

On Mar 28, 2020, at 7:16 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Also to compare it to our own Elisa would be useful, maybe start running a comparison with the NHPs (we already have the elisa results for these, ask Vicky)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Friday, March 27, 2020 at 7:27 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Port, Julia (NIH/NIAID) [F]" <[redacted] (b) (6)
Subject: Re: Updated serology

Can we ask him for some of that serum for looking at cross-neutralization with Michael's pseudotype system? Would be nice to compare with the NHP and mice serum.

Cheers,
Steph

Sent via Skynet

On Mar 27, 2020, at 8:16 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

FYI

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, March 27, 2020 at 8:46 AM
To: '[redacted] (b) (6) <[redacted] (b) (6) "Plowright, Raina"
<[redacted] (b) (6)
Subject: Updated serology

[redacted] (b) (4)

Tony

[redacted] (b) (4)

<image001.png>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 28 Mar 2020 09:50:01 -0600
To: Schountz, Tony
Cc: Seifert, Stephanie (NIH/NIAID) [E]; Port, Julia (NIH/NIAID) [F]
Subject: Re: Artibeus sera

Sounds good, we'll take anything you can spare and support your study!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz < [redacted] (b) (6)
Date: Saturday, March 28, 2020 at 9:16 AM
To: ' [redacted] (b) (6) < [redacted] (b) (6)
Cc: Tony Schountz < [redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" < [redacted] (b) (6) "Port, Julia (NIH/NIAID) [F]" < [redacted] (b) (6)
Subject: Re: Artibeus sera

Vinnie, that should be fine depending on how much you need and how much we have. I'll have to check with Miles when he gets in on Monday to see how much he collected from each at terminal bleed.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Mar 28, 2020, at 8:18 AM, Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6) wrote:

Hi Tony,

Can you spare some sera from your SARS-CoV-2 seropositive Artibeus? We can do he pseudotype assay here, would like to see how this compares to your and our Elisa,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 27 Mar 2020 09:34:21 -0600
To: Schountz, Tony
Cc: Plowright, Raina
Subject: Re: Updated serology

Yes, very similar to humans. Depends on species though, rhesus look better than cyno's

https://www.biorxiv.org/content/10.1101/2020.03.21.001628v1

fast CPE on the cells!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz < [redacted] (b) (6)
Date: Friday, March 27, 2020 at 9:32 AM
To: ' [redacted] (b) (6) < [redacted] (b) (6)
Cc: Tony Schountz < [redacted] (b) (6) "Plowright, Raina"
< [redacted] (b) (6)
Subject: Re: Updated serology

[redacted] (b) (4) They are on our to-do list but my graduate student [redacted] (b) (6) has been in quarantine since [redacted] (b) (6). She should be back in the lab on Wednesday next week to relieve me of my lab duties.

Crazy viral loads on primates. Do the NHPs get disease?

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Mar 27, 2020, at 9:26 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Let me know if there is anything we can do on our end, if your studies look good we'll start at RML too and will be able to supplement the CSU work.

[redacted] (b) (4)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, March 27, 2020 at 9:23 AM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6) "Plowright, Raina"
<[redacted] (b) (6)
Subject: Re: Updated serology

[redacted] (b) (4)

I have mostly been swamped with writing grants and supplements request.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692

[redacted] (b) (6)
[redacted] (b) (6)

On Mar 27, 2020, at 9:17 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

[redacted] (b) (4)

Any more info on the shedding? And live virus recovered?

Good work

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, March 27, 2020 at 8:46 AM
To: "[redacted] (b) (6) <[redacted] (b) (6) "Plowright, Raina"
<[redacted] (b) (6)
Subject: Updated serology

[redacted] (b) (4)

Tony

DPI	Bat1	Bat2	Bat3
14	1600	100	3200
24	6400	800	>12800

<image001.png>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology

College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 26 Mar 2020 09:38:21 -0600
To: Letko, Michael (NIH/NIAID) [F]; Seifert, Stephanie (NIH/NIAID) [E]
Subject: FW: Referee reports from Nature Reviews Microbiology - NRMICRO-18-165V3
Attachments: Munster_PR_1585208349_8.docx, 40739_2_art_0_q6kbxc.docx

We are getting there,

Haven't looked at it yet, but any update on SARS-CoV-2 might be nice (although very limited info on the interface for now)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Reply-To: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Date: Thursday, March 26, 2020 at 1:39 AM
To: '(b) (6) <(b) (6)
Subject: Referee reports from Nature Reviews Microbiology - NRMICRO-18-165V3

Dear Vincent,

Manuscript number: NRMICRO-18-165V3
Title: Bat-borne viruses: mechanisms of spillover and emergence
Author(s): Vincent Munster, Michael Letko, Stephanie Seifert, Kevin Olival, and Raina Plowright
Submission date for revisions: 23d April 2020

I now have the peer-review comments on your Review article entitled "Bat-borne viruses: mechanisms of spillover and emergence" for Nature Reviews Microbiology, which are presented in the attached Word file. The referees have raised some points that I would like you to address before we proceed. I therefore invite you to revise the manuscript and provide a formal rebuttal to all points raised by the referees. You should detail how you have addressed each comment, including your reasons for not making any of the suggested changes, by adding your comments after each point in the Word document.

I have attached the version of your article with page and line numbers to help you navigate the referees' comments and would be most grateful if you could make your changes to this document, ensuring that you use the 'track changes' function.

(b) (5)

be more than enough I think.

I would like to receive your revised manuscript and rebuttal by 23d April 2020; please contact me if this deadline presents any problems.

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ORCID
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We hope that you will support this initiative and supply the required information. Should you have any query or comments, please do not hesitate to contact me.

To submit your revised manuscript, please click on the link below:
(b) (6)

I look forward to receiving your revised manuscript. Please don't hesitate to get in touch if you wish to discuss any of the points raised in this letter or in the referees' reports.

Best wishes and I hope all of you are alright,
Ursula

Ursula Hofer, MD PhD
Chief Editor, Nature Reviews Microbiology
4 Crinan Street
London
N1 9XW

e-mail:ursula.hofer1@nature.com
tel: +44 (0)20 7014 6648
http://www.nature.com/nrmicro

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As a result of the significant disruption that is being caused by the COVID-19 pandemic we are very aware that many researchers will have difficulty in meeting the timelines associated with our peer review process during normal times. Please do let us know if you need additional time. Our systems will continue to remind you of the original timelines but we intend to be highly flexible at this time.

This email has been sent through the Springer Nature Tracking System NY-610A-NPG&MTS

(b) (4), (b) (6)

[redacted]

(b) (4), (b) (6)

[redacted]

(b) (4), (b) (6)

[redacted]

(b) (4), (b) (6)

[redacted]

(b) (4), (b) (6)

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(b) (4), (b) (6)

[redacted]

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[redacted]

(b) (4), (b) (6)

[redacted]

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 25 Mar 2020 12:28:34 -0600
To: Schountz, Tony
Subject: Re: Bat experiment

Any overt signs of disease?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz < (b) (6)
Date: Wednesday, March 25, 2020 at 12:28 PM
To: ' (b) (6) < (b) (6)
Subject: Re: Bat experiment

Inoculated 21 bats on Monday. Euthanized the first 3 today.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Mar 25, 2020, at 12:24 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Any update on your bat experiment yet?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 24 Mar 2020 14:00:53 -0600
To: Schountz, Tony
Subject: Re: Aj cell suscpetibility

[redacted] (b) (4)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 3/24/20, 11:17 AM, "Schountz,Tony" <[redacted] (b) (6) wrote:

[redacted] (b) (4)

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 23 Mar 2020 07:33:40 -0600
To: Emily Gurley; Plowright, Raina
Cc: Alison Peel; [redacted] (b) (6)
Subject: Re: N95s and field work

Papr's would be perfect (and reusable), we use them in congo.

Might be challenging in Oz, due to the looks?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Emily Gurley <[redacted] (b) (6)
Date: Sunday, March 22, 2020 at 5:54 PM
To: "Plowright, Raina" <[redacted] (b) (6)
Cc: '[redacted] (b) (6) <[redacted] (b) (6) Alison Peel <[redacted] (b) (6) '[redacted] (b) (6) <[redacted] (b) (6)
Subject: RE: N95s and field work

We were thinking of PAPRs – those could be used while they're processing bats, but not for catching them.

From: Plowright, Raina <[redacted] (b) (6)
Sent: Sunday, March 22, 2020 7:33 PM
To: Emily Gurley <[redacted] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) Alison Peel <[redacted] (b) (6) [redacted] (b) (6)
Subject: Re: N95s and field work

Vincent — any other types of options we could work on? If no other options, they will have to shut down field work.

On Mar 22, 2020, at 5:27 PM, Emily Gurley <[redacted] (b) (6) wrote:

This is a good effort – I hope that kind of protocol will be useful for folks who need this equipment.

I don't think we have any to decontaminate as all supplies have gone to the hospital, as far as I know.

I'll catch up with Rajib tomorrow.

Emily

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Sunday, March 22, 2020 11:01 AM
To: Emily Gurley [redacted] (b) (6)
Cc: Plowright, Raina <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
[redacted] (b) (6)
Subject: Re: N95s and field work

Yes, you'll need N95s

Currently working on decon procedures for PPE, hydrogen peroxide and high intensity UV. This will potentially allow re-use for a couple of times.

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Emily Gurley <[redacted] (b) (6)
Date: Saturday, March 21, 2020 at 2:39 PM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Plowright, Raina" <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
[redacted] (b) (6)
Subject: N95s and field work

Vincent,

I know that we had long discussion about this, but wanted to check in and confirm that we require N95s for bat sampling. Obviously, this requirement means we stop sampling in the field until the global N95 shortage is solved, so wanted to check in for reporting back to DARPA.

Best,
Emily

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 23 Mar 2020 07:29:47 -0600
To: Ausraful Islam; Emily Gurley; Plowright, Raina
Cc: Alison Peel
Subject: Re: N95s and field work

For now, just daily decon with 70% ethanol and drying should work (make it really wet). Just make sure you check the integrity of the mask before using (seals etc)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Ausraful Islam <(b) (6)
Date: Sunday, March 22, 2020 at 9:34 PM
To: Emily Gurley <(b) (6) "Plowright, Raina" <(b) (6)
Cc: '(b) (6) <(b) (6) Alison Peel
<(b) (6)
Subject: Re: N95s and field work

Hi Emily,

We have three boxes and by these, we will be able to continue the work until next month. If we can decontaminate and use the masks, that will be great. I am also trying to purchase masks locally.

Thanks

Rajib

From: Emily Gurley <(b) (6)
Sent: Monday, March 23, 2020 5:54:42 AM
To: Plowright, Raina
Cc: Munster, Vincent (NIH/NIAID) [E]; Alison Peel; Ausraful Islam
Subject: RE: N95s and field work

We were thinking of PAPRs – those could be used while they're processing bats, but not for catching them.

From: Plowright, Raina <[redacted] (b) (6)
Sent: Sunday, March 22, 2020 7:33 PM
To: Emily Gurley <[redacted] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
[redacted] (b) (6)
Subject: Re: N95s and field work

Vincent — any other types of options we could work on? If no other options, they will have to shut down field work.

On Mar 22, 2020, at 5:27 PM, Emily Gurley [redacted] (b) (6) wrote:

This is a good effort – I hope that kind of protocol will be useful for folks who need this equipment.

I don't think we have any to decontaminate as all supplies have gone to the hospital, as far as I know.

I'll catch up with Rajib tomorrow.

Emily

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Sunday, March 22, 2020 11:01 AM
To: Emily Gurley [redacted] (b) (6)
Cc: Plowright, Raina <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
[redacted] (b) (6)
Subject: Re: N95s and field work

Yes, you'll need N95s

Currently working on decon procedures for PPE, hydrogen peroxide and high intensity UV. This will potentially allow re-use for a couple of times.

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Emily Gurley <[redacted] (b) (6)
Date: Saturday, March 21, 2020 at 2:39 PM
To: "[redacted] (b) (6) <[redacted] (b) (6)

Cc: "Plowright, Raina" [redacted] (b) (6), Alison Peel <[redacted] (b) (6) [redacted] (b) (6)

Subject: N95s and field work

Vincent,

I know that we had long discussion about this, but wanted to check in and confirm that we require N95s for bat sampling. Obviously, this requirement means we stop sampling in the field until the global N95 shortage is solved, so wanted to check in for reporting back to DARPA.

Best,
Emily

From: Rasmussen, Angela L.
Sent: Sun, 22 Mar 2020 23:59:43 +0000
To: Munster, Vincent (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Feldmann, Heinrich (NIH/NIAID) [E]
Cc: Okumura, Atsushi (NIH/NIAID) [V]
Subject: CC mouse COVID model

Hi Emmie, Vincent, and Heinz,

I am writing a white paper for a CDC BAA that is soliciting proposals for a small animal model of COVID. David Threadgill is currently crossing hACE2 transgenics with CC mice. We've got preliminary data on CC lines develop severe disease with high path flu and SARS, so we can make some educated guesses about which lines are more likely to have an extreme phenotype.

Are you interested in collaborating on these studies? Our idea is to propose a screen along with more detailed characterization of disease from several lines with the most relevant phenotypes.

Best,
Angie

From: Schountz,Tony
Sent: Wed, 18 Mar 2020 22:26:11 +0000
To: Kwe Claude, Yinda (NIH/NIAID) [F]
Cc: Schountz, Tony; Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Artibeus ACE2

Hi Kwe, we don't have any marmoset gene data. We also don't have an Aj ACE2 plasmid, but here is its sequence if it is helpful.

atgtcaggctcttcctggctctttctcagccttgttgctgtaactgctgttcaagctcccactgaggaagatgccaggacatttttggagaagttt
aacactgaagctgaagaactgtattatgaaagtgcacttgcttcttggaattataacaccaatattactgaggagaatgtgcaaaaaatgaatg
aggctgaccggaagtggtctaccttttatgaagaacagtccaagcttgccaaagcttacccactagaagcaattaaggatgttaaagtcaagc
atcaattgcaggcccttcagcaaaatggattatcagaagacaaggacaaacgattgcagttgaacacagttctaaatacaatgagcaccatct
acagtactgggaaagtttgtaaaccagataatccacaggaatgcttattacttgcaggaggcttggaagacataatgcacaacagcaaagatt
acaatgaaaggctctgggcttgggaaggctggaggtctaaggttggcaagcagctgaggccattatatgaagagtatgtggtcctgaaaaa
tgagatggcaagagaaaagaattatgaggactatggggattattggagaggagattatgaaacagaggggacaaatggctatgaatatagc
cgcaaccagctgattgaagatgtggaaaatacttttgcagagattaaaccattatatgaacatcttcatgcgtatgtgagggcaaagttgatgg
atacctacccttcccatatcagtccaactggatgcctccctgcccatttgcttggtgatatgtggggtagattttggacaaatctgtatgatttgac
agctccctttgcagataaaccaaccatagatgtcactgctgcaatggttgagaagtcctgggatgcacagaggatattcaaggaggctgaga
agttctttatgtctgtgggcctttttaatatgactcaaggattctgggataactccatgataactaagccagatgatggccgggaagtggtctgc
caccccacagcctgggatctggggaaaaatgacttcaggatcaagatgtgcacaaaggtgacaatggatgacttcctgacagctcatcatg
agatgggacacatccagtatgacatggcatatgccaaccaacccttcctactaagaaatggagcaaatgaagggttccatgaagctgttggg
gaaatcatgtcactttctgtagctacacctaagcatttgaaagttctgggtcttctgccatctgatttccatgaagacaatgaaacagatataaact
tcctactcaaacaagcacttaacattgttggaactctaccattcacctacatgttagaaaagtggaggtggatggtcttcaagggtgaaattccc
aaagagcagtggatgaaaaagtggtgggagatgaagcgagaaatagttggtgtggtggaacctgtgccccatgatgaaacatactgtgatc
ctgcgtctctgttccatgttgctaatgattactcattcatccgttattacacaaggaccatttttcaattccagtttcaagaagccctttgtcgagtag
ctcaacatgaaggtcccctgcacaaatgtgacatttcaaattccaccgcagctggggagaagctgctccaaatgctgaaacttggcaaatcg
gaaccctggacccgtgcattggaagcttctgtagaagaaaagcaaatggatgtaagaccactgctcaagtacttcgagcctttgtttacctgg
ctgaaagaccagaacagggactcttttgtgggatgggacaccgactggagtccatacactgcacaaagcatcaaagtgaggataagccta
aaatcagctcttggagacaaagcatatgaatggaacgacaatgaaatgtacttcttccagtcgtctattgcatatgccatgagagagtatttttc
agatatcaaagaccagatgattccttttagggcggaggacgtgtgggtgagtgatttgaaaccaagagtctccttcaacttctttgtcactttgc
ctaacaatatgtcagacatcattcccagaagtgaagttgaagaggccatcaggaagtcccggggccgcatcaatgatgcttttcgcctggat
gacaacagcctggagtttctgggtattcagcctacactggaacccccttaccagccagctgtcaccatctggctgattgtttttggggttgtgat
gggagcggtggcggctggtattgccgtgctcatcttcaccgggatcagagacagaaggaagaaaaatcaaccgagcagtgaagaaaatc
cttattcttccgtgaatttgagtaaaggagaaaataacccaggattccaaaatggtgaagatcttcaaacttccttttag

MSGSSWLFLSLVAVTAVQAPTEEDARTFLEKFNTEAEELYYESALASWNYNTNITEENV
QKMNEADRKWSTFYEEQSKLAKAYPLEAIKDVKVKHQLQALQQNGLSEDKDKRLQLN
TVLNTMSTIYSTGKVCKPDNPQECLLLAGGLEDIMHNSKDYNERLWAWEGWRSKVGK
QLRPLYEEYVVLKNEMAREKNYEDYGDYWRGDYETEGTNGYEYSRNQLIEDVENTFA
EIKPLYEHLHAYVRAKLMDTYPSHISPTGCLPAHLLGDMWGRFWTNLYDLTAPFADKP
TIDVTAAMVEKSWDAQRIFKEAEKFFMSVGLFNMTQGFWDNSMITKPDDGREVVCHPT
AWDLGKNDFRIKMCTKVTMDDFLTAHHEMGHIQYDMAYANQPFLLRNGANEGFHEA
VGEIMSLSVATPKHLKVLGLLPSDFHEDNETDINFLLKQALNIVGTLPFTYMLEKWRWM
VFKGEIPKEQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVANDYSFIRYYTRTI

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FQFQFQEALCRVAQHEGPLHKCDISNSTAAGEKLLQMLKLGKSEPWTRALEASVEEKQ
MDVRPLLKYFEPLFTWLKDQNRDSFVGWDTDWSPYTAQSIKVRISLKSALGDKAYEWN
DNEMYFFQSSIAYAMREYFSDIKDQMIPFRAEDVWVSDLKPRVSFNFFVTLPNNMSDIIP
RSEVEEAIRKSRGRINDAFRLDDNSLEFLGIQPTLEPPYQPAVTIWLIVFGVVMGAVAAGI
AVLIFTGIRDRRKKNQPSSEENPYSSVNLSKGENNPGFQNGEDLQTSF
```

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Mar 18, 2020, at 4:22 PM, Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) wrote:

Hi Tony,

Hope you are keeping well.
We are wondering if you have marmoset and/or Artibeus ACE2 plasmids.

We want to test their susceptibility/ to nCoV-19.

Thanks
Kwe

From: Broder, Christopher
Sent: Wed, 18 Mar 2020 11:48:35 -0400
To: De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]
Subject: Covid

Hi Emmie / Vincent

In your NHPs with SARS-CoV-2 can you measure viral loads in whole blood of infected animals at any time pts
following challenge?

CB

--
Christopher C. Broder, Ph.
Professor and Chair
Department of Microbiology and Immunology
Uniformed Services University, B4152
4301 Jones Bridge Rd, Bethesda, MD 20814-4799

USU is "America's Medical School"
Email: (b) (6)
https://www.usuhs.edu/national/faculty/christopher-broder-phd
TEL: (b) (6)
FAX: 301-295-3773

Lucille Washington
Administrative Officer
email - (b) (6)
phone - (b) (6)
fax - 301-295-3773

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 18 Mar 2020 08:29:28 -0600
To: Schountz, Tony
Subject: Re: Cancelation of the 3rd International Symposium on Infectious Diseases of Bats

Too bad, but nothing to do about it

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Tuesday, March 17, 2020 at 1:45 PM
To: Tony Schountz <[redacted] (b) (6)
Subject: Cancelation of the 3rd International Symposium on Infectious Diseases of Bats

Dear Colleagues,

As you may have expected, due to the COVID-19 outbreak, the *3rd International Symposium on Infectious Diseases of Bats* has been canceled. We are considering hosting the meeting in the summer of 2021 if the resources are available to do so. If so, I will send another email this fall altering you.

For those of you who have already paid your registration, you will receive a full refund from the Colorado State University Conference Services. I have been told this can take about a month, so if you have not received a refund by April 20, please email me and I will contact Conference Services.

Thank you for your understanding.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Feb 19, 2020, at 4:09 PM, Schountz,Tony < (b) (6) wrote:

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting **This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 18 Mar 2020 07:24:59 -0600
To: Smith, Ina (H&B, Black Mountain); 'Edward Annand'; Alison Peel; John-Sebastian Eden; Plowright, Raina
Subject: Re: Requirements for PanCoVPCR screening of extracted samples under JS at Westmead and confirmatory sequencing.

A true pan-S will be difficult, but we are working on a B-coronovirus pan-S, focusing only on the B-coronas as these are the ones with most zoonotic potential.

That said, we have an updated RdRP one, which works really well so I suggest that one should be used to kickstart this

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Smith, Ina (H&B, Black Mountain)" < (b) (6)
Date: Tuesday, March 17, 2020 at 11:15 PM
To: 'Edward Annand' < (b) (6) Alison Peel < (b) (6) John-Sebastian Eden < (b) (6) "Plowright, Raina" < (b) (6) ' (b) (6) < (b) (6)
Subject: RE: Requirements for PanCoVPCR screening of extracted samples under JS at Westmead and confirmatory sequencing.

Hi All

Vincent, would it be possible to design a coronavirus pan S protein PCR, ideally so that most if not all of this gene is amplified? Then amplicon sequencing could by done in high throughput which would be cheaper.

I was also, thinking that if my airfares etc were covered then I could flying to Brisbane and show Ali how to process the bat poo samples (once all the reagents have been purchased).

Cheers
Ina

Ina Smith, PhD
Senior Research Scientist | Risk Evaluation and Preparedness Program | Health and Biosecurity| CSIRO, Clunies Ross St, Black Mountain ACT 2601 Ph. (b) (6)

From: Edward Annand <[redacted] (b) (6)
Sent: Wednesday, 18 March 2020 3:46 PM
To: Alison Peel <[redacted] (b) (6) John-Sebastian Eden <[redacted] (b) (6) Smith, Ina (H&B, Black Mountain) <[redacted] (b) (6) Plowright, Raina <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Subject: Requirements for PanCoVPCR screening of extracted samples under JS at Westmead and confirmatory sequencing.

Hi all,

Following up after our conversation and Ina and I running the plan by JS.

Ali can you please provide the following for JS so he can be ready to get straight onto setting up approvals given the worry of shut downs etc.:

- Details on the primers and reagents that we want to run – as it is imperative to get them in ASAP due to supply issues. JS says he has all the extracted SARS-CoV-2 human samples (regular ones and the new ones) he can test them on. See further points and consideration of needing to increase to a plan involving multiple primers below.
- Ethics approval for the bat sample collection – a copy of the approval.
- Outline that only extracted samples will be sent.

MTA will only be needed if your institute needs one – otherwise WIMR will not require it.

Even if WIMR shuts down – JS has approval to continue coming in.

[redacted] (b) (4)

JS confirms

[redacted] (b) (4)

However there is an issue around attempting to obtain a full genome sequence where the genome variability is unknown and the Coronavirus genome are big (32kb)

I understand you are expecting a 15% hit rate from 1000 samples leaving 150 for sequencing.

It might be necessary to include additional conventional PCR primers such as was discussed with Ina to capture the regions of interest (ideally a pan-spike protein PCR that would cover the whole protein) in order to allow recovering genome directly from the PCR product and avoid the far higher cost of sequencing from the original extracted sample.

JS is working on a rapid RNA seq protocol that he is using on cases – but it is very expensive – like [redacted] (b) (4)

The ballpark of 5000US was more suited to sequencing 150 pcr products on one RNA seq run rather than Metatranscriptomics of the original extractions.

I will let JS, Vincent and Ina further discussion on that issue and the options.

Cheers

ED

Ed Annand
BVSc(Hons) MANZCVS (Equine Surgery) & (Epidemiology) CertAVP (Equine Stud Medicine) PgCertVPS MRCVS
PhD candidate
One Health Epidemiology and Virology
University of Sydney | School of Veterinary Science
Marie Bashir Institute for Infectious Diseases and Biosecurity (Zoonoses Node)
CSIRO | Health and Biosecurity
E [redacted] (b) (6) **T** [redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 17 Mar 2020 07:34:48 -0600
To: Emily Gurley; Alison Peel; Kwe Claude, Yinda (NIH/NIAID) [F]
Cc: Andrew Cunningham; Ausraful Islam; Plowright, Raina; Cara Brook; Olivier Restif; [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) Tamika Lunn; [redacted] (b) (6) [redacted] (b) (6) McGuire, Liam; Hamish McCallum; [redacted] (b) (6) [redacted] (b) (6) James Wood; Quaye Osbourne; Louise Gibson; Richard D Suu-Ire; LaTrielle, Sara; [redacted] (b) (6) Liam Chirio; Mandy Todd; Remy Brooks; [redacted] (b) (6) [redacted] (b) (6) Fifi Ravelomanantsoa; [redacted] (b) (6) [redacted] (b) (6) Sarah Guth; Wyatt Madden; Manuel Ruiz Aravena; Clif McKee
Subject: Re: PREEMPT Field Team Quarterly meeting - February 2020

Hi Kwe,

I think it would be good if you could be on this call (if you have time)

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Emily Gurley <[redacted] (b) (6)
Date: Tuesday, March 17, 2020 at 7:30 AM
To: Alison Peel <[redacted] (b) (6)
Cc: Andrew Cunningham <[redacted] (b) (6) Ausraful Islam
<[redacted] (b) (6) "Plowright, Raina" <[redacted] (b) (6) Cara Brook
<[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) '[redacted] (b) (6)
<[redacted] (b) (6) "[redacted] (b) (6) <[redacted] (b) (6)
"[redacted] (b) (6) <[redacted] (b) (6) Tamika Lunn <[redacted] (b) (6)
"[redacted] (b) (6) <[redacted] (b) (6) '[redacted] (b) (6)'
<[redacted] (b) (6) "McGuire, Liam" <[redacted] (b) (6) Hamish McCallum
<[redacted] (b) (6) '[redacted] (b) (6)
<[redacted] (b) (6) Steve Luby <[redacted] (b) (6) James Wood
<[redacted] (b) (6) Quaye Osbourne <[redacted] (b) (6) Louise Gibson
<[redacted] (b) (6) Richard D Suu-Ire <[redacted] (b) (6)
"[redacted] (b) (6) <[redacted] (b) (6) "LaTrielle, Sara"
<[redacted] (b) (6) '[redacted] (b) (6) <[redacted] (b) (6) Liam
Chirio <[redacted] (b) (6) Mandy Todd <[redacted] (b) (6) Remy Brooks
<[redacted] (b) (6) '[redacted] (b) (6)
<[redacted] (b) (6) '[redacted] (b) (6) <[redacted] (b) (6)

Fifi Ravelomanantsoa <[redacted] (b) (6) ' [redacted] (b) (6)
<[redacted] (b) (6) ' [redacted] (b) (6) <[redacted] (b) (6) Sarah Guth
<[redacted] (b) (6) Wyatt Madden <[redacted] (b) (6) Manuel
Ruiz Aravena <[redacted] (b) (6) Clif McKee <[redacted] (b) (6)
Subject: RE: PREEMPT Field Team Quarterly meeting - February 2020

Ali,

I'd be delighted to have the chance to think about something other than COVID-19 and would love to hear updates from your results. I can make time for a call next week.

Best,
Emily

From: Alison Peel <[redacted] (b) (6)
Sent: Monday, March 16, 2020 10:47 PM
To: Emily Gurley <[redacted] (b) (6)
Cc: Andrew Cunningham <[redacted] (b) (6) Ausraful Islam <[redacted] (b) (6)
Plowright, Raina <[redacted] (b) (6) Cara Brook <[redacted] (b) (6) Olivier Restif
<[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6); Tamika Lunn
<[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) McGuire, Liam
<[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6)
[redacted] (b) (6) [redacted] (b) (6) James Wood <[redacted] (b) (6) Quaye
Osbourne <[redacted] (b) (6) Louise Gibson <[redacted] (b) (6) Richard D Suu-Ire
<[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) LaTrielle, Sara
<[redacted] (b) (6) [redacted] (b) (6) Liam Chirio <[redacted] (b) (6) Mandy
Todd <[redacted] (b) (6) Remy Brooks <[redacted] (b) (6)
[redacted] (b) (6) [redacted] (b) (6) Fifi Ravelomanantsoa
<[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) Sarah Guth
<[redacted] (b) (6) Wyatt Madden <[redacted] (b) (6) Manuel Ruiz
Aravena <[redacted] (b) (6) Clif McKee <[redacted] (b) (6)
Subject: Re: PREEMPT Field Team Quarterly meeting - February 2020

Hi all,

I'm still keen to touch base with everyone around this time next week to discuss data analyses. However, I'm conscious that there may just be too much going on with COVID-19 for people to commit to this meeting. Please let me know if you're still keen or if you'd prefer to postpone for now.

If nothing else, I could have a solo meeting and just talk about some of our interesting new results from Australia. Alternatively, it could also be an opportunity to discuss how sampling plans are being affected due to COVID-19, and make some decisions on how best to adjust. For example, in Australia, we are likely unable to get most if of not all of our international team members for the peak sampling season this winter, and so will likely need to cut back fieldwork efforts. Deciding which sessions and samples are priority is a discussion that needs to happen amongst Australia-team stakeholders.

Cheers

Ali

On Sun, 1 Mar 2020 at 20:34, Alison Peel <[redacted] (b) (6) wrote:
Thanks Emily. Here are the updated times in case there are any other daylight savings changes:

Sydney, Australia	Tue, 24 Mar 2020 at 7:00 am AEDT
Brisbane, Australia	Tue, 24 Mar 2020 at 6:00 am AEST
Dhaka, Bangladesh	Tue, 24 Mar 2020 at 2:00 am BST
Antananarivo, Madagascar	Mon, 23 Mar 2020 at 11:00 pm EAT
Paris, France	Mon, 23 Mar 2020 at 9:00 pm CET
London, United Kingdom	Mon, 23 Mar 2020 at 8:00 pm GMT
Accra, Ghana	Mon, 23 Mar 2020 at 8:00 pm GMT
Baltimore, USA	Mon, 23 Mar 2020 at 4:00 pm EDT
Denver, USA	Mon, 23 Mar 2020 at 2:00 pm MDT
Los Angeles, USA	Mon, 23 Mar 2020 at 1:00 pm PDT

On Fri, 28 Feb 2020 at 23:18, Emily Gurley <[redacted] (b) (6) wrote:
Thanks, Ali. Look forward to catching up with everyone.

The time is showing up in my calendar as 4pm on the 23rd instead of 3pm – I suspect because we 'spring forward' soon and the time will change here. Just a heads up for others in the US to make sure they have the time right.

All the best,
Emily

From: Alison Peel <[redacted] (b) (6)
Sent: Thursday, February 27, 2020 9:40 PM
To: Emily Gurley <[redacted] (b) (6) Andrew Cunningham <[redacted] (b) (6) Ausraful Islam [redacted] (b) (6) Plowright, Raina <[redacted] (b) (6) Cara Brook <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) Tamika Lunn [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) McGuire, Liam <[redacted] (b) (6) Hamish McCallum [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) James Wood <[redacted] (b) (6) Quaye Osbourne <[redacted] (b) (6) Louise Gibson <[redacted] (b) (6) Richard D Suu-Ire [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) LaTrielle, Sara <[redacted] (b) (6) [redacted] (b) (6) Liam Chirio <[redacted] (b) (6) Mandy Todd <[redacted] (b) (6) Remy Brooks <[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) Fifi Ravelomanantsoa <[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) Sarah Guth [redacted] (b) (6) Wyatt Madden <[redacted] (b) (6) Manuel Ruiz Aravena <[redacted] (b) (6) Clif McKee <[redacted] (b) (6)
Subject: Re: PREEMPT Field Team Quarterly meeting - February 2020

Hi all,

You should have just received an email invite for the rescheduled PREEMPT field data team meeting. It will be held at the time below.

Sydney, Australia	Tue, 24 Mar 2020 at 7:00 am AEDT
Brisbane, Australia	Tue, 24 Mar 2020 at 6:00 am AEST
Dhaka, Bangladesh	Tue, 24 Mar 2020 at 2:00 am BST
Antananarivo, Madagascar	Mon, 23 Mar 2020 at 11:00 pm EAT
Paris, France	Mon, 23 Mar 2020 at 9:00 pm CET
London, United Kingdom	Mon, 23 Mar 2020 at 8:00 pm GMT
Accra, Ghana	Mon, 23 Mar 2020 at 8:00 pm GMT
Baltimore, USA	Mon, 23 Mar 2020 at 4:00 pm EDT
Denver, USA	Mon, 23 Mar 2020 at 2:00 pm MDT
Los Angeles, USA	Mon, 23 Mar 2020 at 1:00 pm PDT

Some items for our agenda for the next meeting are listed below, **but please let me know if there's something specific we should add.**

AGENDA:

- Discuss change of group purpose/title to "Field data collection and analyses" - Is it necessary, or are our meetings just not necessary anymore?
- Update on any revised sampling schemes since initial PREEMPT launch meeting.
- Discuss timing of presentations to PI meetings/DARPA
- Any issues/suggestions with the PREEMPT MAIN google doc
- Presentation of some results/visualisations that the Australia team have been working on

ZOOM LINK:

https://zoom.us/j/(b) (6).?pwd=c1BSZ2s4cCtkbXpmQzFwdGlzeTJLQT09

For those who can make it, I look forward to seeing you then!

Thanks!
Ali

On Wed, 26 Feb 2020 at 14:24, Alison Peel <(b) (6) wrote:
Hi everyone,

Sorry for falling my first task as subgroup leader and for wasting anyone's time earlier today! Yes - Raina is correct - I had the external deadline for a major grant application, when I set the meeting date, had expected that I would have had to submit it internally 1-2 days earlier.

I will confirm availability with the country leads and get back to everyone with a rescheduled time/date and updated zoom link. Currently, I'm thinking of perhaps Monday 16th March/Tuesday 17th March (2 ½ weeks from now).

My apologies again

Ali

On Wed, 26 Feb 2020 at 06:50, Plowright, Raina <[redacted] (b) (6) wrote:
Sorry, I didn't have it on my calendar and so missed this as well. If you have upcoming meetings, cc Sara and ask her to make a calendar invite to share.
I do know Ali has a major grant deadline today and has been burning the midnight oil....so she may not be able to lead a call today.
Raina

On Feb 25, 2020, at 1:04 PM, Emily Gurley <[redacted] (b) (6) wrote:

Hi all,

Tried the zoom link but only Clif and I were there. I must be getting something wrong so please let me know about how to join the call!

Emily

From: Alison Peel <[redacted] (b) (6)
Sent: Thursday, January 30, 2020 1:16 AM
To: Emily Gurley <[redacted] (b) (6) Andrew Cunningham <[redacted] (b) (6) Ausraful Islam [redacted] (b) (6) Mahmudur Rahman <[redacted] (b) (6) Plowright, Raina [redacted] (b) (6) Cara Brook <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6); Tamika Lunn <[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) McGuire, Liam <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) [redacted] (b) (6) Birgit NIKOLAY <[redacted] (b) (6) Henrik SALJE <[redacted] (b) (6) [redacted] (b) (6); James Wood <[redacted] (b) (6) Quaye Osbourne <[redacted] (b) (6) Louise Gibson <[redacted] (b) (6) Richard D Suu-Ire <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) LaTrielle, Sara <[redacted] (b) (6) [redacted] (b) (6) Liam Chirio <[redacted] (b) (6) Mandy Todd [redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) Fifi Ravelomanantsoa <[redacted] (b) (6) [redacted] (b) (6) [redacted] (b) (6) Sarah Guth [redacted] (b) (6) Wyatt Madden <[redacted] (b) (6) Manuel Ruiz Aravena [redacted] (b) (6) Remy Brooks <[redacted] (b) (6)
Subject: PREEMPT Field Team Quarterly meeting - February 2020

Hi all,

If you're not involved with the field teams and think you've received this email by accident, please read on!

Firstly, I'm taking over from Emily as the lead of the PREEMPT field working group, so will take this opportunity to say thanks to Emily for all her hard work wrangling us all together over the past 12+ months! Hopefully, it's as easy as you made it look :)

Secondly, At the annual meeting at Bbar in October, we discussed shifting the group's focus from "Field data collection" to "field data collection and analyses (or visualisation)". Essentially, the idea would be to report on and feed back information that provides key insights into the viral dynamics or bat ecology that would help guide fieldwork planning and implementation. This will need some further discussion to avoid overlap with the modelling groups. I'd like to propose that we discuss this at our next Zoom meeting (in February). So, even those people not currently involved in fieldwork, but who may be interested in analysis of field data may like to attend. With that in mind, **can I please ask that everyone has a look through this email list and (1) identifies anyone on the list that doesn't need to be anymore, or (2) anyone who should be on the list, but isn't. Please let me know.**

Finally, I've listed a proposed time/date for our **quarterly field team call on Tuesday 25th February at 8pm GMT*** (Wednesday 26th in Australia). I think everyone recognises that the time zones are challenging for this group in particular, and my apologies to those for which this time doesn't work. I will rotate the time each quarter. Anyone in the team is welcome to join the call. If you're a country lead and no one from your team can attend at this time, let me know.

Some items for our agenda for the next meeting are listed below, **but please let me know if there's something specific we should add.**

AGENDA:

- Discuss change of group purpose/title to "Field data collection and analyses" - Is it necessary, or are our meetings just not necessary anymore?
- Update on any revised sampling schemes since initial PREEMPT launch meeting.
- Discuss timing of presentations to PI meetings/DARPA
- Any issues/suggestions with the PREEMPT MAIN google doc
- Presentation of some results/visualisations that the Australia team have been working on

ZOOM LINK:

https://zoom.us/j/(b) (6)?pwd=dTlEd1JSdzlEWnN3MU0xSFFsT25MQT09

MEETING TIME

Sydney, Australia	Wed, 26 Feb 2020 at 7:00 am AEDT
Brisbane, Australia	Wed, 26 Feb 2020 at 6:00 am AEST
Dhaka, Bangladesh	Wed, 26 Feb 2020 at 2:00 am BST
Antananarivo, Madagascar	Tue, 25 Feb 2020 at 11:00 pm EAT
Paris, France	Tue, 25 Feb 2020 at 9:00 pm CET
London, United Kingdom	Tue, 25 Feb 2020 at 8:00 pm GMT
Accra, Ghana	Tue, 25 Feb 2020 at 8:00 pm GMT
Baltimore, USA	Tue, 25 Feb 2020 at 3:00 pm EST
Denver, USA	Tue, 25 Feb 2020 at 1:00 pm MST
Los Angeles, USA	Tue, 25 Feb 2020 at 12:00 noon PST

Thanks!

Ali

ALISON PEEL BSc(Vet) BVSc MSc PhD

DECRA Senior Research Fellow, Griffith Wildlife Disease Ecology Group
Environmental Futures Research Institute, Sir Samuel Griffith Centre (N78) 2.23
Griffith University, Nathan Campus, 170 Kessels Rd, Nathan, QLD, 4111, Australia

Office days: Monday - Thursday

E: (b) (6) (b) (6)
W: +(b) (6)
M: (b) (6)
@ali_bat
www.bat1health.org
www.mccallum-disease-ecology.com/alison-peel
experts.griffith.edu.au/7586-alison-peel

If you have received an email from me outside of normal working hours, I'm sending it at a time that suits me. I am not expecting you to read or reply to it until normal working hours.

PREEMPT is inviting you to a scheduled Zoom meeting.

Topic: PREEMPT Field Team Quarterly meeting - February 2020
Time: Feb 26, 2020 06:00 PM Brisbane

Join Zoom Meeting
https://zoom.us/j/(b) (6)?pwd=dTlEd1JSdzlEWnN3MU0xSFFsT25MQT09

Meeting ID: (b) (6)
Password: (b) (6)

One tap mobile
+16465588656,,(b) (6) US (New York)
+16699009128,,(b) (6) US (San Jose)

Dial by your location
    +1 646 558 8656 US (New York)
    +1 669 900 9128 US (San Jose)
Meeting ID: (b) (6)
Find your local number: https://zoom.us/u/adzPR7PsUq

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 16 Mar 2020 15:26:24 -0600
To: Plowright, Raina
Subject: Re: RESPONSE REQUIRED - COVID-19

1. **How is COVID interrupting your PREEMPT work…as many details as possible**

NIH is on lockdown / telework. All non-critical work (non-covid) will be suspended

2. **What is your team doing on COVID, even if outside of PREEMPT work or team or people?**

Fundamental research, diagnostics, capacity building with African partners, animal model development, vaccine development, antiviral development, environmental stability etc etc

3. **What extensions of PREEMPT deadlines would help?**

Extension on the BSL4 animal work as all non-Covid work has been suspended

4) Send ideas of how to pivot PREEMPT work towards COVID (and how you can do this without reneging on HNV contracts—e.g. extend postdoc appointment, hire additional person).

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Monday, March 16, 2020 at 3:22 PM
To: preempt <[redacted] (b) (6)
Subject: Re: RESPONSE REQUIRED - COVID-19

Wow awesome fast responses. Thanks team. **Also include childcare issues.** Just off the phone to colleague about serology for Ro's smaller grant and baby crying in background and he is changing diapers and giving bottles — so stressful. Many of you are balancing school closures with 2 parents working full time... important to state this challenge.

On Mar 16, 2020, at 2:09 PM, Plowright, Raina <[redacted] (b) (6) wrote:

Hi PREEMPT PIs,

Email below is from a colleague on INTERCEPT (another DAPR program). We have not received such an email for PREEMPT but, last week, I made a case to [redacted] (b) (6) to do all of this below, so lets be ahead of the curve and propose this to him first (and note, INTERCEPT were given until 9am tomorrow —typical DARPA timeline! wouldn't be surprised if (b) (6) asks for this later today).

Last week I asked (b) (6) to:

1. free up our HNV deadlines —many of our programs are affected by the pandemic (we can't get people into the field, we are pulling people from some field sites), there are shortages of supplies, and critically, most of us are being pulled into local, national, or international responses. RML lab is going almost exclusively to SARS-2 work.
2. support us financially to work on COVID (along with flexibility in our PREEMPT time-lines) and allow us to report wins on COVID as wins on DARPA PREEMPT. Then it is up to us to strategize deliverables over the two systems.

Other important news.
(b) (6) will give us $500K immediately (b) (6) wants to address preventing the next pandemic, in the same spirit of PREEMPT goals. On a series of calls last week, PIs decided that $500K would go towards developing a complete spatiotemporal data set of CoV shedding from bats (in light of coinfections, stress, etc etc). Focus on Australia and Bangladesh where data sets are most complete. (b) (6) stated that there is a high probability that congress will send them money soon (congress already offered, but DARPA wont promise until money in the bank). I have no guidelines on the focus for the new money.

I'm working on a step plan so they can fund our other projects as money comes in (all the things we originally proposed). I heard loud and clear that folks are concerned about HNV timelines and do not want to be pulled onto other things without additional resources. It is up to us to create a plan that is sustainable and impactful. We shouldn't offer to do anything that stretches our capacity. But we can bolster capacity in ways that will help us deal with the current epidemic and our HNV work (e.g. extending $ to hire postdocs for longer, hiring additional people).

Please email to Sara and I (or reply to all) — or ask your postdoc or student to do this if necessary:

1) How is COVID interrupting your PREEMPT work…as many details as possible
2) What is your team doing on COVID, even if outside of PREEMPT work or team or people?
3) What extensions of PREEMPT deadlines would help?
4) Send ideas of how to pivot PREEMPT work towards COVID (and how you can do this without reneging on HNV contracts—e.g. extend postdoc appointment, hire additional person).

Today would be good. Short response better than none.

Raina

Begin forwarded message:

From: "Connie B. Chang" < (b) (6)
Subject: Fwd: FW: RESPONSE REQUIRED - COVID-19
Date: March 16, 2020 at 11:46:42 AM MDT
To: Raina Plowright < (b) (6)

Raina did you get an email like this from DARPA?

---------- Forwarded message ---------
From: **Brooke, Christopher Byron** < (b) (6)
Date: Mon, Mar 16, 2020 at 10:44 AM
Subject: FW: RESPONSE REQUIRED - COVID-19
To: Hien Tran (b) (6) Koelle, Katharina V. < (b) (6) Ruian Ke
< (b) (6) Laura Fabris < (b) (6) Connie B. Chang
< (b) (6)

Hi everyone, please see below and let me know how you want to respond. Would be best to send a single response from whole team instead of a bunch of individual responses

On 3/16/20, 11:40 AM, " (b) (6) wrote:

Dear Colleagues,
In consideration of the current COVID pandemic, please read the 4 items below closely and provide response or intention to respond by tomorrow (Tuesday, March 17) morning at 9 am eastern.

1) Please notify the DARPA team immediately if COVID-19 is interrupting INTERCEPT work, especially if it involves a university/institution shutdown. Please provide as many details as possible and include estimated length of delay(s).

2) Please update DARPA team on any work related to COVID-19, even if it is not being supported by INTERCEPT/DARPA. Seth would like to maintain awareness of all ongoing performer efforts. More detail is preferred.

3) Many of you have ideas/capabilities for pivoting part of your research program toward COVID response. If you want to assemble a proposed modification to your SoW and Cost Proposal for COVID-19 work under your current INTERCEPT funding. There is not guarantee that this will be approved, but you are welcome to submit ideas.

4) Similarly, you may have ideas/capabilities for new research efforts for COVID. Please feel free to assemble a proposed SoW and Cost Proposal for new COVID-19 work. This is not a promise or guarantee of funding, but we would like to know your capabilities and goals should funding become available.

If any of the above items change after your initial response to DARPA team, please keep us updated as changes occur.

Thank you for your prompt attention to this matter.

[redacted] (b) (6)

[redacted] (b) (6)
Strategic Analysis, Inc.
DARPA/Biological Technologies Office
[redacted] (b) (6)
Office: [redacted] (b) (6)
Mobile: [redacted] (b) (6)

--

Connie B. Chang, PhD (she/her/hers)
Chemical & Biological Engineering
Center for Biofilm Engineering
Montana State University
Bozeman, MT 59717
p: [redacted] (b) (6)
[redacted] (b) (6)
http://www.montana.edu/changlab/

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 16 Mar 2020 15:15:21 -0600
To: Plowright, Raina
Subject: Re: quick heads-up re COVID-19 funding

Yes, should be online this week in NEJM

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 3/16/20, 3:14 PM, "Plowright, Raina" <(b) (6) wrote:

(b)(6) asks — was your viral survival study accepted anywhere yet?

\> On Mar 16, 2020, at 1:41 PM, Plowright, Raina <(b) (6) wrote:
\>
\> OMG. Good to know this. Need to work with (b)(6) Can I get you on a call to him this week. Is it still feasible to get you a postdoc to work on the ideas we set out for (b)(6) a couple of weeks ago. Sounds like a chance congress will send him money to spend. (b)(6) needs to know priorities. INTERCEPT just got told they can transition to COVID. We need to have flexibility to extend hNV work and work on emergency at hand, with cash to do this.
\>
\>\> On Mar 16, 2020, at 1:36 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
\>\>
\>\> I would just stay away from this, no need to throw them under the bus. We'll dazzle them with good science,
\>\>
\>\> Should have some good follow-up environmental data soon, which we can feed to him.
\>\>
\>\> Everything is shutting down, we will be going almost exclusively for SARS-2. Good thing we got the Hendra screen out of the way
\>\>
\>\> Vincent Munster, PhD
\>\> Chief, Virus Ecology Section
\>\> Laboratory of Virology
\>\> Rocky Mountain Laboratories
\>\> NIAID/NIH
\>\>
\>\> On 3/16/20, 1:34 PM, "Plowright, Raina" <(b) (6) wrote:
\>\>
\>\> Vincent I agree… sounds like a waste of money. sounds like the VPR of CSU has convinced (b)(6) to give them money for this… Do you think we should talk to (b)(6) about what they will really learn from this and what may be some better experiments to disentangle the key questions?
\>\>
\>\>\> On Mar 16, 2020, at 1:30 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
\>\>\>
\>\>\> Really didn't want to say anything, but I think the experiment will be not very useful. A lot of assumptions, and they should determine the susceptibility of each individual species first (but unlikely they are going to do this).
\>\>\>
\>\>\> It would basically this experiment:
\>\>\> https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0017643
\>\>\>
\>\>\> Vincent Munster, PhD

>>> Chief, Virus Ecology Section
>>> Laboratory of Virology
>>> Rocky Mountain Laboratories
>>> NIAID/NIH
>>>
>>> On 3/16/20, 1:27 PM, "Plowright, Raina" <(b) (6) wrote:
>>>
>>> I had a chat with Tony on the weekend (ccd here) and his description of the experiment was a little terrifying — throw a bunch of animals and a bunch of virus in a room and see what happens. No follow up studies on susceptibility or really what happened. I wonder how useful the data will be for modeling purposes?
>>> On the other hand, if we see opportunities, we may be able to inform their experimental design so that we can get something out of it.
>>> What kinds of data could be useful for modeling here?
>>> Raina
>>>
>>>> On Mar 16, 2020, at 1:23 PM, Olivier Restif <(b) (6) wrote:
>>>>
>>>> Raina,
>>>>
>>>> Thank you for sharing this. I need to check with Emma and colleagues here but it sounds like her recent work on syndromic surveillance and outbreak detectability might be a nice complement to Alan's work based on his outline below. If it's still an option for Cambridge to be involved I'll send you more info soon on what we could do in that area.
>>>>
>>>> Cheers
>>>>
>>>> Olivier
>>>>
>>>>> On 13 Mar 2020, at 17:38, Plowright, Raina <(b) (6) wrote:
>>>>>
>>>>> PS Integrating with this group is kind of a directive. I think we could work in parallel if needed but there may be data opportunities generated that could help our group.
>>>>>
>>>>> On 3/13/20, 11:20 AM, "Plowright, Raina" <(b) (6) wrote:
>>>>>
>>>>> For now, (b) (6) will fund us separately from CSU (500K to us only, separate seed money to them). But I'm interested in Alan's (VPR CSU) description below. Sounds like there could be some synergy and they could address some issues we cannot.
>>>>> Would love your ideas about how we can integrate with this group. It would also be very good to have some or all of you on the call.
>>>>> Raina
>>>>>
>>>>> On 3/13/20, 11:00 AM, "Rudolph,Alan" <(b) (6) wrote:
>>>>>
>>>>> Raina
>>>>>
>>>>> Could we schedule a call monday?
>>>>>
>>>>> I am happy to send you what we sent it to (b) (6) previously and perhaps you could do the same so we could review this weekend?
>>>>>
>>>>> One area we are eager to explore is to observe spillover events directly in our terraforma mixed ecosystem platform (markets, barnyards) work that we have published and are active on....and was of interest to the PREEMPT program in conception. We can do this with SARS-CoV-2. We can also look at transmissibility in that platform (water, air, ect) as well as persistence in the environment. I would like to include looking at the sars-CoV-2 genome in these experiments to see if there is any genetic drifts....

>>>>>
>>>>> These studies could give us temporal and spatial dynamics of interactions of hosts, reservoirs, environmental influences (we can modulate temp, rain/water drops, and wind in some of the platforms) in a confined ecosystem that will inform us on others.
>>>>>
>>>>> We also have COVID animal model work for vaccine development and vaccine candidate safety and efficacy already underway that we can talk about. It might be interesting to intercede with the virus in the ecosystem through this countermeasure or others. We could also test a Dx in the ecosystem as well which will be informative on viral shedding in the ecosystem and when it is measurable in hosts/reservoirs...
>>>>>
>>>>> I think Tony S also contributed to your request which is important too as he is working hard on the PREEMPT tasks as we speak and has already innoculated bat macrophages and a few species of bats.
>>>>>
>>>>> Let me know if monday would work for you....
>>>>>
>>>>> Thanks
>>>>>
>>>>> Alan
>>>>>
>>>>>
>>>>>
>>>>> Sent from my iPad
>>>>>
>>>>>> On Mar 13, 2020, at 10:29 AM, Plowright, Raina < (b) (6) wrote:
>>>>>>
>>>>>> Hi Alan,
>>>>>> I'm looking forward to learning about your ideas.
>>>>>> I can talk from now until 1pm MT or late this afternoon after 3pm. I could also talk over the weekend or Monday.
>>>>>> Raina
>>>>>>
>>>>>>> On Mar 13, 2020, at 10:21 AM, (b) (6) wrote:
>>>>>>>
>>>>>>> Hi all,
>>>>>>>
>>>>>>> It's looking like we might get a drop of cash from Congress for COVID-19. I like the idea of funding you jointly and have looked over the proposals I rec'd from you, but then of course over the last few weeks was told to hold off as we had no extra money. Now we might. Suggest you consider a joint call (CSU and MSU) to strategize and put together a 2-3 page proposal with clear goals, outputs, timelines, and budget. As MSU is one of our primes, we can move money much faster.
>>>>>>>
>>>>>>> You can always put in extra documentation in back-up. Just a heads-up and will follow up with you next week.
>>>>>>>
>>>>>>> All best,
>>>>>>> (b) (6)
>>>>>>>
>>>>>>> --
>>>>>>> (b) (6)
>>>>>>> Program Manager
>>>>>>> Biological Technologies Office (BTO)
>>>>>>> DARPA
>>>>>>> Office: (b) (6)
>>>>>>> Work mobile: (b) (6)
>>>>>>> Personal mobile: (b) (6)
>>>>>>> (b) (6)

>>>>>>> (b) (6)
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>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 16 Mar 2020 08:49:56 -0600
To: Schulz, Jonathan (NIH/NIAID) [F]; Schountz, Tony
Cc: van Doremalen, Neeltje (NIH/NIAID) [E]
Subject: Re: Aj bats with SARS-CoV-2

Hi Tony,

Can you give Jon an address and POC (if not you).

Jon: send Tony the protocols as well,

Thanks!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Jonathan Schulz <[redacted] (b) (6)
Date: Monday, March 16, 2020 at 8:41 AM
To: '[redacted] (b) (6) <[redacted] (b) (6) Tony Schountz <[redacted] (b) (6)
Cc: Neeltje van Doremalen <[redacted] (b) (6)
Subject: Re: Aj bats with SARS-CoV-2

No problem we'll get it done. We will send it as soon as we have an address.

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Sunday, March 15, 2020 at 9:32 AM
To: "Schountz, Tony" <[redacted] (b) (6) "Schulz, Jonathan (NIH/NIAID) [F]" <[redacted] (b) (6)
Cc: "van Doremalen, Neeltje (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: Re: Aj bats with SARS-CoV-2

Hi Jon,

Can you prepare and ship a package with [redacted] (b) (4) to Tony.

He is doing experimental infections so would like to analyze shedding and quantify the viral loads.

Tony: what address would you like it to be shipped to?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Saturday, March 14, 2020 at 1:04 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Aj bats with SARS-CoV-2

It would be great if you could ship primer/probe plus standards.

We did intranasal with back-tilt position of the bats. Should have gone into the esophagus as well as the trachea. We did the pilot using the vial we got from BEI just for a quick and dirty susceptibility test but will follow up with distinct routes.

Our ELISA is to the NP. We made it using a gBlock of a partial of the NP (pasted below) and expressed in E.coli. Coat with 2 ug/ml in 100 ul overnight at 4C, then block with SuperBlock T21, add serum, then protein-A/G-HRP and ABTS.

We're planning day 2, 4, 7, 10, 14, 21 and 28 day euthanasia points with 3 bats per group. Maybe 5 if we can swing it. We have a loaner ultrasound to identify pregnant bats so we'll exclude those for now.

We'll definitely do the neuts but my experience is they tend to be low or even negative with these bats.

I'll keep you posted.

Thanks,

T.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Mar 14, 2020, at 10:57 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

You might want to do VN as well, to confirm you NP results. We should have an S Elisa as well (not enough to share yet, but soon). We could run them here as well for confirmation

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 3/14/20, 10:49 AM, "Schountz,Tony" <[redacted] (b) (6) wrote:

Vinnie 2 of 3 of our inoculated bats had ELISA antibody titers to NP of 1600 and 3200 on day 14. The third was equivocal (50). We'll bleed again on Monday, day 21. They were all low positive (Ct ~36) by qPCR from oral swabs in days 2 and 4 but negative by rectal. Haven't tested later days yet. The amp curve suggest the CDC primer/probe set is not working for us so we are awaiting a different set to see if that improves it. We're planning a 24 bat study next week with serial necropsies if we get the PCR sorted out.

Sent from my iPhone

VATEGALNTPKDHIGTRNPANNAAIVLQLPQGTTLPKGFYAEGSRGGSQASSRSSSRSRN
SSRNSTPGSSRGTSPARMAGNGGDAALALLLLDRLNQLESKMSGKGQQQQGQTVTKKS
AAEASKKPRQKRTATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGTDYKHWPQIAQFAP
SASAFFGMSRIGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDAYKTFPPTEPKKD
KKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADS

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 14 Mar 2020 13:20:40 -0600
To: Schountz, Tony
Subject: Re: Aj bats with SARS-CoV-2

Sounds good, I'll send the Primers and probes. Let me know if you want us to do serology / pathology.

Let's hope they become infected

On Mar 14, 2020, at 13:04, Schountz,Tony < (b) (6) wrote:

It would be great if you could ship primer/probe plus standards.

We did intranasal with back-tilt position of the bats. Should have gone into the esophagus as well as the trachea. We did the pilot using the vial we got from BEI just for a quick and dirty susceptibility test but will follow up with distinct routes.

Our ELISA is to the NP. We made it using a gBlock of a partial of the NP (pasted below) and expressed in E.coli. Coat with 2 ug/ml in 100 ul overnight at 4C, then block with SuperBlock T21, add serum, then protein-A/G-HRP and ABTS.

We're planning day 2, 4, 7, 10, 14, 21 and 28 day euthanasia points with 3 bats per group. Maybe 5 if we can swing it. We have a loaner ultrasound to identify pregnant bats so we'll exclude those for now.

We'll definitely do the neuts but my experience is they tend to be low or even negative with these bats.

I'll keep you posted.

Thanks,

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692

[redacted] (b) (6)
[redacted] (b) (6)

On Mar 14, 2020, at 10:57 AM, Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6) wrote:

You might want to do VN as well, to confirm you NP results. We should have an S Elisa as well (not enough to share yet, but soon). We could run them here as well for confirmation

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 3/14/20, 10:49 AM, "Schountz,Tony" <[redacted] (b) (6) wrote:

Vinnie 2 of 3 of our inoculated bats had ELISA antibody titers to NP of 1600 and 3200 on day 14. The third was equivocal (50). We'll bleed again on Monday, day 21. They were all low positive (Ct ~36) by qPCR from oral swabs in days 2 and 4 but negative by rectal. Haven't tested later days yet. The amp curve suggest the CDC primer/probe set is not working for us so we are awaiting a different set to see if that improves it. We're planning a 24 bat study next week with serial necropsies if we get the PCR sorted out.

Sent from my iPhone

VATEGALNTPKDHIGTRNPANNAAIVLQLPQGTTLPKGFYAEGSRGGSQASSRSSSRSRN
SSRNSTPGSSRGTSPARMAGNGGDAALALLLLDRLNQLESKMSGKGQQQQGQTVTKKS
AAEASKKPRQKRTATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGTDYKHWPQIAQFAP
SASAFFGMSRIGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDAYKTFPPTEPKKD
KKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADS

From: Schountz,Tony
Sent: Sat, 14 Mar 2020 17:37:20 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Aj bats with SARS-CoV-2

in bsl3. will respond when out. cant type well.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Saturday, March 14, 2020 10:57 AM
To: Schountz,Tony <[redacted] (b) (6)
Subject: Re: Aj bats with SARS-CoV-2

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Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 3/14/20, 10:49 AM, "Schountz,Tony" <[redacted] (b) (6) wrote:

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Sent from my iPhone

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 14 Mar 2020 10:56:28 -0600
To: Schountz, Tony
Subject: Re: Aj bats with SARS-CoV-2

We can help you with qRT-PCR, we have validate primer/probes and standards (so you can do load determination). We can ship on Monday.

What Elisa did you use? Did you do intranasal and intraoral?

My gut feeling is that it will likely be an early infection, so put some focus on the early time points?

Also let me know if you need histo support, we have everything up and running (IHC, ISH etc etc)

Pretty cool!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 3/14/20, 10:49 AM, "Schountz,Tony" <(b) (6) wrote:

> Vinnie 2 of 3 of our inoculated bats had ELISA antibody titers to NP of 1600 and 3200 on day 14. The third was equivocal (50). We'll bleed again on Monday, day 21. They were all low positive (Ct ~36) by qPCR from oral swabs in days 2 and 4 but negative by rectal. Haven't tested later days yet. The amp curve suggest the CDC primer/probe set is not working for us so we are awaiting a different set to see if that improves it. We're planning a 24 bat study next week with serial necropsies if we get the PCR sorted out.
>
> Sent from my iPhone

From: Letko, Michael (NIH/NIAID) [F]
Sent: Thu, 12 Mar 2020 22:25:23 +0000
To: Munster, Vincent (NIH/NIAID) [E]; Foster, Erin (NIH/NIAID) [E]
Cc: Seifert, Stephanie (NIH/NIAID) [E]
Subject: Re: 1 Letko CV (12_7__19).pdf
Attachments: 1 Letko CV (2_24_20).pdf

Attached is a more recent version of my CV in case you need it. Just has a few more papers on it.

-michael

--
Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
(b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Thursday, March 12, 2020 at 4:23 PM
To: "Foster, Erin (NIH/NIAID) [E]" <(b) (6)
Cc: "Seifert, Stephanie (NIH/NIAID) [E]" <(b) (6) "Letko, Michael (NIH/NIAID) [F]" <(b) (6)
Subject: FW: 1 Letko CV (12_7__19).pdf

Hi Erin,

Here is his CV,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Michael Letko <(b) (6)
Date: Thursday, February 20, 2020 at 7:44 AM
To: '(b) (6) <(b) (6)
Subject: 1 Letko CV (12_7__19).pdf

(b) (6)

[redacted]

(b) (6)

[redacted]

(b) (6)

(b) (6)

[redacted]

(b) (6)

[redacted]

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 12 Mar 2020 16:23:29 -0600
To: Foster, Erin (NIH/NIAID) [E]
Cc: Seifert, Stephanie (NIH/NIAID) [E]; Letko, Michael (NIH/NIAID) [F]
Subject: FW: 1 Letko CV (12_7__19).pdf
Attachments: 1 Letko CV (12_7__19).pdf, ATT00001.htm

Hi Erin,

Here is his CV,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Michael Letko <[redacted] (b) (6)
Date: Thursday, February 20, 2020 at 7:44 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: 1 Letko CV (12_7__19).pdf

(b) (6)

[redacted]

(b) (6)

[redacted]

(b) (6)

[redacted]

(b) (6)

[redacted]

(b) (6)

[redacted]

--
Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
(b) (6)

From: Plowright, Raina
Sent: Thu, 12 Mar 2020 20:10:52 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Manuel Ruiz; Kwe Claude, Yinda (NIH/NIAID) [F]; Bushmaker, Trenton (NIH/NIAID) [E]
Subject: Re: Samples for CoV

THanks.

On Mar 12, 2020, at 1:56 PM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

[redacted] (b) (4)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Manuel Ruiz <[redacted] (b) (6)
Date: Thursday, March 12, 2020 at 1:51 PM
To: "Plowright, Raina" <[redacted] (b) (6)
Cc: "[redacted] (b) (6) <[redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6) Trenton Bushmaker <[redacted] (b) (6)
Subject: Re: Samples for CoV

Thanks Kwe and Vincent for the quick replies!
Much appreciated!
M

Manuel Ruiz Aravena
Postdoctoral Researcher
Department of Microbiology and Immunology | Montana State University, USA
Mobile: [redacted] (b) (6)

El jue., 12 mar. 2020 a las 12:42, Plowright, Raina (<[redacted] (b) (6) escribió:
Doing a happy dance!!! Thanks!

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Thursday, March 12, 2020 at 12:39 PM
To: Raina Plowright <[redacted] (b) (6) Manuel Ruiz
<[redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]"
<[redacted] (b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]"
<[redacted] (b) (6)
Subject: Re: Samples for CoV

I would think so (but probably not the ethanol ones), the downstream full genome analyses might prove more difficult but the initial assessment would probably work (pan coronavirus PCR).

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <[redacted] (b) (6)
Date: Thursday, March 12, 2020 at 12:37 PM
To: "[redacted] (b) (6) <[redacted] (b) (6) Manuel Ruiz
<[redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]"
<[redacted] (b) (6) Trenton Bushmaker <[redacted] (b) (6)
Subject: Re: Samples for CoV

Thanks Vincent,
To clarify, the fecal samples have not been put in VTM or buffer or RNA later or anything – plain feces in a zip lock bag. Some went into ethanol.
Could we still get out enough RNA to 1) detect CoVs and 2) sequence a region relevant to developing a phylogeny & downstream analyses in your lab?
If you say yes, I will do a big happy dance all around my office!
Raina

> **From:** "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
> **Date:** Thursday, March 12, 2020 at 12:04 PM
> **To:** Manuel Ruiz <[redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]"
> <[redacted] (b) (6)
> **Cc:** Raina Plowright <[redacted] (b) (6)
> **Subject:** Re: Samples for CoV
>
> 1 no problem, as your screening does RNA/PCR it should hardly be affected by temperature changes etc. Viability, is typically reserved for live

virus which is not that important for this work (of note, coronaviruses are very hard to isolate from bats)

2 Kwe: can you communicate the protocols for Myndi's pan-coronavirus PCR and help Manuel in setting-it up and walk him through the analyses?

3 Media exactly the same as for Henipa, one VTM fits all

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Manuel Ruiz < [redacted] (b) (6)
Date: Thursday, March 12, 2020 at 10:43 AM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" < [redacted] (b) (6) Trenton Bushmaker < [redacted] (b) (6)
Cc: "Plowright, Raina" < [redacted] (b) (6)
" [redacted] (b) (6) < [redacted] (b) (6)
Subject: Samples for CoV

Hi Kwe, Trent and Vincent,

I hope all goes well. I write you to ask for your opinion about the viability of the faecal samples that we have collected in Australia for detection of CoV (preserved in either no-buffer or ethanol at -20). **Raina is currently putting together a proposal which has to be presented to DARPA tomorrow, so a quick response from you will be appreciated.**

Questions;

1.- What's your opinion about the viability of the samples for reliable detection of CoV? (Consider that some of them have been at -80, then - 20 and with potential changes in temperature while archiving and moving from the field and across facilities). If there are doubts of their viability, is there any test we could run to have an idea in a short time?

2.- If the samples are viable (completely or partially), what could be the best approach for their analysis? (For instance, target short or long fragments, etc.) and what depth of results could it give us?

3.- What could be the best sample, media and preservation for CoV ? So we could integrate it into the field protocol.

Thanks for your help in advance,

Raina, please add any point that I could have missed.

Cheers,
Manuel

Manuel Ruiz Aravena
Postdoctoral Researcher
Department of Microbiology and Immunology | Montana State University, USA
Mobile: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 12 Mar 2020 13:59:09 -0600
To: Kwe Claude, Yinda (NIH/NIAID) [F]; Alison Peel; Plowright, Raina; Manuel Ruiz Aravena
Subject: Re: [redacted] (b) (4) Screening results

Great job Kwe, looking forward to see the downstream data analyses of the PhD students,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
Date: Thursday, March 12, 2020 at 12:46 PM
To: Alison Peel <[redacted] (b) (6) "Plowright, Raina" <[redacted] (b) (6)
Manuel Ruiz Aravena <[redacted] (b) (6)
Cc: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: [redacted] (b) (4) Screening results

Dear all,

[redacted] (b) (4)

Details are in attachment.
Let me know if you have any questions.

kwe

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 12 Mar 2020 13:51:58 -0600
To: Jon Epstein; Peter Daszak; Noam Ross; Ariful Islam; Mahmud Rahman; Dr.Mohammad Ziaur Rahman; Meerjady Sabrina Flora , PhD; Broder, Chris (USU-DoD); Kevin Olival, PhD; Eric Laing; Linfa Wang
Cc: Alison Andre; Aleksei Chmura
Subject: Re: Good news regarding our Nipah virus NIH proposal

Good job,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Jon Epstein < (b) (6)
Date: Thursday, March 12, 2020 at 12:36 PM
To: Peter Daszak < (b) (6) Noam Ross < (b) (6)
Ariful Islam < (b) (6) Mahmud Rahman < (b) (6)
"Dr.Mohammad Ziaur Rahman" < (b) (6) " (b) (6)
< (b) (6) "Meerjady Sabrina Flora , PhD" < (b) (6)
"Broder, Chris (USU-DoD)" < (b) (6) "Kevin Olival,"
< (b) (6) Eric Laing < (b) (6) Wang Linfa
< (b) (6)
Cc: Alison Andre < (b) (6) Aleksei Chmura
< (b) (6)
Subject: Good news regarding our Nipah virus NIH proposal

Dear colleagues,

I wanted to share some early and very good news regarding our NIH proposal for continuing our Nipah virus research. Our proposal has been reviewed and we received a strong impact score of 20, putting us in the 6th percentile of proposals. According to the program officer, this should put us solidly within range to be funded, and I'm hopeful that it will indeed be funded. The final decision will be made in May, when the NIAID council meets, but I wanted to take the opportunity to thank you all for your collaboration, patience, and perseverance!

PLEASE keep this confidential until we receive official notification of funding. If funded, we could anticipate a start date around September.

I'll keep you posted if there's any more news.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
460 West 34th Street, Ste. 1701
New York, NY 10001

[redacted] (b) (6) (direct)
[redacted] (b) (6) (mobile)

web: ecohealthalliance.org
Twitter: @epsteinjon
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Plowright, Raina
Sent: Tue, 10 Mar 2020 04:04:56 +0000
To: Colin Parrish
Cc: Alex Washburne; Jamie Lloyd-Smith; Olivier Restif; Munster, Vincent (NIH/NIAID) [E]; LaTrielle, Sara; Barbara Han
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

Is anyone doing some kind of standardization of case definition/testing effort to compare data among countries. e.g. can't get tested in many places unless you traveled internationally to epidemic area (and going to Seattle doesn't count!), but in Korea, you can show up at a drive-thru and get tested.

Much of this is probably driven by availability of tests. Washington State currently can test 100 people a day. Korea can test thousands a day - may explain low death rate in Korea—they are assessing the denominator.

The difference in death rates between countries with similar #'s of cases is so curious. Sth Korea 7,500 cases and 53 deaths whereas Italy 9,000 cases and 463 deaths? Must be partly the ability to assess the denominator, but is it also case definition (e.g. CT vs PCR), age structure, strategies to protect vulnerable people, availability of test kits to treat people who died?

WHO and others must be focused on exactly these issues — must be a preprint out there somewhere on this!

On Mar 9, 2020, at 9:12 PM, Colin Ross Parrish <(b) (6) wrote:

Agree that getting better numbers for mild and subclinical infections is key, and the level of immunity present in different populations (not sure that has been reported to any degree).

The age stratification of the mortality versus age structure of population may be a key risk factor here, relative to who is being infected?

[For the canine flu model dense populations were 100% infected in a few days, and then were solidly immune a few days later, so the infection died out quickly and did not recur].

Colin

Colin R. Parrish
John M. Olin Professor of Virology
College of Veterinary Medicine
Cornell University
Ithaca, NY 14853, USA

Phone: [redacted] (b) (6) (cell anywhere); [redacted] (b) (6)(work); Skype: colinparrish

From: Alex Washburne < [redacted] (b) (6)
Sent: Monday, March 9, 2020 11:02 PM
To: Colin Ross Parrish < [redacted] (b) (6)
Cc: Plowright, Raina < [redacted] (b) (6) Jamie Lloyd-Smith < [redacted] (b) (6)
Olivier Restif < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6)
LaTrielle, Sara < [redacted] (b) (6) Barbara Han < [redacted] (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

The TLDR on this is:

I think case fatality rates are over 100x lower, on account of a very high asymptomatic rate. China didn't succeed via a lockdown, but had herd immunity by Feb 5 and didn't have 20 million deaths we'd expect at the going CFR.

The big anomaly is: this virus grows fast - doubling every 2.1 days everywhere we see it - yet it hasn't led to the deaths or hospital burdens we'd expect from that doubling time. In all places with outbreaks, they may have hit the herd immunity ceiling already (e.g. I predict new cases South Korea are now going to decline).

It's a radical thought, but I can't find any other way to reconcile the fast growth, relatively few hospital visits, and almost perfect prediction of China's peak from Belgium's growth rate.

Look forward to chatting more about it tomorrow!

Sent from miPhone

On Mar 9, 2020, at 8:47 PM, Colin Ross Parrish < [redacted] (b) (6) wrote:

Alex and others,

Not sure about the numbers, but I do agree that a more careful analysis of the likely transmission and increase rates would be useful. Right now so many people are giving "epidemiological advice", and some of it may be causing more harm than good - either to people's health, the economy, or both. Particularly it there was a way to identify how different interventions can most effectively results in outbreaks dying out. (Not sure about the fecal transmission idea but that is being checked as speak I think.)

{We did that analysis of the introduction, spread and fade-out of canine influenza last year, which may have some relevancehttps://www.ncbi.nlm.nih.gov/pubmed/29875234]

Colin

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College of Veterinary Medicine
Cornell University

Ithaca, NY 14853, USA
Phone: (b) (6) (cell anywhere); (b) (6) (work); Skype: colinparrish

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Sent: Monday, March 9, 2020 9:04 PM
To: Plowright, Raina (b) (6)
Cc: Jamie Lloyd-Smith < (b) (6) Colin Ross Parrish < (b) (6) Olivier Restif < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) LaTrielle, Sara < (b) (6) Barbara Han < (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

Hi folks -

I've written up a summary of my latest work on this topic. Let me know if you have any questions - if I'm right (and that's a HUGE if), then learning it in the next week could literally save trillions of dollars from costly interventions.

On Mon, Mar 9, 2020 at 12:17 PM Plowright, Raina < (b) (6) wrote:
Jamie, all fair comments. We have to be very strategic here. Don't want to shoot ourselves in the foot and not deliver on henipaviruses because that will be the model system for understating this problem when COVID in control. I've also been wondering about the time-lines. Will talk to (b) (6) this week and discuss. He is under different pressures than we are so its not clear if that will be an easy sell or not.

Sara – could you make calendar invite/zoom link for this group (10.30am MT). Include Barbara (may not join todays calls).

From: Jamie Lloyd-Smith < (b) (6)
Date: Monday, March 9, 2020 at 11:51 AM
To: Raina Plowright < (b) (6)
Cc: Colin Ross Parrish < (b) (6) Olivier Restif < (b) (6) "Munster, Vincent (NIH/NIAID) [E]" < (b) (6) "LaTrielle, Sara" < (b) (6) Alex Washburne < (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

Hi Raina,

I can do a call tomorrow at 9:30 PDT. I'm not sure how much bandwidth my group will have in the coming months to do hardcore work on the next potential CoV spillover, given the need to focus on the current one (plus other obligations). I'm also getting concerned about the timeline for henipa work, since the covid-19 work has diverted some of my group's effort and has slowed upstream data generation. I feel like one of the most useful things (b) (6) could give us, if he wants fast progress on coronavirus work, is an extended timeline for the henipa work. Though I'm not optimistic that is on the table. Happy to discuss all this in any case.

cheers,
Jamie

On Mon, Mar 9, 2020 at 8:33 AM Plowright, Raina < (b) (6) wrote:
Jamie, Colin, Olivier,

You guys are not on the calls today….but are the critical to moving COVID work forward.

Could you do a call on Tuesday morning? Jamie said he is (was as of last week) able to call Tuesday morning (but not Monday).

9.30-11am PST = 10.30-12pm MT = 12.30-2pm EST
Could you guys do TUESDAY 9.30 PTS/ 10.30 MT/ 12.30 EST?

Vincent, I know you can only do one call….this would be the preference.

Alex has noticed some issues with the COVID projections from other gps and should present some theories to you to get feedback.
Vincent and Jamie, need to see how to move forward with organoid + modeling experiments work for NIH.
Olivier, I think we need to screen samples…want your feedback too.
Need some concrete feedback on DARPA ask. Pasted (b) (6) email below.

Gotta run and teach…

(b) (6)

Thanks. I think for this COVID-19 related work, let's focus on what PREEMPT is trying to do (preempt/prevent spillover). I am thinking of funding along the lines of a DARPA seedling, $300K-500K. In terms of what might be good to show for November (wrt results), how about a stronger understanding of how coronaviruses jump from bats to intermediate reservoirs and to humans. I mean, some of this is already known, I know, but to look at what's unknown, what are the important points along a spillover timeline to elucidate, and how we might block that jump next time. Maybe that sounds too simple, but we know there will be another SARS like virus in humans, so how do we get ahead of that and stop the spillover? A big win, as I see it, would be information to inform a tool to stop this very spillover. Akin to the bat fissioning work you have done, but not necessarily an ecologic intervention, but maybe so! Depends on what the data show. I am sorta spitballing here, but happy to discuss it with you further soon.

From: Colin Ross Parrish < (b) (6)
Date: Thursday, March 5, 2020 at 4:18 PM
To: Jamie Lloyd-Smith < (b) (6) preempt
< (b) (6)
Cc: "Plowright, Raina" < (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

I am also likely to not likely be able to participate as I am visiting another college that day, but am also interested...

Colin

Colin R. Parrish
John M. Olin Professor of Virology
College of Veterinary Medicine
Cornell University
Ithaca, NY 14853, USA
Phone: [redacted] (b) (6) (cell anywhere); [redacted] (b) (6) (work); Skype: colinparrish

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From: Jamie Lloyd-Smith <[redacted] (b) (6)
Sent: Thursday, March 5, 2020 5:34 PM
To: preempt <[redacted] (b) (6)
Cc: Plowright, Raina <[redacted] (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

This is a direct conflict with my department's faculty meeting, where we will be discussing who to hire from a recent search. So I won't be able to make it, and likely will join the PI call quite late. I am definitely interested in pursuing Covid-19 work and funding (and am doing so already) so will need to follow up at a different time or discuss offline.

Sorry, second Monday of the month at noon is terrible timing for me.

Jamie

Jamie

On Thu, Mar 5, 2020 at 2:23 PM Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6) wrote:
I'll try to make it, but will likely only be available for one call,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "LaTrielle, Sara" <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Thursday, March 5, 2020 at 1:43 PM
To: "Plowright, Raina" <[redacted] (b) (6)
[redacted] (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

All,

We decided to have the Corvid 19 call the hour before our PI meeting this coming Monday, March 9th. **This call will be 1-2pm MST and with the PI call 2-3pm MST** (Tony/team presenting during the PI call). A calendar invite will be sent with the Zoom link embedded.

Objective of the call: have a focused strategic discussion for team members directly involved with writing proposals. During the call, we will decide where we are going to lead on this topic, and form sub-teams that can focus on specific things. To note- this call is not an information-sharing session.

Sara/Raina

From: Plowright, Raina < (b) (6)
Sent: Thursday, March 5, 2020 1:10 PM
To: (b) (6) < (b) (6)
Subject: FW: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

Dear team,
We really need to talk and develop strategies for responding to this, and the multiple other calls for funding. We also need to decide how we are going to work together as a group and where we want to be leaders in the response to the epidemic.
DARPA now also wanting to fund us. And there are NIH opportunities as well as other government funding opportunities.
Sara will send doodle poll for us all to talk Monday afternoon or Tuesday.
Raina

From: dmsnews <DMSNEWS@LISTSERV.NSF.GOV> on behalf of Henry Warchall < (b) (6)
Reply-To: dmsnews <DMSNEWS@LISTSERV.NSF.GOV>
Date: Thursday, March 5, 2020 at 12:08 PM
To: "DMSNEWS@LISTSERV.NSF.GOV" <DMSNEWS@LISTSERV.NSF.GOV>
Subject: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

March 4, 2020

Dear Colleague,

In light of the emergence and spread of the coronavirus disease 2019 (COVID-19) in the United States and abroad, the National Science Foundation (NSF) is accepting proposals to conduct non-medical, non-clinical-care research that can be used immediately to explore how to model and understand the spread of COVID-19, to inform and educate about the science of virus transmission and prevention, and to encourage the development of processes and actions to address this global challenge.

NSF encourages the research community to respond to this challenge through existing funding opportunities. In addition, we invite researchers to use the Rapid Response Research (RAPID) funding mechanism, which allows NSF to receive and review proposals having a severe urgency with regard to availability of or access to data, facilities or specialized equipment as well as quick-response research on natural or anthropogenic disasters and similar unanticipated events. Requests for RAPID proposals may be for up to $200K and up to one year in duration. Well-justified proposals that exceed these limits may be entertained. All questions should be directed either to a program officer managing an NSF program with which the research would be aligned or to rapid-covid19@nsf.gov.

Complete guidance on submitting a RAPID proposal may be found in Chapter II.E.1 of the NSF Proposal and Award Policies and Procedures Guide.

We ask that all investigators and organizations maintain awareness of the dynamic nature of this event through regular monitoring of official communications from the Centers for Disease Control and World Health Organization.

NSF has also provided Frequently Asked Questions that address questions associated with NSF proposal submission and award management relevant to research proposals relating to COVID-19 as well as possible impacts of COVID-19 on activities under existing awards and on participation in NSF's merit review panels; that website will be updated as appropriate.

Sincerely,

Dr. France A. Córdova
Director

This document is also available online
at https://www.nsf.gov/publications/pub_summ.jsp?ods_key=nsf20052

--
James O. Lloyd-Smith

Professor
Department of Ecology & Evolutionary Biology
Department of Biomathematics
University of California, Los Angeles
610 Charles E Young Dr South
Box 723905
Los Angeles, CA 90095-7239

Phone: [redacted] (b) (6)

https://www.eeb.ucla.edu/Faculty/lloydsmith/
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From: Plowright, Raina
Sent: Mon, 9 Mar 2020 18:55:47 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

Tomorrow would be most strategic mtg... but would dearly love to have you on both!

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Monday, March 9, 2020 at 12:06 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: Alex Washburne <[redacted] (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

I might be running late today,

Got an urgent last-minute meeting here at NIAID, btw NIH is restricting any travel which is not mission critical.

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Monday, March 9, 2020 at 9:38 AM
To: preempt <[redacted] (b) (6)
Cc: Alex Washburne <[redacted] (b) (6)
Subject: Re: NSF Dear Colleague Letter on the Coronavirus Disease 2019 (COVID-19)

Dear all,

Today's call at 1pm MT is a brainstorm (2pm is a regular report call on immunology). I'm hoping to do another call with Jamie and Colin and Olivier tomorrow morning (they can't make the times today).

Last night, I finally heard back from [redacted] (b) (6) Here is the info he gave. Have lots of ideas about what may and may not be feasible but I want input from all of you.

[redacted] (b) (6) "Thanks. I think for this COVID-19 related work, let's focus on what PREEMPT is trying to do (preempt/prevent spillover). I am thinking of funding along the lines of a DARPA seedling,

$300K-500K. In terms of what might be good to show for November (wrt results), how about a stronger understanding of how coronaviruses jump from bats to intermediate reservoirs and to humans. I mean, some of this is already known, I know, but to look at what's unknown, what are the important points along a spillover timeline to elucidate, and how we might block that jump next time. Maybe that sounds too simple, but we know there will be another SARS like virus in humans, so how do we get ahead of that and stop the spillover? A big win, as I see it, would be information to inform a tool to stop this very spillover. Akin to the bat fissioning work you have done, but not necessarily an ecologic intervention, but maybe so! Depends on what the data show. I am sorta spitballing here, but happy to discuss it with you further soon."

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To: "Plowright, Raina" <[redacted] (b) (6)
"[redacted] (b) (6) <[redacted] (b) (6)
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< (b) (6)
Reply-To: dmsnews <DMSNEWS@LISTSERV.NSF.GOV>
Date: Thursday, March 5, 2020 at 12:08 PM
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Dr. France A. Córdova
Director

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James O. Lloyd-Smith

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https://www.eeb.ucla.edu/Faculty/lloydsmith/
Office: 4135 Terasaki Life Sciences Building
Lab: 4000 Terasaki Life Sciences Building

From: Rasmussen, Angela L.
Sent: Mon, 9 Mar 2020 00:21:30 +0000
To: De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]
Subject: Rhesus samples

Hi Emmie and Vincent,

I'm applying for a NSF RAPID award to cover the cost of sequencing the samples you kindly collected for me in your rhesus experiments. I'm going to push forward with the sequencing before we know for sure that we can get this award, but would it be possible for either (or both) of you to contribute a letter of support for the work?

Michael Kirby is going to be the PI for the NSF award and he will be developing a new algorithm for integrating this with other respiratory data in order to predict disease outcome.

Thanks! I hope all is well. I know you must both be insanely busy…

Angie

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 7 Mar 2020 07:55:34 -0700
To: Broder, Chris (USU-DoD); Schmaljohn, Connie (NIH/NIAID) [E]
Cc: De wit, Emmie (NIH/NIAID) [E]
Subject: Re: SARS-CoV-2

The POC for Fredrick is Connie Smaljohn (CC-Ed)

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Broder, Christopher" <[redacted] (b) (6)
Date: Friday, March 6, 2020 at 4:57 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: Emmie De wit <[redacted] (b) (6)
Subject: Re: SARS-CoV-2

great, thanks Vincent.

is it Lisa Hensley then as a POC for NIAID in Fredrick?

On Fri, Mar 6, 2020 at 6:42 PM Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
No problem, if there are testing requests we send him to the larger NIAID workgroup on this,

Btw 1 will have NHP sera for you if you want it for the Luminex. Will still need to be irradiated etc, but would give you guys a headstart.

Btw 2 planning to apply for coronavirus serology grants? More than happy to provide LOS for NIH/NSF grants,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Broder, Christopher" <[redacted] (b) (6)
Date: Friday, March 6, 2020 at 3:04 PM

To: [redacted] (b) (6) < [redacted] (b) (6)
Cc: Emmie De wit < [redacted] (b) (6)
Subject: Re: SARS-CoV-2

Thanks much Vincent / Emmie

Can I forward your email contact to him ? He may reach out.

it is::
Prof. Trent Munro
Director National Biologics Facility
Program Director Rapid Response Vaccine Pipeline
Australian Institute for Bioengineering and Nanotechnology
The University of Queensland
Brisbane Qld 4072 Australia
O: [redacted] (b) (6)
M: [redacted] (b) (6)
E: [redacted] (b) (6)

On Fri, Mar 6, 2020 at 9:08 AM Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6) wrote:
Yes, we have established rhesus as a very suitable model (lot of URT and LRT shedding),

Probably will take us ~ 2 more weeks to get all the data analyzed,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Broder, Christopher" < [redacted] (b) (6)
Date: Friday, March 6, 2020 at 5:58 AM
To: Emmie De wit < [redacted] (b) (6) " [redacted] (b) (6)
< [redacted] (b) (6)
Subject: SARS-CoV-2

Hey guys

are doing NHPs SARS-CoV-2 ? planning to? a model?
Contacts in Queensland are reaching out. Not sure

what for, but I told them I would touch base with you

Chris

--

Christopher C. Broder, Ph.D.
Professor and Chair
Department of Microbiology and Immunology
Uniformed Services University, B4152
4301 Jones Bridge Rd, Bethesda, MD 20814-4799

USU is "America's Medical School"
Email: [redacted] (b) (6)
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--

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Lucille Washington
Administrative Officer
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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 6 Mar 2020 07:21:35 -0700
To: Letko, Michael (NIH/NIAID) [F]; Seifert, Stephanie (NIH/NIAID) [E]
Subject: FW: Manuscript NRMICRO-18-165V3 out to referees

Its moving,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Reply-To: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Date: Friday, March 6, 2020 at 1:19 AM
To: '(b) (6) <(b) (6)
Subject: Manuscript NRMICRO-18-165V3 out to referees

Dear Vincent,

Manuscript number: NRMICRO-18-165V3
Title: Bat-borne viruses: mechanisms of spillover and emergence
Authors: Vincent Munster, Michael Letko, Stephanie Seifert, Kevin Olival, Raina Plowright

I hope this email finds you well. I just wanted to let you know that your article is now out for peer review. Timings from here can be a bit unpredictable, depending on the schedules of the referees but I hope to be able to send you their comments and our initial decision in the next 3–4 weeks. Please do get in touch if you have any questions in the meantime.

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Further details about how to create and link your ORCID can be found here www.springernature.com/orcid-for-nature-research.

The Nature Reviews journals also are committed to facilitating training in peer review and to ensuring that everyone involved in our peer-review process is appropriately recognised. We have therefore started an initiative to allow and encourage established referees to involve an early-career researcher in our peer-review process. If a reviewer agrees to participate, you will see the following statement when you receive the referee reports: “Nature Reviews are committed to facilitate training in peer review and to ensure that everyone involved in our peer-review process is appropriately recognised. This reviewer co-reviewed one of the listed reports.”

Finally, we would like to inform you that on a case by case basis we coordinate a brief consultation between referees and editors after all referee reports have been received. This is to improve the peer review process and the feedback provided to authors. Referees are given the opportunity to make comments on their peers’ concerns and update their reports to comment on issues raised by the other reviewers. If deemed necessary, your paper might go through this extra step.

Best wishes,
Ursula

Ursula Hofer, MD PhD
Chief Editor, Nature Reviews Microbiology
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N1 9XW
e-mail:ursula.hofer1@nature.com
tel: +44 (0)20 7014 6648
http://www.nature.com/nrmicro

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From: Plowright, Raina
Sent: Thu, 5 Mar 2020 16:02:54 +0000
To: Hector Aguilar-Carreno
Cc: LaTrielle, Sara; Jamie Lloyd-Smith; Munster, Vincent (NIH/NIAID) [E]
Subject: Re: G-P Bozeman-RML July mtg/visit?

It would be very good if you could all come to DC. this is the critical meeting for moving to phase 2. Also good chance to work with Pasteur team and UCD team who will be there. Of course, all contingent on actually being able to travel in May, given COVID situation….

On Mar 5, 2020, at 8:55 AM, Hector Aguilar-Carreno <(b) (6) wrote:

I am pretty sure I can attend the DC meeting in May, unless something extraordinary happens. If Vincent and Jamie can both attend that meeting, then how about having our G-P meeting in May in DC?

Hector

Hector Aguilar-Carreno
Associate Professor
Microbiology and Immunology
College of Veterinary Medicine
Cornell University
Office: (b) (6)

From: LaTrielle, Sara (b) (6)
Sent: Thursday, March 5, 2020 10:51 AM
To: Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6)
(b) (6) <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: G-P Bozeman-RML July mtg/visit?

All,

From discussions a few months back, the G-P team tentatively planned to have a G-P meeting in Bozeman around the same dates as the DARPA review meeting. As we know, that particular mtg shifted to May 4-6 in VA. That said, DARPA (b) (6) will still visit Bozeman, but for a 'site-visit', in Bozeman July 7 and RML July 8th.

Question:
Will you all still be able to have your mini G-P meeting in July- and do you have an interest/time to visit RML? (If this works for VM, of course)

Along with this July 'site visit' by DARPA there is the semi-annual review meeting in May-VA which Hector and/or Vincent 'may' join- so just ceasing out where and when the G-P wants to meet. You are welcome to both locations and meetings of course but know time is a commodity.

Let Raina and I know what is best for the G-P team.

Best,
Sara

From: Plowright, Raina
Sent: Thu, 5 Mar 2020 04:06:30 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2

That's intense. Can't see light at the end of the tunnel...can only see things getting much worse over the next few weeks.
Look after yourself. Hugs to Emmie too, bet she is in the thick of it as well.

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Wednesday, March 4, 2020 at 7:52 PM
To: "Plowright, Raina" <(b) (6)
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2

Lol, actually not that grumpy. More like focused. But a bit higher stress level than normal. Especially as a lot of "normal" stuff still continues.

Largely because of a couple big studies (meaning starting at 7 and then back at 8 at night for treatment).

But thanks for checking, that's really nice of you

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <(b) (6)
Date: Wednesday, March 4, 2020 at 5:36 PM
To: '(b) (6) <(b) (6)
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2

worried about you... you seem grumpy ;-) — must be under extreme pressure right now. are you hanging in there?

On Mar 4, 2020, at 2:29 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Let's hope its of our plate for a while

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology

Rocky Mountain Laboratories
NIAID/NIH

From: Ursula Hofer <Ursula.Hofer1@nature.com>
Date: Friday, February 28, 2020 at 12:03 PM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2

Hi Vincent,

Thank you for sending in the revised version and answering all my queries, in particular in such a busy time. I can imagine you have loads going on.

I'll go through everything in detail early next week and if all looks good all send out a clean version to peer review. I can imagine that peer review will take a little longer than usual. I'll keep you updated.

Take care,
Ursula

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Friday, February 28, 2020 3:44 PM
To: Ursula Hofer
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2

Hi Ursula,

Manuscript resubmitted, let me know what you think. I think after the initial reviews I'd like to highlight the current SARS-2 outbreak a bit better to underscore the gaps and needs in our knowledge (but need a bit more info on this, so hopefully in the next months we know a bit more about the origin),

Hope all is well,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Reply-To: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Date: Tuesday, February 11, 2020 at 5:18 AM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Subject: Editorial feedback for manuscript NRMICRO-18-165V2

Dear Vincent,

Manuscript number: NRMICRO-18-165V2

Title: Bat-borne viruses: mechanisms of spillover and emergence
Authors: Vincent Munster, Michael Letko, Stephanie Seifert, Kevin Olival, and Raina Plowright
Submission date for revisions: 25th February 2020

Apologies again for the delay in sending you feedback on your article. I've been off sick with viral pneumonia (of all things!) for a good two weeks.

(b) (5)

[redacted]

That's it! I hope you find these comments helpful and if you'd like to discuss any of the suggested changes further, please let me know.

I would be grateful if you could return a revised version of the article to me by 25th February 2020.

If at any time you think you will be unable to meet this deadline, please contact me at your earliest convenience to discuss a new date. I know it's an incredible busy time and if you need more time because of the current outbreak, we can arrange an extension.

Please use the following link to upload your revised manuscript:
https://mts-nrmicro.nature.com/cgi-bin/main.plex?el=A6Z5gn4A6TyV3J6A9ftd4v3voV3MJOYTdW1Ye4UzgZ

Thank you very much for all your hard work on this piece so far. Please don't hesitate to contact me if you have any questions or wish to discuss any points in this letter. Finally, I would be very grateful if you could acknowledge receipt of this e-mail and confirm whether you will be able to return your revised draft by the suggested date.

Best wishes,
Ursula

Ursula Hofer, MD PhD
Chief Editor, Nature Reviews Microbiology
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tel: +44 (0)20 7014 6648
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From: Schountz,Tony
Sent: Wed, 4 Mar 2020 13:49:31 +0000
To: Plowright, Raina; Sara LaTrielle; Munster, Vincent (NIH/NIAID) [E]; Hector Aguilar-Carreno; Rynda-Apple, Agnieszka
Cc: Schountz, Tony
Subject: DARPA report
Attachments: Immunology Report March 2020.pptx

Hi Everyone,

Sara has asked me to prepare a 20 min presentation for (b) (6) for March 13. I have attached the draft to this email. Because (b) (6) is new, we need to introduce him to the overall goals of the immunology component, particularly what we have done ("wins") and where we are going next. I would appreciate your comments and revisions to the attached file. If you can get your revisions to me by Saturday, I will get it ready for Monday's group Zoom call and after feedback from that, for the DARPA call on the following Friday.

I'm in Grenada doing a little bat work but will be back to Fort Collins on Sunday.

Thanks

Tony

Montana State University Monthly Update

Preventing emergence and spillover of bat pathogens in high-risk global hot-spots

PREEMPT
March 13, 2020

Introducing team members on call

Raina Plowright
MSU

Tony Schountz
CSU

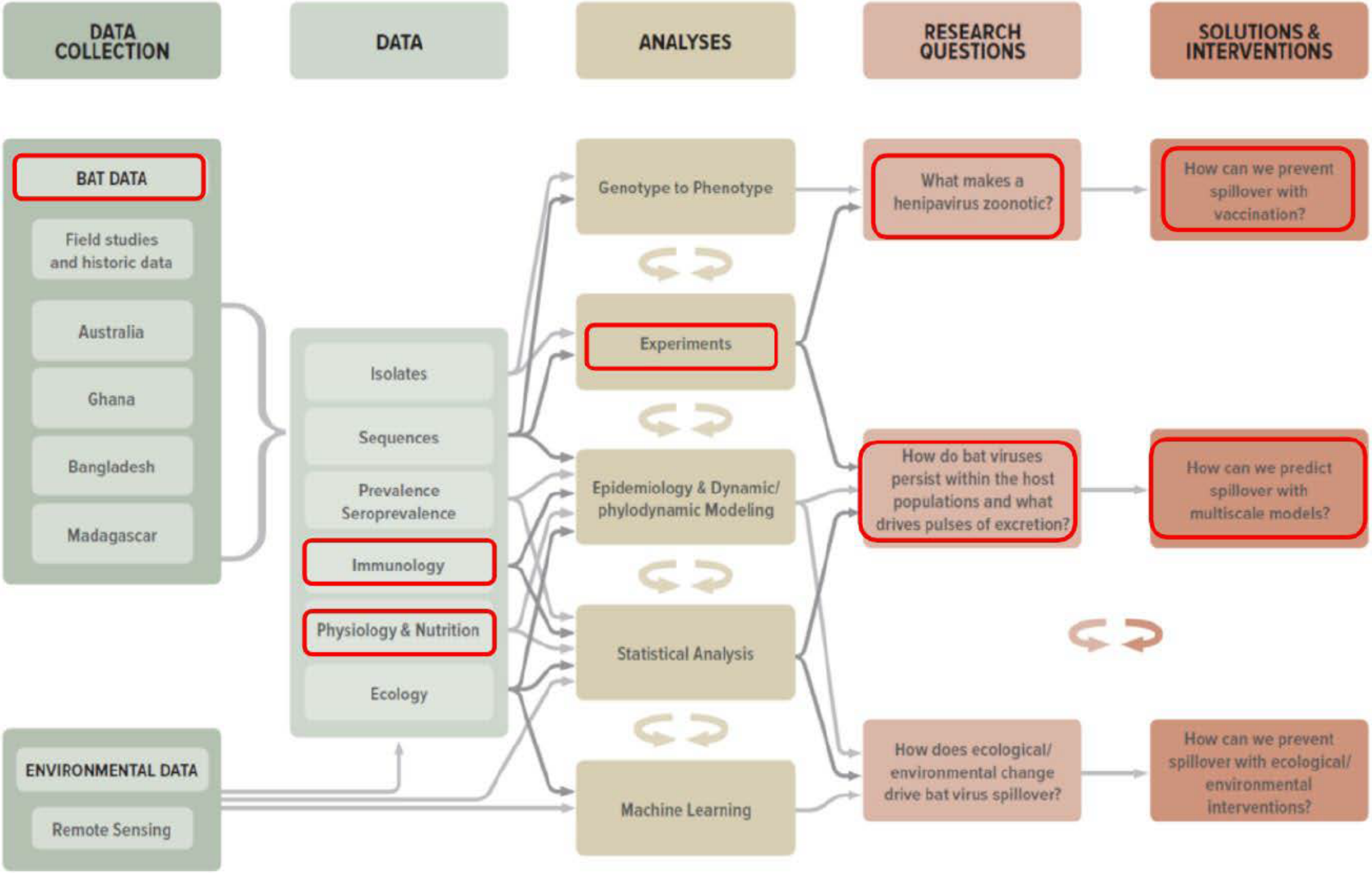
Sara LaTrielle
MSU

Hector Aguilar-Carreno
Cornell University

Agnieszka Rynda-Apple
MSU

Vincent Munster
Rocky Mountain
Laboratories, NIAID

Immunology Role in PREEMPT Project

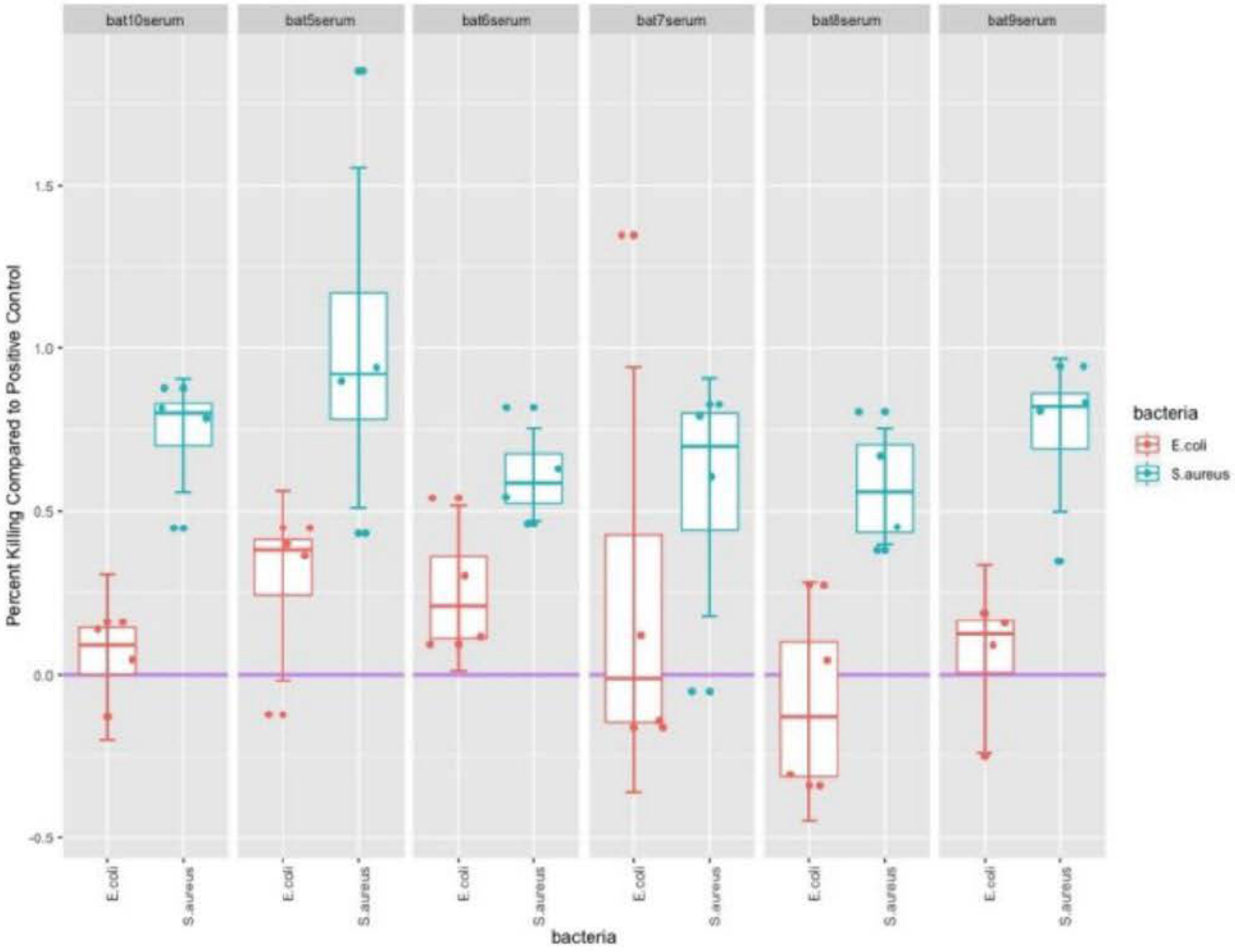


Highlights from the Immunology Component

- Optimized conditions for lab-based assays: BKA and qPCR for bat immunity
- Optimized conditions for sample collections and handling for multiple subprojects
- Determined Immunogenicity of VLPs in hamsters and mice
- Demonstrated susceptibility of Aj bat primary kidney cells to CedV, NiV and HeV
- Showed CedV does not suppress innate response in Aj bat kidney cells whereas NiV and HeV do
- Developed proteomics method for detecting Aj bat cytokines using mass spec
- Demonstrated Cedar virus susceptibility of Jamaican fruit bats

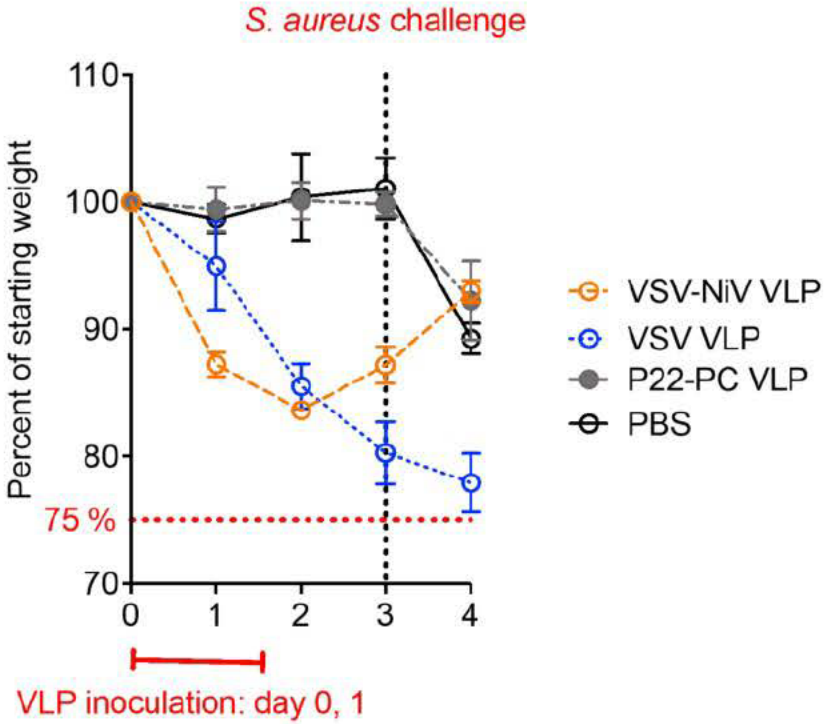
Bactericidal activity of of bat serum

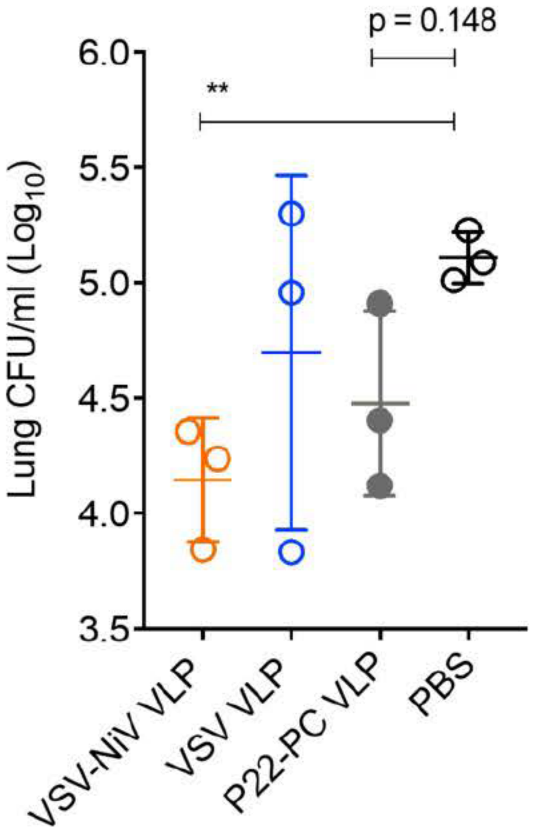
Does bat serum have components that kill bacteria?



Presentation outline

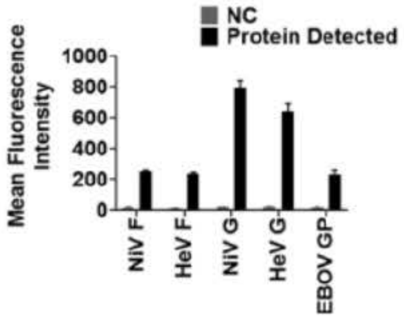
Does stimulation of innate immune responses with Nipah virus VLP enhance pulmonary clearance of *Staphylococcus aureus*?

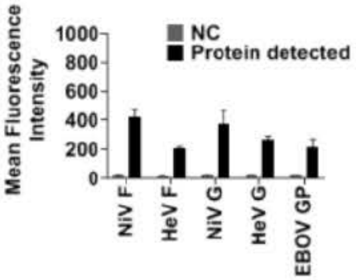


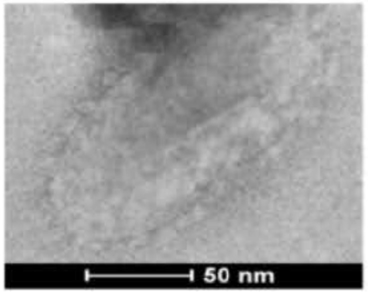


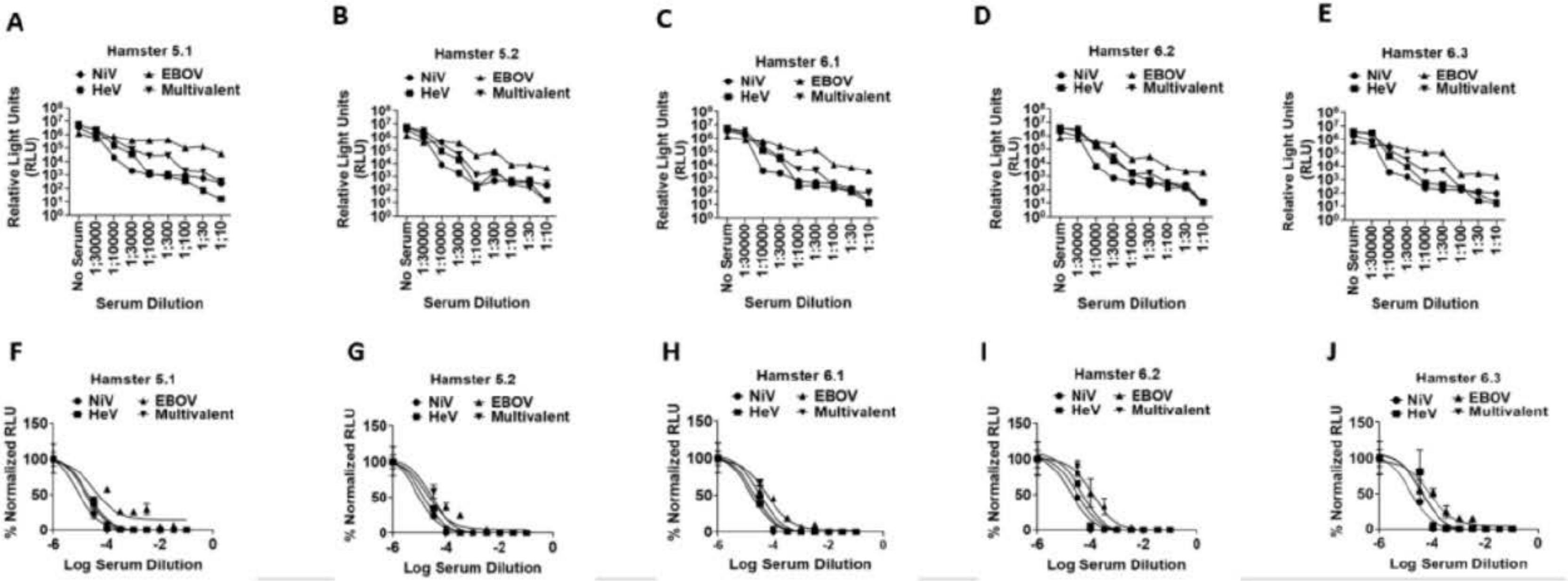
Presentation outline

Does vaccination of hamsters with Nipah virus VLP confer protection?









Demonstrated Susceptibility of Jamaican fruit bats to Cedar Virus

Jamaican fruit bat colony at CSU

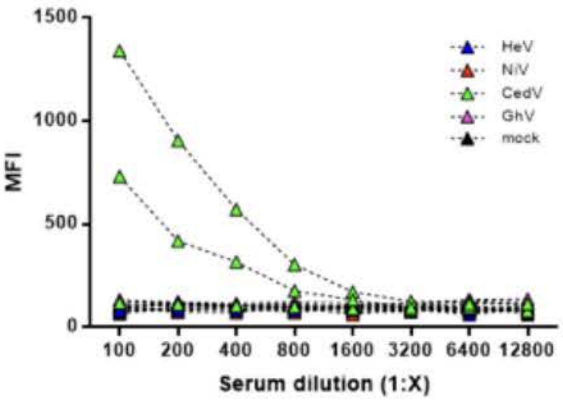
- *Artibeus jamiacensis* (“Aj” bats)
- About 200 bats in the colony

Cedar virus made by Eric Laing (Uniformed Services University)

- BSL-2 in cell culture at CSU
- BSL-3 in animals at CSU
- CedV is missing two genes that that NiV and HeV (and GhV?) use to antagonize a cell’s antiviral system – V and W genes
- It also has different receptor specificities than NiV and CeV

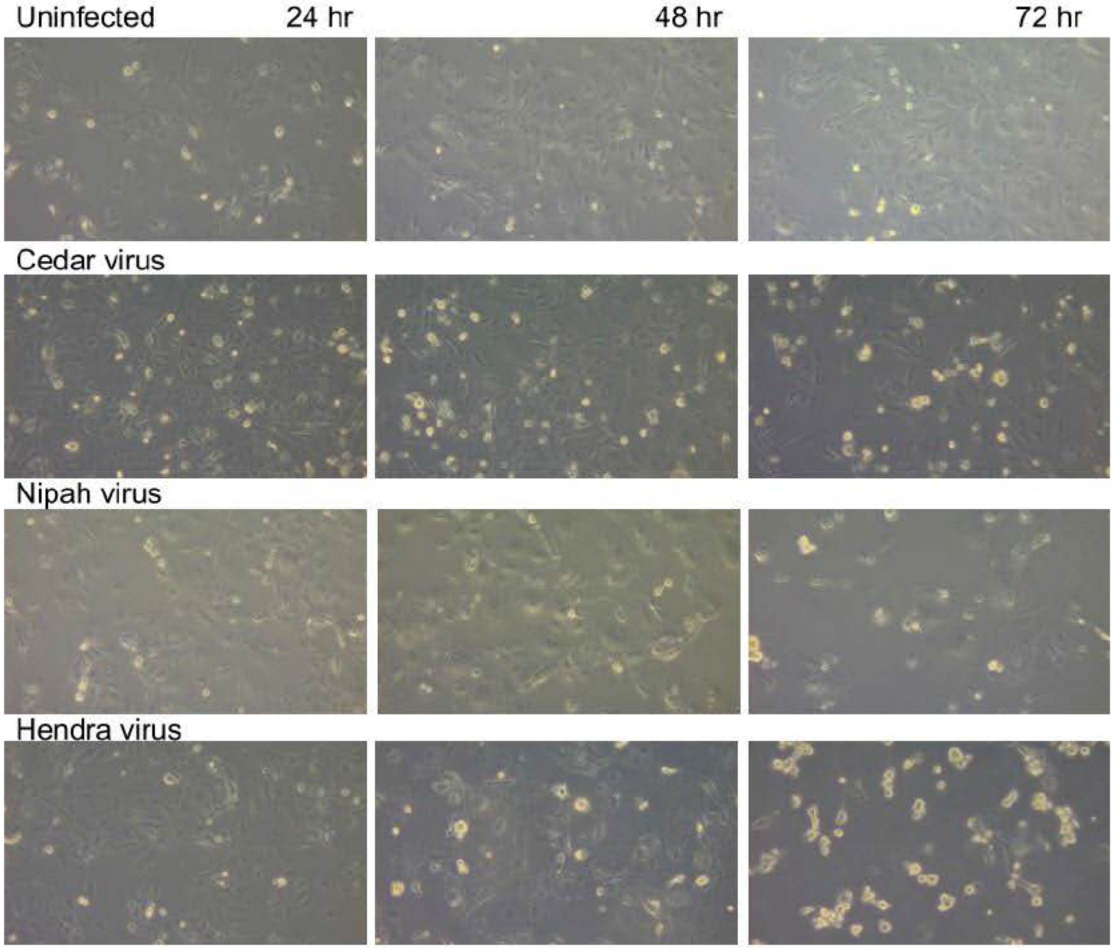
Cedar infection of Aj bats did not cause signs of disease

Bat	Sex	Route	Rectal	Blood
1	F	IN	+	+
2	M	IN	+	-
3	M	IN	+	-
4	F	IP	-	+
5	M	IP	-	+
6	M	IP	-	+



Henipaviruses infect Jamaican fruit bat kidney epithelial cells

Nipah and Hendra viruses induce rapid syncytia formation (48 hr) whereas Cedar virus is slower (72 hr)

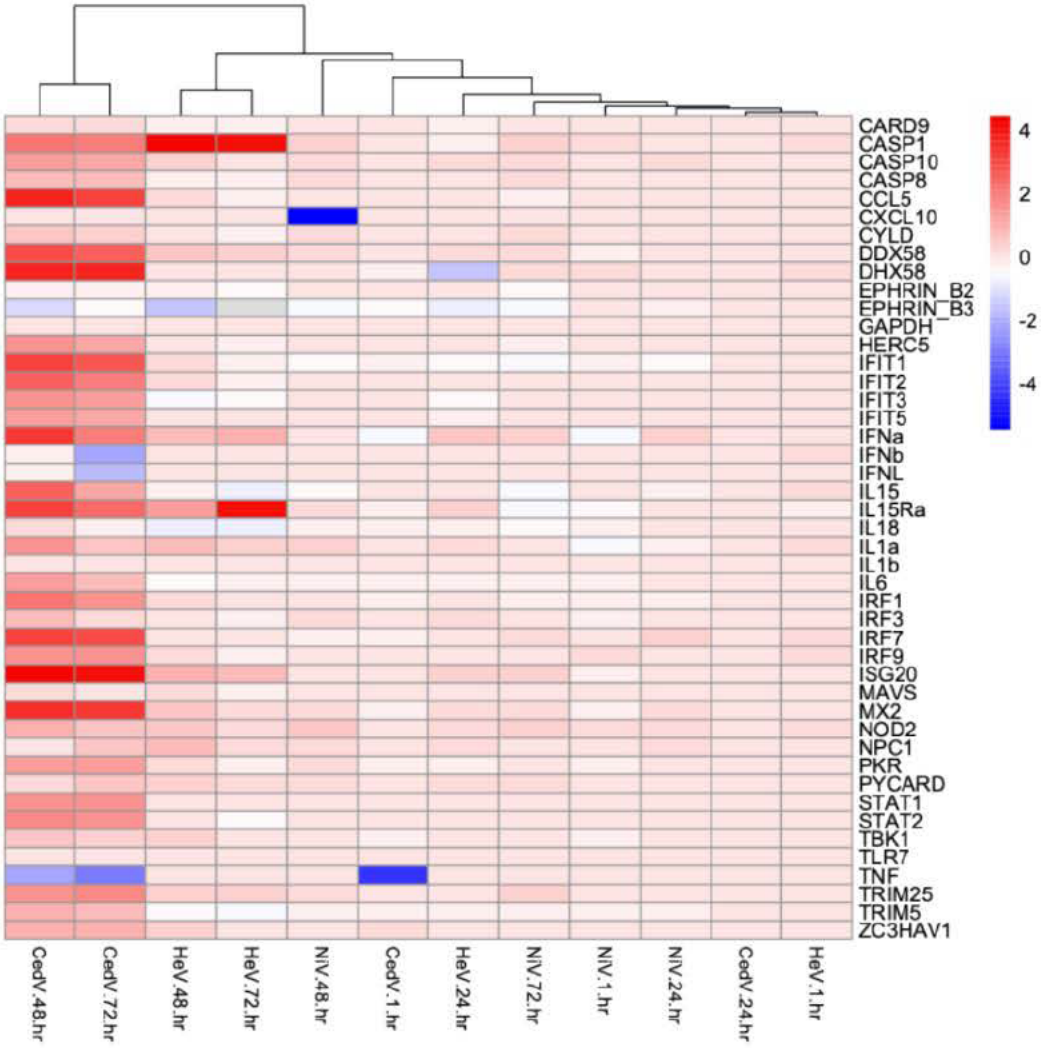


MOI = 0.1

Cells were inoculated with 0.1 MOI for 30 min (media only for uninfected cells), washed once and then cultured with 2% FBS-DMEM for the noted hours.

Henipaviruses infect Jamaican fruit bat kidney epithelial cells

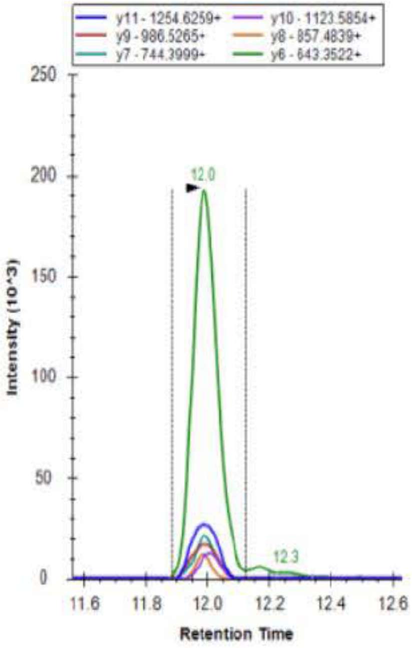
Examination of mRNA expression by qPCR array shows that the bat epithelial cells mount a robust antiviral response to Cedar virus but Nipah or Hendra viruses repress the response



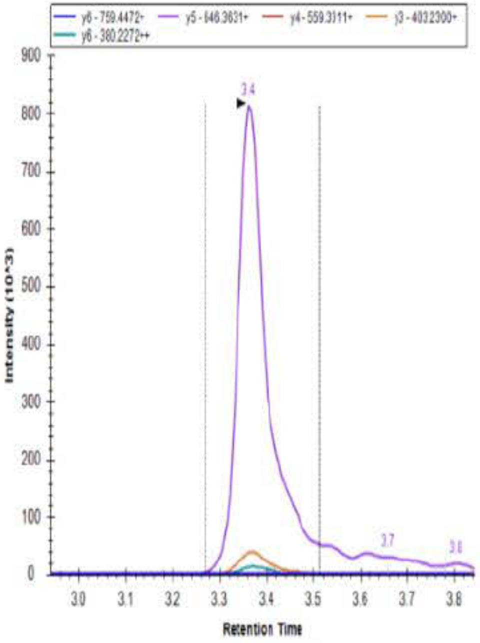
Detection of Aj Cytokines by Mass Spectrometry

Concanavalin A was used to activate spleen cells from an Aj bat
24 hours later, supernatants were collected for MS
Scanned for peptides specific to cytokines

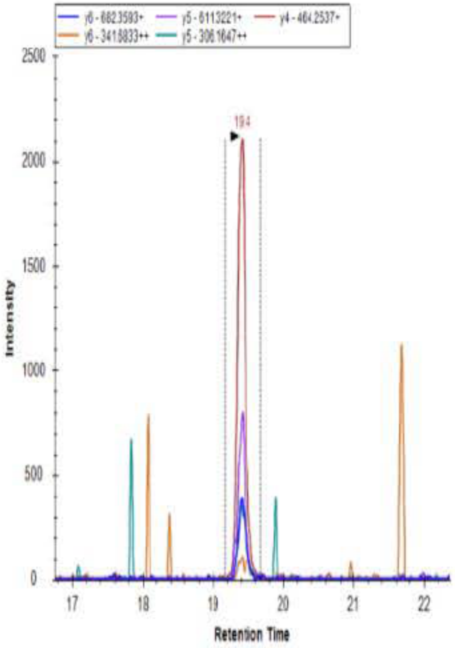
IFNγ



IL-4



IL-10



The Next Year

- What is the role of stress on bat immune responses?
- Experimental protein deprivation in Jamaican fruit bats
    - Challenge with VLPs to assess immune response
        - Will immunity be suppressed compared to non-stressed immune responses?
    - Challenge protein-deprived bats with henipaviruses
        - Does virus shedding increase?
        - Does transmission occur more efficiently?
        - Do VLPs interrupt transmission in stressed bats?

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 28 Feb 2020 08:39:44 -0700
To: Letko, Michael (NIH/NIAID) [F]
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2

Looks good, uploaded it,

I think when there is a bit more clarity and once we have the reviews back we should include more on the recent outbreak.

I think we need to update the intro a bit to incorporate the current outbreak (should be easy), that would sell it better

For now this is good,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Michael Letko <[redacted] (b) (6)
Date: Thursday, February 27, 2020 at 1:42 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2

HI Vincent,

Attached is an updated version of the manuscript. Steph and I made both in-text changes and responded directly to the editor's comments with additional comment boxes, so I have left change-tracking and comments on.

--
Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
[redacted] (b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Tuesday, February 11, 2020 at 8:09 AM
To: "Letko, Michael (NIH/NIAID) [F]" <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: FW: Editorial feedback for manuscript NRMICRO-18-165V2

Lets review, see for some additional panels and return as soon as reasonably possible

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Reply-To: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Date: Tuesday, February 11, 2020 at 5:18 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: Editorial feedback for manuscript NRMICRO-18-165V2

Dear Vincent,

Manuscript number: NRMICRO-18-165V2
Title: Bat-borne viruses: mechanisms of spillover and emergence
Authors: Vincent Munster, Michael Letko, Stephanie Seifert, Kevin Olival, and Raina Plowright
Submission date for revisions: 25th February 2020

Apologies again for the delay in sending you feedback on your article. I've been off sick with viral pneumonia (of all things!) for a good two weeks.

[redacted] (b) (5)

That's it! I hope you find these comments helpful and if you'd like to discuss any of the suggested changes further, please let me know.

I would be grateful if you could return a revised version of the article to me by 25th February 2020.

If at any time you think you will be unable to meet this deadline, please contact me at your earliest convenience to discuss a new date. I know it's an incredible busy time and if you need more time because of the current outbreak, we can arrange an extension.

Please use the following link to upload your revised manuscript:

(b) (6) [redacted]

Thank you very much for all your hard work on this piece so far. Please don't hesitate to contact me if you have any questions or wish to discuss any points in this letter. Finally, I would be very grateful if you could acknowledge receipt of this e-mail and confirm whether you will be able to return your revised draft by the suggested date.

Best wishes,
Ursula

Ursula Hofer, MD PhD
Chief Editor, Nature Reviews Microbiology
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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 28 Feb 2020 08:29:04 -0700
To: Raina Plowright; Letko, Michael (NIH/NIAID) [F]
Subject: Re: CoV proposals moving forward

It's a bit hard to commit to part 1, if there are no funds available for us as this is the most expensive part. If full-genome sequences are generated by the partners then yes, if only positive samples, then no

Organoids, yes, that would fit in my larger program

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <(b) (6)
Date: Thursday, February 27, 2020 at 5:16 PM
To: '(b) (6) <(b) (6) Michael Letko
<(b) (6)
Subject: CoV proposals moving forward

Hi Vincent and Mike,

I'm exploring certain CoV proposals that would build on PREEMPT work and keep the collaboration together and build capacity etc. Wondering if you guys want to be included?

--I'm writing something for screening field samples (based in Australia and Bangladesh). Do you want positive samples to go to RML for phenotypic assessment?
--exploring the bat GIT organoid with folks here who are developing a human GIT organoid on a chip. Only would proceed if you could use organoid for virus work. Its outside my wheelhouse but happy to drive the proposal forward. I'd use it to push some of the immunology. We should chat to the key PIs early next week to decide.

Looking at NIH supplements and a direct connection of MSU to HHS money. Its all incredibly speculative right now.

If you are both overwhelmed and too busy, I'll move forward with in-country testing of samples for CoV. It is a chance to set some screening up in Australia for multiple pathogens and that's desperately needed to relieve pressure on RML.

Raina

Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: (b) (6)
Lab website: http://bzndiseaselab.org
Phone: (b) (6)

From: Letko, Michael (NIH/NIAID) [F]
Sent: Thu, 27 Feb 2020 20:42:09 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Editorial feedback for manuscript NRMICRO-18-165V2
Attachments: 5 NRMICRO-18-165_UH_ML_RP_SNS.docx

HI Vincent,

Attached is an updated version of the manuscript. Steph and I made both in-text changes and responded directly to the editor's comments with additional comment boxes, so I have left change-tracking and comments on.

--
Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
(b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Tuesday, February 11, 2020 at 8:09 AM
To: "Letko, Michael (NIH/NIAID) [F]" <(b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <(b) (6)
Subject: FW: Editorial feedback for manuscript NRMICRO-18-165V2

Lets review, see for some additional panels and return as soon as reasonably possible

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Reply-To: "ursula.hofer1@nature.com" <ursula.hofer1@nature.com>
Date: Tuesday, February 11, 2020 at 5:18 AM
To: '(b) (6) <(b) (6)
Subject: Editorial feedback for manuscript NRMICRO-18-165V2

Dear Vincent,

Manuscript number: NRMICRO-18-165V2
Title: Bat-borne viruses: mechanisms of spillover and emergence
Authors: Vincent Munster, Michael Letko, Stephanie Seifert, Kevin Olival, and Raina Plowright
Submission date for revisions: 25th February 2020

Apologies again for the delay in sending you feedback on your article. I've been off sick with viral pneumonia (of all things!) for a good two weeks.

(b) (5)

That's it! I hope you find these comments helpful and if you'd like to discuss any of the suggested changes further, please let me know.

I would be grateful if you could return a revised version of the article to me by 25th February 2020.

If at any time you think you will be unable to meet this deadline, please contact me at your earliest convenience to discuss a new date. I know it's an incredible busy time and if you need more time because of the current outbreak, we can arrange an extension.

Please use the following link to upload your revised manuscript:

(b) (6)

Thank you very much for all your hard work on this piece so far. Please don't hesitate to contact me if you have any questions or wish to discuss any points in this letter. Finally, I would be very grateful if you could acknowledge receipt of this e-mail and confirm whether you will be able to return your revised draft by the suggested date.

Best wishes,
Ursula

Ursula Hofer, MD PhD
Chief Editor, Nature Reviews Microbiology
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London

N1 9XW
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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 27 Feb 2020 12:59:59 -0700
To: Raina Plowright; Caylee Falvo; Schountz, Tony
Cc: Dan Crowley; Bushmaker, Trenton (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: Re: Question about samples

Hi Raina, it is the other way around, the irradiation should not affect the antibodies. That was initial Dan's question, irradiation will take place on dry ice and no change in antibody titer of activity should take place.

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <[redacted] (b) (6)
Date: Thursday, February 27, 2020 at 10:35 AM
To: '[redacted] (b) (6) <[redacted] (b) (6) Caylee Falvo <[redacted] (b) (6) Tony Schountz <[redacted] (b) (6)
Cc: Dan Crowley <[redacted] (b) (6) Trenton Bushmaker <[redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
Subject: Re: Question about samples

Vincent or Trent,
Can you explain the comment on antibodies? Does the radiation destroy the structure of the antibodies so they can't be used to generate rabbit antibodies to IgG/IgA?
Raina

> **From:** "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
> **Date:** Wednesday, February 26, 2020 at 8:05 AM
> **To:** Caylee Falvo <[redacted] (b) (6) Raina Plowright <[redacted] (b) (6) "Schountz, Tony" <[redacted] (b) (6)
> **Cc:** Dan Crowley <[redacted] (b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]" <[redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
> **Subject:** Re: Question about samples
>
> Hi team,

Just for future refences (again), these samples could have been inactivated or extracted in Australia already. It is a huge commitment from Kwe's and Trent's end to deal with all of these requests while they are doing a massive amount of work getting all the Australian and Bangladesh samples screened because of demands of the program. As a reminder, Kwe is a post-doctoral research and his work is doing research (not just extracting someone else's samples), Trent is a high-end research technician, but NOT paid by the PREEMPT project, and currently he is urgently needed with our coronavirus work.

In addition, I doubt it that Tony will be able to make antibodies from sera (if he can, he'll be a wizard). Sera will need to be irradiated, again we can do this but again a lot of work (involves multiple outside people).

As always, we will get it done, but you guys really need to be a little bit more mindful here. Typically, this is also a stakeholder issue here, if you can include Kwe more directly into this research rather than just asking him to spend his time extracting your samples it would likely speed-up things considerably.

Always open to suggestions,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Caylee Falvo <(b) (6)
Date: Tuesday, February 25, 2020 at 12:55 PM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6)
Cc: Raina Plowright <(b) (6), "(b) (6)
<(b) (6) Dan Crowley <(b) (6) Tony Schountz
<(b) (6)
Subject: Question about samples

Hi Kwe,

I was hoping to request particular samples from the Australian samples that were just sent to RML. Few questions: How long does the RNA extraction take, and is there a certain number that is easiest to do as a batch? **Dan and I want to ensure when we request samples we aren't making it extra difficult for RML.** If we could understand the extraction protocol and inactivation steps that would help. For example, how long does the inactivation (for serum and blood clots) take, and is a certain number easiest to do as a batch?

I can send a list of specific samples, **or** just request an entire box if that is easier for you.

In addition, there are 8 serum samples that we are sending to Tony at CSU to develop antibodies for us. Could those be sent straight to him, or is it easier to send to MSU along with other samples?

Please let me know what you're thinking for a timeline -- I don't have a good sense of how long processing the samples take, and how much time you have at the moment, given the other projects going on.

Feel free to give me a call if that is easier: [redacted] (b) (6)

Thank you,
Caylee

--

Caylee Falvo, MSc
Ph.D. Student | Bozeman Disease Ecology Lab
Department of Microbiology & Immunology
Montana State University

From: Schountz,Tony
Sent: Tue, 25 Feb 2020 23:06:21 +0000
To: Schountz, Tony
Cc: Seifert, Stephanie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]
Subject: Re: artibeus
Attachments: Cyt B Sequences.docx

Looks like they are Ajs.

T.

—

Tony Schountz, PhD
Associate Professor
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[redacted] (b) (6)
[redacted] (b) (6)

On Feb 13, 2020, at 10:31 AM, Schountz,Tony <[redacted] (b) (6) wrote:

Yes, Cytb will be done. (That's what I meant to type in the first place!)

—

Tony Schountz, PhD
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[redacted] (b) (6)

On Feb 13, 2020, at 10:29 AM, Seifert, Stephanie (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Hi Tony,

"I'm certain there are females because at least one had a pup attached to her." Laughing over here; that's a pretty good clue!

Would it be possible for your team to sequence cytb as well?

Glad that everything is working out so far! Hopefully we have space again in BSL4 soon to proceed with the studies.

Best wishes,
Steph

From: "Schountz,Tony" < (b) (6)
Date: Thursday, February 13, 2020 at 10:21 AM
To: "Munster, Vincent (NIH/NIAID) [E]" < (b) (6)
Cc: "Schountz, Tony" < (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" < (b) (6)
Subject: Re: artibeus

I'm certain there are females because at least one had a pup attached to her. I didn't see any carollia's but I didn't go in the room (it's under quarantine). We were told it would take another permit to get them shipped, too.

We got ours from the Denver Zoo. We weren't told where they got them, but I suspect from another zoo.

I have my CDC permit for SARS-CoV-2 and got IBC approval yesterday (attached). Were you planning to ship to Dick or to me?

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
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(b) (6)
(b) (6)

On Feb 13, 2020, at 10:02 AM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Btw, did they send males and females, or juts males? Did they manage to add some carolia?

Where are your Artibeus from originally? I'll email the zoo to see if they have some info where these are from (if they have managed to keep records),

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Thursday, February 13, 2020 at 9:57 AM
To: [redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]"
<[redacted] (b) (6)
Subject: Re: artibeus

Yes, I think we will bleed a few and look at a few genes. Cytochrome C genes for sure. Any others you're aware of? I can scan the artibeus literature to see what markers are used for species-level ID. I know Aj has a large number of subspecies and can hybridize with A. planirostris (producing a fertile hybrid, A. schwartzi).

—

Tony Schountz, PhD
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[redacted] (b) (6)
[redacted] (b) (6)

On Feb 13, 2020, at 9:50 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Maybe sequence them? Just to make sure?

Although there are quite some cryptic species as they all look alike? Maybe literatus?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz < (b) (6)
Date: Thursday, February 13, 2020 at 9:41 AM
To: " (b) (6) < (b) (6)
Cc: Tony Schountz < (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]"
< (b) (6)
Subject: Re: artibeus

Vinnie, your bats seem to be a little bit bigger than ours. I wonder if they might be a different species? Otherwise, only one dead on arrival yesterday and today there do not appear to be any deaths.

T.

—

Tony Schountz, PhD
Associate Professor
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(b) (6)
(b) (6)

On Jan 10, 2020, at 12:49 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Btw, as soon as we have a study date, it might then be a good time for you to come by and do the experiments.

We would have both Steph and Trent in BSL4 to help you (and Kwe), I think its scheduled for early February

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz < (b) (6)
Date: Friday, January 10, 2020 at 9:30 AM
To: " (b) (6) < (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" < (b) (6)
Subject: Re: artibeus

That shouldn't be a problem. I'll get the paperwork started to ship 34 bats to you. We'll try to get a 2:1 M:F ratio for you.

We can do a genotype comparison but if they are really Ajs then the mitochondrial sequences should tell us. Might do a Y-chromosome gene, too, but I'll have to look into that. If they're Ajs, I suspect they are derived from the same source. The zoos tend to share their stocks.

T.

—
Tony Schountz, PhD
Associate Professor
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College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" < [redacted] (b) (6)
Date: Friday, January 10, 2020 at 7:30 AM
To: "Seifert, Stephanie (NIH/NIAID) [E]" < [redacted] (b) (6) "Schountz,Tony" < [redacted] (b) (6)
Subject: Re: artibeus

If possible,

We would like 2 -4 additional bats for fresh tissue samples and protocol development. Also in case smtg might go wrong with some of the animals to make sure we have appropriate groupsizes.

Any idea how we would go about comparing the new Florida Artibeus with your colony? Do we know whether they might have come from the same stock? Pretty important given the cryptic Artibeus species flying around and they all look the same to me.

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Seifert, Stephanie (NIH/NIAID) [E]" < [redacted] (b) (6)
Date: Thursday, January 9, 2020 at 4:41 PM
To: Tony Schountz < [redacted] (b) (6)
Cc: "Haddock, Elaine (NIH/NIAID) [E]" < [redacted] (b) (6) [redacted] (b) (6) < [redacted] (b) (6) Dana Scott < [redacted] (b) (6) "LaCasse, Rachel (NIH/NIAID)

[E]" < (b) (6)
Subject: Re: artibeus

Hi Tony,

If acquiring females will be a problem, particularly with this being a pilot study, then we can work with a 2:1 ratio or even all male. The primary goal with these first studies is to determine whether the bats are susceptible to NiV & HeV.

RMVB is working on the shipment, the latest news is that the problem is in the CSU permit for shipping from Colorado to Montana. I have looped in Dana Scott and Rachel LaCasse who have more information.

Thanks again!

Cheers,
Steph

From: "Schountz,Tony" < (b) (6)
Date: Thursday, January 9, 2020 at 4:29 PM
To: "Seifert, Stephanie (NIH/NIAID) [E]" < (b) (6)
Cc: "Haddock, Elaine (NIH/NIAID) [E]" < (b) (6) "Munster, Vincent (NIH/NIAID) [E]" < (b) (6)
Subject: Re: artibeus

That should be fine. However, it could take us some time to find females that are not pregnant if that is important to you. We can sonogram them but that will miss very early pregnancies. Most of the females that are of reproductive age (>11 months) will be pregnant. We tend to do our studies with a 2:1 M:F ratio because the females are so valuable for sustaining the colony.

Will you be able to arrange shipment?

Let me know how you want to proceed.

T.

—
Tony Schountz, PhD
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(b) (6)
(b) (6)

From: "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Thursday, January 9, 2020 at 3:52 PM
To: "Schountz,Tony" <[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Cc: "Haddock, Elaine (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: Re: artibeus

Hi Tony,

Thank you! I think a 50/50 ratio would be great for this pilot study.

We really appreciate it!

Cheers,
Steph

From: "Schountz,Tony" <[redacted] (b) (6)
Date: Thursday, January 9, 2020 at 1:27 PM
To: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Cc: "Haddock, Elaine (NIH/NIAID) [E]" <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: Re: artibeus

Yes, we sure do. What ratio of M:F would you like?

T.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
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College of Veterinary Medicine
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3185 Rampart Road
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[redacted] (b) (6)
[redacted] (b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Thursday, January 9, 2020 at 10:58 AM
To: "Schountz,Tony" <[redacted] (b) (6)
Cc: "Haddock, Elaine (NIH/NIAID) [E]" <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: artibeus

Hi Tony,

Our arrival of Artibeus to CSU appear to be delayed, would you have 26 – 30 Artibeus bats available for the DARPA Nipah and Hendra infection?

We have the study planned for early February,

Let me know what you think,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

Bat A

TTATTAAAAATTATCAATAGCTCATTCGTAGACCTTCCTGCTCCCTCAAGCCTTTCATCATGATGAAACTTTGGTTCT
CTTTTAGGAGTTTGTTTGGGCGTACAAATTCTAACAGGACTATTCCTAGCTATACATTATACATCCGACACAGCTAC
CGCATTCAACTCTGTCACCCATATCTGTCGAGACGTCAACTATGGATGATTACTTCGATACCTCCATGCCAACGGAG
CCTCTATATTTTTTATCTGCCTCTACCTCCACGTAGGCCGAGGCCTATATTATGGATCCTATACATATTCAGAAACAT
GAAACATTGGCATTCTCCTCCTCTTTGCTGTCATAGCAACAGCATTTATAGGCTATGTCCTACCATGAGGACAAATA
TCATTCTGAGGAGCTACAGTCATCACCAATCTCCTCTCTGCCATCCCCTATATCGGAACAGATTTAGTACAATGAAT
CTGAGGTGGCTTTTCCGTAGACAAAGCAACTCTCACCCGATTCTTCGCCTTCCATTTTCTACTTCCCTTCATTGTAAC
AGCTCTAGTAATAGTCCACCTTTTATTTCTACACGAAACAGGATCTAACAACCCCACAGGCATTCCATCAGACCCAG
ACATAATTCCATTCCACCCCTACTATACTATTAAAGATATTCTAGGATTTTTAGTTATACTTACAGCCCTAGCTACTCT
AGTCTTATTTTCACCAGACCTCCTAGGAGACCCAGACAATTATATTCCAGCAAATCCACTTAATACCCCTCCCCATAT
TAAGCCAGAATGATACTTCCTTTTTGCTTATGCTATTTTACGCTCTATTCCAAACAAACTAGGAGGAGTCCTAGCTCT
AGTAATATCTATCCTAATCCTAGCCATCGTACCAATTCTTCACATATCTAAACAACGAAGTATAATATTTCGCCCTCT
CAGCCAATGCTTATTCTGACTTCTTGTAGCAGTCCTTTTTACATTAACATGAATTGGAGGACAACCAGTAGAGCACC
CCTATATTATTATCGGCCAAACAGCATCCGTCCTATATTTCTTAATTATCCTATTCCTTATACCAATAATTAGCCT

Bat B

CCTGCTCCCTCAAGCCTTTCATCATGATGAAACTTTGGTTCTCTTTTAGGAGTTTGTTTGGGCGTACAAATTCTAACA
GGACTATTCCTAGCTATACATTATACATCCGACACAGCTACCGCATTCAACTCTGTCACCCATATCTGTCGAGACGT
CAACTATGGATGATTACTTCGATACCTCCATGCCAACGGAGCCTCTATATTTTTTATTTGCCTCTACCTCCACGTAGG
CCGAGGCCTATATTATGGATCCTATACATATTCAGAAACATGAAACATTGGCATTCTCCTCCTCTTTGCTGTCATAG
CAACAGCATTTATAGGCTATGTCCTACCATGAGGACAAATATCATTCTGAGGAGCTACAGTCATCACCAATCTCCTC
TCTGCCATCCCCTATATCGGAACAGATTTAGTACAATGAATCTGAGGTGGCTTTTCCGTAGACAAAGCAACTCTCAC
CCGATTCTTCGCCTTCCATTTTCTACTTCCCTTCATTGTAACAGCTCTAGTAATAGTCCACCTTTTATTTCTACACGAA
ACAGGATCTAACAACCCCACAGGCATTCCATCAGACCCAGACATAATTCCATTCCACCCCTACTATACTATTAAAGA
TATTCTAGGATTTTTAGTTATACTTACAGCCCTAGCTACTCTAGTCTTATTTTCACCAGACCTCCTAGGAGACCCAGA
CAATTATATTCCAGCAAATCCACTTAATACCCCTCCCCATATTAAGCCAGAATGATACTTCCTTTTTGCTTATGCTATT
TTACGCTCTATTCCAAACAAACTAGGAGGAGTCCTAGCTCTAGTAATATCTATCCTAATCCTAGCCATCGTACCAAT
TCTTCACATATCTAAACAACGAAGTATAATATTTCGCCCTCTCAGCCAATGCTTATTCTGACTTCTTGTAGCAGTCCT
TTTTACATTAACATGAATTGGAGGACAACCAGTAGAGCACCCCTATATTATTATCGGCCAAACAGCATCCGTCCTAT
ATTTCTTAATTATCCTATTCCTTATACCA

Bat C

TTATTAAAAATTATCAATAGCTCATTCGTAGACCTTCCTGCTCCCTCAAGCCTTTCATCATGATGAAACTTTGGTTCT
CTTTTAGGAGTTTGTTTGGGCGTACAAATTCTAACAGGACTATTCCTAGCTATACATTATACATCCGACACAGCTAC
CGCATTCAACTCTGTCACCCATATCTGTCGAGACGTCAACTATGGATGATTACTTCGATACCTCCATGCCAACGGAG
CCTCTATATTTTTTATTTGCCTCTACCTCCACGTAGGCCGAGGCCTATATTATGGATCCTATACATATTCAGAAACAT
GAAACATTGGCATTCTCCTCCTCTTTGCTGTCATAGCAACAGCATTTATAGGCTATGTCCTACCATGAGGACAAATA
TCATTCTGAGGAGCTACAGTCATCACCAATCTCCTCTCTGCCATCCCCTATATCGGAACAGATTTAGTACAATGAAT
CTGAGGTGGCTTTTCCGTAGACAAAGCAACTCTCACCCGATTCTTCGCCTTCCATTTTCTACTTCCCTTCATTGTAAC

AGCTCTAGTAATAGTCCACCTTTTATTTCTACACGAAACAGGATCTAACAACCCCACAGGCATTCCATCAGACCCAG
ACATAATTCCATTCCACCCCTACTATACTATTAAAGATATTCTAGGATTTTTAGTTATACTTACAGCCCTAGCTACTCT
AGTCTTATTTTCACCAGACCTCCTAGGAGACCCAGACAATTATATTCCAGCAAATCCACTTAATACCCCTCCCCATAT
TAAGCCAGAATGATACTTCCTTTTTGCTTATGCTATTTTACGCTCTATTCCAAACAAACTAGGAGGAGTCCTAGCTCT
AGTAATATCTATCCTAATCCTAGCCATCGTACCAATTCTTCACATATCTAAACAACGAAGTATAATATTTCGCCCTCT
CAGCCAATGCTTATTCTGACTTCTTGTAGCAGTCCTTTTTACATTAACATGAATTGGAGGACAACCAGTAGAGCACC
CCTATATTATTATCGGCCAAACAGCATCCGTCCTATATTTCTTAATTATCCTATTCCTTATACCAATAATTAGCCT

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 25 Feb 2020 13:49:18 -0700
To: Caylee Falvo; Kwe Claude, Yinda (NIH/NIAID) [F]
Cc: Raina Plowright; Dan Crowley; Schountz, Tony
Subject: Re: Question about samples

Hi Caylee,

Please address specific questions regarding sample inactivation to Trent as he is our poc for this. Kwe can help with the inventory, be he is not our POC

Thanks,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Caylee Falvo <[redacted] (b) (6)
Date: Tuesday, February 25, 2020 at 12:55 PM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
Cc: Raina Plowright <[redacted] (b) (6) "[redacted] (b) (6)
<[redacted] (b) (6) Dan Crowley <[redacted] (b) (6) Tony Schountz
<[redacted] (b) (6)
Subject: Question about samples

Hi Kwe,

I was hoping to request particular samples from the Australian samples that were just sent to RML. Few questions: How long does the RNA extraction take, and is there a certain number that is easiest to do as a batch? **Dan and I want to ensure when we request samples we aren't making it extra difficult for RML**. If we could understand the extraction protocol and inactivation steps that would help. For example, how long does the inactivation (for serum and blood clots) take, and is a certain number easiest to do as a batch?

I can send a list of specific samples, **or** just request an entire box if that is easier for you.

In addition, there are 8 serum samples that we are sending to Tony at CSU to develop antibodies for us. Could those be sent straight to him, or is it easier to send to MSU along with other samples?

Please let me know what you're thinking for a timeline -- I don't have a good sense of how long processing the samples take, and how much time you have at the moment, given the other projects going on.

Feel free to give me a call if that is easier: [redacted] (b) (6)

Thank you,
Caylee

--

Caylee Falvo, MSc
Ph.D. Student | Bozeman Disease Ecology Lab
Department of Microbiology & Immunology
Montana State University

From: Plowright, Raina
Sent: Tue, 25 Feb 2020 19:39:28 +0000
To: (b) (6)
Cc: LaTrielle, Sara; Emily Gurley; Peter Hudson; Munster, Vincent (NIH/NIAID) [E]; (b) (6); (b) (6)
Subject: Re: site visit- same dates in July

Excellent! I have told our team to hold the dates. We will book a room.
I suggest booking a downtown hotel ASAP as the central hotels book out very quickly (otherwise you will be stuck out near the airport).
The Lark or The Element hotels are best.
If you can stay an extra day, we would be happy to take you to Yellowstone National Park. Our research group includes collaborators who work on diseases in wolves and bison and elk.
Raina

> On Feb 25, 2020, at 12:35 PM, (b) (6) wrote:
>
> Dear Raina,
>
> Good to know re the logistics. But looking forward and sounds great! It will be myself and (b) (6), and maybe (b) (6) as well.
>
> Best,
> (b) (6)
>
> -----Original Message-----
> From: Plowright, Raina <(b) (6)
> Sent: Tuesday, February 25, 2020 2:33 PM
> To: (b) (6)
> Cc: LaTrielle, Sara <(b) (6) Emily Gurley <(b) (6) Peter Hudson <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
> Subject: Re: site visit- same dates in July
>
> Hi (b) (6)
> Those dates are blocked out for our meeting so this works for me.
> It is a 4 hour drive to RML from here. You should fly in to Bozeman and out of Missoula.
> It will be great to have you in Montana!
> Raina
>
>> On Feb 25, 2020, at 12:27 PM, (b) (6) wrote:
>>
>> Hi Raina,
>>
>> As you know we had originally planned for our PI Review meeting on July 6-7 with a follow-on visit to RML on July 8. As you had blocked out those dates, are you still game for us to do a site visit on Tues July 7 to MSU, and with a follow-on at RML on Wed July 8? I have to be in the office on Monday July 6, else I would suggest we keep the original dates altogether. ;-)
>>
>> Thanks much,
>> (b) (6)
>

From: Schountz,Tony
Sent: Fri, 21 Feb 2020 15:52:01 +0000
To: Port, Julia (NIH/NIAID) [F]
Cc: Seifert, Stephanie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Rynda-Apple, Agnieszka; Hector Aguilar
Subject: Re: New post-doc at RML

Hi Julia, welcome aboard.

We have an Immunology Zoom call on the fourth Monday of each moth at 2:00 PM MST for the PREEMPT group. You're welcome to join if you like. We each provide a brief update on projects and it gives us an opportunity to exchange ideas as the project evolves.

https://zoom.us/j/ (b) (6)

Thanks,

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Feb 20, 2020, at 4:46 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Hi team,

I would like to introduce Dr. Julia Port, who is the newest addition to the team. She has a background in cellular immunology of high containment pathogens (in particular Lassa virus) and will start working on bat immunology as part of PREEMPT,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 21 Feb 2020 08:41:41 -0700
To: Schountz, Tony
Subject: Re: Bat ID symposium

Sounds good, good luck

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, February 21, 2020 at 8:07 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Bat ID symposium

Well do both at the same time. Just 3 bats for initial susceptibility testing and to work out the qPCR. The big study will be with the stock that we make.

Sent from my iPhone

On Feb 21, 2020, at 7:46 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

You're not growing a stock frst?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Thursday, February 20, 2020 at 5:10 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Bat ID symposium

Thanks Vinnie, I appreciate your support.

We got the virus from BEI today. I never heard back from Les so I'll send him an email and cc you on it letting him know he doesn't need to ship it to us. We'll put it in a few bats on Monday. I'll keep you posted.

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 20, 2020 4:54 PM
To: Schountz,Tony <(b) (6)
Subject: Re: Bat ID symposium

More than happy to do a talk!

Just waive the fee, can pay for the lodging (or you can find a sundowner with that)

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 2/20/20, 9:46 AM, "Schountz,Tony" <(b) (6) wrote:

Hi Vinnie, just following up on this email. I now realize I have 3 different email addresses for you, so hopefully one of these will get through!

We have peripheral blood DNA extracted from a few of the bats and will get the sequencing back next week.

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine

Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

> On Feb 11, 2020, at 4:46 PM, Schountz,Tony <(b) (6) wrote:
>
> Hi Vinnie,
>
> I have been awarded some money to subsidize the bat meeting. If you can give a talk, I can waive your registration fee and cover three nights of lodging.
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
> 3185 Rampart Road
> Fort Collins, CO 80523-1692
> (b) (6)
> (b) (6)
>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 21 Feb 2020 07:45:53 -0700
To: Schountz, Tony; Shupert, W. Lesley (NIH/NIAID) [E]
Subject: Re: artibeus

Thanks Tony

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Thursday, February 20, 2020 at 5:11 PM
To: "Shupert, W. Lesley (NIH/NIAID) [E]" <[redacted] (b) (6)
Cc: '[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: artibeus

Hi Les,

We received the virus from BEI today so no need to ship it to us.

Thanks,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
(b) (6)

From: Schountz,Tony <[redacted] (b) (6)
Sent: Thursday, February 13, 2020 12:15 PM
To: Shupert, W. Lesley (NIH/NIAID) [E] <[redacted] (b) (6)
Cc: Schountz,Tony <[redacted] (b) (6) Bennett,Susi <[redacted] (b) (6)
Subject: Re: artibeus

Hi Les,

Susi Bennett is our designated recipient for viruses. Here's the shipping information:

Susi Bennett
200 West Lake Street
1692 Campus Delivery
Colorado State University
Fort Collins, CO 80523-1692
[redacted] (b) (6)

My FedEx account number is [redacted] (b) (6). I've attached my CDC Import Permit and IBC approval in case you need them. Let me know what else you need and I will provide it.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Feb 13, 2020, at 10:27 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Hi Les,

Dr Schountz from CSU has a request for the novel coronavirus.

Can you arrange the necessary paperwork and shipping from RML to CSU,

Kind regards,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 20 Feb 2020 16:59:21 -0700
To: Julia Port; Seifert, Stephanie (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]; Avanzato, Victoria (NIH/NIAID) [F]; Purushotham, Jyothi (NIH/NIAID) [F]; van Doremalen, Neeltje (NIH/NIAID) [E]; Matson, Jeremiah (NIH/NIAID) [F]; Letko, Michael (NIH/NIAID) [F]; De wit, Emmie (NIH/NIAID) [E]; Bushmaker, Trenton (NIH/NIAID) [E]; Fischer, Robert (NIH/NIAID) [F]; Rosenke, Kyle (NIH/NIAID) [F]
Cc: Schountz, Tony
Subject: FW: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

This meeting is scheduled straight after ASV, in Fort Collins

However, if you would like to go you have to write an abstract and present (poster/oral). To reduce costs and environmental impact, car travel / NIH-van would be the preferred travel method.

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <(b) (6)
Date: Wednesday, February 19, 2020 at 4:10 PM
To: Tony Schountz <(b) (6)
Subject: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting **This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Nov 14, 2019, at 10:52 AM, Schountz,Tony <[redacted] (b) (6) wrote:

Dear colleagues,

I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.

We are currently finalizing details of the symposium but I wanted to send this email so that you can add the dates to your calendar if you are interested in attending. The American Society for Virology Annual Conference will also be hosted at CSU in 2020 and it ends on Wednesday, June 17 at noon. Thus, the Bat ID Symposium will follow with a reception on the evening of June 17th and two days of talks and posters on the 18th and 19th. As with previous meetings, we will end each day with an open discussion about bats and their infectious agents.

Should you have questions, please do not hesitate to contact me.

We look forward to hosting you next summer.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 14 Feb 2020 12:27:07 -0700
To: Raina Plowright
Cc: Emily Gurley; Jamie Lloyd-Smith; Alison Peel; Barbara Han; Colin Parrish; Hamish McCallum; Hector Aguilar-Carreno; LaTrielle, Sara; Letko, Michael (NIH/NIAID) [F]; Olivier Restif; Peter Hudson; Schountz, Tony
Subject: Re: CoV proposal for DARPA

Nope, so not of interest for me

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <(b) (6)
Date: Friday, February 14, 2020 at 12:12 PM
To: '(b) (6) <(b) (6)
Cc: Emily Gurley <(b) (6) Jamie Lloyd-Smith <(b) (6) Alison Peel <(b) (6) Barbara Han <(b) (6) Collin Parrish <(b) (6) Hamish McCallum <(b) (6) Hector Aguilar-Carreno <(b) (6) "LaTrielle, Sara" <(b) (6) Michael Letko <(b) (6) Olivier Restif <(b) (6) Peter Hudson <(b) (6) Tony Schountz <(b) (6)
Subject: Re: CoV proposal for DARPA

Can you take $$ from NIH? I assume not. So we would have to focus on the bats/spillover and not the host range?
Our department is well-funded by NIH and we could piggy back onto some existing grants on mammalian viruses. I'm working some channels and will see what we can do.

On Feb 14, 2020, at 12:08 PM, Munster, Vincent (NIH/NIAID) [E] (b) (6) wrote:

Of note,

The supplements can also be off scope, so not directly in line with the grant you hold

Obviously, not for me

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories

From: Emily Gurley [redacted] (b) (6)
Date: Friday, February 14, 2020 at 12:02 PM
To: Raina Plowright < [redacted] (b) (6) Jamie Lloyd-Smith < [redacted] (b) (6)
Cc: Alison Peel < [redacted] (b) (6) Barbara Han [redacted] (b) (6) Collin Parrish < [redacted] (b) (6) Hector Aguilar-Carreno < [redacted] (b) (6) "LaTrielle, Sara" < [redacted] (b) (6) Michael Letko < [redacted] (b) (6) " [redacted] (b) (6) < [redacted] (b) (6) Olivier Restif < [redacted] (b) (6) Peter Hudson < [redacted] (b) (6) Tony Schountz < [redacted] (b) (6)
Subject: RE: CoV proposal for DARPA

Sorry, I can't help with NIH add-ons, sadly.

I would guess that many USG funding streams are holding off on making funding decisions until they see how the proposed budget cuts shake out. We submitted a short proposal from Bangladesh for some human sample testing as an add-on to another NIH funded project, but they haven't decided if there will be any funds for that yet either.

I recently introduced my contact from the USAID One Health office to [redacted] (b) (6) at his request, so that they could talk shared funding strategies. I could reach out to USAID and gauge what they're thinking in terms of funding for COVID-19.

Emily

From: Raina Plowright < [redacted] (b) (6)
Sent: Friday, February 14, 2020 1:14 PM
To: Jamie Lloyd-Smith < [redacted] (b) (6)
Cc: Alison Peel < [redacted] (b) (6) Barbara Han < [redacted] (b) (6) Colin Parrish < [redacted] (b) (6) Emily Gurley [redacted] (b) (6) Hamish McCallum < [redacted] (b) (6) Hector Aguilar-Carreno < [redacted] (b) (6) LaTrielle, Sara < [redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6) Olivier Restif < [redacted] (b) (6) Peter Hudson < [redacted] (b) (6) Schountz, Tony < [redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

We can address these research objectives in their call:

- Studies on the evolution and emergence of 2019-nCoV viruses including the identification of factors that affect viral host-range and virulence;
- Virologic and serologic surveillance studies of the distribution and natural history of 2019-nCoV viruses in animal populations and in humans at the human/animal interface with particular emphasis on host reservoirs and understanding cross-species transmission events;

It says: intended to provide funds for NIH grantees applying to expand the scope of their active grant.

Anyone have an active NIH grant for which expansion to CoV sounds sensible? Colin/Hector/Emily/Tony?

Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: (b) (6)
Lab website: http://bzndiseaselab.org
Phone: (b) (6)

On Feb 14, 2020, at 10:51 AM, Jamie Lloyd-Smith <(b) (6) wrote:

Hi all,

There is this:
https://grants.nih.gov/grants/guide/notice-files/NOT-AI-20-030.html

I don't fully understand the criterion for competitive revisions, but it seems like this is a mechanism to quickly request funds for COVID-related work, attaching to existing grants on topics that are close but not CoV-related. Maybe also an opportunity to attach to recent unfunded proposals? Haven't read all the fine print since I have neither. But if some member of the team does, then this might provide a path.

Colin or Hector, you're our extramural NIAID gurus - any insights?

Jamie

On Fri, Feb 14, 2020 at 9:35 AM Raina Plowright <(b) (6) wrote:
Well, team, what a shame—for those not cc'd on (b) (6) email, DARPA do not have funds for this right now. We are asking for so little to do so much. Given CDC director's quotes today here, and calls for action like this, I think we are on the right track and should keep pursuing opportunities. It sounds like (b) (6)s still trying to support us so we shouldn't give up home on DARPA funds.

Re: the other people cc'd on there... Tony was kind to alert me and try to get me into the middle of that conversation but they had their own channels. The (b) (6), used to be director of the biotech office at DARPA and he was trying to get one of their proposals funded (a CoV proposal from (b) (6) not funded in the original round of PREEMPT). I did not receive any correspondence from (b) (6) great efforts to facilitate that (b) (6) also didn't mention this merging of proposals until the email we received last night. It sounds like (b) (6) has some complimentary ideas but if he wants to collaborate with us, he must reach out to us directly.

Does anyone have ideas for other avenues of funding? We could put in a comprehensive proposal that addresses CoV from bats to bat populations to people and ask for a few million dollars. that is peanuts compared to escalating cost of the outbreak.

Raina

Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: (b) (6)
Lab website: http://bzndiseaselab.org
Phone: (b) (6)

On Feb 12, 2020, at 10:23 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Nice write-up on Michael's work, should be out in Nature microbiology soon

https://www.wired.com/story/can-a-database-of-animal-viruses-help-predict-the-next-pandemic/

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Collin Parrish <(b) (6)
Date: Wednesday, February 12, 2020 at 6:55 AM
To: "(b) (6) <(b) (6) Raina Plowright <(b) (6) Emily Gurley (b) (6) "LaTrielle, Sara" <(b) (6) Olivier Restif <(b) (6) Alison Peel (b) (6)
Cc: Barbara Han <(b) (6) Hamish McCallum <(b) (6) Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6) Michael Letko <(b) (6) "Peter J. Hudson" <(b) (6) Tony Schountz <(b) (6)
Subject: Re: CoV proposal for DARPA

Yes agree with Vincent (and others) on this - they have been pushing their global modeling and hotspot prediction for years, and some of it is useful and much is not, along with the random sequencing of everything and the bat-centric view of global reservoirs.

No real benefit in just pushing back on them, but doing a good and more thoughtful and reality-based job based on this team's expertise and data is good - better science stands the test of time and makes the impact in the end...

Can certainly

Colin R. Parrish
John M. Olin Professor of Virology
College of Veterinary Medicine
Cornell University
Ithaca, NY 14853, USA
Phone: (b) (6) (cell anywhere); (b) (6)0 (work); Skype: colinparrish

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From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, February 11, 2020 10:46 PM
To: Raina Plowright <(b) (6) Colin Ross Parrish <(b) (6) Emily Gurley <(b) (6) LaTrielle, Sara <(b) (6) Olivier Restif <(b) (6) Alison Peel <(b) (6)
Cc: Barbara Han <(b) (6) Hamish McCallum <(b) (6) Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6) Letko, Michael (NIH/NIAID) [F] <(b) (6) Peter J. Hudson <(b) (6) Schountz, Tony <(b) (6)
Subject: Re: CoV proposal for DARPA

I actually there should be way more nuance in the story as realistically those viruses are not everywhere. They typically are a very small subset of viruses with baseline zoonotic or pathogenic potential. Claiming that these viruses are everywhere (or that every host/bat is similar) is just not correct and completely misses the point. In addition, the often claimed line that there is direct global health benefit from this work should be approached very carefully, as a taxpayer I should be quite upset about the tens of millions of USAID dollars fed into Chinese bat work on the premise of preventing spillover, and then realizing that nothing what was claimed was actually achieved (similar with Ebola, or with Nipah viru)s. Complex problems just don't have easy solutions, but hopefully good quality data will help us understand the patterns and drivers and may eventually help us to prepare better. This should be one of our main obligations to the people we train, that even though there appear to be a lot of talking heads with datafree statements, quality data is what should drive us rather than trying to be a fact free voice.

From the basic medical science work it similar to claiming that the pathway you discovered might eventually aid countermeasures (it typically never does) or that you vaccine is the best ever (unless you have a public-private partnership nobody is magically going to get your vaccines through clinical pipelines and the scientific world is filled with shelfed "experimental" vaccines).

Just my five (happily) cynic cents,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology

Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <[redacted] (b) (6)
Date: Tuesday, February 11, 2020 at 4:43 PM
To: Collin Parrish <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) "LaTrielle, Sara" <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Michael Letko <[redacted] (b) (6)
"[redacted] (b) (6) <[redacted] (b) (6) "Peter J. Hudson" <[redacted] (b) (6)
Tony Schountz <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Great idea Emily. We can help/support you.

Colin, yes, we should be more strategic. I'm always put off by the EcoHealth/WCS type opportunism/handwaving/storytelling (very active right now) and want to be the antithesis of that, but a well-reasoned opinion by our team would be valuable right now. The story is that these viruses are everywhere and it is our interaction with bats and the pressures we place on their populations that will determine if we continue to see new spillovers.

I have an opinion written about this that is designed to be submitted with Peggy's paper – without her paper, the mechanisms driving spillover are not substantiated...and we are hoping to get her paper into Science so I don't want to destroy those chances. But maybe this is about timing and a more general message. I'll read through it and think about it.

From: Colin Ross Parrish <[redacted] (b) (6)
Date: Tuesday, February 11, 2020 at 2:57 PM
To: Emily Gurley <[redacted] (b) (6) Raina Plowright <[redacted] (b) (6)
"LaTrielle, Sara" <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6)
Alison Peel <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) "Letko, Michael (NIH/NIAID) [F]" <[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6) "Peter J. Hudson" <[redacted] (b) (6) "Schountz, Tony" <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

If any of us have information that is directly relevant to the coronavirus story (disease ecology, spillover, evolution to host adaptation, etc.) this would be a good time - it seems that right now there are a lot of people making stuff up as they go along, and having more solidly supported information out there can only be useful.

The Royal Society volume is now open-access, and some of those papers are relevant and can be promoted.

Colin

Colin R. Parrish
John M. Olin Professor of Virology
College of Veterinary Medicine
Cornell University
Ithaca, NY 14853, USA
Phone: [redacted] (b) (6) (cell anywhere); [redacted] (b) (6) (work); Skype: colinparrish

---

From: Emily Gurley [redacted] (b) (6)
Sent: Tuesday, February 11, 2020 4:37 PM
To: Raina Plowright < [redacted] (b) (6) LaTrielle, Sara < [redacted] (b) (6) Olivier Restif < [redacted] (b) (6) Alison Peel < [redacted] (b) (6)
Cc: Barbara Han < [redacted] (b) (6) Colin Ross Parrish < [redacted] (b) (6) Hamish McCallum < [redacted] (b) (6) Hector Aguilar-Carreno < [redacted] (b) (6) >; Jamie Lloyd-Smith < [redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6) Peter J. Hudson < [redacted] (b) (6) Schountz, Tony < [redacted] (b) (6)
Subject: RE: CoV proposal for DARPA

I've been thinking about a short letter to the editor, editorial article pitching One Health as the ultimate public health tool for primary prevention of emerging zoonotic infections. The pitch is to the public health community, so was thinking about submitting to American Journal of Epidemiology, or something similar. Thoughts?

From: Raina Plowright < [redacted] (b) (6)
Sent: Tuesday, February 11, 2020 3:57 PM
To: LaTrielle, Sara < [redacted] (b) (6) Olivier Restif < [redacted] (b) (6) Alison Peel < [redacted] (b) (6)
Cc: Barbara Han < [redacted] (b) (6) Colin Parrish < [redacted] (b) (6) Emily Gurley [redacted] (b) (6) Hamish McCallum < [redacted] (b) (6) Hector Aguilar-Carreno < [redacted] (b) (6) Jamie Lloyd-Smith < [redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] < [redacted] (b) (6) Peter J. Hudson < [redacted] (b) (6) Schountz, Tony < [redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Right Sara!!! Its exactly what our group is doing but I don't feel we can broadcast it until Peggy's work is published.... I have a perspective piece on this written but it doesn't make sense without

Peggy's ecology papers out and that is still months away I think. Perhaps others have ideas of how we could promote these concepts from a place of solid scientific standing before the science is published.

From: "LaTrielle, Sara" <[redacted] (b) (6)
Date: Tuesday, February 11, 2020 at 12:54 PM
To: Raina Plowright <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6)
Alison Peel <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Colin Parrish <[redacted] (b) (6)
Emily Gurley <[redacted] (b) (6) Hamish McCallum
<[redacted] (b) (6) Hector Aguilar-Carreno
<[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) "Letko,
Michael (NIH/NIAID) [F]" <[redacted] (b) (6) "Munster, Vincent
(NIH/NIAID) [E]" <[redacted] (b) (6) "Peter J. Hudson"
<[redacted] (b) (6) "Schountz, Tony" <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Thanks Ali.

I especially enjoyed this in the conclusion, "it seems a proper time for the scientific community studying "bat-associated" viruses to move the conversation from bat spillover risk assessments to the planning of pro-biodiversity and subsequently pro-ecosystem strategies aiming to mitigate spillover risk."...

Yep! Just one of many aspects our team is working on... thanks to years+ to Peggy/team for advocating/educating in just this area... with more work to follow of course.

And nice to see TS's paper cited- and surely others I missed.

Sara

Get Outlook for iOS

From: Raina Plowright <[redacted] (b) (6)
Sent: Tuesday, February 11, 2020 11:57:27 AM
To: Olivier Restif <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Colin Parrish <[redacted] (b) (6) Emily
Gurley <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6)
Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith
<[redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6)
Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) Peter J. Hudson
<[redacted] (b) (6) LaTrielle, Sara <[redacted] (b) (6) Schountz, Tony
<[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Good to see something coming out of PREDICT that is addresses dynamics (although looks like they combine many cross sectional sampling events to make inferences on temporal dynamics—such a typical epidemiologist approach!). Amazing that there are no spatiotemporal studies of CoVs in bats and only a handful of temporal studies. Thanks for forwarding Ali.

From: Olivier Restif < (b) (6)
Date: Tuesday, February 11, 2020 at 2:24 AM
To: Alison Peel (b) (6)
Cc: Raina Plowright < (b) (6) Barbara Han < (b) (6) Colin Parrish < (b) (6) Emily Gurley < (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno < (b) (6) Jamie Lloyd-Smith < (b) (6) "Letko, Michael (NIH/NIAID) [F]" < (b) (6) "Munster, Vincent (NIH/NIAID) [E]" < (b) (6) "Peter J. Hudson" < (b) (6) Sara LaTrielle < (b) (6) "Schountz, Tony" < (b) (6)
Subject: Re: CoV proposal for DARPA

Thank you Ali, looks like an interesting pre-ncoV study from PREDICT. Also a timely reminder about One Health Outlook which wasn't on my radar (though I'm sure someone had mentioned this new journal a couple of months ago). We ought to do more sampling in Ghana across bats and domestic animals, I'll follow up with Vincent.

Cheers

Olivier

On 11 Feb 2020, at 09:14, Alison Peel < (b) (6) wrote:

A paper of interest

https://onehealthoutlook.biomedcentral.com/articles/10.1186/s42522-019-0008-8

On Sat, 8 Feb 2020 at 11:38 am, Raina Plowright < (b) (6) wrote:
Thanks Jamie! I forgot we had house guests tonight so I'll submit later than planned~ 9.30 MT.

Sent from my iPhone

On Feb 7, 2020, at 6:23 PM, Jamie Lloyd-Smith < (b) (6) wrote:

Hi Raina,

Here's a version with substantial edits to the UCLA bit, and other minor tweaks throughout. Vincent, if you happen to be online, it would be great to get a quick read to make sure I haven't over-promised based on your earlier email responses. I tried to leave plenty of wiggle room, while emphasizing the opportunities and major leverage they'd get on their further investment.

Looks great!
Jamie

On Fri, Feb 7, 2020 at 2:39 PM Raina Plowright < (b) (6) wrote:
Hi Everyone,

I've attached the proposal. Now that (b) (6) has a summary (I have not heard anything from him), I feel less time-pressured. How about I send this around 7pm MT tonight. If anyone needs more time, let me know. Any edits/shortening/proofreading/formatting appreciated. They will ask for more details if DARPA decide to provide money so this doesn't have to be perfect.

Have a great weekend!

Raina

On Feb 7, 2020, at 3:15 PM, Alison Peel < (b) (6) wrote:

Thanks for the inclusion Raina. I very much appreciate it! I think it reads well and will keep fingers crossed!

On Sat, 8 Feb 2020 at 7:14 am, Jamie Lloyd-Smith < (b) (6) wrote:
Hi Raina and all,

Just emerging from a joyful morning of dept committee/admin work. This email is great, and I echo Olivier in thanking you for your excellent leadership. How could Ro resist this enticing menu?

I can clear some time this afternoon to edit/elaborate - best window is sometime between 2:30-5:30 PST. Sounds like there are some major rearrangements pending, so please let me know if/when there'll be a new version to work on.

Vincent: referring back to our earlier exchange, it sounded like you agreed about testing in human airway and bronchial organoids could be an option. I think this would be hugely valuable to include, to assess zoonotic potential. I'll follow up separately about some other ideas and details.

cheers,
Jamie

On Fri, Feb 7, 2020 at 11:19 AM Raina Plowright <[redacted] (b) (6)
wrote:
This is what I just sent. I'm adding Ali on here because I added potential budget for multi-viral work in Australia (at very bottom)... never know who they may be talking to and what sources of funding they may conjure!

Dear [redacted] (b) (6)

Our team discussed priorities for Coronavirus (CoV) research and what we can do to help stop this outbreak and prevent the next one.

We can address four fundamental knowledge gaps:

1) Phenotypic assessment of the zoonotic potential of coronaviruses circulating in bats

2) Understanding the host-pathogen relationship between 2019-NCoV and bats, and the factors that drive viral shedding

3) The distribution of the 2019-NCoV relatives (and ancestors) in bats

4) Detection and control of the current pandemic spread and future spillover events

All of the proposed projects can start immediately because we are already involved in 2019-nCoV work and we can leverage our ongoing work on henipaviruses. Vincent Munster (RML) has an isolate of 2019-nCoV (first lab to receive isolate from CDC; see here & perspective in NEJM). His team characterized the host receptor and published this 12 days after the sequences were released. Currently RML is leading the USG/NIH/NIAIDs response to the novel coronavirus. Tony Schountz at CSU, has an IACUC approved to run a coronavirus experiments in bats and has bats in hand and ready to infect.

On the epidemiology side, Jamie Lloyd-Smith's group published a preprint on the efficacy of various traveler screening methods for 2019-nCoV and released an open access app for evaluating methods of screening. UCLA and RML can collaborate to extend the genotype-to-phenotype modeling to inform work on 2019-nCoV. Olivier Restif's group at Cambridge has a modeling framework for detecting syndromic clusters that his group can adapt for CoV.

Moreover, we have ongoing field sampling of bats in multiple countries. I suspect we could do more to respond to CoV than DARPA can fund. Therefore, we have added a couple of options for funding that could be implemented if other funds can be leveraged. What sets our team apart is our transdisciplinary approach and our multi-scale, molecules to landscapes, understanding of these systems. The budgets below are stretched over multiple performers to ensure we keep this approach but I do worry that we will be stretched and we need to leverage additional funds.

Below is a very brief summary of the proposal and I will send a detailed version with explanation and cost breakdown shortly. We can cut components to get to your target budget. Do you have any feedback before I send a full proposal?

Sincerely,

Raina and the Bat One Health team

Proposal 1: Translating Surveillance into Knowledge: generating a genotype-to-phenotype pipeline for novel coronaviruses

Leverage existing samples from field studies

- In-country testing of CoV (Hopkins/icddr,b)
- Rapid VirCapseq to obtain spike and full-genome sequences for characterization (RML)

Assess cross-species transmission potential

- synthesize, clone sequences of spike receptor binding region, use VLPs to measure cell entry (RML)

Modeling framework to inform experiments, provide epidemiological insights, and maximize inferences from experimental data

- Mathematical modeling disease transmission and dispersal that might result from different biological changes (UCLA)

Preferred Additions: Develop organoid system of bat intestines, Investigate drivers of evolution and host adaptation of coronaviruses

Total Cost $225,000 plus potential additions

Project 2: Understanding the host-pathogen relationship between 2019-NCoV and bats and factors that drive shedding

2019-NCoV experiments in bats

- Replication kinetics, shedding and host response in bats and assess the relationship between stress, susceptibility, and shedding (Colorado State University)

Develop deployable immunology tools to assess relationship between bat immune defense, stress, and shedding that can be transported to the field (bat roosts or wet market)

- develop transportable *ex vivo* cell-based assays and lab-based mass spec for assessing bat immune defense (Montana State University)

Develop modeling framework for CoV in bats

- machine learning and mechanistic framework to inform future field studies and to incorporate data from lab and field studies (Cambridge, includes cost of syndromic surveillance model, Cary Institute needs no additional funding)

Preferred Additions: deep sequencing for bat experiments, travel budget for Cary/Cambridge interaction

Total Cost: $114,000 plus potential additions

Project 3: Human syndromic surveillance for rapid detection of pandemic spread of nCoV (and future diseases)

Combine UCLA screening model with Cambridge syndromic surveillance model to detect clusters of suspect cases in countries with limited resources

- To maximize the impact of data generated in the field and the lab, we also propose modeling frameworks that will help improve the detection and control of the current pandemic spread and future spillover events (Cambridge)

Total Cost: included in Project 2 (postdoc salary)

———

If further funds can be leveraged, the projects below would be extraordinary — they would leverage the millions of dollars that DARPA has invested in our work on viruses in wild bat populations to extend inferences made on henipaviruses to CoVs.

Project 4: Spatiotemporal dynamics of CoVs in wild bat populations

Extend Bangladesh sampling by 4 months to get 12 month longitudinal dataset on lineage B betacoronaviruses in high-risk global hotspot for emergence

Cost: $100,000 (Hopkins/icddr,b)

In-country testing of existing spatiotemporal samples from Australian bats to understand relationship between CoV shedding, stress, and co-infections
Cost: $180,000 (Griffith, CSIRO, University of Sydney)

On Feb 7, 2020, at 11:54 AM, Raina Plowright <[redacted] (b) (6) wrote:

As V said, it is "the wrath of the pangolins"!

Very good comments and I'm quickly incorporating — OR, made your point #4 knowledge gap so control is much more highlighted; EG, good idea to delete specific $$, will give totals here only, also thx for edit to clarify. CP, using OR language to highlight control.

Sending with comment that full proposal will follow shortly... I'll send at 12 in case anyone else has comments in next 7 minutes!

thx, as always, team!

Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: [redacted] (b) (6)
Lab website: http://bzndiseaselab.org
Phone: [redacted] (b) (6)

On Feb 7, 2020, at 10:55 AM, Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6) wrote:

There are indeed closely related sequences observed in pangolin, these are one of the most hunted animals on earth for Chinese traditional medicine (and food) and driven to extinction. So it could be a combination of scenario's (but likely a palm-civet scenario).

bat to pangolin to human (of note pangolins are not farmed, apparently impossible) bat to intermediate unknown host (unknown) to pangolin and human

bat to human and pangolin

for now we are exploring the pangolin option and have the pangolin ACE2 on the way,

cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Collin Parrish <(b) (6)
Date: Friday, February 7, 2020 at 10:32 AM
To: Olivier Restif <(b) (6) Raina Plowright <(b) (6)
Cc: "(b) (6) <(b) (6) Emily Gurley <(b) (6) Tony Schountz <(b) (6) Barbara Han <(b) (6) Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6) Hamish McCallum <(b) (6) Michael Letko <(b) (6) "Peter J. Hudson" <(b) (6) Sara LaTrielle <(b) (6)
Subject: Re: CoV proposal for DARPA

Agree this is good - and with Olivier's and Emily's suggestions. Highlighting the way the modeling can assist in immediate control efforts is important - as an outcome of this teams efforts and of potentially high impact for outbreak control.

The question of whether this is a bat-derived virus is in play (again) as there are rumors of closely related sequences from pangolins (but also closely related viruses from bats apparently). Not sure where that will all end up, but should likely leave the question of reservoirs open for the moment...

Colin

Colin R. Parrish
John M. Olin Professor of Virology

College of Veterinary Medicine
Cornell University
Ithaca, NY 14853, USA
Phone: (b) (6) (cell anywhere); (b) (6) (work);
Skype: colinparrish

From: Olivier Restif <(b) (6)
Sent: Friday, February 7, 2020 12:23 PM
To: Raina Plowright <(b) (6)
Cc: Colin Ross Parrish <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Emily Gurley (b) (6) Schountz, Tony <(b) (6) Barbara Han <(b) (6) Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6) Hamish McCallum <(b) (6) Letko, Michael (NIH/NIAID) [F] <(b) (6) Peter J. Hudson <(b) (6) Sara LaTrielle <(b) (6)
Subject: Re: CoV proposal for DARPA

Thank you Raina, looks great. Amazing value for money: we're proposing to do the same as our PREEMPT grant for less than 3% of the cost!!

Suggestion: selfishly, I would rewrite this sentence

> In addition, we propose modeling frameworks that can impact the current outbreak and its control.

as

"To maximize the impact of data generated in the field and the lab, we propose modeling frameworks that will help improve the detection and control of the current pandemic spread and future spillover events."

Good luck and thank you (as always) for your exceptional leadership.

Olivier

--

James O. Lloyd-Smith

Professor
Department of Ecology & Evolutionary Biology
Department of Biomathematics

University of California, Los Angeles
610 Charles E Young Dr South
Box 723905
Los Angeles, CA 90095-7239

--

James O. Lloyd-Smith

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Phone: (b) (6)

https://www.eeb.ucla.edu/Faculty/lloydsmith/
Office: 4135 Terasaki Life Sciences Building
Lab: 4000 Terasaki Life Sciences Building

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 13 Feb 2020 10:29:15 -0700
To: Schountz, Tony; Richard Bowen
Subject: Re: artibeus

Update on the virus:

Deep sequenced: the same as the initial sequence from CDC, no contaminants

Titer: 10E5.5

Grows well on vero's, DMEM / 2% FBS

We are still looking for the best cells for titration as the CPE is late to form (and the titer might be a bit higher on other cells)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Thursday, February 13, 2020 at 10:20 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]"
<[redacted] (b) (6)
Subject: Re: artibeus

I'm certain there are females because at least one had a pup attached to her. I didn't see any carollia's but I didn't go in the room (it's under quarantine). We were told it would take another permit to get them shipped, too.

We got ours from the Denver Zoo. We weren't told where they got them, but I suspect from another zoo.

I have my CDC permit for SARS-CoV-2 and got IBC approval yesterday (attached). Were you planning to ship to Dick or to me?

Thanks,

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory

Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Feb 13, 2020, at 10:02 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Btw, did they send males and females, or juts males? Did they manage to add some carolia?

Where are your Artibeus from originally? I'll email the zoo to see if they have some info where these are from (if they have managed to keep records),

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Thursday, February 13, 2020 at 9:57 AM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]"
<[redacted] (b) (6)
Subject: Re: artibeus

Yes, I think we will bleed a few and look at a few genes. Cytochrome C genes for sure. Any others you're aware of? I can scan the artibeus literature to see what markers are used for species-level ID. I know Aj has a large number of subspecies and can hybridize with A. planirostris (producing a fertile hybrid, A. schwartzi).
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692

[redacted] (b) (6)
[redacted] (b) (6)

On Feb 13, 2020, at 9:50 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Maybe sequence them? Just to make sure?

Although there are quite some cryptic species as they all look alike? Maybe literatus?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Thursday, February 13, 2020 at 9:41 AM
To: [redacted] (b) (6)
Cc: Tony Schountz <[redacted] (b) (6) "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: Re: artibeus

Vinnie, your bats seem to be a little bit bigger than ours. I wonder if they might be a different species? Otherwise, only one dead on arrival yesterday and today there do not appear to be any deaths.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Jan 10, 2020, at 12:49 PM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Btw, as soon as we have a study date, it might then be a good time for you to come by and do the experiments.

We would have both Steph and Trent in BSL4 to help you (and Kwe), I think its scheduled for early February

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, January 10, 2020 at 9:30 AM
To: [redacted] (b) (6), "Seifert, Stephanie (NIH/NIAID) [E]" <[redacted] (b) (6)
Subject: Re: artibeus

That shouldn't be a problem. I'll get the paperwork started to ship 34 bats to you. We'll try to get a 2:1 M:F ratio for you.

We can do a genotype comparison but if they are really Ajs then the mitochondrial sequences should tell us. Might do a Y-chromosome gene, too, but I'll have to look into that. If they're Ajs, I suspect they are derived from the same source. The zoos tend to share their stocks.

T.

—
Tony Schountz, PhD
Associate Professor
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[redacted] (b) (6)
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Sent: Thu, 13 Feb 2020 10:27:21 -0700
To: Schountz, Tony; Shupert, W. Lesley (NIH/NIAID) [E]
Subject: Re: artibeus

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Dr Schountz from CSU has a request for the novel coronavirus.

Can you arrange the necessary paperwork and shipping from RML to CSU,

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Attachments: SARS-CoV-2 IBC approval.pdf, file.pdf

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Agent Approval Notice

Institutional Biosafety Committee

Date: 2020-2-13

Investigator	Tony Schountz
Department	Microbiology, Immunology, and Pathology
Approval date	2020-02-12
Agent	SARS-CoV-2
Strains	Any

Biosafety Officer/IBC Chair and date of signature

Christine Johnson
IBC Coordinator
(b) (6)

DEPARTMENT OF HEALTH AND HUMAN SERVICES
PUBLIC HEALTH SERVICE

Centers for Disease Control and Prevention
Office of Health and Safety, MS A-46
Atlanta, Georgia 30333
TEL: (b) (6); FAX: 404-718-2093; Email: (b) (6)

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Permit to Import Infectious Biological Agents, Infectious Substances, and Vectors

In accordance with 42 CFR Section 71.54 of the Public Health Service Foreign Quarantine Regulators, cited on the bottom of this permit, permission is granted the permittee to import into any port under control of the United States, or to receive by transfer within the United States, the material described in Item 1 below.

PHS PERMIT NO. : 20200204-0405A
ISSUED DATE: 02/04/2020
EXPIRATION DATE: 02/04/2021

1. DESCRIPTION OF MATERIAL	ISOLATES OF NOVEL CORONAVIRUS (2019-NCOV).
2. PERMITTEE (NAME, ORGANIZATION, ADDRESS AND CONTACT INFORMATION)	**TONY SCHOUNTZ** (b) (6) **AUTHORIZED USER: ECKLEY MILES** (b) (6) **AUTHORIZED USER: LEWIS JULIETTE** (b) (6) **COLORADO STATE UNIVERSITY** **200 WEST LAKE STREET, 1692 CAMPUS DELIVERY** **FORT COLLINS CO 805231692**
3. SOURCE OF MATERIAL (NAME, ORGANIZATION, ADDRESS, COUNTRY)	RESOURCES BEI (b) (6) BEI RESOURCES 10801 UNIVERSITY BOULEVARD MANASSAS VA 20110-2209 UNITED STATES VINCENT MUNSTER (b) (6) NIAID 903 SOUTH 4TH STREET HAMILTON MT 59840 UNITED STATES
4. TYPE OF PERMIT AND INSTRUCTIONS FOR USE	SINGLE IMPORTATION INTO THE U.S. A. RECORD OF EACH IMPORTATION SHALL BE MAINTAINED ON PERMANENT FILE BY PERMITTEE. B. USDA/APHIS MAY REQUIRE ADDITIONAL PERMITS FOR MATERIALS FROM ANIMALS, MATERIALS EXPOSED TO ANIMAL PRODUCTS/BYPRODUCTS, AND AGENTS THAT ARE INFECTIOUS TO ANIMALS OR PLANTS.U.S.FISH AND WILDLIFE SERVICE MAY REQUIRE ADDITIONAL PERMITS FOR MATERIALS FROM ENDANGERED ANIMALS.
5. CONDITIONS OF ISSUANCE ITEMS APPLICABLE WHEN CHECKED	PACKAGING MUST CONFORM TO 49 CFR SECTIONS 171-180. WORK WITH THE AGENT(S) DESCRIBED SHALL BE RESTRICTED TO AREAS AND CONDITIONS MEETING REQUIREMENTS IN THE CDC/NIH PUBLICATION "BIOSAFETY IN MICROBIOLOGICAL AND BIOMEDICAL LABORATORIES. AS THE PERMITTEE, YOUR FACILITY WILL BE SUBJECT TO INSPECTION AT SOME TIME IN THE FUTURE TO CONFIRM THAT THE IMPORTERS BIOSAFETY MEASURES ARE COMMENSURATE WITH THE HAZARD POSED BY THE ITEMS TO BE IMPORTED AND THE LEVEL OF RISK GIVEN ITS INTENDED USE. SUBSEQUENT DISTRIBUTION WITHIN THE U.S. OF THE MATERIAL DESCRIBED IN THIS PERMIT IS PROHIBITED WITHOUT PRIOR AUTHORIZATION BY THE PUBLIC HEALTH SERVICE. ALL MATERIAL IS FOR LABORATORY USE ONLY - NOT FOR USE IN THE PRODUCTION OF BIOLOGICS FOR HUMANS OR ANIMALS. WORK SHOULD BE CONDUCTED IN ACCORDANCE WITH THE INTERIM RISK ASSESSMENT, HTTPS://WWW.CDC.GOV/CORONAVIRUS/2019-NCOV/LAB-BIOSAFETY-GUIDELINES.HTML.
6.SIGNATURE OF ISSUING OFFICER	(b) (6) SAMUEL S. EDWIN, PH.D. DIRECTOR, DIVISION OF SELECT AGENTS AND TOXINS

CDC 0728 (F 13.40) REV. 4-13

42 CFR 71.54. Permit to Import Biological Agents, Infections Substances, and Vectors
A person may not import into the United States any infectious biological agent, infectious substance, or vector unless: It is accompanied by a permit issued by the Centers for Disease Control and Prevention (CDC). The possession of a permit issued by the CDC does not satisfy permitting requirements placed on materials by the U.S. Department of Agriculture that may pose hazards to agriculture or agricultural production in addition to hazards to human health.

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 13 Feb 2020 08:16:48 -0700
To: Baric, Ralph
Subject: 2019-nCoV

Hi Ralph,

Was anyone from the US involved in the name giving? I see potentially big CFs, with DSAT with SARS and SARS-2. Obviously, hard to address as it might “wake-up” DSAT.

Hope all is well, first NHP start tomorrow,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 12 Feb 2020 10:23:41 -0700
To: Colin Ross Parrish; Raina Plowright; Emily Gurley; LaTrielle, Sara; Olivier Restif; Alison Peel
Cc: Barbara Han; Hamish McCallum; Hector Aguilar-Carreno; Jamie Lloyd-Smith; Letko, Michael (NIH/NIAID) [F]; Peter J. Hudson; Schountz, Tony
Subject: Re: CoV proposal for DARPA

Nice write-up on Michael's work, should be out in Nature microbiology soon

https://www.wired.com/story/can-a-database-of-animal-viruses-help-predict-the-next-pandemic/

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Collin Parrish <(b) (6)
Date: Wednesday, February 12, 2020 at 6:55 AM
To: '(b) (6) <(b) (6) Raina Plowright <(b) (6) Emily Gurley <(b) (6) "LaTrielle, Sara" <(b) (6) Olivier Restif <(b) (6) Alison Peel <(b) (6)
Cc: Barbara Han <(b) (6) Hamish McCallum <(b) (6) Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6) Michael Letko <(b) (6) "Peter J. Hudson" <(b) (6) Tony Schountz <(b) (6)
Subject: Re: CoV proposal for DARPA

Yes agree with Vincent (and others) on this - they have been pushing their global modeling and hotspot prediction for years, and some of it is useful and much is not, along with the random sequencing of everything and the bat-centric view of global reservoirs.

No real benefit in just pushing back on them, but doing a good and more thoughtful and reality-based job based on this team's expertise and data is good - better science stands the test of time and makes the impact in the end...

Can certainly

Colin R. Parrish

John M. Olin Professor of Virology

College of Veterinary Medicine

Cornell University

Ithaca, NY 14853, USA

Phone: [redacted] (b) (6) (cell anywhere); [redacted] (b) (6) (work); Skype: colinparrish

---

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Tuesday, February 11, 2020 10:46 PM
To: Raina Plowright <[redacted] (b) (6) Colin Ross Parrish <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) LaTrielle, Sara <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6) Peter J. Hudson <[redacted] (b) (6) Schountz, Tony <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

I actually there should be way more nuance in the story as realistically those viruses are not everywhere. They typically are a very small subset of viruses with baseline zoonotic or pathogenic potential. Claiming that these viruses are everywhere (or that every host/bat is similar) is just not correct and completely misses the point. In addition, the often claimed line that there is direct global health benefit from this work should be approached very carefully, as a taxpayer I should be quite upset about the tens of millions of USAID dollars fed into Chinese bat work on the premise of preventing spillover, and then realizing that nothing what was claimed was actually achieved (similar with Ebola, or with Nipah viru)s. Complex problems just don't have easy solutions, but hopefully good quality data will help us understand the patterns and drivers and may eventually help us to prepare better. This should be one of our main obligations to the people we train, that even though there appear to be a lot of talking heads with datafree statements, quality data is what should drive us rather than trying to be a fact free voice.

From the basic medical science work it similar to claiming that the pathway you discovered might eventually aid countermeasures (it typically never does) or that you vaccine is the best ever (unless you have a public-private partnership nobody is magically going to get your vaccines through clinical pipelines and the scientific world is filled with shelfed "experimental" vaccines).

Just my five (happily) cynic cents,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <[redacted] (b) (6)
Date: Tuesday, February 11, 2020 at 4:43 PM
To: Collin Parrish <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) "LaTrielle, Sara"

<[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Alison Peel
<[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Hamish McCallum
<[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Michael Letko <[redacted] (b) (6)
"[redacted] (b) (6) <[redacted] (b) (6) "Peter J. Hudson" <[redacted] (b) (6)
Tony Schountz <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Great idea Emily. We can help/support you.

Colin, yes, we should be more strategic. I'm always put off by the EcoHealth/WCS type opportunism/handwaving/storytelling (very active right now) and want to be the antithesis of that, but a well-reasoned opinion by our team would be valuable right now. The story is that these viruses are everywhere and it is our interaction with bats and the pressures we place on their populations that will determine if we continue to see new spillovers.

I have an opinion written about this that is designed to be submitted with Peggy's paper – without her paper, the mechanisms driving spillover are not substantiated...and we are hoping to get her paper into Science so I don't want to destroy those chances. But maybe this is about timing and a more general message. I'll read through it and think about it.

> **From:** Colin Ross Parrish <[redacted] (b) (6)
> **Date:** Tuesday, February 11, 2020 at 2:57 PM
> **To:** Emily Gurley <[redacted] (b) (6) Raina Plowright <[redacted] (b) (6)
> "LaTrielle, Sara" <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6)
> Alison Peel <[redacted] (b) (6)
> **Cc:** Barbara Han <[redacted] (b) (6) Hamish McCallum
> <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie
> Lloyd-Smith <[redacted] (b) (6) "Letko, Michael (NIH/NIAID) [F]"
> <[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]"
> <[redacted] (b) (6) "Peter J. Hudson" <[redacted] (b) (6) "Schountz, Tony"
> <[redacted] (b) (6)
> **Subject:** Re: CoV proposal for DARPA
>
> If any of us have information that is directly relevant to the coronavirus story (disease ecology, spillover, evolution to host adaptation, etc.) this would be a good time - it seems that right now there are a lot of people making stuff up as they go along, and having more solidly supported information out there can only be useful.
>
> The Royal Society volume is now open-access, and some of those papers are relevant and can be promoted.
>
> Colin

Colin R. Parrish

John M. Olin Professor of Virology

College of Veterinary Medicine

Cornell University

Ithaca, NY 14853, USA

Phone: [redacted] (b) (6) (cell anywhere); [redacted] (b) (6) (work); Skype: colinparrish

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From: Emily Gurley <[redacted] (b) (6)
Sent: Tuesday, February 11, 2020 4:37 PM
To: Raina Plowright <[redacted] (b) (6) LaTrielle, Sara <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Alison Peel [redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Colin Ross Parrish <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) Peter J. Hudson <[redacted] (b) (6) Schountz, Tony <[redacted] (b) (6)
Subject: RE: CoV proposal for DARPA

I've been thinking about a short letter to the editor, editorial article pitching One Health as the ultimate public health tool for primary prevention of emerging zoonotic infections. The pitch is to the public health community, so was thinking about submitting to American Journal of Epidemiology, or something similar. Thoughts?

From: Raina Plowright <[redacted] (b) (6)
Sent: Tuesday, February 11, 2020 3:57 PM
To: LaTrielle, Sara <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Alison Peel <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Colin Parrish <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) Peter J. Hudson <[redacted] (b) (6) Schountz, Tony <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Right Sara!!! Its exactly what our group is doing but I don't feel we can broadcast it until Peggy's work is published…. I have a perspective piece on this written but it doesn't make sense without Peggy's ecology papers out and that is still months away I think. Perhaps others have ideas of how we could promote these concepts from a place of solid scientific standing before the science is published.

From: "LaTrielle, Sara" (b) (6)
Date: Tuesday, February 11, 2020 at 12:54 PM
To: Raina Plowright <(b) (6) Olivier Restif <(b) (6) Alison Peel <(b) (6)
Cc: Barbara Han (b) (6) Colin Parrish <(b) (6) Emily Gurley <(b) (6) Hamish McCallum <(b) (6) Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6) "Letko, Michael (NIH/NIAID) [F]" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Peter J. Hudson" <(b) (6) "Schountz, Tony" <(b) (6)
Subject: Re: CoV proposal for DARPA

Thanks Ali.

I especially enjoyed this in the conclusion, "it seems a proper time for the scientific community studying "bat-associated" viruses to move the conversation from bat spillover risk assessments to the planning of pro-biodiversity and subsequently pro-ecosystem strategies aiming to mitigate spillover risk."...

Yep! Just one of many aspects our team is working on... thanks to years+ to Peggy/team for advocating/educating in just this area... with more work to follow of course.

And nice to see TS's paper cited- and surely others I missed.

Sara

Get Outlook for iOS

From: Raina Plowright <(b) (6)
Sent: Tuesday, February 11, 2020 11:57:27 AM
To: Olivier Restif <(b) (6) Alison Peel (b) (6)
Cc: Barbara Han <(b) (6) Colin Parrish <(b) (6) Emily Gurley <(b) (6) Hamish McCallum <(b) (6) Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6) Letko, Michael (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Peter J. Hudson <(b) (6) LaTrielle, Sara <(b) (6) Schountz, Tony <(b) (6)
Subject: Re: CoV proposal for DARPA

Good to see something coming out of PREDICT that is addresses dynamics (although looks like they combine many cross sectional sampling events to make inferences on temporal dynamics—such a typical epidemiologist approach!). Amazing that there are no spatiotemporal studies of CoVs in bats and only a handful of temporal studies. Thanks for forwarding Ali.

From: Olivier Restif <[redacted] (b) (6)
Date: Tuesday, February 11, 2020 at 2:24 AM
To: Alison Peel <[redacted] (b) (6)
Cc: Raina Plowright <[redacted] (b) (6) Barbara Han <[redacted] (b) (6) Colin Parrish <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) "Letko, Michael (NIH/NIAID) [F]" <[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6) "Peter J. Hudson" <[redacted] (b) (6) Sara LaTrielle <[redacted] (b) (6) "Schountz, Tony" <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Thank you Ali, looks like an interesting pre-ncoV study from PREDICT. Also a timely reminder about One Health Outlook which wasn't on my radar (though I'm sure someone had mentioned this new journal a couple of months ago). We ought to do more sampling in Ghana across bats and domestic animals, I'll follow up with Vincent.

Cheers

Olivier

On 11 Feb 2020, at 09:14, Alison Peel [redacted] (b) (6) wrote:

A paper of interest

https://onehealthoutlook.biomedcentral.com/articles/10.1186/s42522-019-0008-8

On Sat, 8 Feb 2020 at 11:38 am, Raina Plowright <[redacted] (b) (6)
wrote:
Thanks Jamie! I forgot we had house guests tonight so I'll submit later than planned~ 9.30 MT.

Sent from my iPhone

On Feb 7, 2020, at 6:23 PM, Jamie Lloyd-Smith <[redacted] (b) (6) wrote:

Hi Raina,

Here's a version with substantial edits to the UCLA bit, and other minor tweaks throughout. Vincent, if you happen to be online, it would be great to get a quick read to make sure I haven't over-promised based on your earlier email responses. I tried to leave plenty of wiggle room, while emphasizing the opportunities and major leverage they'd get on their further investment.

Looks great!
Jamie

On Fri, Feb 7, 2020 at 2:39 PM Raina Plowright <[redacted] (b) (6) wrote:
Hi Everyone,

I've attached the proposal. Now that [redacted] (b)(6) has a summary (I have not heard anything from him), I feel less time-pressured. How about I send this around 7pm MT tonight. If anyone needs more time, let me know. Any edits/shortening/proofreading/formatting appreciated. They will ask for more details if DARPA decide to provide money so this doesn't have to be perfect.

Have a great weekend!

Raina

On Feb 7, 2020, at 3:15 PM, Alison Peel <[redacted] (b) (6) wrote:

Thanks for the inclusion Raina. I very much appreciate it! I think it reads well and will keep fingers crossed!

On Sat, 8 Feb 2020 at 7:14 am, Jamie Lloyd-Smith <[redacted] (b) (6)
wrote:
Hi Raina and all,

Just emerging from a joyful morning of dept committee/admin work. This email is great, and I echo Olivier in thanking you for your excellent leadership. How could [redacted] (b)(6) resist this enticing menu?

I can clear some time this afternoon to edit/elaborate - best window is sometime between 2:30-5:30 PST. Sounds like there are some major rearrangements pending, so please let me know if/when there'll be a new version to work on.

Vincent: referring back to our earlier exchange, it sounded like you agreed about testing in human airway and bronchial organoids could be an option. I think this would be hugely valuable to include, to assess zoonotic potential. I'll follow up separately about some other ideas and details.

cheers,
Jamie

On Fri, Feb 7, 2020 at 11:19 AM Raina Plowright < (b) (6)
wrote:
This is what I just sent. I'm adding Ali on here because I added potential budget for multi-viral work in Australia (at very bottom)... never know who they may be talking to and what sources of funding they may conjure!

Dear (b) (6)

Our team discussed priorities for Coronavirus (CoV) research and what we can do to help stop this outbreak and prevent the next one.

We can address four fundamental knowledge gaps:

1) Phenotypic assessment of the zoonotic potential of coronaviruses circulating in bats

2) Understanding the host-pathogen relationship between 2019-NCoV and bats, and the factors that drive viral shedding

3) The distribution of the 2019-NCoV relatives (and ancestors) in bats

4) Detection and control of the current pandemic spread and future spillover events

All of the proposed projects can start immediately because we are already involved in 2019-nCoV work and we can leverage our ongoing work on henipaviruses. Vincent Munster (RML) has an isolate of 2019-nCoV (first lab to receive isolate from CDC; see here & perspective in NEJM). His team characterized the host receptor and published this 12 days after the sequences were released. Currently RML is leading the USG/NIH/NIAIDs response to the novel coronavirus. Tony Schountz at CSU, has an IACUC approved to run a coronavirus experiments in bats and has bats in hand and ready to infect.

On the epidemiology side, Jamie Lloyd-Smith's group published a preprint on the efficacy of various traveler screening methods for 2019-nCoV and released an open access app for evaluating methods of screening. UCLA and RML can collaborate to extend the genotype-to-phenotype modeling to inform work on 2019-nCoV. Olivier Restif's group at Cambridge has a modeling framework for detecting syndromic clusters that his group can adapt for CoV.

Moreover, we have ongoing field sampling of bats in multiple countries. I suspect we could do more to respond to CoV than DARPA can fund. Therefore, we have added a couple of options for funding that could be implemented if other funds can be leveraged. What sets our team apart is our transdisciplinary approach and our multi-scale, molecules to landscapes, understanding of these systems. The budgets below are stretched over multiple performers to ensure we keep this approach but I do worry that we will be stretched and we need to leverage additional funds.

Below is a very brief summary of the proposal and I will send a detailed version with explanation and cost breakdown shortly. We can cut components to get to your target budget. Do you have any feedback before I send a full proposal?

Sincerely,

Raina and the Bat One Health team

<u>**Proposal 1: Translating Surveillance into Knowledge: generating a genotype-to-phenotype pipeline for novel coronaviruses**</u>

<u>Leverage existing samples from field studies</u>

- In-country testing of CoV (Hopkins/icddr,b)
- Rapid VirCapseq to obtain spike and full-genome sequences for characterization (RML)

<u>Assess cross-species transmission potential</u>

- synthesize, clone sequences of spike receptor binding region, use VLPs to measure cell entry (RML)

<u>Modeling framework to inform experiments, provide epidemiological insights, and maximize inferences from experimental data</u>

- Mathematical modeling disease transmission and dispersal that might result from different biological changes (UCLA)

Preferred Additions: Develop organoid system of bat intestines, Investigate drivers of evolution and host adaptation of coronaviruses

Total Cost $225,000 plus potential additions

<u>**Project 2: Understanding the host-pathogen relationship between 2019-NCoV and bats and factors that drive shedding**</u>

<u>2019-NCoV experiments in bats</u>

- Replication kinetics, shedding and host response in bats and assess the relationship between stress, susceptibility, and shedding (Colorado State University)

<u>Develop deployable immunology tools to assess relationship between bat immune defense, stress, and shedding that can be transported to the field (bat roosts or wet market)</u>

- develop transportable *ex vivo* cell-based assays and lab-based mass spec for assessing bat immune defense (Montana State University)

Develop modeling framework for CoV in bats

- machine learning and mechanistic framework to inform future field studies and to incorporate data from lab and field studies (Cambridge, includes cost of syndromic surveillance model, Cary Institute needs no additional funding)

Preferred Additions: deep sequencing for bat experiments, travel budget for Cary/Cambridge interaction

Total Cost: $114,000 plus potential additions

Project 3: Human syndromic surveillance for rapid detection of pandemic spread of nCoV (and future diseases)
Combine UCLA screening model with Cambridge syndromic surveillance model to detect clusters of suspect cases in countries with limited resources

- To maximize the impact of data generated in the field and the lab, we also propose modeling frameworks that will help improve the detection and control of the current pandemic spread and future spillover events (Cambridge)

Total Cost: included in Project 2 (postdoc salary)

———

If further funds can be leveraged, the projects below would be extraordinary — they would leverage the millions of dollars that DARPA has invested in our work on viruses in wild bat populations to extend inferences made on henipaviruses to CoVs.

Project 4: Spatiotemporal dynamics of CoVs in wild bat populations
Extend Bangladesh sampling by 4 months to get 12 month longitudinal dataset on lineage B betacoronaviruses in high-risk global hotspot for emergence
Cost: $100,000 (Hopkins/icddr,b)

In-country testing of existing spatiotemporal samples from Australian bats to understand relationship between CoV shedding, stress, and co-infections
Cost: $180,000 (Griffith, CSIRO, University of Sydney)

On Feb 7, 2020, at 11:54 AM, Raina Plowright <[redacted] (b) (6) wrote:

As V said, it is “the wrath of the pangolins”!

Very good comments and I'm quickly incorporating — OR, made your point #4 knowledge gap so control is much more highlighted; EG, good idea to delete specific $$, will give totals here only, also thx for edit to clarify. CP, using OR language to highlight control.

Sending with comment that full proposal will follow shortly... I'll send at 12 in case anyone else has comments in next 7 minutes!

thx, as always, team!

Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: [redacted] (b) (6)
Lab website: http://bzndiseaselab.org
Phone: [redacted] (b) (6)

On Feb 7, 2020, at 10:55 AM, Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6) wrote:

There are indeed closely related sequences observed in pangolin, these are one of the most hunted animals on earth for Chinese traditional medicine (and food) and driven to extinction. So it could be a combination of scenario's (but likely a palm-civet scenario).

bat to pangolin to human (of note pangolins are not farmed, apparently impossible)

bat to intermediate unknown host (unknown) to pangolin and human

bat to human and pangolin

for now we are exploring the pangolin option and have the pangolin ACE2 on the way,

cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Collin Parrish <[redacted] (b) (6)
Date: Friday, February 7, 2020 at 10:32 AM

To: Olivier Restif <[redacted] (b) (6) Raina Plowright
<[redacted] (b) (6)
Cc: "[redacted] (b) (6) <[redacted] (b) (6) Emily
Gurley <[redacted] (b) (6) Tony Schountz
<[redacted] (b) (6) Barbara Han <[redacted] (b) (6)
Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith
<[redacted] (b) (6) Hamish McCallum
<[redacted] (b) (6) Michael Letko
<[redacted] (b) (6) "Peter J. Hudson" <[redacted] (b) (6) Sara
LaTrielle [redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Agree this is good - and with Olivier's and Emily's suggestions. Highlighting the way the modeling can assist in immediate control efforts is important - as an outcome of this teams efforts and of potentially high impact for outbreak control.

The question of whether this is a bat-derived virus is in play (again) as there are rumors of closely related sequences from pangolins (but also closely related viruses from bats apparently). Not sure where that will all end up, but should likely leave the question of reservoirs open for the moment...

Colin

Colin R. Parrish
John M. Olin Professor of Virology
College of Veterinary Medicine
Cornell University
Ithaca, NY 14853, USA
Phone: [redacted] (b) (6) (cell anywhere); [redacted] (b) (6) (work);
Skype: colinparrish

From: Olivier Restif <[redacted] (b) (6)
Sent: Friday, February 7, 2020 12:23 PM
To: Raina Plowright <[redacted] (b) (6)
Cc: Colin Ross Parrish <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6) Emily Gurley [redacted] (b) (6); Schountz, Tony
<[redacted] (b) (6) Barbara Han [redacted] (b) (6)
Hector Aguilar-Carreno <[redacted] (b) (6) Jamie Lloyd-Smith
<[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6)
Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6) Peter J. Hudson
<[redacted] (b) (6) Sara LaTrielle <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Thank you Raina, looks great. Amazing value for money: we're proposing to do the same as our PREEMPT grant for less than 3% of the cost!!

Suggestion: selfishly, I would rewrite this sentence

> In addition, we propose modeling frameworks that can impact the current outbreak and its control.

as

"To maximize the impact of data generated in the field and the lab, we propose modeling frameworks that will help improve the detection and control of the current pandemic spread and future spillover events."

Good luck and thank you (as always) for your exceptional leadership.

Olivier

--
James O. Lloyd-Smith

Professor
Department of Ecology & Evolutionary Biology
Department of Biomathematics
University of California, Los Angeles
610 Charles E Young Dr South
Box 723905
Los Angeles, CA 90095-7239

Phone: (b) (6)

https://www.eeb.ucla.edu/Faculty/lloydsmith/
Office: 4135 Terasaki Life Sciences Building
Lab: 4000 Terasaki Life Sciences Building

--
James O. Lloyd-Smith

Professor
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Office: 4135 Terasaki Life Sciences Building
Lab: 4000 Terasaki Life Sciences Building

<Proposals to DARPA on novel coronavirus_Feb_5th_CRP_OR_RP_jls.docx>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 12 Feb 2020 09:41:30 -0700
To: LaTrielle, Sara; Seifert, Stephanie (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]; Alison Peel; Emily Gurley; Cara Brook; Olivier Restif
Cc: Plowright, Raina; Amandine Gamble
Subject: Re: URGENT: Fw: Field samples information request

Hi Sara,

Can you relay back to DoD that I typically don't see the need for last minute requests unless a public health emergency. We are currently very busy here and would like a normal turn-around time for these requests.

These requests can be quite disruptive and do not help a normal work flow,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "LaTrielle, Sara" <(b) (6)
Date: Wednesday, February 12, 2020 at 9:09 AM
To: "Seifert, Stephanie (NIH/NIAID) [E]" <(b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) Alison Peel <(b) (6) Emily Gurley <(b) (6) Cara Brook <(b) (6) Olivier Restif <(b) (6)
Cc: "Plowright, Raina" <(b) (6) Amandine Gamble <(b) (6) "(b) (6) <(b) (6)
Subject: URGENT: Fw: Field samples information request

All,

Morning! We need your quick assistance as we have a 'quick turn around' request from DARPA for information on our samples, numbers of collected/sampled et al. We need to get this back to them no later than COB today (eek) as they are presenting to DARPA on Thurs. Just a few numbers so hopefully not too much.

<u>Here is what I need from each of you:</u>

Field Site leads: Please update the [PREEMPT SAMPLE google doc](#) Samples collected.

Kwe: Please add in your numbers of samples tested on the same google PREEMPT SAMPLE google doc Please include the number of virus pos and neg, and assay used to determine (serotyping vs PCR or other). Kwe, if you have this in a different format, please just send what you have- no need in taking time to transfer to the google doc if you already have your own tables.

Stephanie: Provide Cell types for the samples, per DARPA's request, "Please point out whether sequencing vs infection of cell lines, (and if so, which cell lines) is being done in order to generate the data for gen-to-phen model development".

Feel free to pass off to another team member, as long as they use the google link- all should be set.

Many thanks for the quick turn-around- by COB today.

Best,

Sara LaTrielle

Program Manager
PREEMPT Project
Montana State University

(b) (6)

On 2/12/20, 8:06 AM, "Plowright, Raina" < (b) (6) wrote:

Hi (b) (6)

Here is a flow chart of virology samples from each field site. This does not include samples for immunology/nutrition/energetics (these samples go to MSU via RML).

I have attached a schematic of the genotype-to-phenotype approach. Data for genotype-to-phenotype model development come from sequences, cell culture experiments, and in vivo experiments. We are currently doing cell-culture experiments at RML (in BSL4) but we are always feeding new sequences through the pipeline. We will get a list of the cell types being used. We were due to start our first in vivo experiments this month but that work has been delayed because of the leading role RML is playing with the coronavirus outbreak.

The number of samples collected is changing daily so we will reach out to each field team manager for latest numbers.

Raina

On 2/11/20, 9:39 PM, [redacted] (b) (6) wrote:

Hi Raina/ Sara,

Can you please send the following information:

A flowchart describing what is being done with samples collected in the 4 countries. Please point out whether sequencing vs infection of cell lines (and if so, which cell lines) is being done in order to generate the data for gen-to-phen model development. I recall that these have been / will be shipped to RML? Please make a note about where your team is currently standing in the flowchart.
Also, please provide the number of samples collected to date. Please include number of virus pos and neg, and assay used to determine (serotyping vs PCR or other). This is important for our review meeting on Thursday, to have a clear picture of where the team is in regards to the surveillance component.

Thank you!

[redacted] (b) (6)

[redacted] (b) (6)
Lead Scientist
Support to Biological Technologies Office, DARPA
Science and Technology Associates, Inc.
[redacted] (b) (6)

From: Broder, Christopher
Sent: Tue, 11 Feb 2020 16:56:39 -0500
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Your article has been published by Oxford University Press

Hey did you get that email from Peter about signing the letter
of support for our Chinese virologists,,,,

DoD told us no way can I or Eric sign it.

I head from Linfa last night, but nothing from Zhengli since a few weeks ago.
The ICID meeting in KL next week was just cancelled today.

CB

On Tue, Feb 11, 2020 at 4:46 PM Munster, Vincent (NIH/NIAID) [E]
<(b) (6) wrote:

Thanks Chris!

Although I only facilitated it ☺, all the work was Michael's (post-doc in my lab for another 4 months and then PI at WSA, Pullman, WA)

Vincent Munster, PhD

Chief, Virus Ecology Section

Laboratory of Virology

Rocky Mountain Laboratories

NIAID/NIH

From: "Broder, Christopher" <(b) (6)
Date: Tuesday, February 11, 2020 at 2:42 PM
To: "(b) (6) <(b) (6)
Subject: Re: FW: Your article has been published by Oxford University Press

thanks much Vincent,

and great work on the first RBS data on nCoV, one of our EID students went over it today in journal club, Eric and I saw it a while ago, but today reminded me to relay congrats.

all best

CB

On Sun, Feb 9, 2020 at 11:38 AM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Dear co-authors,

Please find attached the final published version of our manuscript,

Cheers,

Vincent Munster, PhD

Chief, Virus Ecology Section

Laboratory of Virology

Rocky Mountain Laboratories

NIAID/NIH

From: Oxford University Press <noreply@academic.oup.com>
Date: Sunday, February 9, 2020 at 9:33 AM
To: (b) (6) <(b) (6)
Cc: "jid@oup.com" <jid@oup.com>
Subject: Your article has been published by Oxford University Press

Dear Author,

I am pleased to inform you that Oxford University Press has published your article in The Journal of Infectious Diseases.

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--

Christopher C. Broder, Ph.D.
Professor and Chair

Department of Microbiology and Immunology
Uniformed Services University, B4152
4301 Jones Bridge Rd, Bethesda, MD 20814-4799

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https://www.usuhs.edu/national/faculty/christopher-broder-phd

TEL: (b) (6)
FAX: 301-295-3773

Lucille Washington

Administrative Officer

email - (b) (6)

phone - (b) (6)

fax - 301-295-3773

--
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FAX: 301-295-3773

Lucille Washington
Administrative Officer

email - [redacted] (b) (6)
phone - [redacted] (b) (6)
fax - 301-295-3773

From: Broder, Christopher
Sent: Tue, 11 Feb 2020 16:52:44 -0500
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Letko, Michael (NIH/NIAID) [F]
Subject: Re: Your article has been published by Oxford University Press

yes of course, congrats Mike!
Eric told me all about it this other week, very cool.!

Chris

On Tue, Feb 11, 2020 at 4:46 PM Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6) wrote:

Thanks Chris!

Although I only facilitated it ☺, all the work was Michael's (post-doc in my lab for another 4 months and then PI at WSA, Pullman, WA)

Vincent Munster, PhD

Chief, Virus Ecology Section

Laboratory of Virology

Rocky Mountain Laboratories

NIAID/NIH

From: "Broder, Christopher" <[redacted] (b) (6)
Date: Tuesday, February 11, 2020 at 2:42 PM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: FW: Your article has been published by Oxford University Press

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in journal club, Eric and I saw it a while ago, but today reminded me to relay congrats.

all best

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FAX: 301-295-3773

Lucille Washington
Administrative Officer
email - [redacted] (b) (6)
phone - [redacted] (b) (6)
fax - 301-295-3773

From: Rasmussen, Angela L.
Sent: Mon, 10 Feb 2020 11:05:37 +0000
To: De wit, Emmie (NIH/NIAID) [E]
Cc: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: nCoV transcriptomics?

Hi Emmie,

No problem at all and I totally get the extremely tight timeline. I think I'll have Atsu collect the samples anyway. We can shoot for an extremely quick turnaround but if you need to rush it out before, we can always publish the transcriptomic data as a short report separately. Sound good?

I'll let Atsu know and start talking to our sequencing provider here to find out what kind of rush order is possible. Thanks!
Angie

On Feb 9, 2020, at 16:18, De wit, Emmie (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Hi Angie,
Yes, we are planning to start a rhesus study soon (still growing the virus for now). If Atsu wants to collect samples with you, I have no problem with that. I am not really sure right now how this is going to go. We are in a real hurry to get this done because of the pressure to test the efficacy of remdesivir in NHPs. But I am also counting on the Chinese having already started NHP modeling. So, I am not sure what to advise you. On the one hand I can't promise you that we can include the data in a publication. On the other hand, to have any shot at that we would probably indeed need the data really quickly.
Let me know what you think.
Emmie

From: Rasmussen, Angela L. <[redacted] (b) (6)
Sent: Friday, February 7, 2020 10:43 AM
To: De wit, Emmie (NIH/NIAID) [E] <[redacted] (b) (6)
Subject: nCoV transcriptomics?

Hi Emmie,

Hope all is well with you. Atsu tells me that you are doing a nCoV monkey study. Any interest in doing a little host response study like we did previously for MERS? I should be able to cover the cost of the transcriptomics. We could rush it for publication.

Let me know what you think!
Cheers,
Angie

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sun, 9 Feb 2020 09:38:10 -0700
To: Schulz, Jonathan (NIH/NIAID) [F]; Seifert, Stephanie (NIH/NIAID) [E]; John Thompson; Avanzato, Victoria (NIH/NIAID) [F]; Sterling, Spencer; Letko, Michael (NIH/NIAID) [F]; Matson, Jeremiah (NIH/NIAID) [F]; Fischer, Robert (NIH/NIAID) [F]; Janine Seetahal; Vernie Ramkissoon; Tracey Goldstein; Anthony, Simon J.; Jon Epstein; Eric Laing; Broder, Chris (USU-DoD); Christine Carrington; Schountz, Tony
Subject: FW: Your article has been published by Oxford University Press
Attachments: jiz648.pdf

Dear co-authors,

Please find attached the final published version of our manuscript,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Oxford University Press <noreply@academic.oup.com>
Date: Sunday, February 9, 2020 at 9:33 AM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: "jid@oup.com" <jid@oup.com>
Subject: Your article has been published by Oxford University Press

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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 8 Feb 2020 08:06:51 -0700
To: Schountz, Tony; Richard Bowen
Subject: Re: PLEASE RESPOND re: 2019_nCoV

Thanks,

You can refer them to this website:

https://www.beiresources.org/Catalog/animalviruses/NR-52281.aspx

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Saturday, February 8, 2020 at 8:03 AM
To: '[redacted] (b) (6) <[redacted] (b) (6) Richard Bowen
<[redacted] (b) (6)
Subject: Re: PLEASE RESPOND re: 2019_nCoV

Sorry Vincent. I won't mention it to anyone else.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Saturday, February 8, 2020 7:44 AM
To: Schountz,Tony <[redacted] (b) (6) Richard Bowen <[redacted] (b) (6)
Subject: FW: PLEASE RESPOND re: 2019_nCoV

Tony: will you please not refer people to me asking for virus? In case you don't realise (and I guess you don't). it is a huge undertaking to prepare virus, quality control it and make sure all the proper paperwork is in place.

The USG has BEI resources for this in place, as I said I only send it to people who either do work critical for public health response or direct collaborators (like you and dick).

Thanks,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Weiss, Susan" <(b) (6)
Date: Saturday, February 8, 2020 at 1:15 AM
To: '(b) (6) <(b) (6)
Subject: PLEASE RESPOND re: 2019_nCoV

Vincent

Tony Schountz told me that you have the new 2019_nCoV. Would you be able to send me an aliquot?
Please let me know ether way –

Thanks
susan

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 7 Feb 2020 08:54:37 -0700
To: Schountz, Tony; Richard Bowen
Subject: Re: 2019 nCoV

IFA kinda sucks, I would just do a growth curve. No antibodies yet still weeks out.

You might want to design an ISH for artibeus ACE2 as well, we couldn't get Rousettus infected with WIV1 which also uses ACE2 (look at the ace 2 staining and the antibody, this is smtg you can do rapidly with Artibeus)

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6316779/

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, February 7, 2020 at 8:47 AM
To: '[redacted] (b) (6) <[redacted] (b) (6) Richard Bowen
<[redacted] (b) (6)
Subject: Re: 2019 nCoV

Will do. We tested one of our 7 Aj cells for ACE2 expression by PCR and it appears to be there but very low. This could be low level expression of all the cells, or expression by only a small number of cells (they are not likely clonal). It would be helpful to have an antibody to the virus for IFA. Do you have one, by chance? We've started on making NP with Brian Geiss for an ELISA/WB and to make antibodies for IHC.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Friday, February 7, 2020 8:36 AM
To: Schountz,Tony <[redacted] (b) (6) Richard Bowen <[redacted] (b) (6)
Subject: Re: 2019 nCoV

Throw it on cells first, I'm not sure whether your bats will actually be able to support infection

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <[redacted] (b) (6)
Date: Friday, February 7, 2020 at 8:35 AM
To: '[redacted] (b) (6) <[redacted] (b) (6) Richard Bowen
<[redacted] (b) (6)
Subject: Re: 2019 nCoV

Thanks Vincent. I hope to also have IBC approval Wednesday. IACUC approval is already in place.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Friday, February 7, 2020 7:52 AM
To: Richard Bowen <[redacted] (b) (6) Schountz,Tony <[redacted] (b) (6)
Subject: Re: 2019 nCoV

Hi Dick,

We just got the virus in and are growing a stock and doing some quality control. I think we should eb able to send out samples to you and tony (as long-term collaborator, apparently everyone else has to go through BEI). Make sure you have all the appropriate paperwork in place and I'll have our people contact your people ☺.

I'll keep you posted,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Richard Bowen <(b) (6)
Date: Thursday, February 6, 2020 at 9:42 PM
To: '(b) (6) <(b) (6)
Subject: 2019 nCoV

Have you been able to get ahold of the virus yet or have any news on that front?

Thanks Vincent,

Dick

--
Richard Bowen
Department of Biomedical Sciences
Colorado State University
3107 Rampart Road
Fort Collins, CO 80521
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 7 Feb 2020 08:20:18 -0700
To: Richard Bowen
Cc: Schountz, Tony
Subject: Re: 2019 nCoV
Attachments: Short report qRT-PCR assays.docx

Perfect, we'll send to you and then you can share with Tony,

Email Jeff Thurston for SLA / paperwork, just do one for both of you

Thruston, Jeffrey (NIH/NIAID) [E] (b) (6)

Attached find the qRT-PCRs we set-up, so you can easily order and set-up your own assays

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Richard Bowen <(b) (6)
Date: Friday, February 7, 2020 at 8:14 AM
To: '(b) (6) <(b) (6)
Subject: Re: 2019 nCoV

Thanks a bunch - should have IBC approval next Wednesday.

Best,

Dick

On Fri, Feb 7, 2020 at 7:52 AM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
Hi Dick,

We just got the virus in and are growing a stock and doing some quality control. I think we should eb able to send out samples to you and tony (as long-term collaborator, apparently everyone else has to go through BEI). Make sure you have all the appropriate paperwork in place and I'll have our people contact your people □.

I'll keep you posted,

Vincent Munster, PhD
Chief, Virus Ecology Section

Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Richard Bowen <[redacted] (b) (6)
Date: Thursday, February 6, 2020 at 9:42 PM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Subject: 2019 nCoV

Have you been able to get ahold of the virus yet or have any news on that front?

Thanks Vincent,

Dick

--
Richard Bowen
Department of Biomedical Sciences
Colorado State University
3107 Rampart Road
Fort Collins, CO 80521
[redacted] (b) (6)

--
Richard Bowen
Department of Biomedical Sciences
Colorado State University
3107 Rampart Road
Fort Collins, CO 80521
[redacted] (b) (6)

Detection of 2019-nCoV by qRT-PCR

Assays

Assays used were published on the WHO website on January 13, 2020 by the lab of Christian Drosten, Charité Virology, Berlin Germany: https://www.who.int/docs/default-source/coronaviruse/wuhan-virus-assay-v1991527e5122341d99287a1b17c111902.pdf?sfvrsn=d381fc88_2
This assay described three qRT-PCR primer/probe sets for the detection of 2019-nCoV based on the E, RdRp and N gene.

Testing at RML

All three primer/probe sets described in the document above were ordered and tested at RML using our standard Rotorgene qRT-PCR reagents and cycler:

Per reaction (25ul total volume):

Forward Primer 20pmol/ul	1ul
Reverse Primer 20pmol/ul	1ul
Probe 5pmol/ul	1ul
Quantifast multiplex mastermix	12.5ul
Quantifast RT Mix	0.25ul
RNase free water	4.25ul
RNA	5ul

Cycling conditions in FAM(Green****) channel:

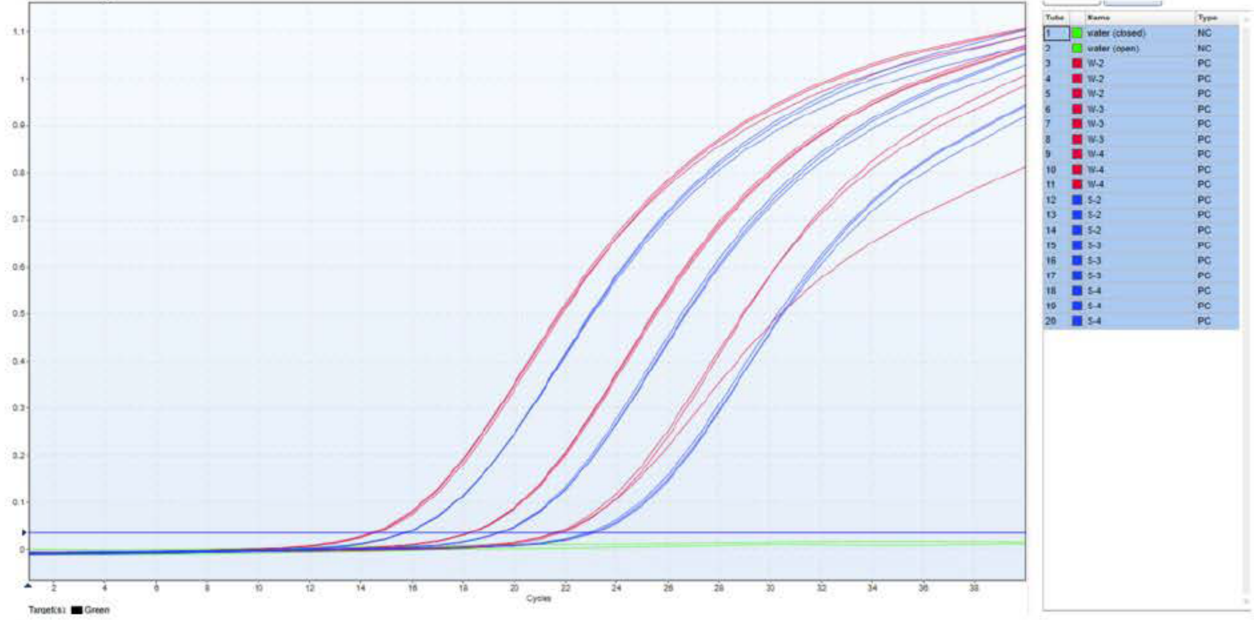
RT	10 min	50ºC
Activation	5 min	95ºC
2-step cycling (40 x)		
Denaturation	10 s	95ºC
Annealing/extension	30 s	60ºC

Test material

RNA extracted from bat coronaviruses WIV1 and SHC014 was used as positive control. RNA was serially diluted 10-fold and the 10^{-2}, 10^{-3} and 10^{-4} dilution were assayed.
qRT-PCR curves are displayed below. Red lines are dilutions of WIV1 RNA; blue lines are dilutions of SCH014 RNA.

Results: E assay

Forward primer ACAGGTACGTTAATAGTTAATAGCGT
Probe FAM-ACACTAGCCATCCTTACTGCGCTTCG
Reverse primer ATATTGCAGCAGTACGCACACA



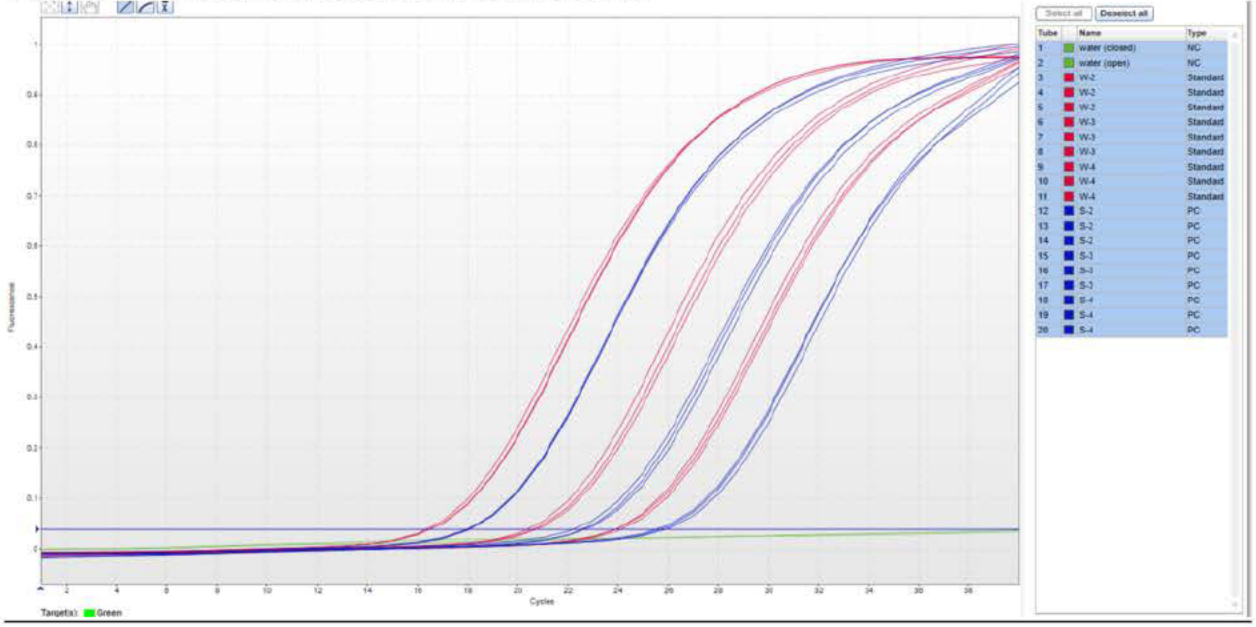
Tube		Name	Type
1	🟩	water (closed)	NC
2	🟩	water (open)	NC
3	🟥	W-2	PC
4	🟥	W-2	PC
5	🟥	W-2	PC
6	🟥	W-3	PC
7	🟥	W-3	PC
8	🟥	W-3	PC
9	🟥	W-4	PC
10	🟥	W-4	PC
11	🟥	W-4	PC
12	🟦	S-2	PC
13	🟦	S-2	PC
14	🟦	S-2	PC
15	🟦	S-3	PC
16	🟦	S-3	PC
17	🟦	S-3	PC
18	🟦	S-4	PC
19	🟦	S-4	PC
20	🟦	S-4	PC

Results: RdRp assay

Of note, the RdRp assay as described uses two probes.

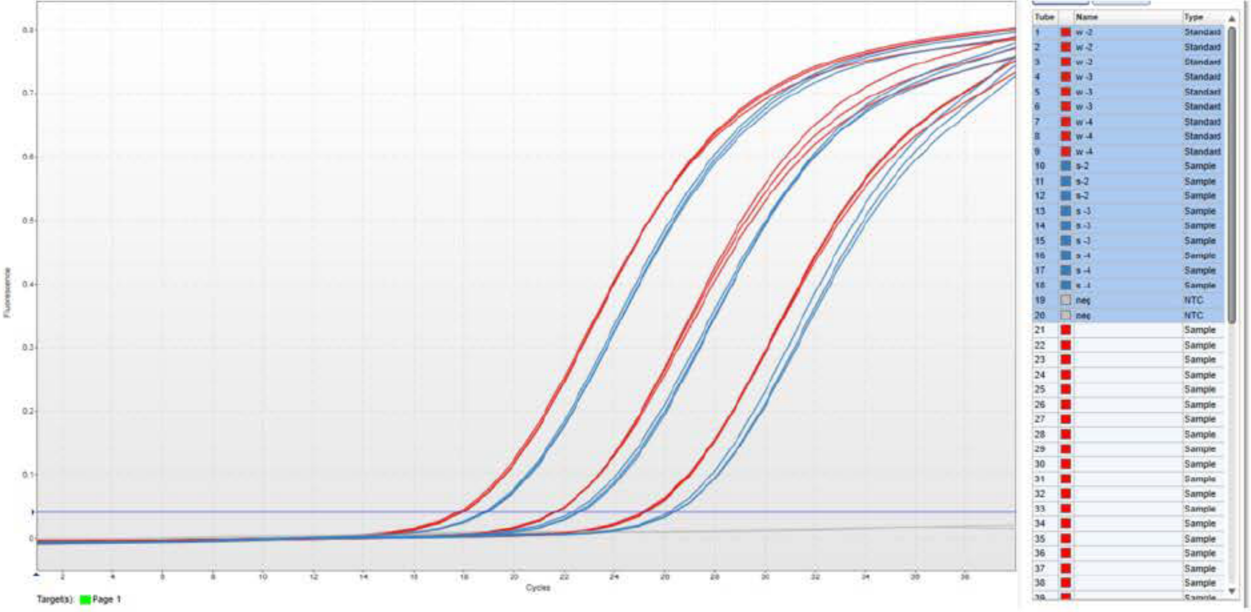
Forward primer GTGARATGGTCATGTGTGGCGG
Probe 1 FAM-CCAGGTGGWACRTCATCMGGTGATGC
Probe 2 FAM-CAGGTGGAACCTCATCAGGAGATGC
Reverse primer CARATGTTAAASACACTATTAGCATA

Results when both probes are included are as follows:



Tube		Name	Type
1	🟩	water (closed)	NC
2	🟩	water (open)	NC
3	🟥	W-2	Standard
4	🟥	W-2	Standard
5	🟥	W-2	Standard
6	🟥	W-3	Standard
7	🟥	W-3	Standard
8	🟥	W-3	Standard
9	🟥	W-4	Standard
10	🟥	W-4	Standard
11	🟥	W-4	Standard
12	🟦	S-2	PC
13	🟦	S-2	PC
14	🟦	S-2	PC
15	🟦	S-3	PC
16	🟦	S-3	PC
17	🟦	S-3	PC
18	🟦	S-4	PC
19	🟦	S-4	PC
20	🟦	S-4	PC

Using Probe 1 alone also works:

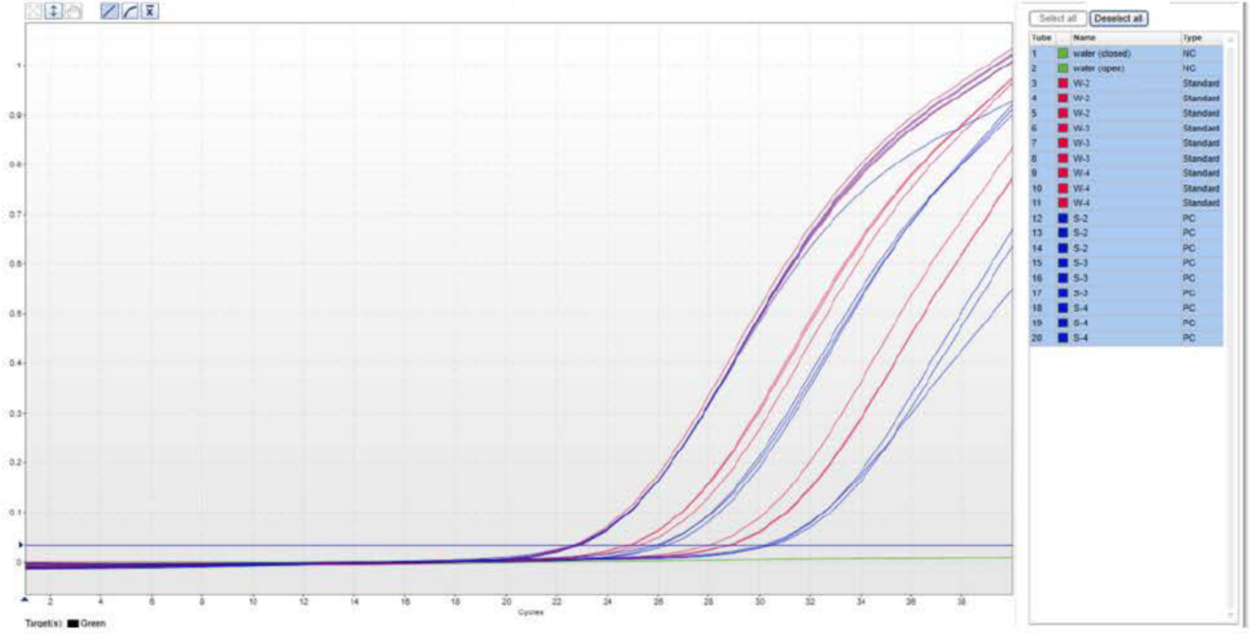


Tube		Name	Type
1	🟥	w -2	Standard
2	🟥	w -2	Standard
3	🟥	w -2	Standard
4	🟥	w -3	Standard
5	🟥	w -3	Standard
6	🟥	w -3	Standard
7	🟥	w -4	Standard
8	🟥	w -4	Standard
9	🟥	w -4	Standard
10	🟦	s-2	Sample
11	🟦	s-2	Sample
12	🟦	s-2	Sample
13	🟦	s -3	Sample
14	🟦	s -3	Sample
15	🟦	s -3	Sample
16	🟦	s -4	Sample
17	🟦	s -4	Sample
18	🟦	s -4	Sample
19	⬜	neg	NTC
20	⬜	neg	NTC
21	🟥		Sample
22	🟥		Sample
23	🟥		Sample
24	🟥		Sample
25	🟥		Sample
26	🟥		Sample
27	🟥		Sample
28	🟥		Sample
29	🟥		Sample
30	🟥		Sample
31	🟥		Sample
32	🟥		Sample
33	🟥		Sample
34	🟥		Sample
35	🟥		Sample
36	🟥		Sample
37	🟥		Sample
38	🟥		Sample

N assay

Forward primer	CACATTGGCACCCGCAATC
Probe	FAM-ACTTCCTCAAGGAACAACATTGCCA
Reverse primer	GAGGAACGAGAAGAGGCTTG

There is a mismatch in the N reverse primer with the WIV1 and SCH014 sequence. This may explain why these curves don't look as nice as with the previous two assays.



Tube		Name	Type
1	🟩	water (closed)	NC
2	🟩	water (open)	NC
3	🟥	W-2	Standard
4	🟥	W-2	Standard
5	🟥	W-2	Standard
6	🟥	W-3	Standard
7	🟥	W-3	Standard
8	🟥	W-3	Standard
9	🟥	W-4	Standard
10	🟥	W-4	Standard
11	🟥	W-4	Standard
12	🟦	S-2	PC
13	🟦	S-2	PC
14	🟦	S-2	PC
15	🟦	S-3	PC
16	🟦	S-3	PC
17	🟦	S-3	PC
18	🟦	S-4	PC
19	🟦	S-4	PC
20	🟦	S-4	PC

Work in progress

We are preparing T7 RNA transcribed standards for all three assays for use as positive controls. These will include a barcode sequence to detect contamination from this positive control.

From: Plowright, Raina
Sent: Thu, 6 Feb 2020 20:02:40 +0000
To: Maureen Kessler
Cc: Alison Peel; Mandy Todd; Mcguire, Liam; Adrienne D; Devin Jones MSU; Munster, Vincent (NIH/NIAID) [E]; Bushmaker, Trenton (NIH/NIAID) [E]
Subject: Re: UR fecal samples

We are working on a CDC permit for MSU (restarting the one we submitted before PREEMPT).

On Feb 6, 2020, at 10:26 AM, Maureen Kessler <[redacted] (b) (6) wrote:

Hi Ali & Mandy,

Attached are our fecal sample requests. I'm so sorry this took so long -- I was struggling with the different versions of the sample existence files (I only had access to the older version on Box, not the most recent one...) & shipping files, so tracking down where certain samples were located was tough!

I have organised these lists by including ALL the fecal samples for the accession number we're interested in, rather than specifying a random assortment of samples someone has to dig around for. My understanding was that we wanted to keep samples together where possible, but please let me know if that's changed and you'd prefer this parsed down more specifically. I'm not interested in all of these in the immediate sense, so we're happy to do so.

If possible, please let us know how many samples can squeeze into this round, and how many will have to wait. We can prioritise the more important ones.

Any way to cut down on samples going through RML?

- **Vincent & Trent,** from your perspective, is this too many samples?
- Manuel mentioned that the courier shipping costs $2/tube.
- if we had a CDC permit for MSU, would we be able to ship all inactivated samples straight to MSU? If there's a way I can help make this happen to lessen costs, happy to discuss.
    - The UR samples for diet analysis can go into formalin (inactivated)
    - Individual samples for cortisol analysis go into ethanol, and so do the swabs (also inactivated). If there's a way to Fedex these to MSU (or ship some other way), that's also a possibility.
    - This would require someone at Griffith to help subset samples into formalin and EtOH, which Trent is currently doing for us at RML

UR Samples

- Diet: I have included a list of samples from the first accession numbers we're hoping to process for microscopic diet analysis. **Adrienne**, I'm not sure which accession numbers or samples you were interested in, so please take a look! I'd hate to take something you might need later. I'm more than happy to discuss sample splitting, too. I'll only need a small portion of the total fecal sample.

- These are also only the first set of accession numbers we're tackling. I'll be wanting samples from more, so as Adrienne starts to select things it would be good to discuss how to share samples.
- Fecal cortisol**: Adrienne and Liam** - I have my protocol & lab supplies organized for the cort analysis of individuals, and I'm aiming to process the first samples within the next 2 or so weeks (pending RML availability to ship things over). I'd love to discuss the protocol with you to make sure we're on the same page. There also may be some opportunity to process a lot of your UR samples at MSU as well, so it would be good to chat. Are you guys (and maybe Ali) free for a quick Zoom call soon?

Capture samples

- If deciding between whether to send one or both samples from the same individual, we have a STRONG preference for the "fresh" sample. These are pretty critical for Devin's microbiome analyses.
- Both the bagged feces and swabbed feces are needed. The bagged feces are what will be used for the cortisol extractions, while swabs are used for sequencing.

As always, thank you all so much for everything. Teamwork makes the dream work!

Maureen (and Devin)

Maureen Kessler, ScM
Ph.D. Student | Bozeman Disease Ecology Lab
Department of Ecology
Montana State University

On Tue, Jan 28, 2020 at 7:45 AM Maureen Kessler <[redacted] (b) (6) wrote:
Gotcha. I'll only pick ones that I'm happy to be subdivided and brought to MSU immediately, too. Thanks!

On Mon, Jan 27, 2020 at 8:20 PM Alison Peel <[redacted] (b) (6) wrote:
Hi Maureen,
Brief email as in a rush today
Yes that would be good. cc Adrienne and Liam and Raina in the email. Also cc Vincent and Trent to keep them in the loop about what samples to expect. I know that they were concerned about the number of samples coming through RML.
We are preparing another shipment now, so please send **ASAP.** Or at least give an indication of the numbers of samples
looking forward to chatting!
Cheers
Ali

On Mon, 27 Jan 2020 at 04:54, Maureen Kessler <[redacted] (b) (6) wrote:
Hi Ali,

I've tried to coordinate with Adrienne about how we want to divvy up all the UR fecal samples, without much luck (and I think Devin has, too). At this point, would it be best if I just send you guys a list of the UR fecal samples I'd like to have shipped to MSU for our projects here, and Adrienne can work around or figure out how to share these?

I thought there were some UR samples already at RML, but I was mistaken -- I'm working on trialing the microscopy with some of the larger individual samples. Do we know when the next shipment is likely to come through...? I know the last one was held up and shipped back, so I'm not sure if it's messed with the timeline of things.

Finally, Brooklin, Tamika, and I had a nice meeting last week to talk about the project idea. We think we've refined her proposed plan a bit more, and we're probably at the stage where it's worth discussing things with you again (and possibly Liam?). Given that she'll need space and time for more frequent sampling, it would be good to chat about the winter sampling plans and how she might fit in with that. My schedule is flexible; Brooklin is most free Mondays and Fridays, or after 5 pm Bozeman time on other days.

Happy New Year! Hope all is well. Sending my love to the poor smoked out batties :(

Maureen

Maureen Kessler, ScM
Ph.D. Student | Bozeman Disease Ecology Lab
Department of Ecology
Montana State University

--
Maureen Kessler, ScM
Ph.D. Student | Bozeman Disease Ecology Lab
Department of Ecology
Montana State University

<2020-02-04_fecal_sample_request_UR.xlsx><2020-02-04_fecal_sample_request_capture.xlsx>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 5 Feb 2020 15:53:16 -0700
To: Raina Plowright; Emily Gurley; Schountz, Tony
Cc: Barbara Han; Colin Parrish; Hector Aguilar; Jamie Lloyd-Smith; Olivier Restif; Hamish McCallum; Letko, Michael (NIH/NIAID) [F]; Peter Hudson; Sara LaTrielle
Subject: Re: CoV proposal for DARPA

Then again, he should be proud to fund this world class team (or stupid not to),

Quality doesn't come cheap, although arguably we deliver quite the bang for the buck!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <[redacted] (b) (6)
Date: Wednesday, February 5, 2020 at 3:50 PM
To: '[redacted] (b) (6) <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Tony Schountz <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Collin Parrish <[redacted] (b) (6) Hector Aguilar <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Michael Letko <[redacted] (b) (6) Peter Hudson <[redacted] (b) (6) Sara LaTrielle <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

This helps thanks. [redacted] (b) (6) said up to 300K but more likely 150-200K. Getting the people to do the work and publish the papers is key! Will get all the numbers together then we can massage down to something doable.

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Wednesday, February 5, 2020 at 3:47 PM
To: Raina Plowright <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) "Schountz, Tony" <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Colin Parrish <[redacted] (b) (6) Hector Aguilar <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) "Letko, Michael (NIH/NIAID) [F]" <[redacted] (b) (6) Peter Hudson <[redacted] (b) (6) Sara LaTrielle <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

In order of appearance:

Baseline costs:
1 vircapseq: $10,000
2 organoids: $5000
3 phenotype screening: $30,000
4 evolution: $5000

baseline costs does not include hands, e.g post-doc ~ 55,000/year so it will probably need at least one post-doc (preferably for a minimum of 2 years or longer),

cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <(b) (6)
Date: Wednesday, February 5, 2020 at 3:29 PM
To: '(b) (6) <(b) (6) Emily Gurley <(b) (6) Tony Schountz <(b) (6)
Cc: Barbara Han <(b) (6) Collin Parrish <(b) (6) Hector Aguilar <(b) (6) Jamie Lloyd-Smith <(b) (6) Olivier Restif <(b) (6) Hamish McCallum <(b) (6) Michael Letko <(b) (6) Peter Hudson <(b) (6) Sara LaTrielle <(b) (6)
Subject: Re: CoV proposal for DARPA

Can you give me ball park today (I don't know if we are talking thousands, tens of thousands, or hundreds of thousands ☺)... a range of $$ off top of your head would help so I can structure 1 to 2 proposals within their budget range. Tomorrow will need accurate estimates. I think we should submit Friday at the latest unless there is a very good reason to wait until the weekend. I have heard that other groups are lining up for this funding!

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Wednesday, February 5, 2020 at 3:24 PM
To: Raina Plowright <(b) (6) Emily Gurley <(b) (6) "Schountz, Tony" <(b) (6)
Cc: Barbara Han <(b) (6) Colin Parrish <(b) (6) Hector Aguilar <(b) (6) Jamie Lloyd-Smith <(b) (6) Olivier Restif <(b) (6) Hamish McCallum <(b) (6) "Letko, Michael (NIH/NIAID) [F]" <(b) (6) Peter Hudson <(b) (6) Sara LaTrielle

<(b) (6)
Subject: Re: CoV proposal for DARPA

What timeline? Today or tomorrow,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <(b) (6)
Date: Wednesday, February 5, 2020 at 3:20 PM
To: Emily Gurley <(b) (6) "(b) (6)
<(b) (6) Tony Schountz <(b) (6)
Cc: Barbara Han <(b) (6) Collin Parrish <(b) (6)
Hector Aguilar <(b) (6) Jamie Lloyd-Smith
<(b) (6) Olivier Restif <(b) (6) Hamish McCallum
<(b) (6) Michael Letko <(b) (6)
Peter Hudson <(b) (6) Sara LaTrielle <(b) (6)
Subject: Re: CoV proposal for DARPA

I need cost estimates from everyone (Emily, I can use the one you gave me earlier…but need to add IDC to that—estimate of 3mths field work plus lab analyses in Bangladesh plus report indirect separately).

Tony, Vincent, need ball park costs from you too (& IDCs).

Olivier, thanks for the estimate and the modeling ideas.

Jamie, what are your thoughts on contributing? – I can create a space in the draft for you to add something tonight.

I'm looking at the draft now with great edits from Vincent and Tony and will resend for comments and specific inputs.

From: Emily Gurley <(b) (6)
Date: Wednesday, February 5, 2020 at 3:03 PM
To: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Raina Plowright <(b) (6) "Schountz, Tony"
<(b) (6)
Cc: Barbara Han <(b) (6) Colin Parrish
<(b) (6) Hector Aguilar <(b) (6) Jamie Lloyd-

Smith <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6)
Hamish McCallum <[redacted] (b) (6) "Letko, Michael (NIH/NIAID) [F]" <[redacted] (b) (6) Peter Hudson <[redacted] (b) (6) Sara LaTrielle <[redacted] (b) (6)
Subject: RE: CoV proposal for DARPA

Proposal looks good from my perspective. Please advise how else we can support getting it ready.

Emily

From: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Sent: Wednesday, February 05, 2020 2:42 PM
To: Raina Plowright <[redacted] (b) (6) Schountz, Tony <[redacted] (b) (6)
Cc: Barbara Han <[redacted] (b) (6) Colin Parrish <[redacted] (b) (6) Hector Aguilar <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6) Peter Hudson <[redacted] (b) (6) Sara LaTrielle <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

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T.
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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 5 Feb 2020 13:47:32 -0700
To: Jamie Lloyd-Smith
Cc: Raina Plowright; Schountz, Tony; Barbara Han; Colin Parrish; Hector Aguilar; Emily Gurley; Olivier Restif; Hamish McCallum; Letko, Michael (NIH/NIAID) [F]; Peter Hudson; Sara LaTrielle
Subject: Re: CoV proposal for DARPA

Very quick replies:

A few questions, mostly for Vincent, Michael and Tony:
- would you plan to test these viral traits in human/NHP airway epithelial cells, or better yet human-like organoid systems? It strikes me that the applied interest is less on bat intestines (since these viruses do fine in bats) and more on which coronaviruses can infect humans.

Yes (although there are currently no good of the shelf lung organoids, we are looking at bronchial tissue organoids), actually a good point as rather than solely focusing on bat intestinal tract it's the comparison between bat intestinal tract and human bronchial organoids is where the money is. E.g. comparison of the general receptors of coronaviruses and co-factors (proteases like TPMRSII) in mucosal tissues of lung vs intestine (or vise versa)

- what is the potential to do live virus experiments to test how insights from entry assays etc scale up to determine fitness? As for the current henipa project, we can't know how well our models without some live virus data.

Yes, interestingly the virus seems not to like many species (based on Michael's prelim data), so the initial data will be backed-up by live virus work (a bit more complicated as we need to make sure the the ACE2 is actually expressed on the surface as well to draw true conclusions).

- any data from in vivo challenges is of interest, including control arms of vaccine/drug trials (or even the non-control arms, in a pinch). Even if it's going to happen independent from this supplement request, it would be valuable to know about.

This will be generated, but will need to know what data would actually be useful. We have a vaccine paper (MERS-CoV) currently under review at Science advances which will give you a good idea what data we have)

- you said that NHP studies would have very low N, which makes sense. We may be able to model resulting data to maximize insights gained. You also said there might be humanized mouse expts or similar, which could allow for dose-response etc. Again that would be interesting. Even dose-response on cell culture or organoids might be of value -- would be interested in hearing your views on that. But bottom line is that any models would need some 'outcome data' to compare them to, or else they're just making untested and unsatisfying predictions.

Agreed, if we get $$$ we can invest in a bit more hands-on support for this. That could then be a post-doc focus, although that needs to be discussed with (b)(6) **as from my end it doesn't make sense to have post-docs less then 5 years (training and investment etc).**

Lastly, we are fast-tracking a whole set of aerosol and surface stability with MERS, SARS and 2019-NCoV for general public health information. Obviously, this data would be available for modeling if someone would be interested (but don't pin me down on the n of replicates, typically 3, its already quite complicated to run these studies in high containment with these kind of viruses).

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From: Jamie Lloyd-Smith <[redacted] (b) (6)
Date: Wednesday, February 5, 2020 at 1:34 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: Raina Plowright <[redacted] (b) (6) Tony Schountz <[redacted] (b) (6) Barbara Han <[redacted] (b) (6) Collin Parrish <[redacted] (b) (6) Hector Aguilar <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Michael Letko <[redacted] (b) (6) Peter Hudson <[redacted] (b) (6) Sara LaTrielle <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

Hi all,

Just catching up with this thread. Sounds like some exciting possibilities out of RML, which could fit nicely with on-going efforts on g-to-p modeling. Note that I've recruited a new modeler, Dylan Morris, who is focusing his initial work on linking molecular/in vitro data to in vivo data as a way of assessing host range for henipas. In the first round he will be focusing on dose-response relationships as a readout of fitness in a given host species. We are hoping to build mechanistically informed dose-response models that build on Amandine's work. [redacted] (b) (6) and will do his final chapter on this problem, then will join my lab as a postdoc. He is an excellent modeler and deep thinker.)

Quick question for Raina
- what timeline are we thinking about here? given [redacted] (b) (6) focus on 'the next one' does that mean this funding could extend beyond the end date of our current project?

A few questions, mostly for Vincent, Michael and Tony:
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cheers,
Jamie

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Phone: (b) (6)

https://www.eeb.ucla.edu/Faculty/lloydsmith/
Office: 4135 Terasaki Life Sciences Building
Lab: 4000 Terasaki Life Sciences Building

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Attachments: Proposals to DARPA on novel coronavirus.docx

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(b) (4), (b) (6)

[redacted]

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[redacted]

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[redacted]

From: Letko, Michael (NIH/NIAID) [F]
Sent: Wed, 5 Feb 2020 18:13:45 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: CoV proposal for DARPA
Attachments: figure.png

Here's an overview figure

-michael

--
Michael Letko, Ph.D
Postdoctoral IRTA
Dr. Vincent Munster Laboratory
Virus Ecology Unit, Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903S 4th Street
Hamilton MT 59840
[redacted] (b) (6)

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From: Tony Schountz <(b) (6)
Date: Wednesday, February 5, 2020 at 10:07 AM
To: Raina Plowright <(b) (6) "(b) (6) <(b) (6) Barbara Han <(b) (6) Collin Parrish <(b) (6) Hector Aguilar <(b) (6) Emily Gurley <(b) (6) Jamie Lloyd-Smith <(b) (6) Olivier Restif <(b) (6) Hamish McCallum <(b) (6) Michael Letko <(b) (6) Peter Hudson <(b) (6)
Cc: Sara LaTrielle <(b) (6) Tony Schountz <(b) (6)
Subject: Re: CoV proposal for DARPA

All, I've put in a couple of paragraphs for the first two items for you to review. There are a few comments for your consideration, as well.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Feb 5, 2020, at 9:34 AM, Raina Plowright <(b) (6) wrote:

V, can u and mike write this up or modify attached proposal?
In defense of cell line/immunology suggested—we want to do this but underfunded this part of our hnv work.

Sent from my iPhone

On Feb 5, 2020, at 8:06 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

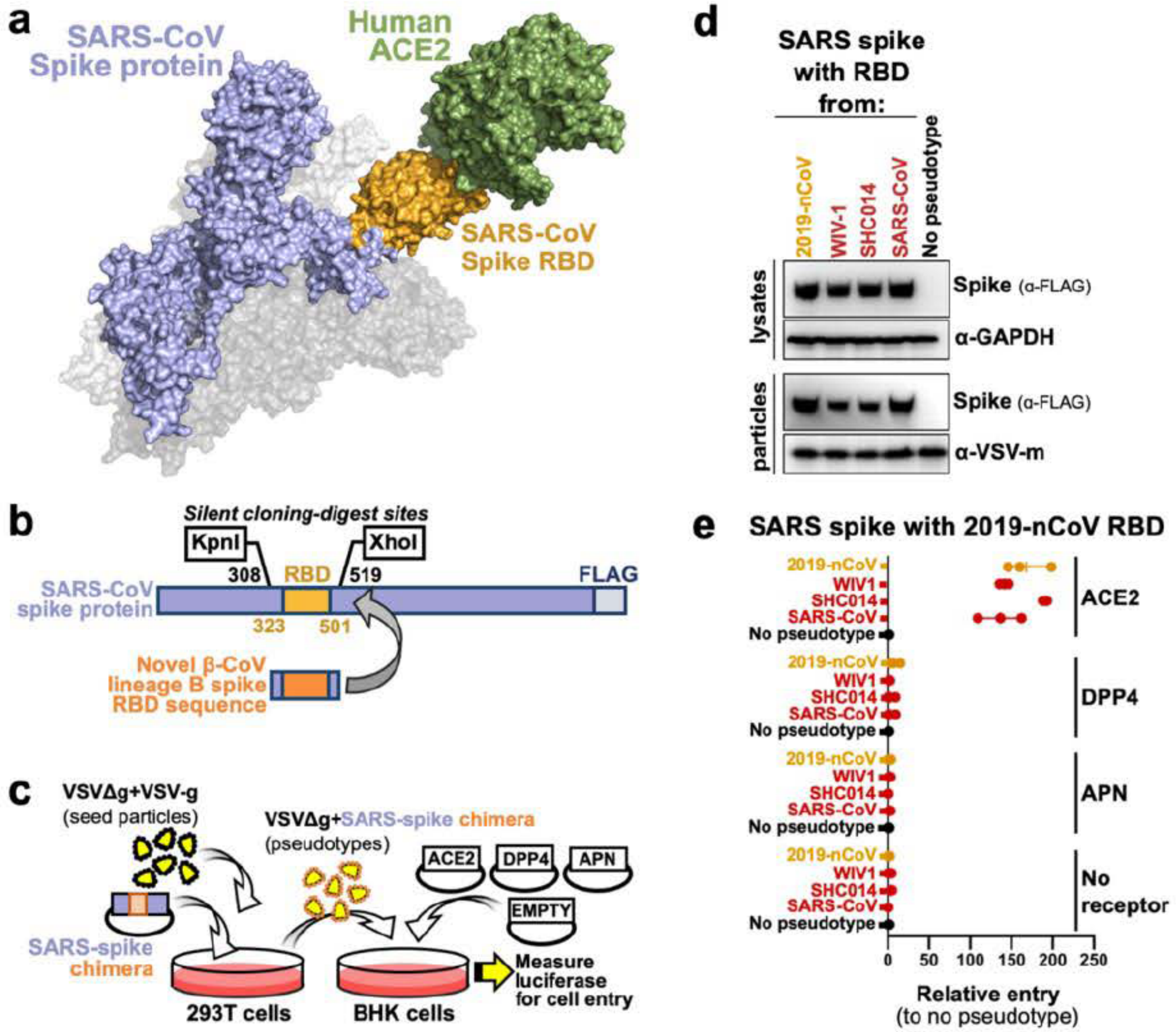
From my end, we should work on smtg which is currently the biggest question with emergence of these viruses otherwise it will be a lot of work which we al have plenty of already, 1 spatiotemporal dynamics, and that would bolster the Bangladesh team (in country analyses and full genome sequencing at RML), and potentially serology. This would be supported by most up-to-date assays developed at RML.

2 genotype-to-phenotypse analyses focused at the first step (entry) and second step (innate), the problem is that there are very few labs with up-to-date experience here as this would involve a very large part working on synthetic biology (reverse genetics), we have the spike part covered with Michael), but the innate part is a whole another beast (both form an experimental as a well a legislative and permit side) and I think simple growth-curve analyses would not be terribly informative here (and most cells might not be susceptible).

Cheers,

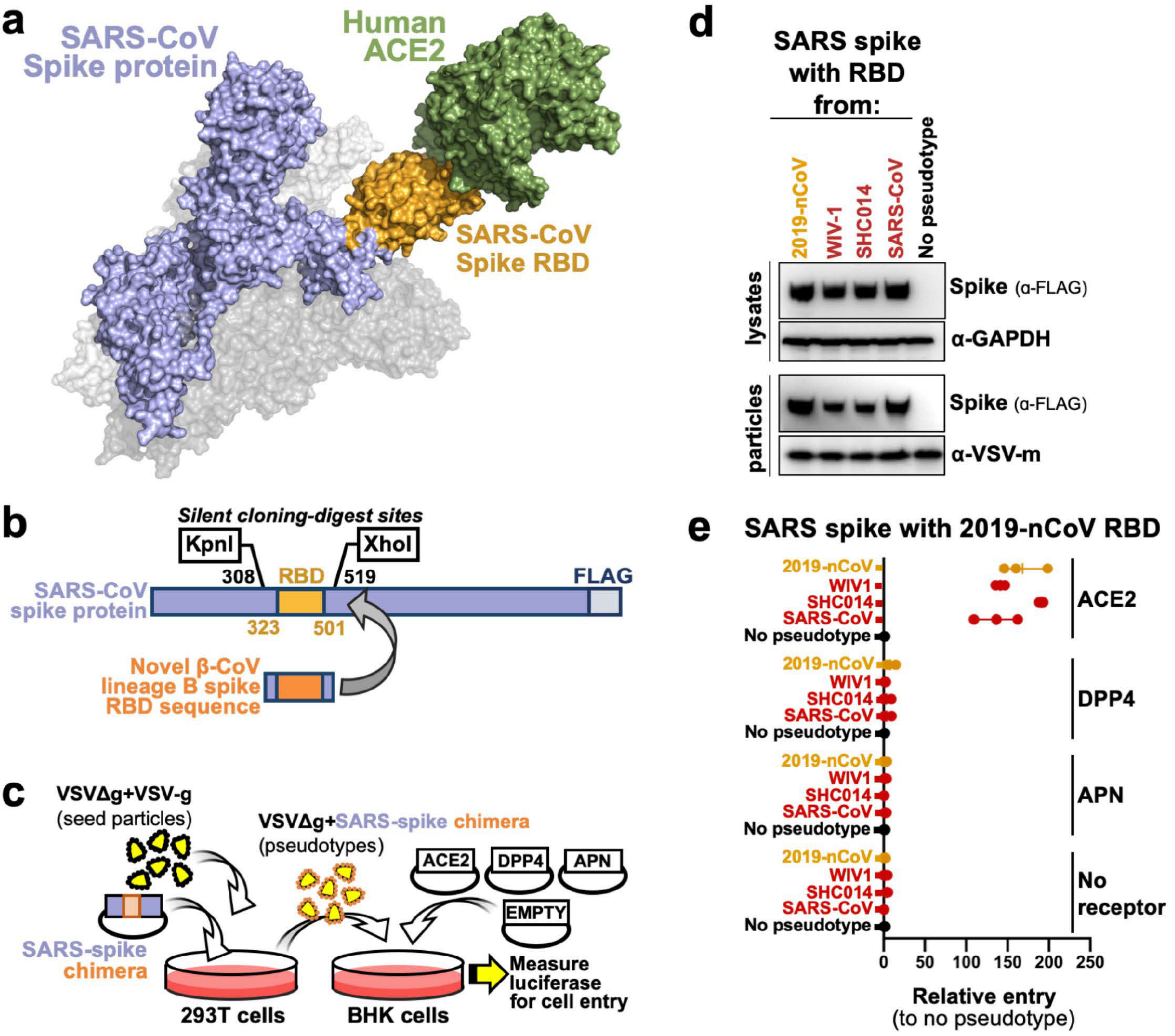
Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

2019-nCoV enters cells expressing human ACE2



a, β-Coronaviruses, including SARS-CoV, interact with the host cell receptor via the Receptor Binding Domain (RBD) in spike (PDB: 5X5B, 2AJF) . **b,** SARS-CoV spike was engineered with silent mutations to facilitate cloning novel RBD sequences in place of the SARS spike RBD. SARS spike amino acid numbers are indicated for silent cloning sites and the RBD in grey and orange, respectively. **c,** outline of experimental workflow. **d,** Expression and pseudotype incorporation of SARS-S-2019-nCoV RBD chimera. **e,** Pseudotypes were used to infect cells expressing human ACE2, DPP4, APN, or empty vector.

2019-nCoV enters cells expressing human ACE2



a, β-Coronaviruses, including SARS-CoV, interact with the host cell receptor via the Receptor Binding Domain (RBD) in spike (PDB: 5X5B, 2AJF) . **b,** SARS-CoV spike was engineered with silent mutations to facilitate cloning novel RBD sequences in place of the SARS spike RBD. SARS spike amino acid numbers are indicated for silent cloning sites and the RBD in grey and orange, respectively. **c,** outline of experimental workflow. **d,** Expression and pseudotype incorporation of SARS-S-2019-nCoV RBD chimera. **e,** Pseudotypes were used to infect cells expressing human ACE2, DPP4, APN, or empty vector.

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 5 Feb 2020 08:25:12 -0700
To: [redacted] (b) (6)
Cc: Plowright, Raina
Subject: Re: Bat1health: Future shipment and analysis plans

Hi Ali and Raina,

Realistically (and mentioned several times before) we are currently stretched to the max of our capacity (and far beyond what is covered by DARPA), so at this point we cannot take-on any more pan-paramyxo screening here at this lab. Just as a reminder: we are screening several 1000s of bat samples from Oz and Bangladesh (with pressure to prioritize from your end), doing pan-paramyxo screen on the Bangladesh samples, doing large-scale sequencing analyses, doing the majority of the cell work in BSL4 for Hector and Jaimie's work and will be doing bat infection in 4. It would be good to realize that these are not computer models we run but involve huge hands-on time-investments from my people.

We keep running into the same discussing with Hector and Jamie as well, there appears to be a clear knowledge gap in how much work it actually is to do experimental work.

In short: you can do qRT-PCRs on cDNA or we can just ship the RNA, both will be fine,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Alison Peel <[redacted] (b) (6)
Reply-To: '[redacted] (b) (6) <[redacted] (b) (6)
Date: Tuesday, February 4, 2020 at 5:30 PM
To: '[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Plowright, Raina" <[redacted] (b) (6)
Subject: Re: Bat1health: Future shipment and analysis plans

Hi Vincent,
Sorry to labour the point, but I'm still not 100% clear on what you're saying. I think you're saying Option 1 below, but I want to clarify the implications in terms of DARPA milestones.
Option 1: RML generates cDNA from all samples and ship all sample cDNA to Australia. The focus of my multiviral study is dynamics of a selection of PMV over time, so I don't have funding for family PMV PCRs and sequencing as well as the multiviral testing. Rather, I think we will likely run 1-2 multiplexed qPCRs.
Option 2: RML undertakes family PCRs to identify positives. RML ships cDNA to Australia. We could probably fund the sequencing (Sanger?). From a DARPA perspective, I thought you were keen to do the family PMV PCRs to get more sequences for the pipeline.
Your call, I just wanted to make sure I understood

Cheers,
Ali

On Wed, 5 Feb 2020 at 10:18, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
Agreed,

For the PCRs we would send cDNA and then the testing could be done in Oz

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <[redacted] (b) (6)
Date: Tuesday, February 4, 2020 at 5:12 PM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Cc: "[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Bat1health: Future shipment and analysis plans

Re FTA cards. Can you please send. Shouldn't be big deal for Trent to bring them here on his next trip. We are doing those in the lab here and they are already decontaminated.
CDC permit will take time and DNA extraction for this project can be done right now.

On Feb 4, 2020, at 5:07 PM, Alison Peel <[redacted] (b) (6) wrote:

Thanks Vincent.

Just to confirm:
- Ok to send FTA cards to RML?
- you'd do family PMV PCRs then generate cDNA on positives to send to Australia? or you don't want to do the family PCRs?

On Wed, 5 Feb 2020 at 10:03, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
Sounds good,

For the other screening, we would probably generate cDNA and send it for analyses in Oz

Lets see if we can add the language to the MTAs and move from there,

Cheers,

Vincent Munster, PhD

Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Alison Peel <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Tuesday, February 4, 2020 at 4:58 PM
To: "[redacted] (b) (6) <[redacted] (b) (6)
Cc: "Plowright, Raina" <[redacted] (b) (6)
Subject: Re: Bat1health: Future shipment and analysis plans

No. They have agreed in principle but it is not currently covered by MTAs. Sounds like there might be a bit more to-ing and fro-ing with each state about the wording in the MTA, but it's a step forward at least!

Vincent/Raina: Re: the Bartonella screening on the FTA cards - would it be preferable to send to RML or wait til CDC permits are in place at MSU and send directly there? I'd have to check whether they are covered by our current export permits and whether they could be included in the shipment planned for Monday

Vincent - re the PMV screening, I'm trying to remember the details of what prompted this to come up again. I think during a discussion about Hendra and Cedar on our call, Sarah enquired about what we knew about other viruses. I think there was then a discussion about possibly doing the generic PMV PCR as a screening test for the presence of other PMV. That could either target the samples to have cDNA created for further screening back in Australia, or possibly request sequencing at RML. I know your capacity is stretched. What would be your preference for moving forward with that if you had the opportunity to run the PMV family PCR?

On Wed, 5 Feb 2020 at 09:54, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
So we are good then? Just double and triple checking before we start isolating Hendra!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" <[redacted] (b) (6)
Date: Tuesday, February 4, 2020 at 2:58 PM
To: Alison Peel <[redacted] (b) (6)
Cc: "[redacted] (b) (6) <[redacted] (b) (6)
Subject: Re: Bat1health: Future shipment and analysis plans

Bloody AWESOME!!!!! well done Ali!

On Feb 4, 2020, at 2:52 PM, Alison Peel <[redacted] (b) (6) wrote:

Good news. Now we need to get MTAs to permit for this work on retrospective samples.

---------- Forwarded message ---------
From: **Sarah Britton** <[redacted] (b) (6)
Date: Wed, 5 Feb 2020 at 7:01 am
Subject: Re: Bat1health: Future shipment and analysis plans
To: Plowright, Raina <[redacted] (b) (6)
Cc: Alison Peel <[redacted] (b) (6) Allison Crook - Department of Agriculture and Fisheries
([redacted] (b) (6) <[redacted] (b) (6) THOMPSON Fiona
<[redacted] (b) (6) Paul Freeman <[redacted] (b) (6)

Hi Alison and Raina,

I apologise for the delay in replying to your emails and pleased to say that Mark , Fiona/Allison and I have discussed the details of your proposal . Thank you for your patience and supplying the additional information as requested. We do support the research requests as outlined below to be undertaken at Rocky Mountain Laboratories.

1. Hendra and Cedar PCR and sequencing (as previously requested and approved)
2. Hendra and Cedar virus isolation from samples that have tested positive in PCR assays- further detail below
3. PCRs and sequencing of blood-borne bacteria in the genera Borrelia and Bartonella (from dried blood spots)
4. Regarding testing for the nine known paramyxoviruses in bats, I understand that Alison Peel will write a separate proposal and send shortly?

Both NSW and QLD will contact you separately to discuss the MTA and any specific requirements for each jurisdiction. We look forward to continuing to work with you on this important research.

Kind regards

Sarah

arah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: [redacted] (b) (6) | M: [redacted] (b) (6)
E: [redacted] (b) (6)
W: www.dpi.nsw.gov.au

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On Fri, 17 Jan 2020 at 05:51, Plowright, Raina <[redacted] (b) (6) wrote:
Dear Sarah, Allison, and Fiona,

Let me know if I can answer any questions for you.

Whole genome sequencing (only possible from isolates) is a high-priority for us and we can't move the phylodynamic modeling forward without this. We will learn so much by having full genome sequences of Hendra virus (e.g. sequence of Hendra virus from bat of known age —aged through Alison Peel's teeth analyses—may help us resolve if bats are persistently infected with Hendra virus).

With isolates, we can also do simple viral survival experiments at microclimates found in horse paddocks. These experiments will tell us how long horses should be separated from trees that bats are feeding in. We tried to get AAHL to do these experiments a few years ago but they couldn't allocate the funding to it. RML is willing to provide us with this useful information, despite the considerable expense.

Best,

Raina

On Jan 12, 2020, at 6:18 PM, Alison Peel <[redacted] (b) (6) wrote:

Dear Sarah, Allison and Fiona,

Firstly, Allison, I wanted to thank you again in your assistance on Christmas Eve in getting our shipment being processed at customs. Our application was processed that day and the samples are safely back in the freezer, while we re-organise a new shipment date. We are extremely grateful to everyone who helped make that happen!

Secondly, I wanted to follow up on our previous request regarding virus isolation. Would a conference call be the best way to progress this? As discussed in my previous email, we hope that the following amendments to any future MTAs will address any concerns that you or Mark may have:

- **Griffith to notify CVOs of any viruses isolated**
    - I propose that this is explicitly included as one of the conditions of export approval from CVOs. ie. Export approval is provided with the following conditions:
        - use the written approval to accompany each shipment.
        - send notification in writing immediately following the despatch of specimens to the United States of America including the details of the specimens despatched.
        - notify of results as they arise***, including isolation of any viruses***
        - meet the requirements of the "Policy for the Transfer of Biological Specimens to Overseas Laboratories for Infectious and Parasitic Disease Testing".

- **RML to provide any viral isolates to AAHL on request.**
    - To address this, the following sentence has been added to the MTA: "*Subject to availability and reasonable request of Griffith, the Recipient may provide viral isolates obtained from the Material to the Commonwealth Scientific and Industrial Research Organisation Australian Animal Health Laboratory, Geelong.*" (see track changes in the attached document).
    - I would be happy to notify an appropriate person at AAHL of the isolation, or CVOs could pass on the notification
    - Transfer of isolates from RML to AAHL could be performed under an SLA ("Simple Letter Agreement"). I have attached an example SLA here. (Also, note that in the previous email, I expanded the acronym "SLA" incorrectly as Service Level Agreement).

If the MTA and procedural amendments proposed above are acceptable, then we will also draft comparable amendments to existing MTAs to cover samples that have previously been shipped to RML.

Please let me know if you have any questions. I'd be happy to discuss any of this over the phone or on a conference call if it's easier than emails.

Many thanks, Happy New Year, and all the best regarding the remainder of the fire season.

Alison

On Tue, 17 Dec 2019 at 16:18, Alison Peel < (b) (6) wrote:
Dear Sarah, Allison and Fiona,

I wanted to provide an update regarding our request to attempt Hendra and Cedar virus isolation and sequencing from samples that have tested positive in PCR assays at RML. One of your questions was regarding controls over the use of isolated viruses outside of Australia. We have confirmed with the legal team at RML that formal Amendments could be made to existing and future MTAs regarding the Agreed Purpose (permitted use) of samples. These amendments could state that virus isolation is permitted on nominated previously shipped samples, but that any viruses isolated may only be used for the purposes specified in the Amendment. e.g. only for sequencing and phenotypic characterization of isolated strains associated with microclimate survival studies. RML would be required to report any successful isolations to Griffith University, and it is already a condition of CVO approval of shipments that I would notify you of any results — which would include those isolations. The RML legal team have confirmed that a condition could be included in the Amendment stating that RML would offer aliquots of any viruses isolated to AAHL. This would be administered between RML and AAHL via a Service Level Agreement.

We, as researchers, feel that results from these BSL-4 studies will represent significant gains in understanding and prediction of local risk factors for Hendra virus spillover risk, and justify the considerable laboratory expenditure associated with them. In order to achieve this, we are happy to continue discussions to identify an approach and set of agreements that are acceptable to you all, and to Mark. I welcome any feedback you have at this point, but recognising pressures in the lead up to Christmas shut-down periods, I am happy to raise it again with you in the New Year. I will continue working with the legal teams to develop the amendments and can present those to you then.

Wishing you a relaxing and enjoyable break over the holiday period!

Kind Regards,

Alison

On Fri, 22 Nov 2019 at 13:21, Alison Peel < (b) (6) wrote:
Dear Sarah, Allison and Fiona,

A short answer is that, under the MTAs, all samples and their derivatives *can only be used for the specific testing stipulated in the MTA* and all unused samples etc must be destroyed. Therefore, the use of the samples (or any derivatives of them) for any other purposes would constitute a breach of contract. For virus isolation, the isolated viruses would be considered a derivative, and therefore, under your guidance, we can explicitly state how those viruses could be used. e.g. only for whole genome sequencing and virus survival studies, for example. We could also include a clause that AAHL will be notified (through whatever mechanism is preferable to you all) of viruses isolated and that aliquots of these viruses be made available to AAHL on request. Vincent Muster at RML is very happy to do that, as AAHL have previously shared viruses with him.

More generally, the arrangements within our research subcontracts mean that (1) each research entity will own the IP each creates and (2) because the research is funded by a US agency, the US government also has rights to use, adapt and modify all IP created.
However, the isolated virus and the sequencing information generated from it are generally not considered to be IP under Australian and US legislation. More intervention/creation needs to involved than simple isolation and sequencing of something that exists in nature.

Regarding making sequences publically available, this is usually required as part of the publication process (made public in an online repository such as genbank after the paper is published). Our MTA has a Special Condition (#3, on page 4 of the MTA) regarding the release of test data. i.e., RML must provide Griffith with test results and Griffith will notify the Australian and State CVOs of these test results. Prior to publication or public disclosure of test results, Griffith retains the right to remove confidential information (e.g. this could include information about the specific source of the sample). Also under the Australian Policy for the Transfer of Biological Specimens to Overseas Laboratories, Griffith requires approval from the State CVOs prior to the release of test results suggesting the presence of an infectious agent not known to occur in Australia.

Hopefully, this answers all the questions sufficiently. I would be keen to hear your thoughts on potential conditions surrounding virus isolation (as proposed in my first paragraph above), but suspect it may take a little bit more time to finalise the exact wording and get it incorporated into a future MTA (or an addendum to existing MTAs). Because we are keen to get a shipment away early next week so that we can keep the PCR screening rolling along, I will submit a request to you both for sending samples - but just for the range of testing that we have already obtained approval for on other samples. We can then work through discussions about the other components.

Thanks
Alison

On Fri, 22 Nov 2019 at 10:56, Sarah Britton < (b) (6) wrote:

Hi Alison,

Yes I think that would be helpful. I have also copied Fiona and Allison in too in case they have any comments

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: (b) (6) | M: (b) (6)
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W: www.dpi.nsw.gov.au
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On Fri, 22 Nov 2019 at 11:33, Alison Peel < (b) (6) wrote:
Hi Sarah,

Would it help if there was a clause within the MTA on what the viruses could be used for, and also if aliquots of the viruses be made available for transferral to AAHL?

Thanks
Alison

On Fri, 22 Nov 2019 at 10:26 am, Sarah Britton < (b) (6) wrote:
HI Alison,

The main concern is that currently most of the viruses (ie Hendra/ Cedar/Menangle samples) sit at AAHL and Mark expressed concern that if virus is isolated o/s from Aust samples then this could be used for other purposes and is outside the control of Australia.
Also as you state , the control of info that would be released into the public domain.

Kind regards

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
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On Fri, 22 Nov 2019 at 10:34, Alison Peel < (b) (6) wrote:
Hi Sarah,

I'm expecting more feedback from the uni this morning, but to make sure we get all the information we need, can I clarify if there is a specific concern? Is it primarily about the process by which sequences would or would not be released into the public domain?

I am around today to discuss (though there may be a small child in the background!), and will hopefully get back to you later this morning once I've heard from our legal team.

Thanks
Alison

On Wed, 20 Nov 2019 at 9:11 pm, Alison Peel (b) (6) wrote:
Hi Sarah,

Many thanks for your efforts in getting that conversation to happen, and for your positive feedback. I have some understanding about the IP situation, but will clarify things with our lawyers to be certain and will get back to you by Friday.

Kind Regards,

Alison

On Wed, 20 Nov 2019 at 20:58, Sarah Britton < (b) (6) wrote:
Hi Alison and Raina,

Managed to speak to both Allison and Mark today. We support the research you are doing and keen to see it progress. The question Mark had was about who owns the IP of the virus and phylogenetic data? I can chat to you on Friday about this if suits, as I am in the field tomorrow.

Kind regards

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
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On Wed, 20 Nov 2019 at 08:46, Sarah Britton <[redacted] (b) (6) wrote:
Hi Alison,

I apologise for the delay in replying but have been trying to catch Allison and Mark to discuss this. I have managed to catch Allison and we need to run it past Mark- as soon as we have done that , I will contact you. It should be this week as he is away next week .

Kind regards,

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: [redacted] (b) (6) | M: [redacted] (b) (6)
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On Mon, 18 Nov 2019 at 09:53, Alison Peel [redacted] (b) (6) wrote:
Hi Sarah,

I hope to be submitting a shipment request to you later this week. We are in the process of getting the required MTAs finalised and it would be helpful to hear your thoughts on which of the following sample testing you consider reasonable to request (further details in the previous emails in this thread):

1. Hendra and Cedar PCR and sequencing (as previously requested and approved)
2. Hendra and Cedar virus isolation from samples that have tested positive in PCR assays
3. PCRs and sequencing of blood-borne bacteria in the genera Borrelia and Bartonella (from dried blood spots)

Thanks very much,

Alison

On Thu, 7 Nov 2019 at 22:01, Alison Peel (b) (6) wrote:
Dear Sarah,

Following on from my previous email, I've included some further information below on the rationale behind our request for permission to undertake virus isolation at Rocky Mountain Laboratories.

- **Hendra virus evolution**
    - Currently, there is only very limited full genome data available for Hendra virus (fewer than 11 full genomes). The lack of available genomes hampers our ability to understand the continuous evolution of Hendra virus and the assessment of effective countermeasures (that is, the monoclonal antibody used as post-exposure prophylaxis in high-risk human cases (M102.4) and the Hendra horse vaccine). The ability to sequence full genomes from Hendra virus is directly related to the amount of virus in the sample. Viral replication during viral isolation increases the amount of virus in the sample, meaning that subsequent full genome sequencing yields the highest quality of full genome sequences with the highest success rate.
- **Hendra virus survival**
    - Limited phenotypic data is available on the environmental stability of Hendra viruses, or the variation in environmental stability between different Hendra virus lineages. However, environmental stability is a crucial layer between the release of the virus in urine from the bat to the infection of the horse. In order to understand this critical step in cross-species transmission of Hendra virus we have unique and sophisticated set-up in the NIH, RML BSL4 laboratory consisting of an environmental chamber (with the ability to manipulate temperature and humidity and therefore the effect of those on viral survival) and a so-called Goldberg drum, which keeps virus is suspension and studies the effect of said environmental parameters on the survival (viability) of Hendra virus. The current set-up is the only set-up available in a maximum containment facility. This is an exciting opportunity to better understand the role of Hendra virus survival under different microclimatic conditions in explaining the discrepancy between high rates of Hendra virus excretion from flying foxes, yet low numbers of successful spillover to horses. In order to understand phenotypic differences associated with enhanced environmental survival and subsequent spillover to horses, we would need virus isolates.

I hope this further explanation is helpful and I look forward to hearing your thoughts.

Kind Regards,

Alison

On Wed, 6 Nov 2019 at 09:15, Alison Peel < (b) (6) wrote:
Dear Sarah,

Thanks for your interest in our research and for the positive feedback during our call yesterday. I have attached the spillover response pamphlet and the multiviral paper that we discussed.

Regarding isolation of Hendra and Cedar virus (for whole genome sequencing and virus survival studies), should we add that to our next shipment request or does this need discussion with Mark Schipp? I can provide further details on the methods if helpful. I also mentioned isolation to Allison Crook this week so it would be worth discussing if you two meet.

Regarding testing for the nine known paramyxoviruses in bats, I will write a separate proposal and send to you shortly.

One last matter that was just brought to my attention is the collection of blood droplets on FTA cards — we hope to extract DNA from these dried blood spots to detect the presence of blood-borne bacteria of flying foxes in the genera *Borrelia* and *Bartonella*. We hope to use presence and quantity of these bacteria as an indicator of health (alongside a number of immune and body condition metrics). The purpose is to get a holistic picture of flying fox health that we can then compare to the ecological and virological (Hendra virus status) information. Is this a reasonable request? It is not absolutely essential to our project but we do have a postdoc who raised the money to do the DNA extractions and PCR and it would add another layer of information into our project.

Thanks,
Alison

ALISON PEEL BSc(Vet) BVSc MSc PhD

DECRA Senior Research Fellow, Griffith Wildlife Disease Ecology Group
Environmental Futures Research Institute, Sir Samuel Griffith Centre (N78) 2.23
Griffith University, Nathan Campus, 170 Kessels Rd, Nathan, QLD, 4111, Australia

Office days: Monday - Thursday

E: (b) (6) (b) (6)
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@ali_bat
www.bat1health.org
www.mccallum-disease-ecology.com/alison-peel
https://experts.griffith.edu.au/academic/a.peel

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<SLA Provider.docx><2019 Draft MTA to allow virus isolation.docx>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 5 Feb 2020 08:14:09 -0700
To: Letko, Michael (NIH/NIAID) [F]
Subject: FW: CoV proposal for DARPA
Attachments: Proposals to DARPA on novel coronavirus.docx

Put a big stamp on this and make sure you get money for at least 1-2 PhD student in there (and consumables)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <(b) (6)
Date: Tuesday, February 4, 2020 at 6:03 PM
To: '(b) (6) <(b) (6) Barbara Han <(b) (6) Tony Schountz <(b) (6) Collin Parrish <(b) (6) Hector Aguilar-Carreno <(b) (6) Emily Gurley <(b) (6) Jamie Lloyd-Smith <(b) (6) Olivier Restif <(b) (6) Hamish McCallum <(b) (6) Michael Letko <(b) (6)
Cc: "LaTrielle, Sara" <(b) (6) Peter Hudson <(b) (6)
Subject: CoV proposal for DARPA

Hi all,

I had exactly 35 minutes of free time since our call, so please understand that this is written in extreme haste but we must get started so we can submit something by Friday.

Please slash and burn reshape/edit this 1pager. G-P section needs to be developed (Vincent, Jamie, Tony et al.). Reply -to-all to keep the momentum!

We could pitch these 2 ideas to (b) (6) so he can pick and choose sections or fund as a block. If the G-P section doesn't improve, perhaps we can include it as a section in spatiotemporal dynamics and change the overall heading to "Translating surveillance into knowledge".

Budgets: I reached out to (b) (6) for specifics he said exactly this: **"Aim for under 300K and maybe closer to 150-200."** This is small change when you add in IDCs. :-(But its an amazing start given how much of this piggy backs on current work, and remember that (b) (6) is already talking about a PREEMPT II!

Please take quick look and share your ideas and edits. **Return by end of tomorrow** so we can do an extra round on Thursday and submit by Friday.

Thanks,

Raina

PS I worry about our other pitch on serology and Hector's strip diagnostics as I really want to see that funded but I think the CoV is a different pot coming straight from Brad (BTO head). I will check with (b) (6) this week.

____
Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: (b) (6)
Lab website: http://bzndiseaselab.org
Phone: (b) (6)

(b) (4), (b) (6)

(b) (4), (b) (6)

[redacted]

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 5 Feb 2020 08:06:39 -0700
To: Raina Plowright; Schountz, Tony
Cc: Barbara Han; Colin Parrish; Hector Aguilar-Carreno; Emily Gurley; Jamie Lloyd-Smith; Olivier Restif; Hamish McCallum; Letko, Michael (NIH/NIAID) [F]; LaTrielle, Sara; Peter Hudson
Subject: Re: CoV proposal for DARPA

From my end, we should work on smtg which is currently the biggest question with emergence of these viruses otherwise it will be a lot of work which we al have plenty of already,

1 spatiotemporal dynamics, and that would bolster the Bangladesh team (in country analyses and full genome sequencing at RML), and potentially serology. This would be supported by most up-to-date assays developed at RML.
2 genotype-to-phenotypse analyses focused at the first step (entry) and second step (innate), the problem is that there are very few labs with up-to-date experience here as this would involve a very large part working on synthetic biology (reverse genetics), we have the spike part covered with Michael), but the innate part is a whole another beast (both form an experimental as a well a legislative and permit side) and I think simple growth-curve analyses would not be terribly informative here (and most cells might not be susceptible).

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Raina Plowright <[redacted] (b) (6)
Date: Wednesday, February 5, 2020 at 7:25 AM
To: Tony Schountz <[redacted] (b) (6)
Cc: '[redacted] (b) (6) <[redacted] (b) (6) Barbara Han <[redacted] (b) (6) Collin Parrish <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Michael Letko <[redacted] (b) (6) "LaTrielle, Sara" <[redacted] (b) (6) Peter Hudson <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

I think its worth discussing the Bangladesh sampling. I am very keen to get more money to Bangladesh but 3 months of additional sampling would take ~50-75% of the available funds. It would be great to get a spatiotemporal dataset on CoV but it would be at the cost of other opportunities. An alternative approach could be to bolster the immunology studies by getting bat cell lines from a few species (HNV and CoV reservoir hosts) and doing cell culture experiments for immune gene expression and for G-P work. This would push our henipa work forward. I'm open to different ideas so lets discuss what is most strategic for our group.

On Feb 5, 2020, at 7:10 AM, Schountz,Tony <[redacted] (b) (6) wrote:

This is great news. I'll put in the bat infections and send out my proposed section to everyone this morning.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

From: Raina Plowright <[redacted] (b) (6)
Sent: Wednesday, February 5, 2020 7:00 AM
To: Vincent Munster <[redacted] (b) (6) Barbara Han <[redacted] (b) (6) Schountz,Tony <[redacted] (b) (6) Colin Parrish <[redacted] (b) (6) Hector Aguilar-Carreno <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Olivier Restif <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6) Letko, Michael (NIH/NIAID) [F] <[redacted] (b) (6)
Cc: LaTrielle, Sara <[redacted] (b) (6) Peter Hudson <[redacted] (b) (6)
Subject: Re: CoV proposal for DARPA

From DARPA ACURO liaison re: can we expedite CoV proposals: "We won't need to expedite. ACURO has sped up reviews significantly and is now reviewing submissions basically as soon as they are submitted. Once I see the submission go through I will send another email to ACURO letting them know it is a priority."

On Feb 4, 2020, at 6:04 PM, Raina Plowright <[redacted] (b) (6) wrote:

Use this version (hadn't saved b4 attaching).
Raina

<Proposals to DARPA on novel coronavirus.docx>

____
Raina Plowright BVSc MS PhD
Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: [redacted] (b) (6)

Lab website: http://bzndiseaselab.org
Phone: (b) (6)

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Assistant Professor
Department of Microbiology & Immunology
Montana State University
Email: (b) (6)
Lab website: http://bzndiseaselab.org
Phone: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 5 Feb 2020 07:45:49 -0700
To: Schountz, Tony
Subject: Re: CoV proposal for DARPA

Caveat, the artibeus cells don't seem to be permissive with pseudo types (we'll confirm with live virus soon), obviously its just pseudo types and kidney cells (for which we don't know the ACE2 expression)

That doesn't mean you should put in the proposal (as you should), but just to give an heads-up

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Tony Schountz <(b) (6)
Date: Wednesday, February 5, 2020 at 7:18 AM
To: Raina Plowright <(b) (6) '(b) (6)
<(b) (6) Barbara Han <(b) (6) Collin Parrish
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Email: [redacted] (b) (6)
Lab website: http://bzndiseaselab.org
Phone: [redacted] (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 4 Feb 2020 16:54:27 -0700
To: Plowright, Raina; Alison Peel
Subject: Re: Bat1health: Future shipment and analysis plans

So we are good then? Just double and triple checking before we start [redacted] (b) (4)

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" < [redacted] (b) (6)
Date: Tuesday, February 4, 2020 at 2:58 PM
To: Alison Peel < [redacted] (b) (6)
Cc: ' [redacted] (b) (6) < [redacted] (b) (6)
Subject: Re: Bat1health: Future shipment and analysis plans

Bloody AWESOME!!!!! well done Ali!

On Feb 4, 2020, at 2:52 PM, Alison Peel < [redacted] (b) (6) wrote:

Good news. Now we need to get MTAs to permit for this work on retrospective samples.

---------- Forwarded message ---------
From: **Sarah Britton** < [redacted] (b) (6)
Date: Wed, 5 Feb 2020 at 7:01 am
Subject: Re: Bat1health: Future shipment and analysis plans
To: Plowright, Raina < [redacted] (b) (6)
Cc: Alison Peel < [redacted] (b) (6) Allison Crook - Department of Agriculture and Fisheries ([redacted] (b) (6) < [redacted] (b) (6) THOMPSON Fiona < [redacted] (b) (6) Paul Freeman < [redacted] (b) (6)

Hi Alison and Raina,

I apologise for the delay in replying to your emails and pleased to say that Mark , Fiona/Allison and I have discussed the details of your proposal . Thank you for your patience and supplying the additional information as requested. We do support the research requests as outlined below to be undertaken at Rocky Mountain Laboratories.

1. Hendra and Cedar PCR and sequencing (as previously requested and approved)

2. Hendra and Cedar virus isolation from samples that have tested positive in PCR assays- further detail below
3. PCRs and sequencing of blood-borne bacteria in the genera Borrelia and Bartonella (from dried blood spots)
4. Regarding testing for the nine known paramyxoviruses in bats, I understand that Alison Peel will write a separate proposal and send shortly?

Both NSW and QLD will contact you separately to discuss the MTA and any specific requirements for each jurisdiction. We look forward to continuing to work with you on this important research.

Kind regards

Sarah

arah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: (b) (6) M: (b) (6)
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On Fri, 17 Jan 2020 at 05:51, Plowright, Raina (b) (6) wrote:
Dear Sarah, Allison, and Fiona,

Let me know if I can answer any questions for you.

Whole genome sequencing (only possible from isolates) is a high-priority for us and we can't move the phylodynamic modeling forward without this. We will learn so much by having full genome sequences of Hendra virus (e.g. sequence of Hendra virus from bat of known age —aged through Alison Peel's teeth analyses—may help us resolve if bats are persistently infected with Hendra virus).

With isolates, we can also do simple viral survival experiments at microclimates found in horse paddocks. These experiments will tell us how long horses should be separated from trees that bats are feeding in. We tried to get AAHL to do these experiments a few years ago but they couldn't allocate the funding to it. RML is willing to provide us with this useful information, despite the considerable expense.

Best,

Raina

On Jan 12, 2020, at 6:18 PM, Alison Peel <(b) (6) wrote:

Dear Sarah, Allison and Fiona,

Firstly, Allison, I wanted to thank you again in your assistance on Christmas Eve in getting our shipment being processed at customs. Our application was processed that day and the samples are safely back in the freezer, while we re-organise a new shipment date. We are extremely grateful to everyone who helped make that happen!

Secondly, I wanted to follow up on our previous request regarding virus isolation. Would a conference call be the best way to progress this? As discussed in my previous email, we hope that the following amendments to any future MTAs will address any concerns that you or Mark may have:

(b) (4)

(b) (4) I have attached an example SLA here. (Also, note that in the previous email, I expanded the acronym "SLA" incorrectly as Service Level Agreement).

If the MTA and procedural amendments proposed above are acceptable, then we will also draft comparable amendments to existing MTAs to cover samples that have previously been shipped to RML.

Please let me know if you have any questions. I'd be happy to discuss any of this over the phone or on a conference call if it's easier than emails.

Many thanks, Happy New Year, and all the best regarding the remainder of the fire season.

Alison

On Tue, 17 Dec 2019 at 16:18, Alison Peel <[redacted] (b) (6) wrote:
Dear Sarah, Allison and Fiona,

I wanted to provide an update regarding [redacted] (b) (4) – [redacted]

[redacted] to you all, and to Mark. I welcome any feedback you have at this point, but recognising pressures in the lead up to Christmas shut-down periods, I am happy to raise it again with you in the New Year. I will continue working with the legal teams to develop the amendments and can present those to you then.

Wishing you a relaxing and enjoyable break over the holiday period!

Kind Regards,

Alison

On Fri, 22 Nov 2019 at 13:21, Alison Peel <[redacted] (b) (6) wrote:
Dear Sarah, Allison and Fiona,

A short answer is that, [redacted] (b) (4)

[redacted] (b) (4)

Hopefully, this answers all the questions sufficiently. I would be keen to hear your thoughts on [redacted] (b) (4) We can then work through discussions about the other components.

Thanks
Alison

On Fri, 22 Nov 2019 at 10:56, Sarah Britton [redacted] (b) (6) wrote:
Hi Alison,

Yes I think that would be helpful. I have also copied Fiona and Allison in too in case they have any comments

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: [redacted] (b) (6) | M: [redacted] (b) (6)
E: [redacted] (b) (6)
W: www.dpi.nsw.gov.au

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On Fri, 22 Nov 2019 at 11:33, Alison Peel <[redacted] (b) (6) wrote:
Hi Sarah,

Would it help if there was a [redacted] (b) (4)

Thanks
Alison

On Fri, 22 Nov 2019 at 10:26 am, Sarah Britton <[redacted] (b) (6) wrote:
HI Alison,

The main concern is that currently most of the viruses (ie Hendra/ Cedar/Menangle samples) sit at AAHL and Mark expressed concern that if virus is isolated o/s from Aust samples then this could be used for other purposes and is outside the control of Australia.
Also as you state , the control of info that would be released into the public domain.

Kind regards

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: [redacted] (b) (6) | M: [redacted] (b) (6)
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On Fri, 22 Nov 2019 at 10:34, Alison Peel <[redacted] (b) (6) wrote:
Hi Sarah,

I'm expecting more feedback from the uni this morning, but to make sure we get all the information we need, can I clarify if there is a specific concern? Is it primarily about the process by which sequences would or would not be released into the public domain?

I am around today to discuss [redacted] (b) (6) and will hopefully get back to you later this morning once I've heard from our legal team.

Thanks
Alison

On Wed, 20 Nov 2019 at 9:11 pm, Alison Peel <[redacted] (b) (6) wrote:
Hi Sarah,

Many thanks for your efforts in getting that conversation to happen, and for your positive feedback. I have some understanding about the IP situation, but will clarify things with our lawyers to be certain and will get back to you by Friday.

Kind Regards,

Alison

On Wed, 20 Nov 2019 at 20:58, Sarah Britton [redacted] (b) (6) wrote:
Hi Alison and Raina,

Managed to speak to both Allison and Mark today. We support the research you are doing and keen to see it progress. The question Mark had was about who owns the IP of the virus and phylogenetic data? I can chat to you on Friday about this if suits, as I am in the field tomorrow.

Kind regards

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
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On Wed, 20 Nov 2019 at 08:46, Sarah Britton < (b) (6) wrote:
Hi Alison,

I apologise for the delay in replying but have been trying to catch Allison and Mark to discuss this. I have managed to catch Allison and we need to run it past Mark- as soon as we have done that , I will contact you. It should be this week as he is away next week .

Kind regards,

Sarah

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On Mon, 18 Nov 2019 at 09:53, Alison Peel < [redacted] (b) (6) wrote:
Hi Sarah,

I hope to be submitting a shipment request to you later this week. We are in the process of getting the required MTAs finalised and it would be helpful to hear your thoughts on which of the following sample testing you consider reasonable to request (further details in the previous emails in this thread):

[redacted] (b) (4)

Thanks very much,

Alison

On Thu, 7 Nov 2019 at 22:01, Alison Peel [redacted] (b) (6) wrote:
Dear Sarah,

Following on from my previous email, I've included some further information below on the rationale behind our request for permission to undertake virus isolation at Rocky Mountain Laboratories.

[redacted] (b) (4)

[redacted] (b) (4)

I hope this further explanation is helpful and I look forward to hearing your thoughts.

Kind Regards,

Alison

On Wed, 6 Nov 2019 at 09:15, Alison Peel [redacted] (b) (6) wrote:
Dear Sarah,

Thanks for your interest in our research and for the positive feedback during our call yesterday. I have attached the spillover response pamphlet and the multiviral paper that we discussed.

[redacted] (b) (4)

[redacted] (b) (4) I will write a separate proposal and send to you shortly.

One last matter that was just brought to my attention is the [redacted] (b) (4)– Is this a reasonable request? It is not absolutely essential to our project but we do have a postdoc who [redacted] (b) (4) and it would add another layer of information into our project.

Thanks,
Alison

ALISON PEEL BSc(Vet) BVSc MSc PhD

DECRA Senior Research Fellow, Griffith Wildlife Disease Ecology Group
Environmental Futures Research Institute, Sir Samuel Griffith Centre (N78) 2.23
Griffith University, Nathan Campus, 170 Kessels Rd, Nathan, QLD, 4111, Australia

Office days: Monday - Thursday

E: [redacted] (b) (6) [redacted] (b) (6)
W: [redacted] (b) (6)
M: [redacted] (b) (6)
@ali_bat
www.bat1health.org
www.mccallum-disease-ecology.com/alison-peel
https://experts.griffith.edu.au/academic/a.peel

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<SLA Provider.docx><2019 (b) (4).docx>

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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 4 Feb 2020 16:51:41 -0700
To: [redacted] (b) (6) Raina Plowright
Subject: Re: Bat1health: Future shipment and analysis plans

Woohoo!!!!

Great job team!

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Alison Peel < [redacted] (b) (6)
Reply-To: ' [redacted] (b) (6) < [redacted] (b) (6)
Date: Tuesday, February 4, 2020 at 2:54 PM
To: Raina Plowright < [redacted] (b) (6) " [redacted] (b) (6)
< [redacted] (b) (6)
Subject: Fwd: Bat1health: Future shipment and analysis plans

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1. Hendra and Cedar PCR and sequencing (as previously requested and approved)
2. Hendra and Cedar virus isolation from samples that have tested positive in PCR assays-further detail below
3. PCRs and sequencing of blood-borne bacteria in the genera Borrelia and Bartonella (from dried blood spots)

4. Regarding testing for the nine known paramyxoviruses in bats, I understand that Alison Peel will write a separate proposal and send shortly?

Both NSW and QLD will contact you separately to discuss the MTA and any specific requirements for each jurisdiction. We look forward to continuing to work with you on this important research.

Kind regards

Sarah

arah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: [redacted] (b) (6) M: [redacted] (b) (6)
E: [redacted] (b) (6)
W: www.dpi.nsw.gov.au

***We work flexibly.** If you have received an email from me outside of normal business hours, I'm sending it at a time that suits me. Unless it's urgent, I'm not expecting you to read or reply until normal business hours.*

On Fri, 17 Jan 2020 at 05:51, Plowright, Raina < [redacted] (b) (6) wrote:
Dear Sarah, Allison, and Fiona,

Let me know if I can answer any questions for you.

[redacted] (b) (4)

[redacted] (b) (4) RML is willing to provide us with this useful information, despite the considerable expense.

Best,

Raina

On Jan 12, 2020, at 6:18 PM, Alison Peel <[redacted] (b) (6) wrote:

Dear Sarah, Allison and Fiona,

Firstly, Allison, I wanted to thank you again in your assistance on Christmas Eve in getting our shipment being processed at customs. Our application was processed that day and the samples are safely back in the freezer, while we re-organise a new shipment date. We are extremely grateful to everyone who helped make that happen!

Secondly, I wanted to follow up on our previous request regarding virus isolation. Would a conference call be the best way to progress this? As discussed in my previous email, we hope that the following amendments to any future MTAs will address any concerns that you or Mark may have:

[redacted] (b) (4)

[redacted] (b) (4). I have attached an example SLA here. (Also, note that in the previous email, I expanded the acronym "SLA" incorrectly as Service Level Agreement).

If the MTA and procedural amendments proposed above are acceptable, then we will also draft comparable amendments to existing MTAs to cover samples that have previously been shipped to RML.

Please let me know if you have any questions. I'd be happy to discuss any of this over the phone or on a conference call if it's easier than emails.

Many thanks, Happy New Year, and all the best regarding the remainder of the fire season.

Alison

On Tue, 17 Dec 2019 at 16:18, Alison Peel <[redacted] (b) (6) wrote:
Dear Sarah, Allison and Fiona,

I wanted to provide an update regarding [redacted] (b) (4) – [redacted]

[redacted] (b) (4) In order to achieve this, we are happy to continue discussions to identify an approach and set of agreements that are acceptable to you all, and to Mark. I welcome any feedback you have at this point, but recognising pressures in the lead up to Christmas shut-down periods, I am happy to raise it again with you in the New Year. I will continue working with the legal teams to develop the amendments and can present those to you then.

Wishing you a relaxing and enjoyable break over the holiday period!

Kind Regards,

Alison

On Fri, 22 Nov 2019 at 13:21, Alison Peel <[redacted] (b) (6) wrote:
Dear Sarah, Allison and Fiona,

A short answer is that, [redacted] (b) (4)

[redacted] (b) (4)

Hopefully, this answers all the questions sufficiently. I would be keen to hear your thoughts [redacted] (b) (4)

Thanks
Alison

On Fri, 22 Nov 2019 at 10:56, Sarah Britton <[redacted] (b) (6) wrote:
Hi Alison,

Yes I think that would be helpful. I have also copied Fiona and Allison in too in case they have any comments

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: [redacted] (b) (6) | M: [redacted] (b) (6)
E: [redacted] (b) (6)
W: www.dpi.nsw.gov.au

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On Fri, 22 Nov 2019 at 11:33, Alison Peel [redacted] (b) (6) wrote:
Hi Sarah,

[redacted] (b) (4)

Thanks
Alison

On Fri, 22 Nov 2019 at 10:26 am, Sarah Britton < [redacted] (b) (6) wrote:
HI Alison,

The main concern is that currently most of the viruses (ie Hendra/ Cedar/Menangle samples) sit at AAHL and Mark expressed concern that if virus is isolated o/s from Aust samples then this could be used for other purposes and is outside the control of Australia.
Also as you state , the control of info that would be released into the public domain.

Kind regards

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: [redacted] (b) (6) | M: [redacted] (b) (6)
E: [redacted] (b) (6)
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On Fri, 22 Nov 2019 at 10:34, Alison Peel <[redacted] (b) (6) wrote:
Hi Sarah,

I'm expecting more feedback from the uni this morning, but to make sure we get all the information we need, can I clarify if there is a specific concern? Is it primarily about the process by which sequences would or would not be released into the public domain?

I am around today to discuss [redacted] (b) (6) and will hopefully get back to you later this morning once I've heard from our legal team.

Thanks
Alison

On Wed, 20 Nov 2019 at 9:11 pm, Alison Peel <[redacted] (b) (6) wrote:
Hi Sarah,

Many thanks for your efforts in getting that conversation to happen, and for your positive feedback. I have some understanding about the IP situation, but will clarify things with our lawyers to be certain and will get back to you by Friday.

Kind Regards,

Alison

On Wed, 20 Nov 2019 at 20:58, Sarah Britton [redacted] (b) (6) wrote:
Hi Alison and Raina,

Managed to speak to both Allison and Mark today. We support the research you are doing and keen to see it progress. The question Mark had was about who owns the IP of the virus and phylogenetic data? I can chat to you on Friday about this if suits, as I am in the field tomorrow.

Kind regards

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800

T: (b) (6) | M: (b) (6)
E: (b) (6)
W: www.dpi.nsw.gov.au
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On Wed, 20 Nov 2019 at 08:46, Sarah Britton < (b) (6) wrote:
Hi Alison,

I apologise for the delay in replying but have been trying to catch Allison and Mark to discuss this. I have managed to catch Allison and we need to run it past Mark- as soon as we have done that , I will contact you. It should be this week as he is away next week .

Kind regards,

Sarah

Sarah Britton | NSW Chief Veterinary Officer and Group Director Animal Biosecurity
NSW Department of Primary Industries | Biosecurity and Food Safety
161 Kite Street | Locked Bag 21 | Orange NSW 2800
T: (b) (6) | M: (b) (6)
E: (b) (6)
W: www.dpi.nsw.gov.au
We work flexibly. *If you have received an email from me outside of normal business hours, I'm sending it at a time that suits me. Unless it's urgent, I'm not expecting you to read or reply until normal business hours.*

On Mon, 18 Nov 2019 at 09:53, Alison Peel < [redacted] (b) (6) wrote:
Hi Sarah,

I hope to be submitting a shipment request to you later this week. We are in the process of getting the required MTAs finalised and it would be helpful to hear your thoughts on which of the following sample testing you consider reasonable to request (further details in the previous emails in this thread):

[redacted] (b) (4)

Thanks very much,

Alison

On Thu, 7 Nov 2019 at 22:01, Alison Peel [redacted] (b) (6) wrote:
Dear Sarah,

Following on from my previous email, I've included some further information below on the rationale behind our request for permission to undertake virus isolation at Rocky Mountain Laboratories.

[redacted] (b) (4)

[redacted] (b) (4)

I hope this further explanation is helpful and I look forward to hearing your thoughts.

Kind Regards,

Alison

On Wed, 6 Nov 2019 at 09:15, Alison Peel [redacted] (b) (6) wrote:
Dear Sarah,

Thanks for your interest in our research and for the positive feedback during our call yesterday. I have attached the spillover response pamphlet and the multiviral paper that we discussed.

[redacted] (b) (4)

[redacted] (b) (4) I will write a separate proposal and send to you shortly.

One last matter that was just brought to my attention is the [redacted] (b) (4)– [redacted] Is this a reasonable request? It is not absolutely essential to our project but we do have a postdoc who [redacted] (b) (4) and it would add another layer of information into our project.

Thanks,
Alison

ALISON PEEL BSc(Vet) BVSc MSc PhD

DECRA Senior Research Fellow, Griffith Wildlife Disease Ecology Group
Environmental Futures Research Institute, Sir Samuel Griffith Centre (N78) 2.23
Griffith University, Nathan Campus, 170 Kessels Rd, Nathan, QLD, 4111, Australia

Office days: Monday - Thursday

E: [redacted] (b) (6) [redacted] (b) (6)
W: [redacted] (b) (6)
M: [redacted] (b) (6)
@ali_bat
www.bat1health.org
www.mccallum-disease-ecology.com/alison-peel
https://experts.griffith.edu.au/academic/a.peel

If you have received an email from me outside of normal working hours, I'm sending it at a time that suits me. I am not expecting you to read or reply to it until normal working hours.

<SLA Provider.docx><2019 (b) (4).docx>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 4 Feb 2020 08:02:17 -0700
To: [redacted] (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F]
Cc: Wyatt Madden; LaTrielle, Sara; Plowright, Raina
Subject: Re: Next Hendra batch of testing

Hi Ali,

That makes completes sense, other than that you probably has the best idea who would qualify as co-author. For us it is important that all significant contributions get acknowledged. Form our end I do not feel comfortable making that decision (as I'm sure you wouldn't feel comfortable making that decision for the contributions from our end).

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Alison Peel <[redacted] (b) (6)
Reply-To: '[redacted] (b) (6) <[redacted] (b) (6)
Date: Monday, February 3, 2020 at 5:47 PM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
Cc: Wyatt Madden <[redacted] (b) (6) "LaTrielle, Sara" <[redacted] (b) (6) "[redacted] (b) (6) <[redacted] (b) (6) "Plowright, Raina" <[redacted] (b) (6)
Subject: Re: Next Hendra batch of testing

Hi Kwe,

Thanks for this. I think we need to explain the stakeholder table in a bit more detail
For you to generate the results that you've listed, you needed the input of all those people that were involved in collection of the samples. And, presumably for your analyses, you also need metadata on date of collection, location etc. This information is contained in other tables within the database and the appropriate tables will identify who collected those samples, and therefore those people those who are potential stakeholders in any analyses that come from it.
The table is intended to list everyone who should either be a co-author or be acknowledged on the paper that comes from this work. So, for the row in the table that you've filled out, you would put 'First author' under the 'Acknowledgements' heading, and then have another row for Vincent, with 'Last author' under the 'Acknowledgements' heading (I presume). There should be a new row for each person.
For the field data, there will be some people listed in the databse as contributors but who made only minor contributions (e.g. volunteers), they would be listed as 'Acknowledgement' etc.

Does that make sense?

Thanks
Ali

On Tue, 4 Feb 2020 at 08:24, Kwe Claude, Yinda (NIH/NIAID) [F] <[redacted] (b) (6) wrote:
Hi Wyatt,

Find attached is a copy of the data sharing agreement.

Cheers

--

Kwe

From: Wyatt Madden <[redacted] (b) (6)
Date: Friday, January 31, 2020 at 11:17 AM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
Cc: "LaTrielle, Sara" <[redacted] (b) (6) "[redacted] (b) (6)
<[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
"Plowright, Raina" <[redacted] (b) (6)
Subject: Re: Next Hendra batch of testing

Hi Kwe,

No rush on the agreement - and feel free to just upload it to the box folder and let me know.

Regarding the script - still need to wrap it up. Sorry it's taken so long, been a little swamped with stuff lately! But I will try to get it over asap.

Best,
Wyatt

On Fri, Jan 31, 2020 at 11:07 AM Kwe Claude, Yinda (NIH/NIAID) [F] <[redacted] (b) (6) wrote:
Wyatt,
I have filled the form. I will have Vincent look at it before I sent to you. He is out of the office and hopefully next week he is in.

Thanks

--

Kwe

PS: Any progress with the script you had to write for me?

From: Wyatt Madden <[redacted] (b) (6)
Date: Thursday, January 30, 2020 at 9:38 AM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
Cc: "LaTrielle, Sara" <[redacted] (b) (6) "[redacted] (b) (6)
<[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
"Plowright, Raina" <[redacted] (b) (6)
Subject: Re: Next Hendra batch of testing

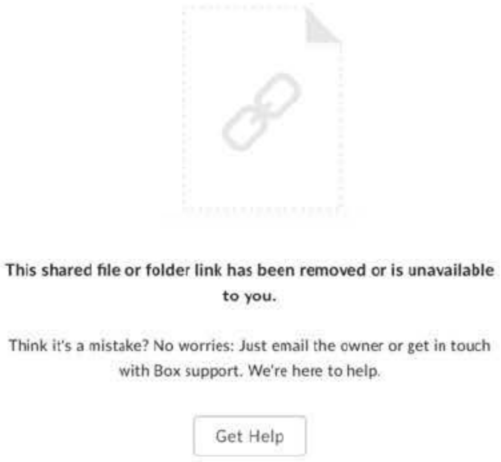
Hi Kwe,

I've connected you with the current data dictionary, as well as the data sharing agreement template, both on Box. If you could please fill out the template, including the first column of the "Stackholder" table (stating which tables you would like to be connected to). I will fill out the remainder of the columns in the table, except for the last one titled "Acknowledgement", which will be filled in prior to signing. Please let me know if you have any questions or suggestions.

Thanks!
Wyatt

On Thu, Jan 30, 2020 at 8:44 AM Kwe Claude, Yinda (NIH/NIAID) [F] <[redacted] (b) (6) wrote:
Thanks Sara,

I tried to login and this what it says:



This shared file or folder link has been removed or is unavailable to you.

Think it's a mistake? No worries: Just email the owner or get in touch with Box support. We're here to help.

--
Kwe

From: "LaTrielle, Sara" <[redacted] (b) (6)
Date: Wednesday, January 29, 2020 at 8:39 PM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6) "[redacted] (b) (6)

[redacted] (b) (6), "Munster, Vincent (NIH/NIAID) [E]" < [redacted] (b) (6)
Cc: "Plowright, Raina" < [redacted] (b) (6) Wyatt Madden
< [redacted] (b) (6)
Subject: Re: Next Hendra batch of testing

Here is the link to the BOX folder, 'PREEMPT: public release of Australian data'

https://montana.box.com/s/8yvb1ze3wbsc8p5q79a8yu7qf8ap2kpa

Please share the link with those you want to give access to. Let me know if there are any issues with the settings.

Sara

Get Outlook for iOS

From: Kwe Claude, Yinda (NIH/NIAID) [F] < [redacted] (b) (6)
Sent: Thursday, January 30, 2020 2:29:15 AM
To: [redacted] (b) (6) < [redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E]
< [redacted] (b) (6)
Cc: Plowright, Raina < [redacted] (b) (6) LaTrielle, Sara < [redacted] (b) (6)
Wyatt Madden < [redacted] (b) (6)
Subject: Re: Next Hendra batch of testing

Thanks so mush Ali,

I already mentioned to you that I tried a phylogeographic analysis on the F and G sequences we've got so far. The time vs genetic signal in this F and G sequences is not great, that is why we are trying our best to get full genomes.

However, when I concatenate F and G (for samples that we've sequenced both genes) the signal is slightly better and I could do some preliminary phylogenetic/phytogeographic analysis.

If you won't mind I can send you a draft Abstract.

Sara, let me know when you have created a box folder for this.

Wyatt, I will be waiting to hear from you.

Thanks

--

Kwe

From: Alison Peel <(b) (6)
Reply-To: "(b) (6) <(b) (6)
Date: Tuesday, January 28, 2020 at 4:08 PM
To: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Cc: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) Raina Plowright
<(b) (6) "LaTrielle, Sara"(b) (6) Wyatt
Madden <(b) (6)
Subject: Re: Next Hendra batch of testing

Ok, great, thanks. That's great that you've got some good results to present. I'll look forward to hearing more about how you're interpreting the results so far :)

So, from the perspective of the Australian CVOs, that should be fine, but it would be good if I could forward the abstract to them when you submit it, and also forward some key slides to them when you've prepared them for presentation.

Sara - would you please be able to create a new Box folder called "PREEMPT - Public release of Australian data" and have the settings so that I can invite others to join it? Would it be possible for me to share links for certain files so that people outside of our group (like the CVOs) can view particular files? I think that will reduce having to send large powerpoints over emails.

Kwe - Regarding the content of the abstract/presentation, from my perspective, as long as you've consulted with others working on phylogeny-related projects, then that is totally fine with me. I'd suggest posting your abstract/slides on slack too to keep others in the loop. In terms of including the shedding prevalences in your presentation for context, then that's also fine with me. Moving forward, if you're thinking about a publication on this work, there are several publications in the pipeline that will be looking at prevalence over space and time, so I think the publication committee (being led by Pete I think?) would be best to consult about what types of analyses, level of detail, and timing etc would be appropriate for your to include in a publication.

I've also cc'd Wyatt in here - Wyatt, perhaps you could share the data sharing agreement for the database with Kwe, including the templates for proposed work. Kwe - Wyatt's documentation should explain this in more detail, but the purpose of this is to identify all the team members involved in generation of the data, and write a publication plan for your analyses and co-authorship, so that this is transparent across the group and doesn't rely on forgetful people like me to keep track of everything! :)

We're still working all this out, so let me know if you have any suggestions!

Cheers

Ali

On Wed, 29 Jan 2020 at 02:37, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

It's an abstract for a virology conference with adjacent Tony's bat meeting.

Cheers,

Vincent

On Jan 28, 2020, at 15:38, Kwe Claude, Yinda (NIH/NIAID) [F] <[redacted] (b) (6) wrote:

Sorry, I did not right ASV in full it is for American Society of Virology Conference.

Thanks

--

Kwe

From: Alison Peel [redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Tuesday, January 28, 2020 at 1:37 AM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)
Cc: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6) Raina Plowright
<[redacted] (b) (6)
Subject: Re: Next Hendra batch of testing

Hi Kwe,

Thanks for getting in touch. You may have to clarify what you mean re: "short story/abstract" - is this a publication, or a blog post or something for a conference? I"m not quite sure.

Thanks

Ali

On Fri, 24 Jan 2020 at 05:05, Kwe Claude, Yinda (NIH/NIAID) [F] <[redacted] (b) (6) wrote:

Hi Ali,

I am planning to write a short story/abstract for ASV on the phylogeny of HeVs F and G we have recovered so and possibly the shedding/prevalence of HeV in AUS.

I thought I should check if that is ok for.

Also, from March 15 to April 7, I will be in Congo for field work and sample processing will be a little slow within this time.

Thanks

--

Kwe

From: Alison Peel <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Wednesday, January 22, 2020 at 5:26 AM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6) "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]" <[redacted] (b) (6) Raina Plowright <[redacted] (b) (6)
Cc: Mandy Todd <[redacted] (b) (6) Tamika Lunn <[redacted] (b) (6) Hamish McCallum <[redacted] (b) (6)
Subject: Next Hendra batch of testing

Hi Vincent, Kwe and Trent,

Tamika is in the last year of her PhD now, and unfortunately, the shipment that got rejected at the border included samples that she needs for her analyses. We're still trying to reorganise shipment of samples to you guys, but as we work towards that, I wanted to check in with you what your workload was in the coming months? I know you've got a lot of different commitments that you're juggling, and I wonder if there are any particular time windows that would be better than others for processing Australian samples?

Thanks

Ali

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 3 Feb 2020 10:29:20 -0700
To: [redacted] (b) (6) Raina Plowright
Subject: Re: Update on ability to culture

Thanks Ali,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Alison Peel <[redacted] (b) (6)
Reply-To: "[redacted] (b) (6) <[redacted] (b) (6)
Date: Sunday, February 2, 2020 at 7:51 PM
To: "[redacted] (b) (6) <[redacted] (b) (6) Raina Plowright
<[redacted] (b) (6)
Subject: Re: FW: Update on ability to culture

Hi Vincent,

No, I haven't gotten any response this time around. I will need to write to them again in a few days to notify them of re-export of samples. So can bring it up again then.

Cheers

Ali

From: Munster, Vincent (NIH/NIAID) [E]
Sent: 03 February 2020 02:40:36 (UTC+10:00) Brisbane
To: Raina Plowright; Alison Peel
Subject: Update on ability to culture

Hi Ali,

Any update on the permission from CVOs to culture HeV from our samples?

Hope all is well,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 3 Feb 2020 10:25:20 -0700
To: [redacted] (b) (6)
Cc: Letko, Michael (NIH/NIAID) [F]
Subject: Re: 2019-nCov: can we do something for it?

* General approach (e.g., augmenting surveillance in China, markets, or wherever makes sense); where and what kind of surveillance and to what end

I would do Cambodia, Vietnam and Laos wet market surveillance and have WCS as a partner (using the leftover PREDICT framework) . For us, an inventory of lineage B betacoronaviruses within Pteropid bats (although microbats are more important). Most importantly is identifying labs who will do the pcr analyses (Ghana and Bangladesh and then partner labs in SE Asia are well suited and we at RML have updated nested-PCR sets and qRT-PCRs specific for 2019-NCoV). Translating surveillance into knowledge (functional spike assays). Understanding the drivers of evolution in particular functional assessment of recombination events of the RBD.

* Team/players (can be you and your current subs or others if you can get them on contract fairly quickly)

WCS (Laos, Vietnam and Cambodia and respective partners) & Dr. Michael Letko at Pullmann

* Period of performance/timeframe

2 years?
* Cost
$500,000?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

On 2/3/20, 9:39 AM, "Plowright, Raina" <[redacted] (b) (6) wrote:

> Dear PIs,
> Let's use 30 minutes on our call today to discuss this. Olivier, sorry to shorten your report time to 30 minutes but this is obviously critical in timing.
> I think we can identify areas we can address then form a subgroup to develop a proposal.
> Raina
>
> On 2/3/20, 7:36 AM, [redacted] (b) (6) wrote:
>
> > Hi all,
> >
> > Hope you are each well wherever you are! We in DARPA/BTO are discussing our approach to supporting the response to the new coronavirus. There is the possibility for extra funding for related work, as I understand.
> >
> > Two categories, at least, of interest for our office (BTO) are medical countermeasures (MCMs) and diagnostics/surveillance. In the 2nd category and given your expertise and the work you are supporting in PREEMPT, there may be an oppty for some work by your team, esp as you have assets and expertise in this area. If you are interested in potentially supporting this work, I'd welcome a 1-2 pager that covers the following topics:

- General approach (e.g., augmenting surveillance in China, markets, or wherever makes sense); where and what kind of surveillance and to what end
- Team/players (can be you and your current subs or others if you can get them on contract fairly quickly)
- Period of performance/timeframe
- Cost

My guess is that there won't be a lot of money for this, but I think it's worth putting forward a proposal! If DARPA leadership provides some funding, I'd love to be able to do more with you related to helping support surveillance or related for the current virus, but even more likely to mitigate/prevent the next one!

If you can send me something within a week that would be great... maybe by end of next weekend? Happy to chat or email further if you want clarification. Right now this is exploratory...

Best,
(b) (6)

From: Plowright, Raina
Sent: Mon, 3 Feb 2020 16:48:46 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: FW: 2019-nCov: can we do something for it?

Need to be strategic here. Thinking your work, Jamie's modeling, hector (strips), Tony's bats. Focused stuff that helps us with our henipa stuff too.
Gotta teach half the day today unfortunately. R u back in US? Would be good to chat on phone.

On 2/3/20, 7:36 AM, (b) (6) wrote:

Hi all,

Hope you are each well wherever you are! We in DARPA/BTO are discussing our approach to supporting the response to the new coronavirus. There is the possibility for extra funding for related work, as I understand.

Two categories, at least, of interest for our office (BTO) are medical countermeasures (MCMs) and diagnostics/surveillance. In the 2nd category and given your expertise and the work you are supporting in PREEMPT, there may be an oppty for some work by your team, esp as you have assets and expertise in this area. If you are interested in potentially supporting this work, I'd welcome a 1-2 pager that covers the following topics:

* General approach (e.g., augmenting surveillance in China, markets, or wherever makes sense); where and what kind of surveillance and to what end
* Team/players (can be you and your current subs or others if you can get them on contract fairly quickly)
* Period of performance/timeframe
* Cost

My guess is that there won't be a lot of money for this, but I think it's worth putting forward a proposal! If DARPA leadership provides some funding, I'd love to be able to do more with you related to helping support surveillance or related for the current virus, but even more likely to mitigate/prevent the next one!

If you can send me something within a week that would be great... maybe by end of next weekend? Happy to chat or email further if you want clarification. Right now this is exploratory...

Best,
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 09:03:53 -0700
To: Kendall,Lon; Cisar, Alphie (NIH/OD/ORS) [E]; Schountz, Tony
Subject: Re: Bat shipment Miami-CSU- RML

Thanks guys,

Its all hands-on with the novel coronavirus

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Lon Kendall <[redacted] (b) (6)
Date: Friday, January 31, 2020 at 6:49 PM
To: "Cisar, Alphie (NIH/OD/ORS) [E]" <[redacted] (b) (6) Tony Schountz
<[redacted] (b) (6)
Cc: "LaCasse, Rachel (NIH/NIAID) [E]" <[redacted] (b) (6) "[redacted] (b) (6)
<[redacted] (b) (6)
Subject: RE: Bat shipment Miami-CSU- RML

Sounds good, thanks.

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University
2007 Painter Center
Colorado State University
Fort Collins, CO 80523
Voice: [redacted] (b) (6)
Cell: [redacted] (b) (6)
Fax: 970-491-2496
[redacted] (b) (6)

From: Cisar, Alphie (NIH/OD/ORS) [E] <[redacted] (b) (6)
Sent: Friday, January 31, 2020 6:43 PM
To: Kendall,Lon <[redacted] (b) (6) Schountz,Tony <[redacted] (b) (6)
Cc: LaCasse, Rachel (NIH/NIAID) [E] <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6)
Subject: RE: Bat shipment Miami-CSU- RML

I understand that we won't be transferring bats from CSU to RML at his time.

I'll work to get things finalized from Miami to CSU.
Alf

Alphie Cisar, LATG
NHP & Large Animal Procurement Specialist and Resource Manager
DVR, ORS
NIH Animal Center
Ph: [redacted] (b) (6)
Fax 301-480-0644

From: Kendall,Lon <[redacted] (b) (6)
Sent: Tuesday, January 28, 2020 10:47 AM
To: Cisar, Alphie (NIH/OD/ORS) [E] <[redacted] (b) (6) Schountz, Tony
<[redacted] (b) (6)
Cc: LaCasse, Rachel (NIH/NIAID) [E] <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E]
<[redacted] (b) (6)
Subject: RE: Bat shipment Miami-CSU- RML

Alf-

Arrival 2/12 will work.

We can load the bats destine for RML at that time. Although wouldn't it be easier to just keep 30 of the bats from Miami crated and continue routing to RML rather than uncrate them, then load an additional 30? We could reload food.

Yes we'll need transport crates and 10 per crate seems reasonable, assuming all is well upon arrival from Miami.

Miami should send the health certificate to the CO state vet at [redacted] (b) (6) and please copy me.

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University
2007 Painter Center
Colorado State University
Fort Collins, CO 80523
Voice: [redacted] (b) (6)
Cell: [redacted] (b) (6)
Fax: 970-491-2496
[redacted] (b) (6)

From: Cisar, Alphie (NIH/OD/ORS) [E] <[redacted] (b) (6)
Sent: Tuesday, January 28, 2020 7:45 AM

To: Kendall,Lon < (b) (6) Schountz,Tony < (b) (6)
Cc: LaCasse, Rachel (NIH/NIAID) [E] < (b) (6) Munster, Vincent (NIH/NIAID) [E]
< (b) (6)
Subject: Bat shipment Miami-CSU- RML

Good morning everyone, spoke with Miami and transporter, Looks like we are getting confirmed for a pick up on 2/10 with delivery to CSU on 2/12. Will that work for CSU?

Based on request from RML, the transporter will be picking up bats from CSU for RML when he delivers the bats from Miami. Could either CSU or RML confirm the number that we will be transporting from CSU to RML, I have notes that range from 26-36. Please advise. The bats from CSU will arrive into RML on 2/13.

Lastly, will CSU need transport crates for the animals going to RML, if so, can you confirm that your comfortable shipping about 10 bats per crates as we are from Miami to CSU.

PS, will forward Miami HC as soon as I can so you can obtain the CO. import permit number.

Thanks, I look forward to everyone response.
Alf

Alphie Cisar, LATG
NHP & Large Animal Procurement Specialist and Resource Manager
DVR, ORS
NIH Animal Center
Ph: (b) (6)
Fax 301-480-0644

From: Kendall,Lon < (b) (6)
Sent: Friday, January 24, 2020 6:44 PM
To: Cisar, Alphie (NIH/OD/ORS) [E] < (b) (6) Schountz, Tony
< (b) (6)
Subject: CPW permit

I have the permit in hand!

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University
2007 Painter Center
Colorado State University
Fort Collins, CO 80523
Voice: (b) (6)
Cell: (b) (6)

Fax: 970-491-2496

(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 31 Jan 2020 07:30:18 +0000
To: Plowright, (b) (6); Letko, Michael (NIH/NIAID) [F]; Seifert, Stephanie (NIH/NIAID) [E]
Subject: Re: coronavirus brainstorm
Attachments: RML phylogeny.pptx

last one, slide to put the diversity of the just the B-coronaviruses in perspective (analyses by Steph). Adding Michael & Stephanie here as well. Michael will be starting his own lab soon and would be essential in some of the high-throughput downstream analyses on zoonotic potential if we decide to go that route. Same holds true for Steph, but more from a population genetics pov.

Vincent Munster, PhD
Chief, Virus Ecology Unit
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903 South 4th street
Hamilton, MT 59840
(b) (6)

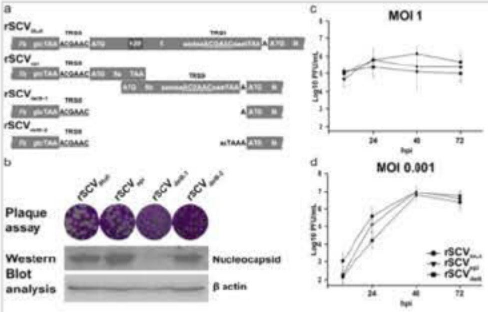
From: Munster, Vincent (NIH/NIAID) [E] (b) (6)
Sent: Friday, January 31, 2020 12:16 AM
To: Plowright, Raina (b) (6) (b) (6)
(b) (6)
Subject: Re: coronavirus brainstorm

I would actually be more upset by the Chinese authorities knowing that had h-t-h transmission as early as half December. Just of note, unless you are in a risk group (diabetic, observed, elderly male etc), you will likely be fine (but no guarantee).

And for the coronavirus, rather than the bats per se the critical steps lie in the adaptation in the intermediate host. Of note, the diversity of coronaviruses in bats will be staggering so it might need some new way of thinking how to study this (e.g. see Michael's paper) and maybe the focus should be more on the intermediate host as well. There are coronaviruses everywhere but they emerge more readily in china or on a different line, what sets horshoe bats apart from other bats?

https://www.nature.com/articles/s41598-018-33487-8

Attenuation of replication by a 29 nucleotide deletion in SARS-coronavirus acquired during the early



stages of human-to-human transmission - Scientific Reports

A 29 nucleotide deletion in open reading frame 8 (ORF8) is the most obvious genetic change in severe acute respiratory syndrome coronavirus (SARS-CoV) during its emergence in humans. In spite of ...

www.nature.com

Vincent Munster, PhD
Chief, Virus Ecology Unit
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903 South 4th street
Hamilton, MT 59840
[redacted] (b) (6)

From: Plowright, Raina [redacted] (b) (6)
Sent: Thursday, January 30, 2020 11:57 PM
To: [redacted] (b) (6)
Subject: Re: coronavirus brainstorm

Vincent, Thanks for the reading list. A very good idea for our team to become versed in the biology of coronaviruses. I will forward to my lab and encourage them to become experts too.

I think we could advance some of our work by framing it around 2019nCoV. E.g, understanding immune defense in bats, links between stress and shedding (some evidence for this with coronaviruses), temporal dynamics of pathogens in bats. We can solve some of these issues, with real funding!

N95 on after reading Jamie's tweet on the asymptotic transmission in Germany, reported in NEJM. Thanks Jamie! Now I can't breathe! Airplane taking off now.

Sent from my iPhone

On Jan 31, 2020, at 12:21 PM, Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6) wrote:

I think realistically if you want to have a productive meeting people should do some significant background reading as coronaviruses are markedly different from henipa's / paramyxo's.

couple of suggested papers:

https://www.biorxiv.org/content/10.1101/2020.01.22.915660v1

Functional assessment of cell entry and receptor usage for lineage B β-coronaviruses, including 2019-nCoV | bioRxiv

Over the past 20 years, several coronaviruses have crossed the species barrier into humans, causing outbreaks of severe, and often fatal, respiratory illness. Since SARS-CoV was first identified in animal markets, global viromics projects have discovered thousands of coronavirus sequences in diverse animals and geographic regions. Unfortunately, there are few tools available to functionally ...

www.biorxiv.org

https://www.ncbi.nlm.nih.gov/pubmed/30110630

https://www.ncbi.nlm.nih.gov/pubmed/30531947

https://www.ncbi.nlm.nih.gov/pubmed/27344959

https://www.ncbi.nlm.nih.gov/pubmed/24172901

https://www.ncbi.nlm.nih.gov/pubmed/30572566

https://www.ncbi.nlm.nih.gov/pubmed/28377531

https://www.ncbi.nlm.nih.gov/pubmed/26976607

https://www.ncbi.nlm.nih.gov/pubmed/26552008

A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence.

1. Nat Med. 2015 Dec;21(12):1508-13. doi: 10.1038/nm.3985. Epub 2015 Nov 9. A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence.

www.ncbi.nlm.nih.gov

SARS-like WIV1-CoV poised for human emergence. - PubMed - NCBI

Proc Natl Acad Sci U S A. 2016 Mar 15;113(11):3048-53. doi: 10.1073/pnas.1517719113. Epub 2016 Mar 14. Comparative Study; Research Support, N.I.H., Extramural

www.ncbi.nlm.nih.gov

Further Evidence for Bats as the Evolutionary Source of Middle East Respiratory Syndrome Coronavirus.

1. MBio. 2017 Apr 4;8(2). pii: e00373-17. doi: 10.1128/mBio.00373-17. Further Evidence for Bats as the Evolutionary Source of Middle East Respiratory Syndrome Coronavirus.

www.ncbi.nlm.nih.gov

SARS-Like Coronavirus WIV1-CoV Does Not Replicate in Egyptian Fruit Bats (Rousettus aegyptiacus).

1. Viruses. 2018 Dec 19;10(12). pii: E727. doi: 10.3390/v10120727. SARS-Like Coronavirus WIV1-CoV Does Not Replicate in Egyptian Fruit Bats (Rousettus aegyptiacus).

www.ncbi.nlm.nih.gov

Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor.

1. Nature. 2013 Nov 28;503(7477):535-8. doi: 10.1038/nature12711. Epub 2013 Oct 30. Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor.

www.ncbi.nlm.nih.gov

SARS and MERS: recent insights into emerging coronaviruses.

1. Nat Rev Microbiol. 2016 Aug;14(8):523-34. doi: 10.1038/nrmicro.2016.81. Epub 2016 Jun 27. SARS and MERS: recent insights into emerging coronaviruses.

www.ncbi.nlm.nih.gov

Origin and evolution of pathogenic coronaviruses.

1. Nat Rev Microbiol. 2019 Mar;17(3):181-192. doi: 10.1038/s41579-018-0118-9. Origin and evolution of pathogenic coronaviruses. Cui J(1), Li F(2), Shi ZL(3).

www.ncbi.nlm.nih.gov

Adaptive Evolution of MERS-CoV to Species Variation in DPP4. - PubMed - NCBI

Cell Rep. 2018 Aug 14;24(7):1730-1737. doi: 10.1016/j.celrep.2018.07.045. Research Support, N.I.H., Extramural

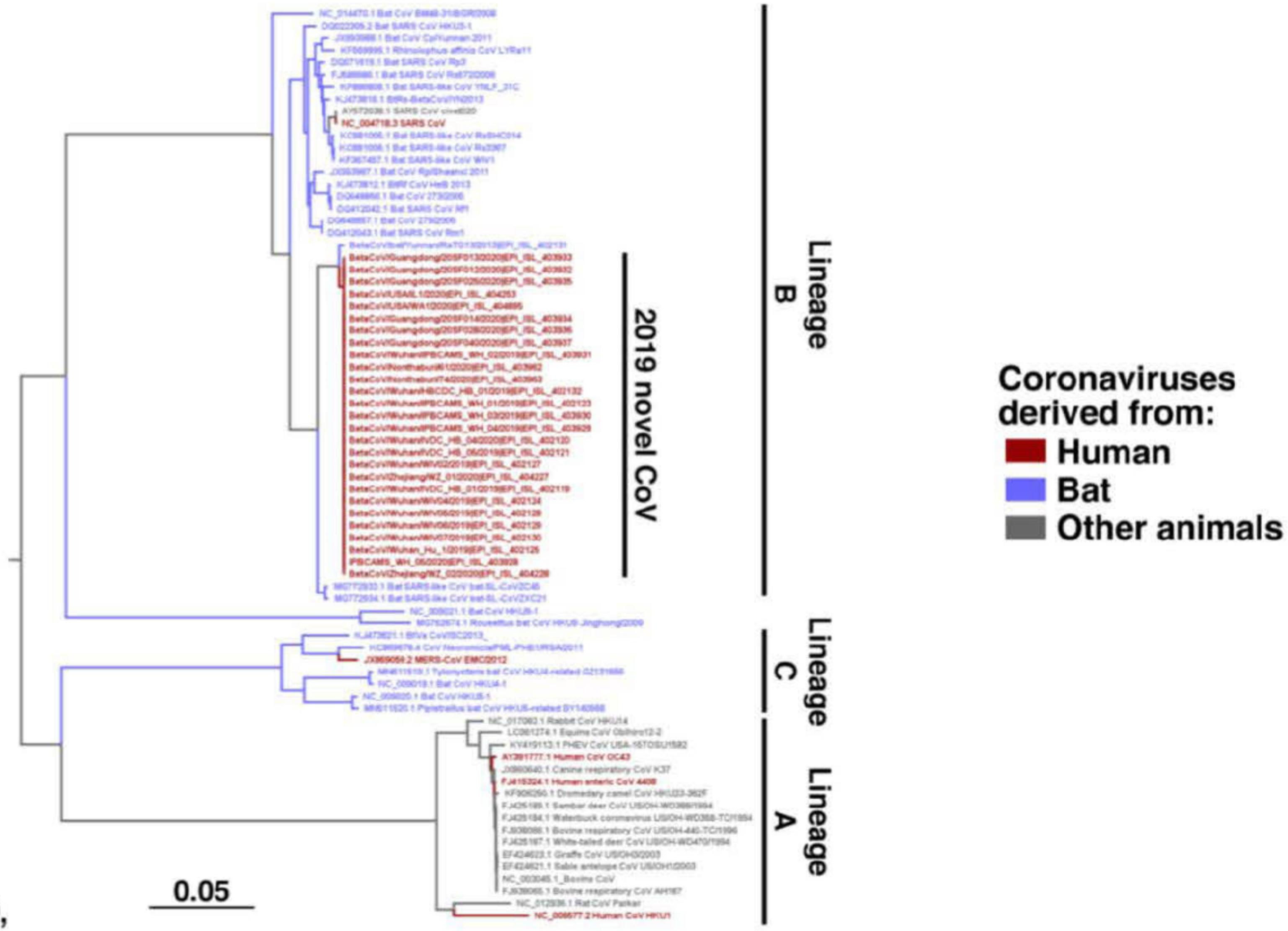
www.ncbi.nlm.nih.gov

Vincent Munster, PhD
Chief, Virus Ecology Unit
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH
903 South 4th street
Hamilton, MT 59840
(b) (6)

From: Plowright, Raina (b) (6)
Sent: Thursday, January 30, 2020 8:06 PM
To: (b) (6)
Subject: coronavirus brainstorm

Just to PREEMPT PIs:
Very briefly as I'm on way to Dhaka airport... we are going to reach out to (b) (6) with some ideas about how our group could be helpful in the emerging coronavirus situation (with increased funding of course). A couple of days ago, we pitched some ideas for funding around serology and rapid diagnostic development – projects that we want funded to progress the henipa project but these tools could easily be transferred to other bat systems. It would be strategic to send a list of ideas and priorities for understanding coronavirus emergence from bats. E.g. Bangladesh will now start storing fecal samples from their longitudinal studies for future analysis of temporal dynamics of coronaviruses (pending funding). Shoot us your ideas and we will prep a bullet point list for (b) (6)
Raina

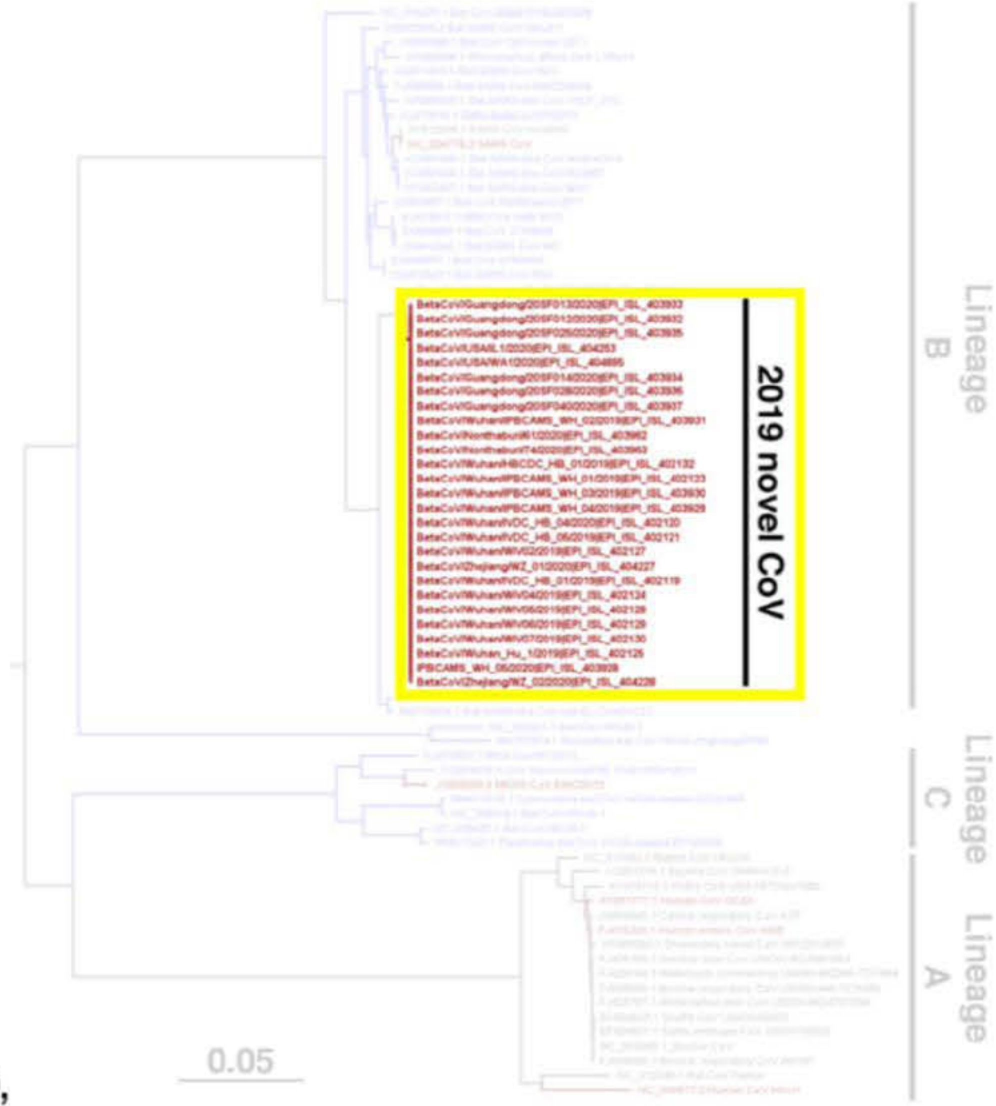
Phylogenetic Analysis of 2019 Novel Coronavirus Within Betacoronaviruses



Analysis by Seifert & Munster, NIH/NIAID,
Virus Ecology Section, 27-Jan-2020

AS Fauci/NIAID

Phylogenetic Analysis of 2019 Novel Coronavirus Within Betacoronaviruses

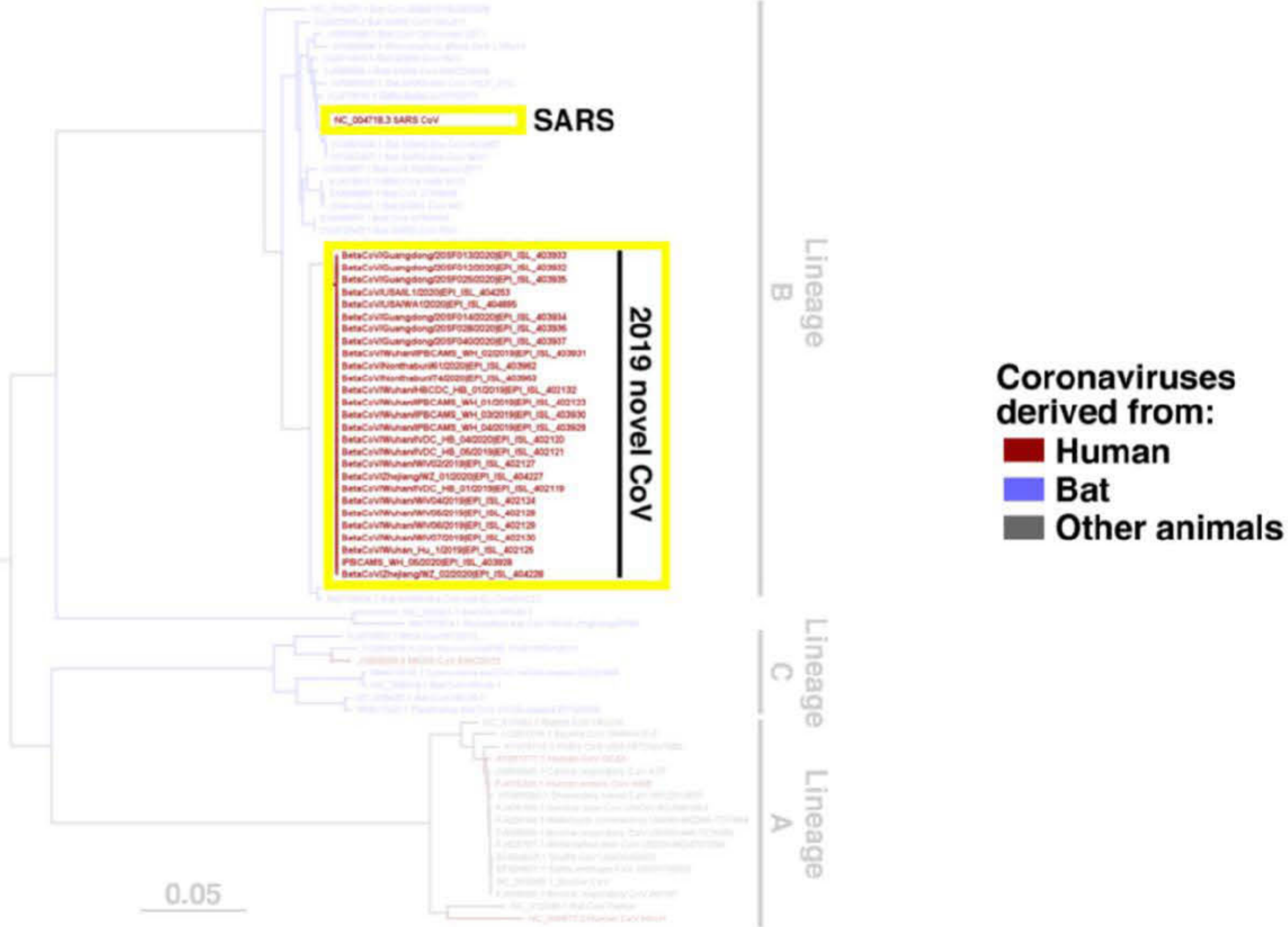


Coronaviruses derived from:
- 🟥 Human
- 🟦 Bat
- ⬛ Other animals

Analysis by Seifert & Munster, NIH/NIAID, Virus Ecology Section, 27-Jan-2020

AS Fauci/NIAID

Phylogenetic Analysis of 2019 Novel Coronavirus Within Betacoronaviruses



Analysis by Seifert & Munster, NIH/NIAID,
Virus Ecology Section, 27-Jan-2020

AS Fauci/NIAID

From: Schountz,Tony
Sent: Thu, 30 Jan 2020 19:50:22 +0000
To: Eric Laing; Munster, Vincent (NIH/NIAID) [E]
Subject: ASV abstract
Attachments: ASV 2019 abstract.docx

Vincent and Eric, my student (b) (6) will be submitting this abstract to ASV for a poster.

Thanks,

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

Title: Primary Jamaican Fruit Bat Kidney Cells are Susceptible and Permissive to Henipavirus Infection

Authors: Juliette Lewis[1], Neeltje van Doremalen[2], Eric Laing[3] Vincent Munster[2] and Tony Schountz[1]

Affiliations: [1]Department of Microbiology, Immunology and Pathology, Colorado State University, [2]Laboratory of Virology, Rocky Mountain Laboratories, NIAID, and (look at PNAS paper for Eric's address)

Introduction: Nipah (NiV) and Hendra henipaviruses (HeV) are pteropid bat-borne viruses that cause fatal encephalitis in humans and livestock. Cedar virus (CedV), another henipavirus that is nonpathogenic in all tested animal models, was recently isolated from pteropid bats. The disparate pathogenicity of CedV and its relatives has yet to be fully investigated. CedV lacks V and W genes found in NiV and HeV that are potent type I interferon pathway antagonists, which may account, in part, for its lack of pathogenicity. **Objectives:** In this study, we investigated CedV susceptibility and anti-viral responses of primary kidney cells (AJKs) from seven Jamaican fruit bats (*Artibeus jamaicensis*). We also compared the replication and anti-viral responses of CedV to NiV and HeV in AJK cells. **Results:** By 72 hours post-infection (hpi), cytopathic effect (CPE) was evident in the cells inoculated with CedV. Both the viral RNA concentrations and virus titers increased over the infection period, revealing that the cells are both susceptible and permissive to CedPV infection. Gene expression analysis showed that at 1 hpi and 24 hpi a slight decrease in expression of many genes of the type I interferon response occurred; however, by 48 hpi several of these genes were dramatically elevated, some more than 1,000-fold. Inoculation of AJK cells with NiV and HeV resulted in pronounced CPE within 48hpi, including syncytia formation. By 72 hpi, cells inoculated with NiV and HeV exhibited extensive CPE and cell death, with increasing viral replication. Gene expression analysis determined that nearly all the examined genes were repressed during NiV and HeV infection. **Conclusion:** This work is the first to show that primary cells from a species of New World bat are susceptible to henipaviruses. CedV elicits a robust antiviral response that appeared to delay onset of CPE but without preventing viral replication. NiV and HeV also replicated in AJK cells but repressed the antiviral response and caused substantial CPE and cell death. This work provides a framework for in vitro studies that may shed light on the mechanisms of henipavirus pathogenesis. Future studies will examine the roles of V and W during infection and examine the susceptibility of Jamaican fruit bats to henipaviruses.

From: Plowright, Raina
Sent: Wed, 29 Jan 2020 11:24:44 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Mandy Todd; Alison Peel; Bushmaker, Trenton (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: Re: Shipping list Dec-2019

Good to have a plan. I'll tell Emily and Rajeeb that there is no rush to send samples from here.

Sent from my iPhone

On Jan 29, 2020, at 3:14 PM, Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6) wrote:

Hi Mandy and Ali,

Do not worry about numbers from your end. I was mainly referring to that [redacted] (b) (4) So, just proceed as planned and we'll screen these samples with priority to make sure all the needs of the students are met.

[redacted] (b) (4)

The timeframe would work from our end,

Cheers,

Vincent

On Jan 29, 2020, at 05:37, Mandy Todd [redacted] (b) (6) wrote:

Hi Vincent and Trent,

Due to the delay from the failed shipment last year, it was my understanding that we re-export the samples as a matter of urgency. I have been working to prepare the shipment before I go on leave from February 13-28, and was aiming to send on Monday the 10th of February (if World Courier approves the paperwork in an efficient manner). Would this timeline work for you to receive the samples later that week?

Kind regards,
Mandy Todd

Senior Technical Officer

Environmental Futures Research Institute
N78_2.11 Sir Samuel Griffith Building
Griffith University
Nathan, QLD 4111

Extension: [redacted] (b) (6)
Phone: [redacted] (b) (6)
Mobile: [redacted] (b) (6)
<Outlook-5lt3zrbu.png>

From: Alison Peel [redacted] (b) (6)
Sent: Tuesday, 28 January 2020 8:29 PM
To: Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6); Plowright, Raina [redacted] (b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] [redacted] (b) (6) Mandy Todd [redacted] (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

Hi Vincent,

Yes, I appreciate the pressure you're all under and I hope that we can time our shipment to work best for you. Thank you for all the hard work that you and your team are putting in. I think we all appreciate that there are so many moving parts in this project, that getting the timing right for everything would be very unexpected! We'd be happy to hear when you'd prefer to receive this next shipment.
My comment in the other email chain about priorities for Tamika, was meant to highlight that, *within our shipment*, there will be some samples that are higher priorities for testing than others.

[redacted] (b) (4)

Cheers

Ali

From: "Munster, Vincent (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Tuesday, 28 January 2020 at 6:55 pm

To: "Plowright, Raina" [redacted] (b) (6)
Cc: [redacted] (b) (6), Mandy Todd [redacted] (b) (6), Alison Peel [redacted] (b) (6), "Kwe Claude, Yinda (NIH/NIAID) [F]" [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

Hi Raina,

As mentioned previously we are under quite a lot of work pressure, including work for hector and Jamie, a bat infection experiment etc.
This in addition to a currently rapidly increasing coronavirus outbreak.

Not everything can be a priority, so be mindful of this. And again, it would be good if we continue the discussion on sampling and numbers [redacted] (b) (4)

Regards,

Vincent

On Jan 28, 2020, at 04:37, Plowright, Raina [redacted] (b) (6) wrote:

Hi from Bangladesh!
I'm not finding the last email in the chain so excuse the leapfrog back in the conversation chain – also limiting email recipients.
[redacted] (b) (4)
I don't think I heard from Mandy and Ali about Australian shipment plan but I apologize if I've missed emails on this.
What I need is an update on timing from the Australians and an update from Vincent on capacity to handle samples right now.
Thanks all,
Raina

From: "Bushmaker, Trenton (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Tuesday, January 21, 2020 at 2:52 PM
To: Mandy Todd [redacted] (b) (6), "Plowright, Raina" [redacted] (b) (6), "alisonpeel@gmail.com" [redacted] (b) (6)
Cc: Manuel Ruiz Aravena [redacted] (b) (6), "Munster, Vincent (NIH/NIAID) [E]" [redacted] (b) (6), "Rynda-Apple, Agnieszka" [redacted] (b) (6), "Kwe Claude, Yinda (NIH/NIAID) [F]" [redacted] (b) (6)
Subject: RE: Shipping list Dec-2019

Mandy,
I'm starting to think you have a camera on me… the package arrived 30 minutes ago.

During the shipment we had a few issues:

1. They PROMISED delivery by Jan 17th. Today is the 21st. I would've liked to skip the US holiday(20th) was the only special request.
2. They go through a contractor in the US who:
   a. I did not have a phone number for so I couldn't call them for a updates.
   b. Only work 8-5 hours.
   c. Had issues with customs in Denver but they figured it out.
3. Promised delivery on Wednesday (22nd) but instead it just arrived today (randomly one day earlier).

Good things:

1. Dry ice looked good. No temperature probe however.
2. The cost is ~$1,300 for one box that would hold ~(10) boxes.

I would stick with the devil we know but what do you think?

-Trent

From: Mandy Todd [redacted] (b) (6)
Sent: Tuesday, January 21, 2020 2:35 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] [redacted] (b) (6); Plowright, Raina [redacted] (b) (6); alisonpeel@gmail.com
Cc: Manuel Ruiz Aravena [redacted] (b) (6); Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6); Rynda-Apple, Agnieszka [redacted] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

Hi Trent,

Has your shipment with SFS Pharma arrived and if so, any feedback on the experience?

Kind regards,

Mandy Todd

Senior Technical Officer

Environmental Futures Research Institute

N78_2.11 Sir Samuel Griffith Building

Griffith University

Nathan, QLD 4111

Extension: (b) (6)

Phone: (b) (6)

Mobile: (b) (6)

<image001.png>

From: Mandy Todd (b) (6)
Sent: Tuesday, 14 January 2020 2:51 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) Plowright, Raina (b) (6); (b) (6)
Cc: Manuel Ruiz Aravena (b) (6); Munster, Vincent (NIH/NIAID) [E] (b) (6); Rynda-Apple, Agnieszka (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6)
Subject: Re: Shipping list Dec-2019

Great thanks Trent, please let us know how it goes. WC were meeting to discuss the failed shipment this afternoon so I'm expecting to hear an update shortly.

Kind regards,

Mandy Todd

Senior Technical Officer

Environmental Futures Research Institute

N78_2.11 Sir Samuel Griffith Building

Griffith University

Nathan, QLD 4111

Extension: (b) (6)

Phone: (b) (6)

Mobile: (b) (6)

<image001.png>

From: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Sent: Tuesday, 14 January 2020 2:58 AM
To: Plowright, Raina (b) (6); (b) (6)
Cc: Mandy Todd (b) (6); Manuel Ruiz Aravena (b) (6) Munster, Vincent (NIH/NIAID) [E] (b) (6) Rynda-Apple, Agnieszka (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6)
Subject: RE: Shipping list Dec-2019

I am doing a shipment of cells from Geelong today or tomorrow via SFS pharma so we can use it as a test shipment. It should be here by the end of the week.

-Trent

From: Plowright, Raina (b) (6)
Sent: Friday, January 10, 2020 2:40 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Cc: Mandy Todd (b) (6); (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6) Manuel Ruiz Aravena (b) (6) Munster, Vincent (NIH/NIAID) [E] (b) (6) Rynda-Apple, Agnieszka (b) (6)
Subject: Re: Shipping list Dec-2019

Hi All,
We have a few projects that are being held up by delay in shipment, so if WC is a problem, let's discuss other solutions so we can get some critical samples here.
I hope WC are nice guys about this!
Raina

On Jan 9, 2020, at 7:38 PM, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:

Mandy,
Thank you for the update. We should be good for shipping whenever. As always, let me know if you need something from me.

Just a quick FYI, I am going to be in Congo ~March 15-April 6th. Doesn't mean you can't ship but just wanted to give you a heads up.

-Trent

From: "Mandy Todd" [redacted] (b) (6)
Date: Thursday, January 9, 2020 at 4:12:24 PM
To: "Bushmaker, Trenton (NIH/NIAID) [E]" [redacted] (b) (6), [redacted] (b) (6)
[redacted] (b) (6)
Cc: "Kwe Claude, Yinda (NIH/NIAID) [F]" [redacted] (b) (6), "Manuel Ruiz Aravena"
[redacted] (b) (6), "Munster, Vincent (NIH/NIAID) [E]" [redacted] (b) (6), "Plowright, Raina"
[redacted] (b) (6), "Rynda-Apple, Agnieszka" [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

Hi Trent,

Thanks for checking in on this and the offer of help. I need to speak with Ali [redacted] (b) (6) [redacted] but my thoughts were that we wouldn't send the shipment until we have sorted out with World Courier how the failed shipment will be paid for. World Courier is still completing an internal investigation into how they approved the erroneous paperwork, however I will prod them a little and see if they have any updates for me.

Kind regards,
Mandy Todd

Senior Technical Officer
Environmental Futures Research Institute
N78_2.11 Sir Samuel Griffith Building
Griffith University
Nathan, QLD 4111

Extension: [redacted] (b) (6)
Phone: [redacted] (b) (6)
Mobile: [redacted] (b) (6)
<Outlook-dpseifau.png>

From: Bushmaker, Trenton (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, 8 January 2020 4:55 AM
To: Mandy Todd [redacted] (b) (6); [redacted] (b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6); Manuel Ruiz Aravena
[redacted] (b) (6); Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6);
Plowright, Raina [redacted] (b) (6); Rynda-Apple, Agnieszka
[redacted] (b) (6)
Subject: RE: Shipping list Dec-2019

Hello and Happy 2020,
Could you update us on what is happening/planning with the re-shipment of samples? Do you need any help from my end?

Hope you are well.

-Trent

Trenton Bushmaker
Biologist, Virus Ecology Unit
Rocky Mountain Laboratories
903 South 4th Street
Hamilton, MT 59840
Phone: (b) (6)
Email: (b) (6)

From: Alison Peel (b) (6)
Sent: Thursday, December 12, 2019 1:25 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6); Mandy Todd (b) (6) Manuel Ruiz Aravena (b) (6) Munster, Vincent (NIH/NIAID) [E] (b) (6) Plowright, Raina (b) (6) Rynda-Apple, Agnieszka (b) (6)
Subject: Re: Shipping list Dec-2019

Thanks very much Trent, this is really helpful. I think Mandy will follow up with them today (she's been juggling this from the field this week).

We had looked into using SFS pharma previously and they are certainly a lot cheaper. If they are an approved courier for you guys, we'd certainly be interested in trying them. Let me know how you find them with your next shipment

Thanks again,
Ali

On Fri, 13 Dec 2019 at 2:09 am, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:
Ali,
I fully agree with assumption. For other shipments we send the brokerage team at World Courier the finial paper work beforehand. They approve the paper work and then, and only then the shipment is sent. I would send them an email to explaining we expect no additional charges for the samples to be re-shipped to RML.

I have just looked back into my notes and we have only had one shipment sent back because of customs issues but it was via DHL, not World Courier.

On another note, I am working on a shipment of cells from Australia via SFS pharma. I will let you know how this goes, this might be an option. We can use it as a test shipment.

Sad situation….

-Trent

From: Alison Peel (b) (6)
Sent: Wednesday, December 11, 2019 9:40 PM
To: Plowright, Raina (b) (6)
Cc: Mandy Todd (b) (6) Bushmaker, Trenton (NIH/NIAID) [E] (b) (6); Manuel Ruiz Aravena (b) (6) Munster, Vincent (NIH/NIAID) [E (b) (6) Rynda-Apple, Agnieszka (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6)
Subject: Re: Shipping list Dec-2019

Thanks Raina.
Mandy and Manuel are the most meticulous people I know, so it seems like we've been given poor advice here.

Trent - my assumption is that, as part of their service, WC should be checking the documents for the shipment and this is part of why they are so expensive. So, I feel like they have some responsibility here. Is this your understanding, have you previously had situations like this?

Cheers

Ali

On Thu, 12 Dec 2019 at 14:26, Plowright, Raina (b) (6) wrote:
I'm so sorry to hear this, given how much work you and Ali and Manuel have done to get it to where it is. I hope the samples are in good condition. Can you troubleshoot the issues and turn it around again?
Raina

On Dec 11, 2019, at 9:16 PM, Mandy Todd (b) (6) wrote:

Hi all,

Unfortunately World Courier have just notified me that the shipment has been rejected by the USFWS and will be returned to us. Please let me know if you'd like to see the rejection notice.

Mandy

From: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Sent: Thursday, December 12, 2019 2:58:15 AM
To: Mandy Todd (b) (6); (b) (6); Manuel Ruiz Aravena (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] (b) (6); Plowright, Raina (b) (6); Rynda-Apple, Agnieszka (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6)
Subject: RE: Shipping list Dec-2019

Thank you Mandy. I will discuss this the brokerage team when they call. Keep me updated if you hear anything.

-Trent

From: Mandy Todd (b) (6)
Sent: Wednesday, December 11, 2019 9:50 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6); (b) (6); Manuel Ruiz Aravena (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] (b) (6) Plowright, Raina (b) (6) Rynda-Apple, Agnieszka (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6)
Subject: Re: Shipping list Dec-2019

Thanks Trent. World Courier have responded and say that the "Cites was stamped by Australian quarantine prior to export" and that it is not possible to export without customs clearance, but we used three permits the WTA's email referred to only one of the permits so it's possible that one was missed.

Kind regards
Mandy Todd

From: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Sent: Thursday, December 12, 2019 2:26:23 AM
To: Mandy Todd (b) (6); (b) (6); Manuel Ruiz Aravena (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] (b) (6); Plowright, Raina (b) (6); Rynda-Apple, Agnieszka (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: RE: Shipping list Dec-2019

Mandy,
I called World Courier to see if I can do anything on my end. The customs brokerage team should be calling me back very soon to discuss.

However, it is does not look good because of the "export documentation was not endorsed by an Australian Border Force official" what they said also. WC said the package might have to be sent back because of this.

If you have any updates or emails from Australian customs please forward.

-Trent

Trenton Bushmaker
Biologist, Virus Ecology Unit
Rocky Mountain Laboratories
903 South 4th Street
Hamilton, MT 59840
Phone: (b) (6)

Email: [redacted] (b) (6)

From: Mandy Todd [redacted] (b) (6)
Sent: Tuesday, December 10, 2019 10:39 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] [redacted] (b) (6); [redacted] (b) (6); Manuel Ruiz Aravena [redacted] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6) Plowright, Raina [redacted] (b) (6) Rynda-Apple, Agnieszka [redacted] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

Hi all,

I've just received an email from the Australian department that issues the CITES permits (the WTA), they advise they have received a request from the US Fish and Wildlife Service regarding two problems with the documentation. The first problem is that the specimen export records that accompany the copy of the permit had lines in them which were handwritten. The last couple of times the WTA has issued me permits the specimen export records have been incomplete/not on watermarked paper, etc. I had them re-issued but they still didn't have the lines in them so I wrote them myself, unaware that it was a requirement for them to be printed.

The second problem is that the export documentation was not endorsed by an Australian Border Force official, which leads me to believe that the samples didn't clear Australian customs. I have emailed World Courier seeking clarification on this.

The WTA representative has advised the USFWS that the samples are in fact authorised under the permits, however the final decision will be with the USFWS.

Kind regards,
Mandy Todd

Senior Technical Officer
Environmental Futures Research Institute
N78_2.11 Sir Samuel Griffith Building
Griffith University
Nathan, QLD 4111

Extension: [redacted] (b) (6)
Phone: [redacted] (b) (6)
Mobile: [redacted] (b) (6)

From: Bushmaker, Trenton (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Tuesday, 10 December 2019 3:07 AM

To: [redacted] (b) (6); Manuel Ruiz Aravena [redacted] (b) (6); Mandy Todd [redacted] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6); Plowright, Raina [redacted] (b) (6); Rynda-Apple, Agnieszka [redacted] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6)
Subject: RE: Shipping list Dec-2019

Update as 12/9/2019 at 10am Mountain Time:

Still not cleared USDA, I will call them this afternoon to push a little bit. WC said deliver still should be Tuesday morning. I will update everyone this afternoon.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Friday, December 06, 2019 1:43 PM
To: [redacted] (b) (6); Manuel Ruiz Aravena [redacted] (b) (6); Mandy Todd [redacted] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6); Plowright, Raina [redacted] (b) (6); Rynda-Apple, Agnieszka [redacted] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6)
Subject: RE: Shipping list Dec-2019

Update as of 12/6/2019 at 1:30pm Mountain Time…

We are looking at delivery of the AUS samples early next week. They have not clear customs. I will monitor the situation over the weekend and update if something changes.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Thursday, December 05, 2019 9:52 AM
To: [redacted] (b) (6); Manuel Ruiz Aravena [redacted] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6); Plowright, Raina [redacted] (b) (6); Rynda-Apple, Agnieszka [redacted] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6); Mandy Todd [redacted] (b) (6)
Subject: RE: Shipping list Dec-2019

Update as of 12/5/2019 at 10am Mountain time….

I have attached the email for World Courier this morning. I have giving them a call and the estimated customs clearance & delivery is this Saturday (7th). Everything is looking good!

Let me know if you have questions.

-Trent

From: Alison Peel (b) (6)
Sent: Monday, December 02, 2019 5:06 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Cc: Manuel Ruiz Aravena (b) (6); Munster, Vincent (NIH/NIAID) [E] (b) (6); Plowright, Raina (b) (6); Rynda-Apple, Agnieszka (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6); Mandy Todd (b) (6)
Subject: Re: Shipping list Dec-2019

Hi Trent,
Thanks for that. Yep - I agree that there a high level of mutual respect on both sides, and I think basically it just comes down to so many things going on and it being hard to keep track of everything -, especially across multiple email threads. No blame in any direction, and no need to apologise :) If we can get requests/instructions off emails and into written protocols, then I think it will be smoother sailing from then :)
Cheers
Ali

On Tue, 3 Dec 2019 at 10:00, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:
Ali,
Kwe and/or me should be around 16th if we required the meeting, just processing Bangladesh samples. Vincent will be in Brazzaville, Congo during this time but might have some availability depending on internet access.

I just want to support Vincent's comments that nothing was directed specifically at your team. Hope you know we think your crew is awesome for getting these samples out in great condition.

My apologies to Manuel and you for any miscommunication that I may have caused. Will be better next shipment.

-Trent

From: Alison Peel (b) (6)
Sent: Monday, December 02, 2019 4:21 PM
To: Manuel Ruiz Aravena (b) (6)
Cc: Plowright, Raina (b) (6); Munster, Vincent (NIH/NIAID) [E] (b) (6); Rynda-Apple, Agnieszka (b) (6); Bushmaker, Trenton (NIH/NIAID) [E] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] (b) (6); Mandy Todd (b) (6)
Subject: Re: Shipping list Dec-2019

Hi all,
Perhaps we should aim to work through all this on a zoom call and modify the protocol on the spot? Would Monday 16th December (afternoon-US)/Tuesday 17th December (morning-Aus) work for everyone?
Cheers
Ali

On Tue, 3 Dec 2019 at 06:51, Alison Peel (b) (6) wrote:

Hi all,

To expand on Manuel's points, yes, the lists of sample numbers weren't finalised til just before the shipment, but I think all the different sample types were included in that original email, so I think that's the time that we need to be having the discussions about sample types.

Since Manuel will be leaving in a few weeks, it would be great to clarify a stepwise protocol for future shipments - including who at RML should be cc'd about shipments, how far in advance and with what level of detail (accounting for the fact that the actual numbers of samples may vary slightly in the week prior to shipment). We can also add a step into the protocol about confirming whether samples should be sent to RML or elsewhere (if permits allow).

Thanks everyone :)

Cheers

Ali

On Tue, 3 Dec 2019 at 06:12, Manuel Ruiz Aravena [redacted] (b) (6) wrote:
Hi everyone,

My apologies Trent for the delay sending the final shipping list. I didn't want to send a list of samples that was changing in length and sample positions until last minute for different contingencies [redacted] (b) (4) In addition, we had the final permits during the last week, therefore numbers could have changed until that moment [redacted] (b) (4) If you are flexible with last minute changes we could share future lists as they are in progress, but this could involve, anyway, that the final list could be available just a few days before the shipment occurs or even as now, when the boxes are leaving Griffith.

So, to move forward, is there any specific timeframe in which receiving the list of samples would make things smoother in your end? (we would add this to our protocols for sample requests and shipment)

About the list format that could have been confusing with the preliminary lists, finally for this shipment I managed to put a few lines of R code to merge data and change formats from ours to the one you use at RML which would make things easier for future shipments.

I personally apologize for any inconveniences, I know how much effort sample management requires, and I hope this didn't make things too complicated in your end.

Please, let me know what needs to be fixed in the list and I would do it today.

Cheers,
M

PS: I'll check the bill # once I get to the office and send it to you.

From: Plowright, Raina [redacted] (b) (6)
Sent: Tuesday, 3 December 2019 5:35 AM
To: Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Alison Peel [redacted] (b) (6); Rynda-Apple, Agnieszka [redacted] (b) (6); Bushmaker, Trenton (NIH/NIAID) [E] [redacted] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6); Mandy Todd [redacted] (b) (6); Manuel Ruiz Aravena [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

We would have to get a CDC import permit for slides. We can do this if you need but I don't have a staff member capable of this kind of thing, so I would have to do all of the paperwork. We can discuss by phone.

On Dec 2, 2019, at 12:32 PM, Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6) wrote:

Hi Raina,

We just figured out that the [redacted] (b) (4) so it would be good to have an idea what to do with these?

Thanks for all the help, especially Ali who has been very responsive. Just making sure thate everyone is aware, that there is a huge effort involved in both the front end (Oz) and back-end (RML), so it would be good that end users of samples are aware of this and that last-minute changes in shipping lists or "new" sample types can cause some confusion / sorting out,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: "Plowright, Raina" [redacted] (b) (6)
Date: Monday, December 2, 2019 at 12:25 PM
To: Alison Peel [redacted] (b) (6)
Cc: [redacted] (b) (6), Trenton Bushmaker [redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" [redacted] (b) (6), Mandy Todd [redacted] (b) (6), Manuel Ruiz Aravena [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

We have no import permit for samples from bats (CDC suggested we go through RML) so slides would have to go through RML. Dan Becker was leading this part of the project but hasn't stayed involved since he left and there is no clear leader on the slides to ensure all protocols are adhered to. We really need a single 'sample tsar' to ensure all samples are cared for under the best protocols, but I think we have been understaffed in this respect and so it is messy, but everyone is stepping up and everyone is doing more than their best effort to pull it off (especially Manuel—thanks Manuel!). Thanks team for the enormous effort to get the samples away.
Raina

On Dec 2, 2019, at 12:15 PM, Alison Peel [redacted] (b) (6) wrote:

Thanks Vincent for the reminder and clarification on that. Similarly, it's quite a task on our end to get the shipments away, with requests (and last minute requests) from many people, changes to shipment lists to [redacted] (b) (4) when results come in from Kwe, and many many layers of permits, agreements and approvals across multiple institutions. All good though, we can continue to refine the process.

I had it in my mind that MSU didn't have all the required import permits, but if they are obtained, then that would be much easier.

Raina- who is our best point of contact at MSU re import permits?

Thanks
Ali

On Tue, 3 Dec 2019 at 5:07 am, Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6) wrote:
Thanks Ali,

This info most have been "lost" then on this end. Thanks for replying so quickly, it is quite the task with multiple shipments coming on to make sure that everything runs smoothly. Just as a reminder that this is nothing directed specifically at your team, we'll have the same scrutiny with [redacted] (b) (4)

Just want to make sure, that once they are at RML, they can only be released following RML established procedures. So anything which can be routed around RML to MSU is easier for us (as every inactivation will take-up significant time of the people here).

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Alison Peel [redacted] (b) (6)
Reply-To: [redacted] (b) (6)
Date: Monday, December 2, 2019 at 11:59 AM
To: [redacted] (b) (6)

Cc: Trenton Bushmaker [redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" [redacted] (b) (6) Mandy Todd [redacted] (b) (6), Manuel Ruiz Aravena [redacted] (b) (6) "Plowright, Raina" [redacted] (b) (6)
Subject: Re: Shipping list Dec-2019

Hi all,

Still early here, so I or Manuel can respond more in full later on but I just wanted to say that we emailed details of the samples in this shipment on November 1st and had a discussion with Trent about the slides and the clots at that time. The slides were not sent on dry ice- just a regular box.

We should have sent the final list prior to shipment, but we did send this draft list well in advance and answered any questions posed by Trent. Let us know what else we can do for next time.

Cheers
Ali

On Tue, 3 Dec 2019 at 4:48 am, Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6) wrote:
Hi Manuel,

You might want to consider sending the slides directly to MSU? That would make it a little bit easier from our end. If Raina can discuss this with their local IRB, if these are not considered infectious than there is no need for a CDC import permit. Also, these will not have to be shipped using a cold-chain. So they could be shipped using a regular package rather than a very expensive dry-ice shipment.

As Trent said, make sure these things are discussed well ahead of time, this would facilitate a better logistics from our end,

cheers

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Trenton Bushmaker [redacted] (b) (6)
Date: Monday, December 2, 2019 at 11:26 AM
To: Manuel Ruiz Aravena [redacted] (b) (6) Mandy Todd [redacted] (b) (6) [redacted] (b) (6)
Cc: [redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" [redacted] (b) (6) "Plowright, Raina" [redacted] (b) (6)
Subject: RE: Shipping list Dec-2019

Hello,
Thank you for packing list, however Manuel I will talk with you individually because we need to have a few things to fixed on the packing list. I just want to reiterate that I need this packing list before the

samples are shipped. This way we can discuss any discrepancies beforehand. This will delay the processing of samples and the results to you guys.

Most important for now....I will need the House Airway bill# and the Job# if you are still sending it via World Courier. I will need to track the package, we have had issues of them sending packages to different locations and via odd routes of travel.

Let me know if you have questions. Thank you again for sending the samples, can't wait to find something!

-Trent

Trenton Bushmaker
Biologist, Virus Ecology Unit
Rocky Mountain Laboratories
903 South 4th Street
Hamilton, MT 59840
Phone: [redacted] (b) (6)
Email: [redacted] (b) (6)

From: Manuel Ruiz Aravena [redacted] (b) (6)
Sent: Sunday, December 01, 2019 9:56 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] [redacted] (b) (6)
Cc: [redacted] (b) (6); Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] [redacted] (b) (6); Plowright, Raina [redacted] (b) (6) Mandy Todd [redacted] (b) (6)
Subject: Shipping list Dec-2019

Hi Trent,

Samples are on their way to RML!

I attach the list of samples.

Samples are packed in a way that whole boxes can be transfer to MSU without moving samples among them. [redacted] (b) (4) for Vicky's experiments are in Box AUS_155 (Locations F01 to F04)

Details of content and destinations are below.

Regards,
Manuel

BoxName	TotalSamples	SampleType	Destination
[redacted]			(b) (4)

(b) (4)