From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 18 Mar 2021 15:34:55 -0600
To: Bushmaker, Trenton (NIH/NIAID) [E]; Dylan H. Morris; Kwe Claude, Yinda (NIH/NIAID) [F]
Cc: Amandine Gamble; Plowright, Raina; Adney, Danielle (NIH/NIAID) [F]; Holbrook, Myndi (NIH/NIAID) [C]; Jamie Lloyd-Smith
Subject: Re: Goldberg drum - WA1, UK, and SA variants

I'll have a look at it tonight, trying to case another B.1.1.7 strain if needed

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

From: Trenton Bushmaker <(b) (6)
Date: Thursday, March 18, 2021 at 3:32 PM
To: "Dylan H. Morris" <(b) (6) "(b) (6) <(b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6)
Cc: Amandine Gamble <(b) (6) "Plowright, Raina" <(b) (6) "Adney, Danielle (NIH/NIAID) [F]" <(b) (6) "Holbrook, Myndi (NIH/NIAID) [C]" <(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Great thank you! I will have some questions but also some more data Monday afternoon!

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Thursday, March 18, 2021 2:49 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Amandine Gamble <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

New plots!

On Mar 17, 2021, at 10:38 PM, Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) wrote:

Here is the titration data for new stock South African variant(B.1.351) for timepoint T0,3hours.

I will have titration date for UKv(B.1.1.7) for T0,8hrs on Monday(22nd).

I will have titration data for new stock South African variant(B.1.351) for timepoint T0,8hours on Wednesday next week.

Happy St. Pats day, hope you all enjoy a green beer!

-Trent

From: Dylan H. Morris < (b) (6)
Sent: Wednesday, March 10, 2021 11:51 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Cc: Amandine Gamble < (b) (6) Plowright, Raina < (b) (6) Adney, Danielle (NIH/NIAID) [F] < (b) (6) Holbrook, Myndi (NIH/NIAID) [C] < (b) (6) Jamie Lloyd-Smith < (b) (6) Munster, Vincent (NIH/NIAID) [E] (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Oops forgot to attach!

On Mar 10, 2021, at 1:50 PM, Dylan H. Morris < (b) (6) wrote:

Here you go. Half-life looks to be above 2h, which would imply losing about 1.2 log10 in 8 h. Only potential problem is the slightly lower T=0. Still, my guess is it will be fine. Worst case scenario, it's right around the LOD. Could probably get resolution by doing a couple extra wells at zero dilution

(e.g. if we're right around the LOD, might get 0 / 4 positive, but probably at least one of 8 wells positive)

On Mar 10, 2021, at 1:05 PM, Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) wrote:

Dylan/Amandine,
Here is the titration data for the UK variant (B.1.1.7) for the timepoint 0, 3hrs.

Could you have a quick look to confirm the later timepoint of 8 hour because I will need to start these runs on this Friday(3/12/21).

Thank you!

In addition, I will have the titrations for timepoint 0,3hrs for the new stockSouth African variant next week Wednesday(3/17/21). However, I will need to start on the T0, 8hour aerosol runs on Tuesday so I can get them done. We have a deadline for a lab recertification coming up.

Let me know if you have questions. Hope all is well!

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Friday, March 5, 2021 10:58 AM
To: Dylan H. Morris <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: IMPORTANT- RE: Goldberg drum - WA1, UK, and SA variants

Dylan/Amandine,
Important part- I will need a quick turn around because I'm starting the SA variant's LATER timepoint on Monday. We will need to figure out what we want to do for this LATER timepoint (8hr, 12-hardest, 18, or 24hrs) before Monday.

Titration sheet is attached.

WA1 has both T0,3hr and T0,8hr, I looks pretty good by eye balling it. I will work independent of you this afternoon to look at the decay for WA1. Dylan you did a really good job with the 8 hr timepoint!

For the SA variant, I redid the titrations but was only able to read 2 of the 3 plates. We had a little issue with the third plate because we missed a row which messed up the rest of the plate. Oh well. I did put all 5 plates on the titration sheet for T0,3hr for you to work with.

Talk with you both soon! Here is my cell phone if you want a quick reply: (b) (6). I will be in BSL4 till 1:30pm MTime today.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Tuesday, March 2, 2021 9:56 AM
To: Dylan H. Morris <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Amandine Gamble <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C]

< (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Thank you crew. Call me if you have questions. Just prepping for these studies today.

-Trent

From: Dylan H. Morris < (b) (6)
Sent: Tuesday, March 2, 2021 9:52 AM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) Amandine Gamble < (b) (6) Jamie Lloyd-Smith < (b) (6) Plowright, Raina (b) (6); Adney, Danielle (NIH/NIAID) [F] < (b) (6) Holbrook, Myndi (NIH/NIAID) [C] < (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

I can try to analyze the PCR data today.

On Mar 2, 2021, at 11:50 AM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Yes, so focus on the UK variant (B.1.1.7). Genotypically the current B.1.351 is weird (we'll have a correct one at the end of this week, but still needs to be grown). Whereas it shouldn't impact on the stability, the recovery sensitivity might be different.

Lets see what it looks like with the PCR data. Waiting until April does not make much sense (as there will likely be another variant)

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

From: Dylan H. Morris < (b) (6)
Sent: Tuesday, March 2, 2021 9:08 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Cc: Amandine Gamble < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Jamie Lloyd-Smith < (b) (6) Plowright, Raina < (b) (6) Adney, Danielle (NIH/NIAID) [F] < (b) (6) Holbrook, Myndi (NIH/NIAID) [C] < (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thanks! Personally, I would suggest getting something out quickly rather than delaying to include CA VOC. B.1.351 and B.1.1.7 very informative for a lot of the other VOC/VOI, since there's so much convergence.

And less stress for Trent too.

On Mar 2, 2021, at 11:03 AM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Here is the qRT-PCR data for the E-assay "Results for UCLA_qRT-PCR_E-assay_Aero WA1 and SAv_2021-02-03".

Two things to keep on the radar:

1. If we add the CA VOC this will have to be done after we get Suite D back from the annual shutdown which is slotted for March 23- ~April 15th. For people that don't speak BSL4 lingo, I am currently booked till March 23rd with the current SAv, UKv, and WA1 strain project. This is already a tight window to get things done. This required annual shutdown will stop all aerosol work between the dates of March 23- ~April 15th.
2. This is mostly for Vincent but if we don't think this SAv (B.1.351) is the correct variant should we omit this upcoming longer timepoint. This can be decided after we see the data normalized with the qRT-PCR.

Thanks everyone for your input, learning a bunch.

-Trent

From: Amandine Gamble <(b) (6)
Sent: Tuesday, March 2, 2021 7:43 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Dylan H. Morris <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Jamie Lloyd-Smith <(b) (6) Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi Trent and Vincent,

Thanks for the info regarding B.1.351. Indeed it would be even better if you can get data for the CA VOC.

Dylan made this plot on the raw titration data. Trent, you can send the PCR data our way (I don't think we got them yet, right?) and we will see how much it changes after normalization.

Looking forward to more data! Thanks again for all the hard work getting the isolates and then in BSL4!

Amandine

Le mar. 2 mars 2021 à 09:19, Munster, Vincent (NIH/NIAID) [E] <(b) (6)> a écrit :
The B.1.351 is a bit weird, as it has several mutations (not fixed) at ~ 80% in the reads in spike (one transitioning the furin cleavage site into a trypsin site, so not the cleavage deletion but still a SNP not reported in the natural variant which might affect our ability to recover it a bit). We are working on getting better strain in. I think we need to repeat the B.1.351 with a fully genetic comparable one.

In addition, we should likely add the 452-CA-VOC as well, to make an even better panel.

Did you try to normalize based on the PCR data? Any good?

Cheers,

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

From: "Dylan H. Morris" <(b) (6)>
Date: Monday, March 1, 2021 at 11:10 PM
To: Trenton Bushmaker <(b) (6)>
Cc: Amandine Gamble <(b) (6)> Jamie Lloyd-Smith <(b) (6)> "(b) (6)" <(b) (6)> "Plowright, Raina" <(b) (6)> "Adney, Danielle (NIH/NIAID) [F]" <(b) (6)> "Holbrook, Myndi (NIH/NIAID) [C]" <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Here are some fits and half-life estimates for B.1.351 and WA1

Definitely need the later timepoint for B.1.351 to be sure, but it looks like there might be a real difference. There also might not.

The model is very uncertain about the half-life of B.1.351 since minimal infectious virus appeared to be lost during the 3 hr experiment.

Best,
Dylan

On Mar 1, 2021, at 5:07 PM, Dylan H. Morris <(b) (6)> wrote:

Excellent. Yes, please send it over!

On Mar 1, 2021, at 1:21 PM, Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) wrote:

Dylan,
Here is the titration data "2021-03-01 Raw data - 22C @ 65%RH- WA1, UK, & SA" for WA1 and SAv (B.1.351). I will be very interested to hear what you think and what you think about the later timepoint.

I have the PCR data done for the WA1 and SAv (B.1.351) samples I you want that data now?

Update for this week:

1. UK variant stock for aerosol runs does not detecting any deletion of the furin site from sequencing. Stock titer is 10^5.7.
2. Aerosol runs for UK variant, for timepoints 0 and 3hrs, is on Monday(today), Wednesday, and Friday.
3. I will starting the titrations on the UKv 0 and 3hr on Friday and will be read next Wednesday(3/10).
4. Titration read out for WA1 0 and 8hour timepoints will be this Wednesday(3/3).

Let me know I you have questions.

-Trent

From: Dylan H. Morris < (b) (6)
Sent: Monday, February 22, 2021 10:24 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6)
Cc: Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Plowright, Raina < (b) (6) Adney, Danielle (NIH/NIAID) [F] < (b) (6) Holbrook, Myndi (NIH/NIAID) [C] < (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Awesome! Thanks so much for your hard work!

On Feb 22, 2021, at 12:20 PM, Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) wrote:

Update for this week:

1. SAvariant titrations will be read on Wednesday, this is the 0 and 3 hours timepoints.
2. WA1 and SAv PCR samples will be extracted this week, this is the 0 and 3 hours timepoints.
3. UK variant stock is grown and I will have titers on Wednesday.
4. UK variant stock will be sequenced this week to look for furin cleavage site.
5. I'm starting the WA1 strain 0 and 8 hour timepoints today. Titrations will be start on Friday and read next Wednesday.

Update everyone later this week with data.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Tuesday, February 9, 2021 5:01 PM
To: Dylan H. Morris <(b) (6)> Jamie Lloyd-Smith <(b) (6)> Amandine Gamble <(b) (6)>
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Subject: RE: Goldberg drum - WA1, UK, and SA variants

What is your estimate for 8 hours? Somewhere between 10^0.75- 10^1? I would be more comfortable around 10^1 – 10^1.25 in case we see a drop.

8 hours can be done but Jamie will owe me tickets to a NHL game jk.

-Trent

From: Dylan H. Morris <(b) (6)>
Sent: Tuesday, February 9, 2021 4:55 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)>
Cc: Jamie Lloyd-Smith <(b) (6)> Amandine Gamble <(b) (6)> Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Got it. Based on our back-of-the-envelope calculations, the best option in that case might be 8 hours. Would that potentially be an option? We can also do a bit more modeling. 9 could work too, but might be a little long.

On Feb 9, 2021, at 5:31 PM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)> wrote:

Dylan,
It looks like all inoculum (WA1, SA, & UK) will be ~1 X10^6. The WA1 was 1.7 x 10^6.

-Trent

From: Dylan H. Morris <(b) (6)>
Sent: Tuesday, February 9, 2021 3:07 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)> Jamie Lloyd-Smith <(b) (6)> Amandine Gamble <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

If we can go high enough, 12 hours is viable, and then we'll get a clearer estimate of the half-life. Otherwise we can do 9.

On Feb 9, 2021, at 5:02 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

In this case, would it be the highest of the lowest? Or WA1 as a standalone?

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

From: Dylan H. Morris < (b) (6)
Sent: Tuesday, February 9, 2021 2:59 PM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

How high do you reckon you can get the WA1 inoculum? That'll determine 9 versus 12.

On Feb 9, 2021, at 4:51 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Sounds good, fingers crossed. Pretty sure we're still one of the only US labs with these viruses

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

From: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6)
Sent: Tuesday, February 9, 2021 2:46 PM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Dylan H. Morris < (b) (6) Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hello crew,
I would like to figure out this extended timepoint (either 9 or 12) by the end of this week if we can? Just need some time to prep.

Plan for now…
Stocks:

- UKvairant- Start 2/12, titrations-2/19, Readout- 2/24

Runs:

- Feb.14-20 - 3x runs of SAvariant at T0,3hr
- Feb. 21-27 - 3x runs of WA1 at T0, 9 or 12hr - this is the timepoint we need to figure out?
- Feb. 28-Mar.6 - 3x runs of UKvariant at T0,3hr
- Mar. 7-13 - 3x runs of SAvariant at T0,??hr
- Mar. 14-10 - 3x runs of UKvariant at T0,??hr

Titrations and readout

- SAvariant at T0,3hr – 2/19, readout 2/24
- WA1 at T0, ??hr – 2/26, readout 3/3
- UKvariant at T0,3hr – 3/5, readout 3/10
- SAvariant at T0,??hr – 3/12, readout 3/17
- UKvariant at T0,??hr – 3/19, readout 3/24

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Monday, February 8, 2021 11:53 AM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Dylan H. Morris
< (b) (6)
Cc: Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

It takes ~1 ½ hours to get the Timepoint 0. It will take the 1 – 1 ½ for the finial timepoint.

As Vincent said 15 hr point is not doable. 6 hour will take some work to do but not preferred. 9 and 12 can be done.

It is looking like our UK strain will be ~ 10^5 for the starting inoculum. Can you run the model with this number for which timepoint you want?

South African will be higher(~10^7) so we should be good on that. Start with the same dilution as we did for the WA1. We will probably start with the SA strain and see if we can increase the inoculum titer for the UK.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Sent: Saturday, February 6, 2021 8:25 AM
To: Dylan H. Morris < (b) (6) Bushmaker, Trenton (NIH/NIAID) [E]
(b) (6)
Cc: Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

With a bit of planning every point might be doable, other than the 15 hour one

Trent: ho long exactly does it take you to start a run?

e.g. prep at 8, start run at 9 am? Sample at 9pm?

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

From: Dylan H. Morris <(b) (6)
Sent: Friday, February 5, 2021 8:24 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

I think 18h is probably too long given the T=0h measurements. I think we'd dip below the LOD. And I'm especially concerned given what you said about smaller initial virus concentrations for the new variant.

Which of the following intervals would be most practical given your protocols in 4?

A) T=0h, T=6h
B) T=0h, T=9h
C) T=0h, T=12h
D) T=0h, T=15h

Something else?

On Feb 5, 2021, at 4:47 PM, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:

Dylan/Amandine,
Thank you again for the quick turnaround for the graphs. It was a big hit today in the presentation I think!

So we need to discuss the later timepoint. What do you think would be a good timepoint? 18hrs?

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Thursday, February 4, 2021 8:41 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Amandine Gamble
<(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Here are some quick figures. Half-life looks to be 1 to 2 hours.

On Feb 4, 2021, at 1:27 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6)> wrote:

I think at the moment anything goes

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)>
Sent: Thursday, February 4, 2021 11:18 AM
To: Dylan H. Morris <(b) (6)> Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Cc: Amandine Gamble <(b) (6)> Jamie Lloyd-Smith <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Good idea Vincent.

-Trent

From: Dylan Morris <(b) (6)>
Date: Thursday, February 4, 2021 at 11:15 AM
To: Vincent Munster <(b) (6)>
Cc: Trenton Bushmaker <(b) (6)> Amandine Gamble <(b) (6)> Jamie Lloyd-Smith <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Could do a virological micropub? Or does that have to be genetics?

Or just a skinny preprint to which we can add B.1.351 when ready.

On Feb 4, 2021, at 1:11 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6)> wrote:

I think we should be able to run the UK variant very soon, we should probably see if that alone would already be good to get a preprint out or at least some communication in the public domain while we work on getting the SA variant plugged in?

Vincent Munster, PhD
Chief Virus Ecology Section

Rocky Mountain Laboratories
NIAID/NIH

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 11:09 AM
To: Dylan H. Morris <(b) (6) Amandine Gamble <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Dylan/Amandine,
Here is the temp and RH for the first (3) run of WA1 at timepoints 0 and 180 minutes.

-Trent

From: Dylan Morris <(b) (6)
Date: Thursday, February 4, 2021 at 10:50 AM
To: Vincent Munster <(b) (6)
Cc: Trenton Bushmaker <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Agreed. Data looks clean; congrats and thanks, Trent! I think we'll get a decent read out here on the half-life, and a good idea of how long to go for the longer run.

On Feb 4, 2021, at 12:48 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Looked pretty solid by eyeballing the data

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 10:42 AM
To: Dylan H. Morris <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thank you! Let me know if you have questions.

-Trent

From: Dylan Morris <(b) (6)
Date: Thursday, February 4, 2021 at 10:41 AM
To: Trenton Bushmaker <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6) Vincent Munster <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Excellent. Thanks, Trent! Will get right on this.

On Feb 4, 2021, at 12:39 PM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Hey crew,
Here is the excel file with the first (3) runs for WA1 at timepoints 0 and 180 minutes. Let me know what you think we should do for the extended timepoint after run through the model.

Dylan/Amadine- As we discussed I would like to include this in my talk tomorrow @ 1pm MT but just let me know if you can't make timeline.

I will get a better idea what the starting inoculum titers will be for the UK and South African variants the middle of next week. Estimate is that we will have to be starting with a lower titer. I will update you when I find out more.

I will start to grow those up at the end of next week. My schedule looks like you should have some data again around the first week of March.

Thank you everyone.

-Trent

From: Trenton Bushmaker <(b) (6)
Date: Wednesday, February 3, 2021 at 1:03 PM
To: Vincent Munster <(b) (6)
Cc: "Plowright, Raina" <(b) (6) "Adney, Danielle (NIH/NIAID) [F]" <(b) (6) "Holbrook, Myndi (NIH/NIAID) [C]" <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Vincent,
Here is the titration data for the first (3) runs of WA1 variant at timepoints 0 or 180 mins. I will send UCLA the excel file once you approve here today.

-Trent

From: Trenton Bushmaker <(b) (6)
Date: Wednesday, January 27, 2021 at 3:44 PM

To: Vincent Munster <(b) (6)
Cc: "Plowright, Raina" <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Vincent,
Updates the on the project:

1. For people helping on the project- Myndi will do the cells-TMEPRESS for titrations plates and the stocks. Danielle and me will do titrations. Kwe will help me with the quant qRT-PCR analysis and some paper writing. Dylan will work on the decay with me and paper writing. Let me know if you are ok with this?

2. For your email attached- For the aerosol stocks I think you already know the issues with the UK stock but the stock is only growing to 10^4 for the BEI isolate from California. Brand, Neeltje, and Myndi already know I need minimum of 120ml of stock of the highest stock. HOWEVER, if we get the South African (SA) variant grown up before the UK is figured out I will start with it.

I'm still projecting to be done with this project by the end of February.

Bob is in charge of the surface stability(according to Kwe) but let me know how you would like to proceed with it.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 7:07 AM
To: Bushmaker, Trenton (NIH/NIAID) [E](b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Maybe ask in todays meeting: just lay-out the tasks and we can see who signs-up?

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

From: Trenton Bushmaker <(b) (6)
Date: Monday, January 11, 2021 at 2:04 PM
To: "(b) (6) <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Vincent,
I'm looking at personnel to help me with this experiment. I'm thinking Myndi to grow stocks because she will be doing it anyways in BSL3. Vicky and Myndi to maintain cells for titrations and do plates(Monday passage, Thursday plate for Friday titrations). Danielle to help me with titrations(Fridays) and reading plates(Wednesdays/Thursdays).

Danielle and Vicky I would like to have involved because it will free up the senior group for other experiments.

Let me know if you agree with this.

Looks like at Goldberg runs on Monday, Thursday, and Friday. Titrations on Friday afternoon. Might have to do a few weekend days to accomidnate for Cara's schedule and school.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Friday, January 8, 2021 11:56 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Dylan H. Morris <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hey guys,

Please do understand the technical limitation of the set-up in a high containment laboratory. I favor shorter experiments, which will allow us to more rapidly determine whether there are differences between the isolates.
Given that the transmission window is likely under 3 hours, I'm not particularly in favor making these experiments longer in duration than absolutely necessary. Anything over a 3 hour window will have massive implication on the way we conduct experiments.

My main priority is not running a model, but a providing good comparison between the different strains, which should be done in under 3 hours. A limited analyses as was done in the NEJM should be sufficient (I'm not against running a model, but human resources are extremely limited and I think it would be best to have an experimental design which would get us the best result with the least effort). Also this data is urgent, and I don't want to have any delays with getting this data out.

Of note, you don't "lose" 2 logs during the spray, that's just the experimental system (from collision to collection), this is fixed for every experiment so no difference is expected there between variants (or viruses)

As discussed this week, at the moment no isolates are in yet (again, try to understand that this is a massive undertaking and is a process of several weeks), but titers are expected in the WA1 range

Cheers,

Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories

NIAID/NIH

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 7, 2021 8:14 PM
To: Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6)
Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Dylan H. Morris
<(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thank you for the quick reply, I like the points you made. I have some time tomorrow in BSL4 from 9-2pm to think and reply, thanks crew.

-Trent

From: "Amandine Gamble" <(b) (6)
Date: Thursday, January 7, 2021 at 7:01:22 PM
To: "Jamie Lloyd-Smith" <(b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]"
<(b) (6) "Dylan H. Morris" <(b) (6) "Munster, Vincent
(NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi everyone,

Thanks Trent for all the info and your work on those new strains (among other things!). I only have two minor thoughts following up on Jamie's e-mail:

- As Jamie noted, the longer we wait before taking the second time point, the more precise our estimate of decay rate / half-life will be (as long as we are still above the LOD), so I would also be tempted to target 4 or 5h rather than 3h based on the data we had for the NEJM paper and the fact that you are now using a more sensitive titration protocol (if we understood well), however that obviously depends on the starting dose (the intercept on the graph Jamie put) so, my question is: **do you have any idea of the stock concentrations for the new variants**, and whether we have any reason to expect more loss during spraying? It looks from the NEJM paper that we lose around 2 log10 during spraying with WA1 (and SARS-CoV-1). I guess you all already thought about this, but just writing down in case (there are lots of things to think about!). Also, if you already have an idea on the stock concentration, Dylan can run some analyses on mock data (as mentioned by Jamie) accounting for this, the loss at spraying and potential decay rates, as pointed by Jamie.

- The second point can be discussed after you got the data as it is only about formatting. I see from the raw data attached to one of the e-mails (the scan of the hand-written data) that some wells are blank, although in the Excel file we received, all

the wells were classified as + or -. I assume that you did not collect data from those blank wells because you could assume they were all positive (based on higher dilutions being positive) or negative (based on lower dilutions being negative), right? Dylan can correct me, but I think his model would run perfectly on the raw data, even if they are "incomplete". In other words, I think we can let the model do what you were already doing when you complete the blank wells so there is no need for you to do this. So in the future, **we are happy to work on the raw data (i.e., with +, - and blanks [that you can note "NA" so we know it is not just a forgotten well]), rather the completed version (with only + and -)**. You can even just send us a scan of your data and we can generate the Excel file if you prefere.

With all this, I also with you all the best for 2021 =)

Amandine

Le jeu. 7 janv. 2021 à 16:53, Jamie Lloyd-Smith <(b) (6) a écrit :
Hi Trent, hi everyone (also copying in Amandine since she's the one on our side with most experience with the raw data),

Great to hear this -- a few quick responses.
- 22/65 makes sense to me
- great to add the SA strain!
- I hope we are planning to collect new data on the WA1 strain, not reuse the NEJM data. There were enough differences in design with the original experiments that I think it would be MUCH stronger science to study all three strains using the same design (updated to avoid some of the challenges of the first round). (Actually from your comment about 'another 9 days' to add a timepoint, i.e. 3 viruses times 3 replicates, I think we're on the same page here.)
- I think the 5% decline in RH due to settling should be OK, if it's basically consistent across the viruses. We can think about whether to account for it in the modelling... my instinct is that we can leave it out of the model unless it differs significantly across replicates and viruses.
- Great to hear about T=0. That's especially crucial if we're just doing the one later time-point.
- Regarding the timing of the later timepoint, I was surprised by your statement, since my memory from the NEJM paper was that the above-LOD detections would have continued well beyond 3 hours. i.e. look at the plots:

<image001.png>
The SARS-CoV-2 data (red) started at a lower titer, but given the slopes it looks like there'd still be useful super-LOD data out to 5 and probably 6 hours. The SARS-CoV-1 data (blue) show the same slope with a higher intercept, and look like they'd stay above LOD out to 6 hours and beyond. Looking at the raw well data, the difference in + counts across time points isn't so striking, i.e. it's not like we're losing a dilution per hour - which makes sense, given the estimated half-life of ~3 hrs. Also if I'm not mistaken, Neetlje or Vincent mentioned that you guys have changed protocols (spin inoculation and different cell line) to get higher sensitivity in culture.
Bottom line: again, it will depend on the titers achievable at T=0, but unless I'm misreading things badly I think there would be value in extending that later timepoint. I know there are complexities about how long you can spend in BSL4, etc, but I'm just talking about the raw information content.

Dylan, Amandine, any further/other thoughts? Dylan, do you want to do a quick analysis with mock data (and reasonable noise) to think about the power we'd have to distinguish differences among variants using this design (i.e. 3 replicates of a single uninterrupted decay window)? And how that might change if we stretch the window to longer time periods? Or if we need more information to get better estimates, do we do as well by adding a 4th replicate at the long time point, rather than adding intermediate time points? (nothing magic about intermediate time points, except for prettier decay graphs. one replicate at 5h might be equivalent to 2 at 2h, in terms of information gained)

cheers,
Jamie

On Thu, Jan 7, 2021 at 3:51 PM Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:
Jamie/Dylan,
First, I have added the pervious email so we can all stay on the same page(UK variant shams).

Next, I have talked with Vincent today but would like your input. For a quick paper, I think we should do condition at 22C @ 65%RH – hospital setting. Is everyone ok with this? This was the same setting as we had in the NEJM paper.

Third, we will do the UK variant (VOC), South African (SA) variants, and the original NEJM paper Washington (WA1) for the comparison.

Four, will a 5% percent decrease over 3 hours of the relative humidity cause issues with anything? This happens when nothing is pulled out of the drum, it just happens because of the time frame of 3 hours with the deposition. It should be ok for this decay model(linear regression) correct? I just want to confirm.

Lastly and most important, we will "for sure" have a timepoint at 0 minutes to check for the start values. However, we need to discuss the last timepoint. The LOD for ourtitrations with our cell culture seems to happen between 180-240 mins, so I would stick with the 180 minute timepoint (titrations attached- "2019-nCoV titrations goldberg drum.jpeg"). Do you agree with this? It would give you two points at timepoint 0 and 180 minutes.

I will collect (4) qRT-PCR per timepoint 0 and (4) more during the later timepoint.

How does this sound? Think about the later timepoint. Each run is a day of work in BSL4 and 10ml of virus. If in addition you want to collect at a middle timepoint this will adding another 9 days of BSL4 work, that will have to be spread out over 3 weeks. We can also think about a later timepoint. The titrations will be useless but qRT-PCR might be interesting. I think this will be usefully for a later experiment because we want to get this out quickly.

-Trent

--

James O. Lloyd-Smith

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<2020-03-24 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

<2021-03-01 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

<Results for UCLA_qRT-PCR_E-assay_Aero WA1 and SAv_2021-02-03.xls>

<2021-03-10 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

<2021-03-17 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 11 Mar 2021 14:25:01 +0000
To: Alison Peel; Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: RE: Hendra-2

Just a reminder (as Kwe already said), don't make too many changes in sample stream. This again is a very big undertaking so I want it completely streamlined in order to do this.

- Full plates
- Don't worry too much if we miss a couple of samples
- Keep communication streamlined

As a reminder, this is still on top of requests from MSU, Bangladesh, UCLA, UK and at the moment we are very understaffed. However, as discussed this is a number 1 priority for us.

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

From: Alison Peel <(b) (6)
Sent: Thursday, March 11, 2021 12:42 AM
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Hendra-2

Hi Kwe,
So here's an updated list, with my own plate numbers. I can update this with your plate numbers if you are able to send through that sheet I mentioned in my previous email.
The "Kwe list with selections" tab should have all the samples you provided to me (in the original order provided), and their allocation into batches of samples (Plate_priority 1, 2, 3, 4 or SKIP)
The pivot table tab shows a list of plates to work through – priority 1, 2, 3 plates should be about 47 plates, and about 4418 samples.
The "Kwe list ONLY priority 1, 2, 3" tab has only the priority 1, 2, 3 samples selected, and sorted so that all the priority 1 plates are first (n = 20), then priority 2 (n = 18), then priority 3 (n = 9).

It would be great if you could feed back results as you start working through the plates, as we may change our sample selections based on early results.

Thanks
Ali

From: Alison Peel <(b) (6)
Date: Thursday, 11 March 2021 at 5:01 pm
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent

(NIH/NIAID) [E] <(b) (6)> Plowright, Raina <(b) (6)>
Subject: Re: Hendra-2

Thanks Kwe – this is really helpful.

That spreadsheet that you shared the screenshot of would be super-helpful because it shows the internal plate numbers that you're already using. In my sample selection, I've arbitrarily allocated my own plate numbers, and worry that this would get confusing because they are close but not the same. It confused me for a while when I was reading your email.
e.g. it looks like the line will need to be shifted up by two rows for the subsequent plates in that spreadsheet (my plate ids of 42, 43, 44 – as these all have 94 samples already)

And apologies, I meant to ask if my plate_id 49 was the incomplete plate (not 48), but it sounds like this is the case.

Anyway, If you're able to share that spreadsheet that shows your extraction numbering ("AUS plate 049" etc), I would prefer use that so it more neatly integrates the plate number selections with the numbers already in your system.

Thanks
Ali

From: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)>
Date: Thursday, 11 March 2021 at 12:52 pm
To: Alison Peel <(b) (6)> Munster, Vincent (NIH/NIAID) [E] <(b) (6)> Plowright, Raina <(b) (6)>
Subject: Re: Hendra-2

Hi Ali,

Thanks so much for your email.

- plate_id 41 has 96 samples on it. Is that correct? (e.g. rows 4361- 4456 in the "MakeExcelSheetForLabResults" tab)

I made the lines to facilitate the choice of plates for rescreening. See the screen shot that these last two samples are the first two samples of plate 49 (our extractions numbering) confirming that it simply an error in the lines.

- Also, can you please check that plate_id 45 and 48 are both incomplete plates with <94 samples on them? Or can you check the plate markers of where red samples starts (spillover response row 4692)?

Plate 45 is an incomplete plate while plate 48 is complete (4998-5091)

- Finally, plates 46/47 seem to have the 'end of plate' line in the wrong place?

Yes, I have corrected this.

Again, I made the lines to ease work of chosen plates for rescreening. We had a rigorous system of assignment samples to plates which involved to different people till Wyatt and I finalized the automated system of assigning samples.

Thanks

Kwe

From: Alison Peel <(b) (6)
Date: Tuesday, March 9, 2021 at 9:48 PM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Hendra-2

Hi Kwe,
I've attached copies of your spreadsheets where I've added a plate reference number. Can you please check a few things for me though, as there are some inconsistencies.

- In "Copy of RML_Template_Shipment_20190709_updated.xlsx"
  - plate_id 41 has 96 samples on it. Is that correct? (e.g. rows 4361- 4456 in the "MakeExcelSheetForLabResults" tab)
  - Also, can you please check that plate_id 45 and 48 are both incomplete plates with <94 samples on them? Or can you check the plate markers of where red samples starts (spillover response row 4692)?
  - Finally, plates 46/47 seem to have the 'end of plate' line in the wrong place?

Do you have alternative plateID numbers? How do you go back to identify a particular sample in a particular plate?
Thanks
Ali

From: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Date: Wednesday, 3 March 2021 at 8:38 am
To: Alison Peel <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Hendra-2

I have adjusted the file and the reds have a line now. These were samples which were screened as emergency outbreak. I had highlighted them and they still remain highlighted.
I have included the other two sheets and they all have lines demarketing plates. I will prefer that we go by plates. This will be helpful because our procedure is semi-automated.

Thanks

Kwe

From: Alison Peel <(b) (6)
Date: Tuesday, March 2, 2021 at 5:55 AM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Hendra-2

Hi Kwe,

This is helpful, thanks. I've been working through sample selections today

Firstly, what is the red colouring for the ARSBK001 and ARBEL001 accessions for? I can't see a plate separation there, but we would likely include those samples in the selection

While I think it is sensible for us to focus on AVL samples, I would also like to include a few samples from across the whole time series – so, including the latter half on 2019 and also in 2020. Can you please also send a spreadsheet showing how those samples separate across extraction plates? If you had a sheet that gives come kind of reference for the plate, that would be helpful (enable me to provide you with a list of plates?)

Finally, I'll going to assume that if there are 90 samples on the plate that we'd like to screen then we would just screen the whole plate. But what about if there is a plate with (for example) 60 samples that have been selected for screening, but also 34 non selected samples (i.e. a whole session, which would be laid out consecutively within the plate). Is it too fiddly if we were to omit those samples an just screen a partial plate, or would it just be preferable to screen the whole plate?

Thanks
Ali

From: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Date: Tuesday, 2 March 2021 at 6:34 am
To: Alison Peel <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina (b) (6)
Subject: Re: Hendra-2

Ali,

Each batch of samples we receive we make extractions plates of 94 samples per plate. In the list attached for example, after 94 sample there is line and representing the end of a plate.

So in this sheet if you choose the samples to be rescreen in reference to plates that will be helpful. This is the list of samples we received in July 2019.

Let me know if that is helpful.
Thanks
Kwe

From: Alison Peel <(b) (6)
Date: Friday, February 26, 2021 at 2:31 PM
To: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Hendra-2

Apologies, here's a zoom link for the meeting now:
https://us02web.zoom.us/j/(b) (6)

From: Alison Peel <(b) (6)
Date: Wednesday, 24 February 2021 at 9:21 am
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Hendra-2

Ok, thanks everyone. Sorry you can't make this time slot Kwe

From: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Date: Wednesday, 24 February 2021 at 12:56 am
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6) Alison Peel <(b) (6)
Subject: Re: Hendra-2

I have necropsy at that time. I think I will hear from Vincent.

Kwe

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Tuesday, February 23, 2021 at 7:38 AM
To: "Plowright, Raina" <(b) (6) Alison Peel <(b) (6)
Cc: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6)
Subject: RE: Hendra-2

Works from my end

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

From: Plowright, Raina <(b) (6)
Sent: Tuesday, February 23, 2021 7:35 AM
To: Alison Peel <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Re: Hendra-2

Yes

Sent from my iPad

On Feb 22, 2021, at 11:57 PM, Alison Peel <(b) (6) wrote:

Hi all,
Does Friday 2:30pm suit everyone?
Thanks
Ali

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, February 23, 2021 12:28:24 AM
To: Alison Peel <(b) (6) Plowright, Raina <(b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: RE: Hendra-2

Hi Ali

Can make Friday at the earliest, let me know if that would work for you. Thought I cancelled it but apparently not.

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

From: Alison Peel <(b) (6)
Sent: Sunday, February 21, 2021 4:59 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Re: Hendra-2

Thanks Vincent.
Sounds good. Let's discuss in more detail this week – can you make the tentative meeting slot on Tuesday afternoon 4pm your time? I've sent a calendar invite, that has a list of items to discuss
We could probably get through it in half an hour
Ali

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Monday, 22 February 2021 at 12:43 am
To: Plowright, Raina <(b) (6)
Cc: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: RE: Hendra-2

The remaining RNA will be still shipped afterwards to Ali so Ina can perform the broad screen.

Cheers,

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

From: Plowright, Raina <(b) (6)
Sent: Saturday, February 20, 2021 3:45 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Re: Hendra-2

Makes sense. Thanks for clarifying.

Sent from my iPhone

On Feb 20, 2021, at 3:10 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Broad paramyxovirus won't work, remember that that is all individual pcr based screen, with putting stuff on gels and sequencing, that's too labor intensive. The Hendra is "easy" as its just a single qRT-PCR. I think it's important to realize that this is "just" a Hendra so we won't be violating any agreement with

the CVO. That said, we have plenty of time to discuss this with the CVOs, as we still need to develop and setup the assays(that might still take a couple of months).

Cheers,

Vincent

On Feb 20, 2021, at 13:17, Plowright, Raina <(b) (6) wrote:

If V has capacity, it would be ideal to do broad paramyxovirus screen. We could ask CVO about this, given V is sending RNA back to Oz to do just that. At this stage I don't think we have anything to lose by asking.

Sent from my iPhone

On Feb 20, 2021, at 1:07 PM, Alison Peel <(b) (6) wrote:

Thanks Vincent,
This is fabulous!!
A couple of quick things as I need to get up and leave for a conference now
- chat would be good. I'm out all day today so earliest would be Monday morning my time
- we need to take guidance on timing of this work from Ed, awaiting a discussion this week with CVOs for approval to screen. But we can certainly get ready in the meantime
- I have thoughts on which samples to prioritise if you can suggest sample size but if it's just as easy to rescreen whole plates then that would be fabulous. We are the only group placed to rapidly see if this is in blacks as well as greys. If sample selection is a preferred, then if Kwe can share plate layout of RNA extracts, then I can take that into consideration with sample selection too.
- I'm concerned about the effect of this screening on my subsequent screening for PMV- freeze thaw, quantity etc. I'd like to have a clear plan for how this fits in with this multiviral work.

Thanks all!
Chat soon
Ali

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Sunday, February 21, 2021 3:09:07 AM
To: Plowright, Raina (b) (6)
Cc: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: RE: Hendra-2

I think it's an important question to address (and would increase the impact of the work), given that the most labor intensive part is already done (the extractions) we should be able to do quite some sample sets.

The most important thing we need to do is:

- Update new assay (which we need to design so it only picks-up this variant and not the other as we need to distinguish)
- Design and generated run-off template RNA positive controls
- Assay validation (so we know the performance of the assay and can report back Ct values AND copy numbers)

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

From: Plowright, Raina <(b) (6)
Sent: Saturday, February 20, 2021 9:21 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Re: Hendra-2

V, so happy to hear you can do this!!! We could do times with higher prevalence and also sheets with mixed species. Ali, happy to do a call tonight or tomorrow night. We could ask Wyatt to generate a list of high likelihood samples. Let me know your availability.
V do u have a sample size in mind? Is the selection process time consuming (eg easier to just do a batch all contained in one part of freezer). Let us know your constraints.

Sent from my iPhone

On Feb 20, 2021, at 8:31 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Hi guys,

As soon as we have an updated primer set (and positive controls) we plan to run some screens on the Australian samples. We can rapidly redo the initial screen on the last samples, but would be good if you would like a targeted approach (e.g. with blacks etc.) or just a blanket approach.

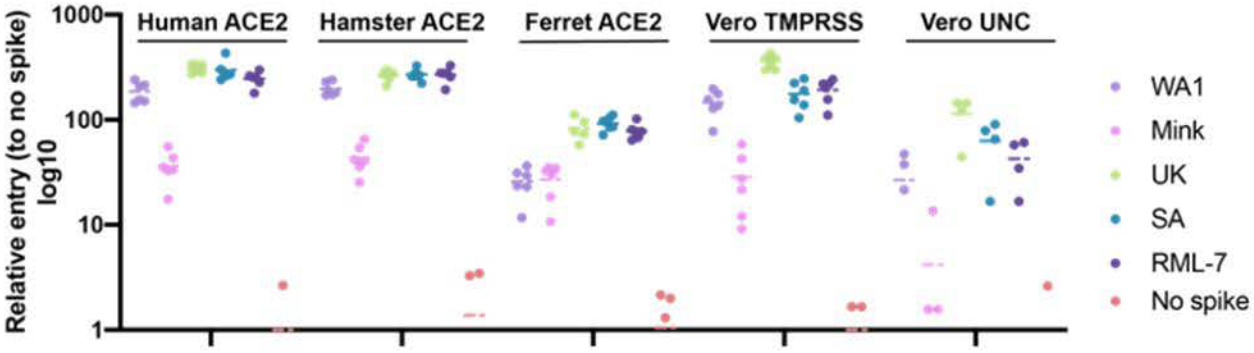
Cheers,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 10 Mar 2021 22:31:12 +0000
To: Jamie Lloyd-Smith
Cc: Dylan H. Morris; Bushmaker, Trenton (NIH/NIAID) [E]; Amandine Gamble; Plowright, Raina; Adney, Danielle (NIH/NIAID) [F]; Holbrook, Myndi (NIH/NIAID) [C]; Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: RE: Goldberg drum - WA1, UK, and SA variants

I was thinking about that as well, obviously if the 0 and 8 hour timepoints behave the same then it should not have an effect. However, if the ID is lowered with the virus, that might have some effect on the aerosol stability. Just not clear how we would tease this out.

This is some of the pseudotype entry data generated by Kwe, suggesting that different strains have different affinity for ACE2 (basically WA1 less, UK and SA more). For some reason this effect seems more pronounced with the TMPSII cells (these are vero's expressing human ACE2 and TMPRSII)



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

From: Jamie Lloyd-Smith <(b) (6)
Sent: Wednesday, March 10, 2021 1:10 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Dylan H. Morris <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Amandine Gamble <(b) (6) Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Interesting point, but wouldn't that play out equally at earlier and later time points? i.e. the overall culture sensitivity might be higher, but the decay in viable virus titer should still reflect inactivation between measurements? Or am I missing something?

In any case, the change over time of the ability to infect cells expressing hACE2 and TMPRSII seems like an important functional proxy for actual human infectivity. These 8-hour time points will be very interesting... see where these posteriors end up. That second replicate on 1.1.7 is having a big influence, I think, but the longer timepoints will provide strong information on whether that's a fluke.

cheers
Jamie

On Wed, Mar 10, 2021 at 12:01 PM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
One of the interesting things with these novel variants is that they bind better to ACE2, so the effect might partly not be a true environmental impact, rather the ability of less infectious virus to still infect (so lowering the threshold).

These samples were titrated on cells expressing human Ace2 and TMPRSII,

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

From: Dylan H. Morris <(b) (6)
Sent: Wednesday, March 10, 2021 11:51 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Amandine Gamble <(b) (6) Plowright, Raina (b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6) Jamie Lloyd-Smith <(b) (6) Munster, Vincent (NIH/NIAID) [E] (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Oops forgot to attach!

On Mar 10, 2021, at 1:50 PM, Dylan H. Morris <(b) (6) wrote:

Here you go. Half-life looks to be above 2h, which would imply losing about 1.2 log10 in 8 h. Only potential problem is the slightly lower T=0. Still, my guess is it will be fine. Worst case scenario, it's right around the LOD. Could probably get resolution by doing a couple extra wells at zero dilution

(e.g. if we're right around the LOD, might get 0 / 4 positive, but probably at least one of 8 wells positive)

On Mar 10, 2021, at 1:05 PM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Dylan/Amandine,
Here is the titration data for the UK variant (B.1.1.7) for the timepoint 0, 3hrs.

Could you have a quick look to confirm the later timepoint of 8 hour because I will need to start these runs on this Friday(3/12/21).

Thank you!

In addition, I will have the titrations for timepoint 0,3hrs for the new stockSouth African variant next week Wednesday(3/17/21). However, I will need to start on the T0, 8hour aerosol runs on Tuesday so I can get them done. We have a deadline for a lab recertification coming up.

Let me know if you have questions. Hope all is well!

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Friday, March 5, 2021 10:58 AM
To: Dylan H. Morris <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: IMPORTANT- RE: Goldberg drum - WA1, UK, and SA variants

Dylan/Amandine,
Important part- I will need a quick turn around because I'm starting the SA variant's LATER timepoint on Monday. We will need to figure out what we want to do for this LATER timepoint (8hr, 12-hardest, 18, or 24hrs) before Monday.

Titration sheet is attached.

WA1 has both T0,3hr and T0,8hr, I looks pretty good by eye balling it. I will work independent of you this afternoon to look at the decay for WA1. Dylan you did a really good job with the 8 hr timepoint!

For the SA variant, I redid the titrations but was only able to read 2 of the 3 plates. We had a little issue with the third plate because we missed a row which messed up the rest of the plate. Oh well. I did put all 5 plates on the titration sheet for T0,3hr for you to work with.

Talk with you both soon! Here is my cell phone if you want a quick reply:(b) (6). I will be in BSL4 till 1:30pm MTime today.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Tuesday, March 2, 2021 9:56 AM
To: Dylan H. Morris <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6) Amandine Gamble <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Plowright, Raina <(b) (6)
Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C]
<(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Thank you crew. Call me if you have questions. Just prepping for these studies today.

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Tuesday, March 2, 2021 9:52 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6); Amandine Gamble
<(b) (6) Jamie Lloyd-Smith <(b) (6) Plowright, Raina
<(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook,
Myndi (NIH/NIAID) [C] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

I can try to analyze the PCR data today.

On Mar 2, 2021, at 11:50 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Yes, so focus on the UK variant (B.1.1.7). Genotypically the current B.1.351 is weird (we'll have a correct one at the end of this week, but still needs to be grown). Whereas it shouldn't impact on the stability, the recovery sensitivity might be different.

Lets see what it looks like with the PCR data. Waiting until April does not make much sense (as there will likely be another variant)

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

From: Dylan H. Morris <(b) (6)
Sent: Tuesday, March 2, 2021 9:08 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)

Cc: Amandine Gamble <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Jamie Lloyd-Smith <(b) (6) Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thanks! Personally, I would suggest getting something out quickly rather than delaying to include CA VOC. B.1.351 and B.1.1.7 very informative for a lot of the other VOC/VOI, since there's so much convergence.

And less stress for Trent too.

On Mar 2, 2021, at 11:03 AM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Here is the qRT-PCR data for the E-assay "Results for UCLA_qRT-PCR_E-assay_Aero WA1 and SAv_2021-02-03".

Two things to keep on the radar:

1. If we add the CA VOC this will have to be done after we get Suite D back from the annual shutdown which is slotted for March 23- ~April 15th. For people that don't speak BSL4 lingo, I am currently booked till March 23rd with the current SAv, UKv, and WA1 strain project. This is already a tight window to get things done. This required annual shutdown will stop all aerosol work between the dates of March 23- ~April 15th.
2. This is mostly for Vincent but if we don't think this SAv (B.1.351) is the correct variant should we omit this upcoming longer timepoint. This can be decided after we see the data normalized with the qRT-PCR.

Thanks everyone for your input, learning a bunch.

-Trent

From: Amandine Gamble <(b) (6)
Sent: Tuesday, March 2, 2021 7:43 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Dylan H. Morris <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Jamie Lloyd-Smith <(b) (6) Plowright, Raina <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi Trent and Vincent,

Thanks for the info regarding B.1.351. Indeed it would be even better if you can get data for the CA VOC.

Dylan made this plot on the raw titration data. Trent, you can send the PCR data our way (I don't think we got them yet, right?) and we will see how much it changes after normalization.

Looking forward to more data! Thanks again for all the hard work getting the isolates and then in BSL4!

Amandine

Le mar. 2 mars 2021 à 09:19, Munster, Vincent (NIH/NIAID) [E] <(b) (6) a écrit :
The B.1.351 is a bit weird, as it has several mutations (not fixed) at ~ 80% in the reads in spike (one transitioning the furin cleavage site into a trypsin site, so not the cleavage deletion but still a SNP not reported in the natural variant which might affect our ability to recover it a bit). We are working on getting better strain in. I think we need to repeat the B.1.351 with a fully genetic comparable one.

In addition, we should likely add the 452-CA-VOC as well, to make an even better panel.

Did you try to normalize based on the PCR data? Any good?

Cheers,

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

From: "Dylan H. Morris" <(b) (6)
Date: Monday, March 1, 2021 at 11:10 PM
To: Trenton Bushmaker <(b) (6)
Cc: Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) "(b) (6) <(b) (6) "Plowright, Raina" (b) (6), "Adney, Danielle (NIH/NIAID) [F]" <(b) (6) "Holbrook, Myndi (NIH/NIAID) [C]" <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Here are some fits and half-life estimates for B.1.351 and WA1

Definitely need the later timepoint for B.1.351 to be sure, but it looks like there might be a real difference. There also might not.

The model is very uncertain about the half-life of B.1.351 since minimal infectious virus appeared to be lost during the 3 hr experiment.

Best,
Dylan

On Mar 1, 2021, at 5:07 PM, Dylan H. Morris <(b) (6) wrote:

Excellent. Yes, please send it over!

On Mar 1, 2021, at 1:21 PM, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:

Dylan,
Here is the titration data "2021-03-01 Raw data - 22C @ 65%RH- WA1, UK, & SA" for WA1 and SAv (B.1.351). I will be very interested to hear what you think and what you think about the later timepoint.

I have the PCR data done for the WA1 and SAv (B.1.351) samples I you want that data now?

Update for this week:

1. UK variant stock for aerosol runs does not detecting any deletion of the furin site from sequencing. Stock titer is 10^5.7.
2. Aerosol runs for UK variant, for timepoints 0 and 3hrs, is on Monday(today), Wednesday, and Friday.
3. I will starting the titrations on the UKv 0 and 3hr on Friday and will be read next Wednesday(3/10).
4. Titration read out for WA1 0 and 8hour timepoints will be this Wednesday(3/3).

Let me know I you have questions.

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Monday, February 22, 2021 10:24 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina (b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Awesome! Thanks so much for your hard work!

On Feb 22, 2021, at 12:20 PM, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:

Update for this week:

1. SAvariant titrations will be read on Wednesday, this is the 0 and 3 hours timepoints.
2. WA1 and SAv PCR samples will be extracted this week, this is the 0 and 3 hours timepoints.
3. UK variant stock is grown and I will have titers on Wednesday.
4. UK variant stock will be sequenced this week to look for furin cleavage site.
5. I'm starting the WA1 strain 0 and 8 hour timepoints today. Titrations will be start on Friday and read next Wednesday.

Update everyone later this week with data.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Tuesday, February 9, 2021 5:01 PM
To: Dylan H. Morris < (b) (6) Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

What is your estimate for 8 hours? Somewhere between 10^0.75- 10^1? I would be more comfortable around 10^1 – 10^1.25 in case we see a drop.

8 hours can be done but Jamie will owe me tickets to a NHL game jk.

-Trent

From: Dylan H. Morris < (b) (6)
Sent: Tuesday, February 9, 2021 4:55 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6)
Cc: Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Got it. Based on our back-of-the-envelope calculations, the best option in that case might be 8 hours. Would that potentially be an option? We can also do a bit more modeling. 9 could work too, but might be a little long.

On Feb 9, 2021, at 5:31 PM, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:

Dylan,
It looks like all inoculum (WA1, SA, & UK) will be ~1 X10^6. The WA1 was 1.7 x 10^6.

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Tuesday, February 9, 2021 3:07 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

If we can go high enough, 12 hours is viable, and then we'll get a clearer estimate of the half-life. Otherwise we can do 9.

On Feb 9, 2021, at 5:02 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

In this case, would it be the highest of the lowest? Or WA1 as a standalone?

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

From: Dylan H. Morris <(b) (6)
Sent: Tuesday, February 9, 2021 2:59 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

How high do you reckon you can get the WA1 inoculum? That'll determine 9 versus 12.

On Feb 9, 2021, at 4:51 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Sounds good, fingers crossed. Pretty sure we're still one of the only US labs with these viruses

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, February 9, 2021 2:46 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Dylan H. Morris <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble

< (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hello crew,
I would like to figure out this extended timepoint (either 9 or 12) by the end of this week if we can? Just need some time to prep.

Plan for now…
Stocks:

- UKvairant- Start 2/12, titrations-2/19, Readout- 2/24

Runs:

- Feb.14-20 - 3x runs of SAvariant at T0,3hr
- Feb. 21-27 - 3x runs of WA1 at T0, 9 or 12hr - this is the timepoint we need to figure out?
- Feb. 28-Mar.6 - 3x runs of UKvariant at T0,3hr
- Mar. 7-13 - 3x runs of SAvariant at T0,??hr
- Mar. 14-10 - 3x runs of UKvariant at T0,??hr

Titrations and readout

- SAvariant at T0,3hr – 2/19, readout 2/24
- WA1 at T0, ??hr – 2/26, readout 3/3
- UKvariant at T0,3hr – 3/5, readout 3/10
- SAvariant at T0,??hr – 3/12, readout 3/17
- UKvariant at T0,??hr – 3/19, readout 3/24

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Monday, February 8, 2021 11:53 AM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Dylan H. Morris
< (b) (6)
Cc: Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

It takes ~1 ½ hours to get the Timepoint 0. It will take the 1 – 1 ½ for the finial timepoint.

As Vincent said 15 hr point is not doable. 6 hour will take some work to do but not preferred. 9 and 12 can be done.

It is looking like our UK strain will be ~ 10^5 for the starting inoculum. Can you run the model with this number for which timepoint you want?

South African will be higher(~10^7) so we should be good on that. Start with the same dilution as we did for the WA1. We will probably start with the SA strain and see if we can increase the inoculum titer for the UK.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Saturday, February 6, 2021 8:25 AM
To: Dylan H. Morris <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

With a bit of planning every point might be doable, other than the 15 hour one

Trent: ho long exactly does it take you to start a run?

e.g. prep at 8, start run at 9 am? Sample at 9pm?

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

From: Dylan H. Morris <(b) (6)
Sent: Friday, February 5, 2021 8:24 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

I think 18h is probably too long given the T=0h measurements. I think we'd dip below the LOD. And I'm especially concerned given what you said about smaller initial virus concentrations for the new variant.

Which of the following intervals would be most practical given your protocols in 4?

A) T=0h, T=6h
B) T=0h, T=9h
C) T=0h, T=12h
D) T=0h, T=15h

Something else?

On Feb 5, 2021, at 4:47 PM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Dylan/Amandine,
Thank you again for the quick turnaround for the graphs. It was a big hit today in the presentation I think!

So we need to discuss the later timepoint. What do you think would be a good timepoint? 18hrs?

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Thursday, February 4, 2021 8:41 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Here are some quick figures. Half-life looks to be 1 to 2 hours.

On Feb 4, 2021, at 1:27 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

I think at the moment anything goes

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 11:18 AM
To: Dylan H. Morris <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Good idea Vincent.

-Trent

From: Dylan Morris <(b) (6)
Date: Thursday, February 4, 2021 at 11:15 AM
To: Vincent Munster <(b) (6)
Cc: Trenton Bushmaker <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Could do a virological micropub? Or does that have to be genetics?

Or just a skinny preprint to which we can add B.1.351 when ready.

On Feb 4, 2021, at 1:11 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

I think we should be able to run the UK variant very soon, we should probably see if that alone would already be good to get a preprint out or at least some communication in the public domain while we work on getting the SA variant plugged in?

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

From: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6)
Sent: Thursday, February 4, 2021 11:09 AM
To: Dylan H. Morris < (b) (6) Amandine Gamble < (b) (6)
Cc: Jamie Lloyd-Smith < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Dylan/Amandine,
Here is the temp and RH for the first (3) run of WA1 at timepoints 0 and 180 minutes.

-Trent

From: Dylan Morris < (b) (6)
Date: Thursday, February 4, 2021 at 10:50 AM
To: Vincent Munster < (b) (6)
Cc: Trenton Bushmaker < (b) (6) Jamie Lloyd-Smith < (b) (6) Amandine Gamble < (b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Agreed. Data looks clean; congrats and thanks, Trent! I think we'll get a decent read out here on the half-life, and a good idea of how long to go for the longer run.

On Feb 4, 2021, at 12:48 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Looked pretty solid by eyeballing the data

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 10:42 AM
To: Dylan H. Morris <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thank you! Let me know if you have questions.

-Trent

From: Dylan Morris <(b) (6)
Date: Thursday, February 4, 2021 at 10:41 AM
To: Trenton Bushmaker <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble
<(b) (6) Vincent Munster <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Excellent. Thanks, Trent! Will get right on this.

On Feb 4, 2021, at 12:39 PM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Hey crew,
Here is the excel file with the first (3) runs for WA1 at timepoints 0 and 180 minutes. Let me know what you think we should do for the extended timepoint after run through the model.

Dylan/Amadine- As we discussed I would like to include this in my talk tomorrow @ 1pm MT but just let me know if you can't make timeline.

I will get a better idea what the starting inoculum titers will be for the UK and South African variants the middle of next week. Estimate is that we will have to be starting with a lower titer. I will update you when I find out more.

I will start to grow those up at the end of next week. My schedule looks like you should have some data again around the first week of March.

Thank you everyone.

-Trent

From: Trenton Bushmaker <(b) (6)
Date: Wednesday, February 3, 2021 at 1:03 PM
To: Vincent Munster <(b) (6)

Cc: "Plowright, Raina" <(b) (6)> "Adney, Danielle (NIH/NIAID) [F]" <(b) (6)> "Holbrook, Myndi (NIH/NIAID) [C]" <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Vincent,
Here is the titration data for the first (3) runs of WA1 variant at timepoints 0 or 180 mins. I will send UCLA the excel file once you approve here today.

-Trent

From: Trenton Bushmaker <(b) (6)>
Date: Wednesday, January 27, 2021 at 3:44 PM
To: Vincent Munster <(b) (6)>
Cc: "Plowright, Raina" <(b) (6)>
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Vincent,
Updates the on the project:

1. For people helping on the project- Myndi will do the cells-TMEPRESS for titrations plates and the stocks. Danielle and me will do titrations. Kwe will help me with the quant qRT-PCR analysis and some paper writing. Dylan will work on the decay with me and paper writing. Let me know if you are ok with this?

2. For your email attached- For the aerosol stocks I think you already know the issues with the UK stock but the stock is only growing to 10^4 for the BEI isolate from California. Brand, Neeltje, and Myndi already know I need minimum of 120ml of stock of the highest stock. HOWEVER, if we get the South African (SA) variant grown up before the UK is figured out I will start with it.

I'm still projecting to be done with this project by the end of February.

Bob is in charge of the surface stability(according to Kwe) but let me know how you would like to proceed with it.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Sent: Tuesday, January 12, 2021 7:07 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Maybe ask in todays meeting: just lay-out the tasks and we can see who signs-up?

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology

Rocky Mountain Laboratories
NIAID/NIH

From: Trenton Bushmaker <(b) (6)
Date: Monday, January 11, 2021 at 2:04 PM
To: "(b) (6) <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Vincent,
I'm looking at personnel to help me with this experiment. I'm thinking Myndi to grow stocks because she will be doing it anyways in BSL3. Vicky and Myndi to maintain cells for titrations and do plates(Monday passage, Thursday plate for Friday titrations). Danielle to help me with titrations(Fridays) and reading plates(Wednesdays/Thursdays).

Danielle and Vicky I would like to have involved because it will free up the senior group for other experiments.

Let me know if you agree with this.

Looks like at Goldberg runs on Monday, Thursday, and Friday. Titrations on Friday afternoon. Might have to do a few weekend days to accomidnate for Cara's schedule and school.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Friday, January 8, 2021 11:56 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Dylan H. Morris <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hey guys,

Please do understand the technical limitation of the set-up in a high containment laboratory. I favor shorter experiments, which will allow us to more rapidly determine whether there are differences between the isolates.
Given that the transmission window is likely under 3 hours, I'm not particularly in favor making these experiments longer in duration than absolutely necessary. Anything over a 3 hour window will have massive implication on the way we conduct experiments.

My main priority is not running a model, but a providing good comparison between the different strains, which should be done in under 3 hours. A limited analyses as was done in the NEJM should be sufficient (I'm not against running a model, but human resources are extremely limited and I think it would be best to have an experimental design which would get us the best result with the least effort). Also this data is urgent, and I don't want to have any delays with getting this data out.

Of note, you don't "lose" 2 logs during the spray, that's just the experimental system (from collision to collection), this is fixed for every experiment so no difference is expected there between variants (or viruses)

As discussed this week, at the moment no isolates are in yet (again, try to understand that this is a massive undertaking and is a process of several weeks), but titers are expected in the WA1 range

Cheers,

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 7, 2021 8:14 PM
To: Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Dylan H. Morris <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thank you for the quick reply, I like the points you made. I have some time tomorrow in BSL4 from 9-2pm to think and reply, thanks crew.

-Trent

From: "Amandine Gamble" <(b) (6)
Date: Thursday, January 7, 2021 at 7:01:22 PM
To: "Jamie Lloyd-Smith" <(b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]" <(b) (6) "Dylan H. Morris" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi everyone,

Thanks Trent for all the info and your work on those new strains (among other things!). I only have two minor thoughts following up on Jamie's e-mail:

- As Jamie noted, the longer we wait before taking the second time point, the more precise our estimate of decay rate / half-life will be (as long as we are still above the LOD), so I would also be tempted to target 4 or 5h rather than 3h based on the data we had for the NEJM paper and the fact that you are now using a more sensitive titration protocol (if we understood well), however that obviously depends on the

starting dose (the intercept on the graph Jamie put) so, my question is: **do you have any idea of the stock concentrations for the new variants**, and whether we have any reason to expect more loss during spraying? It looks from the NEJM paper that we lose around 2 log10 during spraying with WA1 (and SARS-CoV-1). I guess you all already thought about this, but just writing down in case (there are lots of things to think about!). Also, if you already have an idea on the stock concentration, Dylan can run some analyses on mock data (as mentioned by Jamie) accounting for this, the loss at spraying and potential decay rates, as pointed by Jamie.

- The second point can be discussed after you got the data as it is only about formatting. I see from the raw data attached to one of the e-mails (the scan of the hand-written data) that some wells are blank, although in the Excel file we received, all the wells were classified as + or -. I assume that you did not collect data from those blank wells because you could assume they were all positive (based on higher dilutions being positive) or negative (based on lower dilutions being negative), right? Dylan can correct me, but I think his model would run perfectly on the raw data, even if they are "incomplete". In other words, I think we can let the model do what you were already doing when you complete the blank wells so there is no need for you to do this. So in the future, **we are happy to work on the raw data (i.e., with +, - and blanks [that you can note "NA" so we know it is not just a forgotten well]), rather the completed version (with only + and -)**. You can even just send us a scan of your data and we can generate the Excel file if you prefere.

With all this, I also with you all the best for 2021 =)

Amandine

Le jeu. 7 janv. 2021 à 16:53, Jamie Lloyd-Smith < (b) (6) a écrit :
Hi Trent, hi everyone (also copying in Amandine since she's the one on our side with most experience with the raw data),

Great to hear this -- a few quick responses.
- 22/65 makes sense to me
- great to add the SA strain!
- I hope we are planning to collect new data on the WA1 strain, not reuse the NEJM data. There were enough differences in design with the original experiments that I think it would be MUCH stronger science to study all three strains using the same design (updated to avoid some of the challenges of the first round). (Actually from your comment about 'another 9 days' to add a timepoint, i.e. 3 viruses times 3 replicates, I think we're on the same page here.)
- I think the 5% decline in RH due to settling should be OK, if it's basically consistent across the viruses. We can think about whether to account for it in the modelling... my instinct is that we can leave it out of the model unless it differs significantly across replicates and viruses.
- Great to hear about T=0. That's especially crucial if we're just doing the one later time-point.

- Regarding the timing of the later timepoint, I was surprised by your statement, since my memory from the NEJM paper was that the above-LOD detections would have continued well beyond 3 hours. i.e. look at the plots:

<image001.png>
The SARS-CoV-2 data (red) started at a lower titer, but given the slopes it looks like there'd still be useful super-LOD data out to 5 and probably 6 hours. The SARS-CoV-1 data (blue) show the same slope with a higher intercept, and look like they'd stay above LOD out to 6 hours and beyond. Looking at the raw well data, the difference in + counts across time points isn't so striking, i.e. it's not like we're losing a dilution per hour - which makes sense, given the estimated half-life of ~3 hrs. Also if I'm not mistaken, Neetlje or Vincent mentioned that you guys have changed protocols (spin inoculation and different cell line) to get higher sensitivity in culture.
Bottom line: again, it will depend on the titers achievable at T=0, but unless I'm misreading things badly I think there would be value in extending that later timepoint. I know there are complexities about how long you can spend in BSL4, etc, but I'm just talking about the raw information content.

Dylan, Amandine, any further/other thoughts? Dylan, do you want to do a quick analysis with mock data (and reasonable noise) to think about the power we'd have to distinguish differences among variants using this design (i.e. 3 replicates of a single uninterrupted decay window)? And how that might change if we stretch the window to longer time periods? Or if we need more information to get better estimates, do we do as well by adding a 4th replicate at the long time point, rather than adding intermediate time points? (nothing magic about intermediate time points, except for prettier decay graphs. one replicate at 5h might be equivalent to 2 at 2h, in terms of information gained)

cheers,
Jamie

On Thu, Jan 7, 2021 at 3:51 PM Bushmaker, Trenton (NIH/NIAID) [E] <[redacted] (b) (6)
wrote:
Jamie/Dylan,
First, I have added the pervious email so we can all stay on the same page(UK variant shams).

Next, I have talked with Vincent today but would like your input. For a quick paper, I think we should do condition at 22C @ 65%RH – hospital setting. Is everyone ok with this? This was the same setting as we had in the NEJM paper.

Third, we will do the UK variant (VOC), South African (SA) variants, and the original NEJM paper Washington (WA1) for the comparison.

Four, will a 5% percent decrease over 3 hours of the relative humidity cause issues with anything? This happens when nothing is pulled out of the drum, it just happens because of the time frame of 3 hours with the deposition. It should be ok for this decay model(linear regression) correct? I just want to confirm.

Lastly and most important, we will "for sure" have a timepoint at 0 minutes to check for the start values. However, we need to discuss the last timepoint. The LOD for ourtitrations with our cell culture seems to happen between 180-240 mins, so I would stick with the 180 minute timepoint (titrations attached- "2019-nCoV titrations goldberg drum.jpeg"). Do you agree with this? It would give you two points at timepoint 0 and 180 minutes.

I will collect (4) qRT-PCR per timepoint 0 and (4) more during the later timepoint.

How does this sound? Think about the later timepoint. Each run is a day of work in BSL4 and 10ml of virus. If in addition you want to collect at a middle timepoint this will adding another 9 days of BSL4 work, that will have to be spread out over 3 weeks. We can also think about a later timepoint. The titrations will be useless but qRT-PCR might be interesting. I think this will be usefully for a later experiment because we want to get this out quickly.

-Trent

--
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

<2020-03-24 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

<2021-03-01 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

<Results for UCLA_qRT-PCR_E-assay_Aero WA1 and SAv_2021-02-03.xls>

<2021-03-10 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

--
James O. Lloyd-Smith

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Department of Ecology & Evolutionary Biology
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610 Charles E Young Dr South
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Office: 4135 Terasaki Life Sciences Building
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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 9 Mar 2021 21:51:35 +0000
To: (b) (6)
Cc: LaTrielle, Sara; Plowright, Raina
Subject: RE: FY20 Unexpended Funds

correct

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

From: (b) (6)
Sent: Tuesday, March 9, 2021 2:43 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: LaTrielle, Sara <(b) (6) Plowright, Raina <(b) (6)
Subject: RE: FY20 Unexpended Funds

Super. Thanks, Vincent. Also, just to confirm, you have your first tranche of FY21 funding ($255K) in hand now, correct? The remaining ~$60K is nearly through the approval gauntlet at DARPA so I expect that to be awarded soon.

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, March 9, 2021 4:40 PM
To: (b) (6)
Cc: LaTrielle, Sara <(b) (6) Plowright, Raina <(b) (6)
Subject: RE: FY20 Unexpended Funds

Hi (b) (6)

That would be no problem and we fully expect to spend down to the last dollar,

Cheers,

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

From: (b) (6)
Sent: Tuesday, March 9, 2021 1:19 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: LaTrielle, Sara <(b) (6) Plowright, Raina <(b) (6)
Subject: FY20 Unexpended Funds

Hi Vincent. That time of year. As of 5 March, DARPA holds that you have yet to expend $27,412.22 from the $365,702 FY20 funding awarded last year. I wanted to ensure that you would be able to fully expend that funding by the end of FY21. If not, I'll need to initiate a pull-back MIPR for the remaining amount.

Please let me know whether or not you expect to be able to expend that remaining funding by the end of this FY.

Thanks.

(b) (6)
Contractor Support to DARPA BTO
Quantitative Scientific Solutions (QS-2)
(b) (6)
Cell: (b) (6)
Work Mobile: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 9 Mar 2021 19:09:18 +0000
To: Manuel Ruiz; Bushmaker, Trenton (NIH/NIAID) [E]; Plowright, Raina; Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: RE: Options for inactivation of serum samples

Nope, and it shouldn't effect proteins

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

From: Manuel Ruiz <(b) (6)
Sent: Tuesday, March 9, 2021 12:04 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6); Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6); Plowright, Raina <(b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Options for inactivation of serum samples

Hi Vincent,

The immunology team has some concerns about the irradiation breaking down some proteins in the serum samples... which could be influencing some results. They are currently running some experiments with non-irradiated samples from Lubee.

Do you have any other options for inactivation of serum samples that we could explore/discuss as options?

Thank you,
M

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 9 Mar 2021 19:00:21 +0000
To: Manuel Ruiz
Cc: Bushmaker, Trenton (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina; Dan Crowley; Caylee Falvo
Subject: RE: sample processing

Hi Manuel,

we'll will add the blood to the Trizol (they could then bet stored at MSU if needed or processed straight away). At MSU they will continue the extraction with the phasemaker tubes and purelink RNA extraction (makes sense?)

So the order is:

1 add blood to Trizol in 2 ml Sarsted screwcap tubes at RML and Ship to MSU
2 at MSU: add the blood Trizol to the phasemaker tubes and separate aqueous phase
3 add aqueous phase to purelink tubes and elute

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

From: Manuel Ruiz <(b) (6)
Sent: Tuesday, March 9, 2021 11:47 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6) Dan Crowley <(b) (6) Caylee Falvo <(b) (6)
Subject: Re: sample processing

Hi Vincent,

Following up about the RNA P samples, Caylee and Dan had a couple of questions for you that I think it may be easier to ask in direct communication. So I add them in this email.
(Please, let's keep the conversation about numbers of samples out of this thread now, to avoid confusions).

In response to the protocol you Vincent sent us, Caylee asked the following (please, Caylee jump in to clarify questions, etc).

"So they [RML] would add trizol and whole blood to the Phasemaker tubes, then send that to MSU, where we would do the rest? Or would they just put trizol + blood in a plain tube and ship that to MSU?"
"Also would you [Manuel] mind clarifying which steps in the PureLink protocol to follow? There is

a section on “purifying RNA from liquid samples/RNA clean up” which I’m assuming is correct, but want to make sure its the right section, and also that we start on ‘step 1’, since step 1 involves adding lysis buffer (do we skip this lysis step and go directly to step 3?)".

Thanks heaps!
Manuel

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

On Sun, Feb 28, 2021 at 6:33 PM Manuel Ruiz < (b) (6) wrote:
Thanks Vincent.

M

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

On Sun, Feb 28, 2021 at 9:03 AM Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:
total RNA will be extracted from whole blood samples that had sufficient remaining volume with an optimized protocol utilizing Trizol reagent (10-parts Trizol to 1-part blood), Phasemaker

tubes with chloroform phase separation, and PureLink RNA columns (Invitrogen, Thermo Fisher Scientific, Waltham MA USA)

- so you get samples in Trizol (1 ml, which will be 100ul of blood with 900 ul of Trizol)
- spin down on the phasemaker tubes to separate the aqueous phase
- proceed with column base extraction using the purelink mRNA kit

https://www.thermofisher.com/order/catalog/product/A33248?us&en#/A33248?us&en

https://www.thermofisher.com/us/en/home/life-science/dna-rna-purification-analysis/rna-extraction/rna-types/total-rna-extraction/purelink-rna-mini-kit.html

this should yield top quality mRNA / RNA

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

From: Manuel Ruiz (b) (6)
Sent: Friday, February 26, 2021 3:26 PM
To: Munster, Vincent (NIH/NIAID) [E] (b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] < (b) (6) Plowright, Raina (b) (6)
Subject: Re: sample processing

Hi Vincent,

I had a chat with Caylee and Dan and they are ok with doing the extractions here at MSU. Though, they aren't sure at the moment about what of the two options could perform better so they will do an experiment with mouse samples. We currently don't have a protocol for trizol, do you happen to have one that you could share with us for this experiment?

Thank you!
Manuel

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

https://batonehealth.org/

On Tue, Feb 23, 2021 at 3:05 PM Manuel Ruiz <(b) (6) wrote:
Thanks Vincent,

I'll check with Dan and Caylee and get back to you.

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

On Tue, Feb 23, 2021 at 2:53 PM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
1= in Trizol, I believe for quite some time. For the other kits lysis buffer, we'll freeze them and ship them on dry ice. However, for both its probably be better to proceed straight away with extraction.

Btw, Trizol is the gold standard, but you need access to a fume hood. We Have protocols with Trizol and then followed with column based centrifuge extraction.

I'm thinking about between 84 to 168 / month for the sera samples.

Sounds ok?

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

From: Manuel Ruiz <(b) (6)
Sent: Tuesday, February 23, 2021 2:43 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: sample processing

Thanks Vincent, we fully understand how thinly stretched you are. The two options for the RNAP samples sound great to release some pressure from you.

Just two questions: 1) Do you have an idea of for how long the RNAP samples in the buffer (Trizol or Qiagen) would be stable before extraction? (I'll check with Caylee and Dan about how to plan this move) and, 2) How many serum samples do you envision you could process in the monthly round of irradiation?

Thank you again for all your help!
Manuel

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

On Tue, Feb 23, 2021 at 2:06 PM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
Hi Manuel,

I'm looking into this at the moment. The problem is a little bit that the validation and requirement for some of the assays are not clear to me. The blood samples in RNAP could either be suspended in Trizol (typically the gold standard) or your Qiagen kit and shipped directly to MSU for extraction. This would have solved the issue of having to extract these at RML (for which we don't have any bandwidth in the next 3-4 months). This will still take quite some organization, also from your end.

I'm trying to arrange a irradiation session every month, sop we can supply you with a steady stream of irradiated sera.

As a reminder, we get continuous requests from UCLA, Bangladesh, MSU, Australia. We cannot do everything, and need to prioritize. That will also need to be communicated to other PIs who might be waiting a long time on their results (like John Hopkins / Bangladesh).

Cheers,

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

From: Manuel Ruiz <(b) (6)
Sent: Tuesday, February 23, 2021 1:13 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: sample processing

Hi Vincent et al.

Just thought of reviving this conversation. Do you have any ideas about how to plan/proceed?

Thanks,
Manuel

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

On Thu, Feb 11, 2021 at 4:03 PM Manuel Ruiz <(b) (6) wrote:
Thanks Vincent,

Yes, I fully understand and share the view of this not being the ideal use of Kwe's or Trent's time. We really wish we had a way of taking some of this work off your hands... From my end I am doing my best to prioritize samples and keep the lists to the minimum possible number.

The blood samples in RNAP would need to be extracted at RML (Kwe and Trent have been coordinating the protocol for that with Dan and Caylee). initially we were discussing some capacity of processing ~96 every three weeks. I understand this number might not be possible now.

The saliva samples would need to be irradiated to inactivate them. Dan and Caylee are planning a preliminary assay to look for IgA... since it is preliminary, if we can move ~10 samples initially should be enough to test if the assay works.

For serum samples, yes, I am fully aware of the workload that they involve (actually, we are fully aware of the whole workload that we are putting on you guys).

For RNAP samples and serum, the "high priority" samples are ~ 300 of each. I would need to confirm the numbers with Dan and Caylee, but those numbers would allow them to answer some questions substantially.

Cheers,
M

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

On Thu, Feb 11, 2021 at 3:45 PM Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:
Hi Manuel,

How do you foresee moving the blood samples? This is crucial as they are not inactivated.

What is the proposed work-up for saliva samples?

For the sera that's relatively easier, we can start moving batches of irradiated samples (again, this is a massive effort with at least 2-3 people involved and not suited for mass sample numbers).

I'm not making any promises, this is not a job for a postdoc and with the departure of Trent I don't have any capacity to get this solved anytime soon with the ongoing pandemic. Kwe is working 6-7 days a week, so he doesn't really have much time spend between his own studies, the Hendra and Nipah screenings and being involved in the UCLA work (and 100 other things).

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

From: Manuel Ruiz <(b) (6)
Sent: Thursday, February 11, 2021 3:27 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: sample processing

Great, Thank you, Trent for letting me know.

Thanks Vincent, yes, I imagine you are flat out there.

The bulk of samples that we need to move are blood samples in RNA protect and serum samples. There are some minor numbers (<100) saliva samples.

Both RNAP and serum samples are in large numbers (>1000). Maybe we could come up with a plan for moving them at a steady pace over time, or in any way that you find it feasible (?)

How would this work best for you?

Cheers,
Manuel

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

On Thu, Feb 11, 2021 at 3:16 PM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
Lets talk this through, as we have extremely limited capacity at the moment to dedicate time to this with Trent's departure.

What is exactly still needed to be shipped to MSU?

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

From: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Sent: Thursday, February 11, 2021 3:09 PM
To: Manuel Ruiz < (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F]
< (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Subject: RE: sample processing

Manuel,
I will have you start to talking with Kwe about sending samples to MSU, he will be your POC. Please CC me on the emails so I can walk him through the process.

-Trent

From: Manuel Ruiz < (b) (6)
Sent: Thursday, February 11, 2021 2:32 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Subject: sample processing

Hi Trent,

I hope you are keeping warm!

How is your availability to start coordinating a new batch of samples to come to MSU?

Cheers,
Manuel

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

https://batonehealth.org/

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 8 Mar 2021 18:40:03 +0000
To: Schountz, Tony; Feldmann, Heinrich (NIH/NIAID) [E]
Subject: LOS CO6
Attachments: Sharp MX-4141N_20210306_092520.pdf

All good to go!

Cheers,

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

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

March 5, 2020

Gregory Ebel, PhD
Director, Center for Vector-borne Infectious Diseases
Colorado State University
Fort Collins, CO 80523

Dear Dr. Ebel,

It is with utmost pleasure to provide a letter of support for your proposed C06 grant to construct the Colorado State University bat vivarium. Outbreaks of bat-borne zoonotic viruses such as coronaviruses, henipaviruses and filoviruses, have had an enormous impact on human health. The unpredictability of the zoonotic introductions of these bat-borne viruses limits the potential for effective intervention strategies. Within our research at the NIAID's Rocky Mountain Laboratories, we have directly focussed on bat-borne viruses such as Nipah virus, Ebola virus, MERS-CoV and now SARS-CoV-2, the cause of COVID-19. In particular we have extensive knowledge of bat infection models of ß-coronaviruses (MERS-CoV and WIV-1, in *Artibeus* and *Rousettus* bats) and Nipah virus (*Rousettus* bats) and are one of the few facilities which are completely set-up to perform bat studies in high and maximum containment (including long-term husbandry and on-site veterinary staff) and complete downstream immunological, genetic and virological analyses. The addition of facilities for bat breeding colonies, for which demand is significantly increasing, is essential for understanding the risk of spillover of bat viruses to humans.

We are highly enthusiastic to support construction of a vivarium for the breeding of key bat species at CSU. Having access to natural hosts for coronaviruses, henipaviruses and filoviruses will significantly advance research in infectious disease undertaken by our groups and others at RML and the research community as a whole, and we are committed to working with Co-I Dr. Schountz at CSU (long standing research collaborations on zoonotic viruses) to develop and use the resources generated through this C06 proposal. The SARS-CoV-2 pandemic marks an occasion which should put renewed focus on detailed studies of bats as reservoirs of emerging diseases. After SARS-CoV-1, MERS-CoV and Ebola virus in West Africa, we have yet another high impact (both from public health as economic perspective) bat-borne disease which justifies the urgent need for facilities in the US for advanced bat infectious disease studies.

Please feel free to contact us with any questions,

Sincerely,

(b) (6)

Heinz Feldmann, M.D.
Chief, Laboratory of Virology
Chief Scientist of the RML BSL4 Laboratories

(b) (6)

Vincent Munster, Ph.D.
Chief, Virus Ecology Section
Laboratory of Virology

903 S. 4th St., Hamilton, MT 59840
Phone: (b) (6)
Fax: 406-375-9620
Email: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 6 Mar 2021 16:35:17 +0000
To: Feldmann, Heinrich (NIH/NIAID) [E]; Schountz, Tony
Subject: RE: Letter of support for C06 construction grant?

Let me check with them to be on the safe side

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

From: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Sent: Saturday, March 6, 2021 9:34 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Schountz, Tony <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

Extramural has neglected support letters in the past if they were not co-signed by the Director (intrmural). I don't know how this one would go. If this would not be NIH, I wouldn't see any problem.

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Saturday, March 6, 2021 9:24 AM
To: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) Schountz, Tony <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

So it's a bit different from our normal RO1 support letters, as we are not putting any of our time and resources to this grant. Its just to highlight the importance of establishment of bat work at CSU

That said,

I'll send it to Jeff Thruston and see if needs any additional wording / signatures

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

From: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Sent: Saturday, March 6, 2021 9:03 AM
To: Schountz, Tony <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

Since this is going to NIH we may need Steve Holland's signature on the letter. Normally support letters need to be co-signed by the Director which will be arranged through Jeff Thruston for us. The letter also misses some of the usual language that we normally add. The process will take a few days – do we have the time?

I signed the letter (see attachment), but I am not sure if this will be sufficient.

Let me know what you wish to do. We can give it a try and if it comes back on time, we can replace the letter.

Best wishes,
Heinz

From: Schountz,Tony <(b) (6)
Sent: Friday, March 5, 2021 9:22 AM
To: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Letter of support for C06 construction grant?

Thanks Heinz and Vincent. I've attached a draft letter that I modified from one of Vincent's letter for your editing.

Thanks much!

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: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, March 4, 2021 8:43 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Schountz,Tony <(b) (6)
Subject: Re: Letter of support for C06 construction grant?

If you still need something from, please send the draft.

Sent from my iPhone

On Mar 4, 2021, at 11:25 AM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Will do

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

From: Schountz,Tony < (b) (6)
Sent: Thursday, March 4, 2021 10:21 AM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Feldmann, Heinrich (NIH/NIAID) [E] < (b) (6)
Subject: Re: Letter of support for C06 construction grant?

Vinnie, that would be great. Only a few suggested changes:

"letter of support for the CSU bat vivarium."
Can you delete the references to Bowen and Epstein (they are not on the grant and it may confuse reviewers).

Thanks!

Tony

--
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" < (b) (6)
Date: Thursday, March 4, 2021 at 10:13 AM
To: "Schountz,Tony" < (b) (6) "Feldmann, Heinrich (NIH/NIAID) [E]" < (b) (6)
Subject: RE: Letter of support for C06 construction grant?

Would this still work, if so I'll update the data and send straight away

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, March 4, 2021 10:09 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Subject: Letter of support for C06 construction grant?

Hi Heinz and Vinnie,

We're submitting a C06 proposal to NIH in a couple of weeks to secure funds to construct a dedicated bat breeding facility. The building will have three large rooms for housing up to 30 Indian flying foxes each (i.e., 90 total; and more for smaller pteropid bats), and 12 smaller rooms to accommodate microbats, up to about 200 bats per room. The idea for the building is to have capacity to import and breed multiple species of bats to provide to investigators in the USA as a national resource who might need them. If you're willing and able to provide a letter of support, I'll send you a draft letter this afternoon or tomorrow. If possible, we'd like to have the letter by a week from tomorrow (Friday, March 12).

Thanks,

Tony

--
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 5 Mar 2021 17:27:05 +0000
To: Holbrook, Michael (NIH/NIAID) [C]; David Montefiori, Ph.D.
Cc: Vincent, Leah (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; (b) (6) (b) (6) Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; (b) (6) Jason McLellan; (b) (6) (b) (6) (b) (6) Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; (b) (6) Julie McElrath; (b) (6) (b) (6) (b) (6) Matthew Frieman; (b) (6) Baric, Ralph; Richard Webby; Adolfo García-Sastre; (b) (6) Andrew B. Ward; Ali Ellebedy; (b) (6) (b) (6) (b) (6) Aubree Gordon; (b) (6) (b) (6) Schmaljohn, Connie (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Nelson Michael; (b) (6) (b) (6) (b) (6) (b) (6) Patrick C. Wilson; Douek, Daniel (NIH/VRC) [E]; R.A.M. Fouchier; Ghedin, Elodie (NIH/NIAID) [E]; Krogan, Nevan; Graham, Barney (NIH/VRC) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott
Subject: RE: Weekly Meeting polls for Breakout Groups

Hi guys,

The German isolate had the furin cleavage deletion already in the stock we received from BEI,

We have shared a D614G isolate with BEI, but hasn't come-up in their repository (https://www.biorxiv.org/content/10.1101/2021.01.09.426058v1.full.pdf+html), has been validated in hamsters and NHPs. Another isolate of interest for which the p2 is getting sequenced is this one (see below, this is the CA452R). Both isolates are from our backyard surveillance here in Hamilton, MT. We can share these isolates but if multiple requests come in, it might be good to set-up some kind of clearing house where we can send x-number of vials which can then be distributed across labs?

I'll try to make an effort to be part of this group, but the meeting time is a bit rough from my end (and its not my only meeting at these weird timepoints, the WHO likes me to get out of bed at 3:30)

Virus detail	
Virus name:	hCoV-19/USA/MT-RML-34/2021
Accession ID:	EPI_ISL_1113138
Type:	betacoronavirus
Clade	GH
Pango Lineage	B.1.427 (version: 2021-02-21)
AA Substitutions	Spike D614G, Spike L452R, Spike S13I, Spike W152C, N T205I, NS3 Q57H, NSP2 T85I, NSP4 S395T, NSP6 L125F, NSP12 P323L, NSP13 D260Y, NSP13 P53L
Variant	GH/452R.V1 (B.1.429+B.1.427)
Passage details/history:	Original
Sample information	
Collection date:	2021-01-20
Location:	North America / USA / Montana
Host:	Human
Additional location information:	
Gender:	Female
Patient age:	62
Patient status:	unknown
Specimen source:	
Additional host information:	
Outbreak:	
Last vaccinated:	
Treatment:	
Sequencing technology:	Illumina
Assembly method:	
Coverage:	
Comment:	
Institute information	
Originating lab:	Rocky Mountain Laboratories
Address:	903 S 4th street, Hamilton, MT, 59840
Sample ID given by the originating laboratory:	

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

From: Holbrook, Michael (NIH/NIAID) [C] <(b) (6)
Sent: Friday, March 5, 2021 7:57 AM
To: David Montefiori, Ph.D. <(b) (6)
Cc: Vincent, Leah (NIH/NIAID) [E] <(b) (6) Degrace, Marciela (NIH/NIAID) [E] <(b) (6) dbarouch <(b) (6) Paul Thomas <(b) (6) Stacey Schultz-Cherry <(b) (6) Post, Diane (NIH/NIAID) [E] <(b) (6) Stemmy, Erik (NIH/NIAID) [E] <(b) (6) Lampley, Rebecca (NIH/NIAID) [C] <(b) (6) (b) (6) (b) (6) Scheuermann, Richard <(b) (6) Eakin, Ann (NIH/NIAID) [E] <(b) (6) Brown, Liliana (NIH/NIAID) [E] <(b) (6) (b) (6) Jason McLellan <(b) (6) (b) (6) (b) (6) (b) (6) Suthar, Mehul <(b) (6) Pei yong. Shi <(b) (6) McDermott, Adrian (NIH/VRC) [E] <(b) (6) Florian Krammer <(b) (6) (b) (6) Julie McElrath <(b) (6) (b) (6) (b) (6) (b) (6) Matthew Frieman

< (b) (6) (b) (6) Baric, Ralph < (b) (6)
Richard Webby < (b) (6) Adolfo García-Sastre < (b) (6)
(b) (6) Andrew B. Ward < (b) (6) Ali Ellebedy < (b) (6)
(b) (6) (b) (6) (b) (6) Aubree Gordon < (b) (6)
(b) (6) (b) (6) Schmaljohn, Connie (NIH/NIAID) [E]
< (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Koup,
Richard (NIH/VRC) [E] < (b) (6) Seder, Robert (NIH/VRC) [E] < (b) (6)
Alessandro Sette < (b) (6) Adam Godzik < (b) (6) Embry, Alan
(NIH/NIAID) [E] < (b) (6) Roberts, Chris (NIH/NIAID) [E] < (b) (6)
Schotsaert, Michael < (b) (6) MacCannell, Duncan (CDC/DDID/NCEZID/OD)
< (b) (6) Weiss, Carol (FDA/CBER) < (b) (6) Nelson Michael
< (b) (6) (b) (6) (b) (6)
(b) (6) (b) (6) Patrick C. Wilson < (b) (6)
Douek, Daniel (NIH/VRC) [E] < (b) (6) R.A.M. Fouchier < (b) (6);
Ghedin, Elodie (NIH/NIAID) [E] < (b) (6) Krogan, Nevan < (b) (6)
Graham, Barney (NIH/VRC) [E] < (b) (6) Wentworth, David E. (CDC/DDID/NCIRD/ID)
< (b) (6) Michael, Nelson < (b) (6) Zhou, Bin (CDC/DDID/NCIRD/ID)
< (b) (6) Peter Halfmann < (b) (6) Hensley, Lisa (NIH/NIAID) [E]
< (b) (6) Gardner, Meredith Elizabeth Davis < (b) (6)
Weaver, Scott < (b) (6)
Subject: Re: Weekly Meeting polls for Breakout Groups

I believe there are also two NY isolates with the D614G mutation. NR-53516 and NR-53514. We had an issue with the German isolate but I don't remember what that was.

M

++++++++++++++
Mike Holbrook, PhD

Please excuse any typos or grammatical errors.

On Mar 5, 2021, at 09:48, David Montefiori, Ph.D. < (b) (6) wrote:

According to Greg Sempowski, the D614G variant can be requested from BEI Resources by Level 3 registrants.
NR-52370 SARS-Related Coronavirus 2, Isolate Germany/BavPat1/2020

Best,
David

From: Vincent, Leah (NIH/NIAID) [E] < (b) (6)
Sent: Wednesday, March 3, 2021 9:44 AM
To: Degrace, Marciela (NIH/NIAID) [E] < (b) (6) dbarouch
< (b) (6) Paul Thomas < (b) (6) Stacey Schultz-Cherry

< (b) (6) Post, Diane (NIH/NIAID) [E] < (b) (6) Stemmy, Erik (NIH/NIAID) [E] < (b) (6) Lampley, Rebecca (NIH/NIAID) [C] < (b) (6) (b) (6) (b) (6) Scheuermann, Richard < (b) (6) Eakin, Ann (NIH/NIAID) [E] < (b) (6) Brown, Liliana (NIH/NIAID) [E] < (b) (6) (b) (6) Jason McLellan (b) (6); (b) (6) (b) (6) David Montefiori, Ph.D. < (b) (6) (b) (6) Suthar, Mehul < (b) (6) Pei yong. Shi < (b) (6) McDermott, Adrian (NIH/VRC) [E] < (b) (6) Florian Krammer <flor (b) (6) (b) (6) Julie McElrath < (b) (6) (b) (6) (b) (6) (b) (6); Matthew Frieman < (b) (6) (b) (6) Baric, Ralph < (b) (6) Richard Webby < (b) (6) Adolfo García-Sastre < (b) (6) (b) (6) Andrew B. Ward < (b) (6) Ali Ellebedy < (b) (6) (b) (6) (b) (6) (b) (6) Aubree Gordon < (b) (6) (b) (6) (b) (6) Schmaljohn, Connie (NIH/NIAID) [E] < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Koup, Richard (NIH/VRC) [E] < (b) (6) Seder, Robert (NIH/VRC) [E] < (b) (6) Alessandro Sette < (b) (6) Adam Godzik < (b) (6) Embry, Alan (NIH/NIAID) [E] < (b) (6) Roberts, Chris (NIH/NIAID) [E] < (b) (6) Schotsaert, Michael < (b) (6) MacCannell, Duncan (CDC/DDID/NCEZID/OD) < (b) (6) Weiss, Carol (FDA/CBER) < (b) (6) Nelson Michael < (b) (6) (b) (6) (b) (6) (b) (6) il; (b) (6) Patrick C. Wilson < (b) (6) Douek, Daniel (NIH/VRC) [E] < (b) (6) R.A.M. Fouchier < (b) (6) Ghedin, Elodie (NIH/NIAID) [E] < (b) (6) Krogan, Nevan < (b) (6) Graham, Barney (NIH/VRC) [E] < (b) (6) Wentworth, David E. (CDC/DDID/NCIRD/ID) < (b) (6)

Cc: David Montefiori, Ph.D. < (b) (6) Michael, Nelson < (b) (6) Zhou, Bin (CDC/DDID/NCIRD/ID) < (b) (6) Peter Halfmann < (b) (6) Holbrook, Michael (NIH/NIAID) [C] < (b) (6) Hensley, Lisa (NIH/NIAID) [E] < (b) (6) Gardner, Meredith Elizabeth Davis < (b) (6) Weaver, Scott < (b) (6)

Subject: RE: Weekly Meeting polls for Breakout Groups

Good morning all,
Just a reminder that if you have not participated in the Doodle polls (see links below) for weekly breakout meetings, please **do so by 2 PM EST today**.

Thanks,
Leah

From: Vincent, Leah (NIH/NIAID) [E]
Sent: Friday, February 26, 2021 8:13 PM
To: Degrace, Marciela (NIH/NIAID) [E] < (b) (6) dbarouch < (b) (6) Paul Thomas < (b) (6) Stacey Schultz-Cherry < (b) (6) Post, Diane (NIH/NIAID) [E] < (b) (6) Stemmy, Erik (NIH/NIAID) [E] < (b) (6) Lampley, Rebecca (NIH/NIAID) [C]

< (b) (6) (b) (6) (b) (6) Scheuermann, Richard
< (b) (6) Eakin, Ann (NIH/NIAID) [E] < (b) (6) Brown, Liliana (NIH/NIAID)
[E] < (b) (6) (b) (6) Jason McLellan < (b) (6)
(b) (6) (b) (6) (b) (6) (b) (6) Suthar, Mehul
< (b) (6) Pei yong. Shi < (b) (6) McDermott, Adrian (NIH/VRC) [E]
< (b) (6) Florian Krammer < (b) (6)>;
(b) (6) Julie McElrath < (b) (6) (b) (6)
(b) (6) (b) (6) Matthew Frieman
< (b) (6) (b) (6) Baric, Ralph < (b) (6)
Richard Webby < (b) (6) Adolfo García-Sastre (b) (6)
; (b) (6) Andrew B. Ward < (b) (6) Ali Ellebedy
< (b) (6) (b) (6) (b) (6) (b) (6) Aubree Gordon
< (b) (6) (b) (6) (b) (6) Schmaljohn, Connie
(NIH/NIAID) [E] < (b) (6) Munster, Vincent (NIH/NIAID) [E]
< (b) (6) Koup, Richard (NIH/VRC) [E] < (b) (6) Seder, Robert
(NIH/VRC) [E] < (b) (6) Alessandro Sette (b) (6) Adam Godzik
< (b) (6) Embry, Alan (NIH/NIAID) [E] < (b) (6) Roberts, Chris
(NIH/NIAID) [E] < (b) (6) Schotsaert, Michael < (b) (6)
MacCannell, Duncan (CDC/DDID/NCEZID/OD) < (b) (6) Weiss, Carol (FDA/CBER)
< (b) (6) Nelson Michael < (b) (6)
(b) (6) (b) (6) (b) (6)
(b) (6) Patrick C. Wilson < (b) (6) Douek, Daniel (NIH/VRC) [E]
< (b) (6) R.A.M. Fouchier < (b) (6) Ghedin, Elodie (NIH/NIAID) [E]
< (b) (6) Krogan, Nevan < (b) (6) Graham, Barney (NIH/VRC) [E]
< (b) (6) Wentworth, David E. (CDC/DDID/NCIRD/ID) < (b) (6)
Cc: David Montefiori, Ph.D. < (b) (6) Michael, Nelson
< (b) (6) Zhou, Bin (CDC/DDID/NCIRD/ID) < (b) (6) Peter Halfmann
< (b) (6) Holbrook, Michael (NIH/NIAID) [C] < (b) (6) Hensley,
Lisa (NIH/NIAID) [E] < (b) (6) Gardner, Meredith Elizabeth Davis
< (b) (6) Weaver, Scott < (b) (6)
Subject: Weekly Meeting polls for Breakout Groups

Good evening,
Some SAVE investigators would like to participate in more than one of the breakout groups. I am including the doodle polls for all three groups here. Please indicate your availability on at least one breakout scheduling poll, but feel free to fill out the poll for each you are interested in.

Early Detection and Analysis
https://doodle.com/poll/bf5frcrt3v5enktv?utm_source=poll&utm_medium=link
In Vitro
https://doodle.com/poll/a8xtck4supwfe5zf?utm_source=poll&utm_medium=link
In Vivo
https://doodle.com/poll/y77qim2thm5rsgvz?utm_source=poll&utm_medium=link

Best,
Leah

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 5 Mar 2021 16:52:13 +0000
To: Schountz,Tony; Feldmann, Heinrich (NIH/NIAID) [E]
Subject: RE: Letter of support for C06 construction grant?

Hi Heinz,

Just printed and signed it and put it on your desk. If you can sign, just put it on my desk and I'll scan and send to Tony,

Cheers,

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

From: Schountz,Tony <(b) (6)
Sent: Friday, March 5, 2021 9:22 AM
To: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Letter of support for C06 construction grant?

Thanks Heinz and Vincent. I've attached a draft letter that I modified from one of Vincent's letter for your editing.

Thanks much!

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: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, March 4, 2021 8:43 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)

Cc: Schountz,Tony <(b) (6)
Subject: Re: Letter of support for C06 construction grant?

If you still need something from, please send the draft.

Sent from my iPhone

On Mar 4, 2021, at 11:25 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Will do

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, March 4, 2021 10:21 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Subject: Re: Letter of support for C06 construction grant?

Vinnie, that would be great. Only a few suggested changes:

"letter of support for the CSU bat vivarium."
Can you delete the references to Bowen and Epstein (they are not on the grant and it may confuse reviewers).

Thanks!

Tony

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Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Thursday, March 4, 2021 at 10:13 AM
To: "Schountz,Tony" <(b) (6) "Feldmann, Heinrich (NIH/NIAID) [E]" <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

Would this still work, if so I'll update the data and send straight away

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, March 4, 2021 10:09 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Subject: Letter of support for C06 construction grant?

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Thanks,

Tony

--
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

From: Schountz,Tony
Sent: Fri, 5 Mar 2021 16:22:28 +0000
To: Feldmann, Heinrich (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Letter of support for C06 construction grant?
Attachments: CSU project.docx

Thanks Heinz and Vincent. I've attached a draft letter that I modified from one of Vincent's letter for your editing.

Thanks much!

Tony

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

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NIAID/NIH

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Can you delete the references to Bowen and Epstein (they are not on the grant and it may confuse reviewers).

Thanks!

Tony

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Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

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Date: Thursday, March 4, 2021 at 10:13 AM
To: "Schountz,Tony" <(b) (6) "Feldmann, Heinrich (NIH/NIAID) [E]" <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

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Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

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Sent: Thursday, March 4, 2021 10:09 AM
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Subject: Letter of support for C06 construction grant?

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Thanks,

Tony

--
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

March 5, 2020

Gregory Ebel, PhD
Director, Center for Vector-borne Infectious Diseases
Colorado State University
Fort Collins, CO 80523

Dear Dr. Ebel,

It is with utmost pleasure to provide a letter of support for your proposed C06 grant to construct the Colorado State University bat vivarium. Outbreaks of bat-borne zoonotic viruses such as coronaviruses, henipaviruses and filoviruses, have had an enormous impact on human health. The unpredictability of the zoonotic introductions of these bat-borne viruses limits the potential for effective intervention strategies. Within our research at the NIAID's Rocky Mountain Laboratories, we have directly focussed on bat-borne viruses such as Nipah virus, Ebola virus, MERS-CoV and now SARS-CoV-2, the cause of COVID-19. In particular we have extensive knowledge of bat infection models of ß-coronaviruses (MERS-CoV and WIV-1, in *Artibeus* and *Rousettus* bats) and Nipah virus (*Rousettus* bats) and are one of the few facilities which are completely set-up to perform bat studies in high and maximum containment (including long-term husbandry and on-site veterinary staff) and complete downstream immunological, genetic and virological analyses. The addition of facilities for bat breeding colonies, for which demand is significantly increasing, is essential for understanding the risk of spillover of bat viruses to humans.

We are highly enthusiastic to support construction of a vivarium for the breeding of key bat species at CSU. Having access to natural hosts for coronaviruses, henipaviruses and filoviruses will significantly advance research in infectious disease undertaken by our groups and others at RML and the research community as a whole, and we are committed to working with Co-I Dr. Schountz at CSU (long standing research collaborations on zoonotic viruses) to develop and use the resources generated through this C06 proposal. The SARS-CoV-2 pandemic marks an occasion which should put renewed focus on detailed studies of bats as reservoirs of emerging diseases. After SARS-CoV-1, MERS-CoV and Ebola virus in West Africa, we have yet another high impact (both from public health as economic perspective) bat-borne disease which justifies the urgent need for facilities in the US for advanced bat infectious disease studies.

Please feel free to contact us with any questions,

Sincerely,

Heinz Feldmann, M.D.
Chief, Laboratory of Virology
Chief Scientist of the RML BSL4 Laboratories

Vincent Munster, Ph.D.
Chief, Virus Ecology Section
Laboratory of Virology

903 S. 4th St., Hamilton, MT 59840
Phone: (b) (6)
Fax: 406-375-9620
Email: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 5 Mar 2021 15:51:46 +0000
To: Schountz,Tony
Subject: RE: Scanned image from Rocky MTN Labs

That might be easiest, did he respond yet?

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

From: Schountz,Tony <(b) (6)
Sent: Friday, March 5, 2021 8:31 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Scanned image from Rocky MTN Labs

That would be great.

In light of Heinz's email, should I edit the letter so that both of you could sign it?

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] (b) (6)
Sent: Thursday, March 4, 2021 7:49 PM
To: Schountz,Tony <(b) (6)
Subject: Re: Scanned image from Rocky MTN Labs

Yes that's NIAIDs dude, so the one which wil give you the money hopefully

On Mar 4, 2021, at 16:49, Tony Schountz <(b) (6) wrote:

Hi Vinnie, I just noticed the letter is addressed to Dr. Auchincloss! I've attached a revised letter with Greg Ebel's name because he will be the PI on the proposal (PI must be a department or laboratory head).

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

> On Mar 4, 2021, at 10:59 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
>
> And signed!
>
> Vincent Munster, PhD
> Chief Virus Ecology Section
> Rocky Mountain Laboratories
> NIAID/NIH
>
> -----Original Message-----
> From: NIAID RML LAN Support <NIAIDRMLLANSupport@mail.nih.gov> On Behalf Of niaidrmllansupport@
> Sent: Thursday, March 4, 2021 11:24 AM
> To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
> Subject: Scanned image from Rocky MTN Labs
>
> Reply to: niaidrmllansupport@mail.nih.gov <niaidrmllansupport@mail.nih.gov> Device Name: Rocky MTN Labs Device Model: MX-4141N
> Location: Rocky MTN Labs
>
> File Format: PDF (Medium)
> Resolution: 200dpi x 200dpi
>
> Attached file is scanned image in PDF format.
> Use Acrobat(R)Reader(R) or Adobe(R)Reader(R) of Adobe Systems Incorporated to view the document.

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> <Sharp MX-4141N_20210304_112406.pdf><ATPFile_CE6EEE48-3663-4393-AEBB-9A55F7C1723F.token>

<CSU project_Munster.docx>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 4 Mar 2021 17:59:45 +0000
To: Schountz, Tony
Subject: FW: Scanned image from Rocky MTN Labs
Attachments: Sharp MX-4141N_20210304_112406.pdf

And signed!

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

-----Original Message-----
From: NIAID RML LAN Support <NIAIDRMLLANSupport@mail.nih.gov> On Behalf Of niaidrmllansupport@
Sent: Thursday, March 4, 2021 11:24 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Subject: Scanned image from Rocky MTN Labs

Reply to: niaidrmllansupport@mail.nih.gov <niaidrmllansupport@mail.nih.gov> Device Name: Rocky MTN Labs
Device Model: MX-4141N
Location: Rocky MTN Labs

File Format: PDF (Medium)
Resolution: 200dpi x 200dpi

Attached file is scanned image in PDF format.
Use Acrobat(R)Reader(R) or Adobe(R)Reader(R) of Adobe Systems Incorporated to view the document.
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http://www.adobe.com/

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

March 4th, 2021

Dear Dr. Auchincloss,

It is with utmost pleasure to be able to provide a letter of support for the CSU bat vivarium. Past outbreaks of bat-borne zoonotic viruses such as coronaviruses, henipaviruses and filoviruses, have had an enormous impact on human and wildlife health. The unpredictability of the zoonotic introductions of these bat-borne limits the potential for effective intervention strategies. Within my research at the NIAIDs Rocky Mountain Laboratories, I have directly focussed on bat-borne viruses such as Nipah virus, Ebola virus, MERS-CoV and now SARS-CoV-2. In particular we have extensive knowledge of bat infection models of ß-coronaviruses (MERS-CoV and WIV-1, in *Artibeus* and *Rousettus* bats) and Nipah virus (*Rousettus* bats) and are one of the few facilities which are completely set-up to perform bat studies in high and maximum containment (including long-term husbandry and on-site veterinary staff) and complete downstream immunological, genetic and virological analyses. In the absence of suitable breeding facilities at intramural NIAID, the addition of a centre focussed on *in vivo* bat research at CSU deserves the NIAIDs unconditional support.

I am underwriting my enthusiasm to continue to collaborate on the development of a bat resource center including breeding colonies of key bat species, at CSU. Having access to natural hosts for coronaviruses, henipaviruses and filoviruses would significantly advance research in infectious disease undertaken by my group and others at RML, and I am committed to working with Dr. Schountz at CSU (long standing research collaboration on MERS-CoV and SARS-CoV-2) to develop and use the resources generated through this C06 proposal. The SARS-CoV-2 pandemic marks an occasion which should put renewed focus on detailed studies of bats as reservoirs of emerging diseases. After SARS-CoV-1, MERS-CoV and Ebola virus in West Africa, we have yet another high impact (both from public health as economic perspective) bat-borne disease which justifies the urgent need for facilities in the US for advanced bat infectious disease studies.

Please feel free to contact me with any remaining questions,

Sincerely,

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

903 S. 4th St., Hamilton, MT 59840
Phone: (b) (6)
Fax: 406-375-9620
Email: (b) (6)

From: Schountz,Tony
Sent: Thu, 4 Mar 2021 17:41:30 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Letter of support for C06 construction grant?

Yes, that would be the plan but as proof of principle for a grant, we think hACE2 will be better to start with.

T.

--
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Thursday, March 4, 2021 at 10:29 AM
To: "Schountz,Tony" <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

Wouldn't you do a Rhinolophus ACE2?

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, March 4, 2021 10:26 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Letter of support for C06 construction grant?

I now see you sent a Word document and not a PDF. I've included the suggested changes in the attached.

BTW – I have started working with a couple of our animal reproductive biologists to see if they can generate human ACE2 Jamaican fruit bats. They're working on cloning the Aj keratin-18 promotor (in case the mouse version doesn't work in the bats) and determining the best way of freezing sperm cells. Next week they will collect ovaries from a couple of bats to see how the oocytes behave in culture.

T.
--
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Thursday, March 4, 2021 at 10:13 AM
To: "Schountz,Tony" <(b) (6) "Feldmann, Heinrich (NIH/NIAID) [E]" <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

Would this still work, if so I'll update the data and send straight away

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Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

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Sent: Thursday, March 4, 2021 10:09 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
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Thanks,

Tony

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Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

From: Schountz,Tony
Sent: Thu, 4 Mar 2021 17:26:02 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Letter of support for C06 construction grant?
Attachments: CSU project_Munster.docx

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Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

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To: "Schountz,Tony" <(b) (6) "Feldmann, Heinrich (NIH/NIAID) [E]" <(b) (6)
Subject: RE: Letter of support for C06 construction grant?

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NIAID/NIH

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Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

April 1st, 2020

Dear Dr. Auchincloss,

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Please feel free to contact me with any remaining questions,

Sincerely,

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

903 S. 4th St., Hamilton, MT 59840
Phone: (b) (6)
Fax: 406-375-9620
Email: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 4 Mar 2021 17:13:21 +0000
To: Schountz,Tony; Feldmann, Heinrich (NIH/NIAID) [E]
Subject: RE: Letter of support for C06 construction grant?
Attachments: Los bat project_Munster CSU.docx

Would this still work, if so I'll update the data and send straight away

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

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Sent: Thursday, March 4, 2021 10:09 AM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Feldmann, Heinrich (NIH/NIAID) [E] < (b) (6)
Subject: Letter of support for C06 construction grant?

Hi Heinz and Vinnie,

We're submitting a C06 proposal to NIH in a couple of weeks to secure funds to construct a dedicated bat breeding facility. The building will have three large rooms for housing up to 30 Indian flying foxes each (i.e., 90 total; and more for smaller pteropid bats), and 12 smaller rooms to accommodate microbats, up to about 200 bats per room. The idea for the building is to have capacity to import and breed multiple species of bats to provide to investigators in the USA as a national resource who might need them. If you're willing and able to provide a letter of support, I'll send you a draft letter this afternoon or tomorrow. If possible, we'd like to have the letter by a week from tomorrow (Friday, March 12).

Thanks,

Tony

--
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
Colorado State University
(b) (6)
(b) (6)

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

April 1st, 2020

Dear Dr. Auchincloss,

It is with utmost pleasure to be able to provide a letter of support for the CSU bat research center. Past outbreaks of bat-borne zoonotic viruses such as coronaviruses, henipaviruses and filoviruses, have had an enormous impact on human and wildlife health. The unpredictability of the zoonotic introductions of these bat-borne limits the potential for effective intervention strategies. Within my research at the NIAIDs Rocky Mountain Laboratories, I have directly focussed on bat-borne viruses such as Nipah virus, Ebola virus, MERS-CoV and now SARS-CoV-2. In particular we have extensive knowledge of bat infection models of ß-coronaviruses (MERS-CoV and WIV-1, in *Artibeus* and *Rousettus* bats) and Nipah virus (*Rousettus* bats) and are one of the few facilities which are completely set-up to perform bat studies in high and maximum containment (including long-term husbandry and on-site veterinary staff) and complete downstream immunological, genetic and virological analyses. In the absence of suitable breeding facilities at intramural NIAID, the addition of a centre focussed on *in vivo* bat research at CSU deserves the NIAIDs unconditional support.

I am underwriting my enthusiasm to continue to collaborate on the development of a bat resource center including breeding colonies of key bat species, at CSU. Having access to natural hosts for coronaviruses, henipaviruses and filoviruses would significantly advance research in infectious disease undertaken by my group and others at RML, and I am committed to working with Drs. Bowen and Schountz at CSU (long standing research collaboration on MERS-CoV) and Dr. Epstein of EcoHealth Alliance (long standing collaboration on the underlying ecological changes driving spillover events of Nipah virus) to develop and use the resources generated through this C06 proposal. The SARS-CoV-2 pandemic marks an occasion which should put renewed focus on detailed studies of bats as reservoirs of emerging diseases. After SARS-CoV-1, MERS-CoV and Ebola virus in West Africa, we have yet another high impact (both from public health as economic perspective) bat-borne disease which justifies the urgent need for facilities in the US for advanced bat infectious disease studies.

Please feel free to contact me with any remaining questions,

Sincerely,

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

903 S. 4th St., Hamilton, MT 59840
Phone: (b) (6)
Fax: 406-375-9620
Email: (b) (6)

From: Edward Holmes
Sent: Mon, 1 Mar 2021 08:42:35 +0000
To: malik
Cc: Andrew Rambaut; Tong, Suxiang (Sue) (CDC/DDID/NCIRD/DVD); Leo Poon; KONINGS, Frank; (b) (6) (b) (6) Richard Neher; (b) (6) (b) (6) Oliver Pybus; peter ((b) (6) (b) (6) cheryl ((b) (6) Sebastian Maurer-Stroh; (b) (6) (b) (6)-giessen.de; (b) (6) (b) (6) (b) (6) Tulio De Oliveira; Anne von Gottberg ((b) (6) Angie Lackenby ((b) (6) JinalB ((b) (6) Caly, Leon; MacCannell, Duncan (CDC/DDID/NCEZID/OD); gaofu ((b) (6) Druce Julian ((b) (6) w.barclay; sylvie.van-der-werf ((b) (6) Thiel, Volker Earl (VETSUISSE); Munster, Vincent (NIH/NIAID) [E]; Kuhn, Jens (NIH/NIAID) [C]; Post, Diane (NIH/NIAID) [E]; Ann Cullinane; ElMasry, Ihab (NSAH); Erik Alm ((b) (6) Eeva Broberg ((b) (6) B.B. Oude Munnink; M.P.G. Koopmans; MARKLEWITZ, Marco; KAKKAR, Manish; BARAKAT, Amal; Mendez Rico, Dr. Jairo Andres (WDC); Leite, Dr. Juliana (WDC); HERRING, Belinda Louise; EVANS, Roger; Dr VAN KERKHOVE, Maria; BEN EMBAREK, Peter Karim; PERKINS, Mark; SUBISSI, Lorenzo; CARTER, Lisa; PEREYASLOV, Dmitriy; ALEXANDER, Nyka; KHARE, Shagun; ARCHER, Brett; ALLAN, Maya; HAMBLION, Esther
Subject: Re: [WHO] For review | Working Group on naming SARS-CoV-2 variants
Attachments: who sars-cov-2 voi voc nomenclature 02282021 Leo_Sue T_AR.EH.docx

I agree with Andrew.

I made a few edits to the document: there were a few over-generalisations on the opening paragraph on virus evolution.

Cheers,

Eddie

--

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

THE UNIVERSITY OF SYDNEY
Marie Bashir Institute for Infectious Diseases & Biosecurity,
School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia
T (b) (6)
E (b) (6)

On 1 Mar 2021, at 7:29 pm, malik < (b) (6) wrote:

Dear Frank and Andrew,

I think Andrew has raised a valid point for decision.

My own preference is that even if there two lineages which have the same combination of mutants (convergent evolution, which is what seems to be taking place, we should give them different names. Because we cannot be sure how the backbone of the virus subtly influences the phenotype and we will not have all that data in time to make any decision on naming.
So logically, give them two names.

What happens to for e.g. B.1.1.7 (which will be give a name) which then develops for e.g. 484K, that is an issue to be considered.

Malik

From: Andrew Rambaut <(b) (6)
Sent: Monday, March 1, 2021 4:09 PM
To: Tong, Suxiang (Sue) (CDC/DDID/NCIRD/DVD) <(b) (6) Leo Poon <(b) (6) KONINGS, Frank <(b) (6) (b) (6) Richard Neher <(b) (6) (b) (6) Oliver Pybus <(b) (6) peter ((b) (6) <(b) (6) (b) (6) cheryl ((b) (6) <(b) (6) Sebastian Maurer-Stroh <(b) (6) (b) (6) (b) (6); (b) (6) Eddie Holmes <(b) (6) (b) (6) (b) (6) Andrew Rambaut <(b) (6) Tulio De Oliveira <(b) (6) Anne von Gottberg ((b) (6) <(b) (6) Angie Lackenby ((b) (6) <(b) (6) JinalB ((b) (6) <(b) (6) Caly, Leon <(b) (6) MacCannell, Duncan (CDC/DDID/NCEZID/OD) <(b) (6) gaofu ((b) (6) <(b) (6) Druce Julian ((b) (6) (b) (6); malik <(b) (6) w.barclay <(b) (6) sylvie.van-der-werf ((b) (6) <(b) (6) Thiel, Volker Earl (VETSUISSE) <(b) (6) Munster, Vincent (NIH/NIAID) [E] (b) (6) Kuhn, Jens (NIH/NIAID) [C] <(b) (6) Post, Diane (NIH/NIAID) [E] <(b) (6) Ann Cullinane (b) (6) ElMasry, Ihab (NSAH) <(b) (6) Erik Alm ((b) (6) <(b) (6) Eeva Broberg ((b) (6) <(b) (6) B.B. Oude Munnink <(b) (6) M.P.G. Koopmans <(b) (6) MARKLEWITZ, Marco <(b) (6) KAKKAR, Manish <(b) (6) BARAKAT, Amal <(b) (6) Mendez Rico, Dr. Jairo Andres (WDC) <(b) (6) Leite, Dr. Juliana (WDC) <(b) (6) HERRING, Belinda Louise <(b) (6) EVANS, Roger <(b) (6)>; Dr VAN KERKHOVE, Maria <(b) (6) BEN EMBAREK, Peter Karim <(b) (6) PERKINS, Mark <(b) (6) SUBISSI, Lorenzo <(b) (6) CARTER, Lisa <(b) (6) PEREYASLOV, Dmitriy <(b) (6) ALEXANDER, Nyka <(b) (6) KHARE, Shagun <(b) (6) ARCHER, Brett <(b) (6) ALLAN, Maya <(b) (6) HAMBLION, Esther <(b) (6)
Subject: Re: [WHO] For review | Working Group on naming SARS-CoV-2 variants

Dear Frank,

My comments on top of Leo's and Sue's but not Malik's or Oli's (so will need to be merged).

My only substantial comment is whether the terms VOI/VOC (and thus the labels) refer to a genotype with mutations considered likely to have phenotypic effects or a phylogenetic lineage with mutations of interest/concern.

For example, if the same set of mutations of interest/concern arise in different lineage (i.e., evolutionary convergence) are these given the same label? I.e., do synonymous, intergenic or likely inconsequential mutations that distinguish genotypes with identical mutations of concern warrant different VOI/VOC labels?

The example I give is that a VOC has been defined by Public Health England that comprises the B.1.1.7 background with E484K but this has arisen multiple times independently. PHE calls them all the same VOC. Will this be the same with the WHO definition? I think this should be clarified.

I think this should be the case (because otherwise the naming group will need to consider phylogenetics) but this has consequences for the connection of VOCs to the other nomenclatures (not insurmountable ones - just a VOC may be listed as being present in multiple lineages/clades.

One other suggestion - rather than variant of interest, we could use variant of note which would give the acronym 'VON' this is then pronounced as a word like Voc rather than an V.O.I. which has to be spelled out.

Either way - happy to be an author.

Best,
Andrew

On 1 Mar 2021, at 03:36, Tong, Suxiang (Sue) (CDC/DDID/NCIRD/DVD) < (b) (6) wrote:

This email was sent to you by someone outside the University.
You should only click on links or attachments if you are certain that the email is genuine and the content is safe.

Hi Frank,
It is well written. Only minor comments are added to Leo's version.
Thanks,

Sue T

-----Original Message-----
From: Leo Poon < (b) (6)
Sent: Sunday, February 28, 2021 9:25 PM
To: KONINGS, Frank < (b) (6) (b) (6) (b) (6) Richard Neher
< (b) (6) (b) (6) (b) (6) (b) (6) peter
((b) (6) < (b) (6) (b) (6) cheryl ((b) (6) < (b) (6) Sebastian Maurer-
Stroh < (b) (6) (b) (6) (b) (6); (b) (6)
Edward Holmes < (b) (6) (b) (6) (b) (6) Andrew Rambaut ((b) (6)
< (b) (6) Tulio De Oliveira < (b) (6) Anne von Gottberg ((b) (6) < (b) (6)

Angie Lackenby ((b) (6) < (b) (6) JinalB ((b) (6) < (b) (6)
Caly, Leon < (b) (6) MacCannell, Duncan (CDC/DDID/NCEZID/OD) < (b) (6) gaofu
((b) (6) < (b) (6) Druce Julian ((b) (6) < (b) (6) malik
(b) (6); (b) (6) sylvie.van-der-werf (b) (6) < (b) (6)
Thiel, Volker Earl (VETSUISSE) < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Kuhn, Jens (NIH/NIAID) [C] < (b) (6) Post, Diane (NIH/NIAID) [E] < (b) (6) Tong, Suxiang (Sue)
(CDC/DDID/NCIRD/DVD) < (b) (6) Ann Cullinane < (b) (6) ElMasry, Ihab (NSAH)
< (b) (6) Erik Alm ((b) (6) < (b) (6) Eeva Broberg
((b) (6) < (b) (6) B.B. Oude Munnink < (b) (6) M.P.G.
Koopmans ((b) (6) < (b) (6)
Cc: MARKLEWITZ, Marco < (b) (6) KAKKAR, Manish < (b) (6) BARAKAT, Amal
< (b) (6) Mendez Rico, Dr. Jairo Andres (WDC) < (b) (6) Leite, Dr. Juliana (WDC) < (b) (6)
HERRING, Belinda Louise < (b) (6) EVANS, Roger < (b) (6) Dr VAN KERKHOVE, Maria
< (b) (6) BEN EMBAREK, Peter Karim < (b) (6) PERKINS, Mark < (b) (6)
SUBISSI, Lorenzo < (b) (6) CARTER, Lisa < (b) (6) PEREYASLOV, Dmitriy < (b) (6)
ALEXANDER, Nyka < (b) (6) KHARE, Shagun < (b) (6) ARCHER, Brett < (b) (6) ALLAN,
Maya < (b) (6) HAMBLION, Esther < (b) (6)
Subject: RE: [WHO] For review | Working Group on naming SARS-CoV-2 variants

Dear Frank,

It looks good. I have some minor comments on the text.

Best,

Leo

****
Leo Poon
Professor
School of Public Health
The University of Hong Kong
Hong Kong
Tel: (b) (6)
Fax: (852) 2855 9587
****

-----Original Message-----
From: KONINGS, Frank < (b) (6)
Sent: Sunday, 28 February 2021 10:42 PM
To: (b) (6) (b) (6) Richard Neher
< (b) (6) (b) (6) (b) (6) (b) (6) peter
((b) (6) < (b) (6) (b) (6) cheryl ((b) (6) < (b) (6) Sebastian Maurer-
Stroh < (b) (6) (b) (6) (b) (6); (b) (6) Edward
Holmes < (b) (6) (b) (6) (b) (6) Andrew Rambaut ((b) (6)
< (b) (6) Tulio De Oliveira < (b) (6) Anne von Gottberg ((b) (6) < (b) (6)
Angie Lackenby ((b) (6) < (b) (6) JinalB ((b) (6) < (b) (6)
Caly, Leon < (b) (6) (b) (6) gaofu ((b) (6) < (b) (6) Druce Julian
((b) (6) < (b) (6) Leo Poon < (b) (6) malik
(b) (6); (b) (6); sylvie.van-der-werf (b) (6);
Thiel, Volker Earl (VETSUISSE) < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Kuhn, Jens (NIH/NIAID) [C] < (b) (6) Post, Diane (NIH/NIAID) [E] < (b) (6) Tong, Suxiang (Sue)
(CDC/DDID/NCIRD/DVD) < (b) (6) Ann Cullinane < (b) (6) ElMasry, Ihab (NSAH)
< (b) (6) Erik Alm ((b) (6) < (b) (6) Eeva Broberg
((b) (6) < (b) (6) B.B. Oude Munnink < (b) (6) M.P.G.
Koopmans ((b) (6) < (b) (6)
Cc: MARKLEWITZ, Marco < (b) (6) KAKKAR, Manish < (b) (6) BARAKAT, Amal
< (b) (6) Mendez Rico, Dr. Jairo Andres (WDC) < (b) (6) Leite, Dr. Juliana (WDC) < (b) (6)
HERRING, Belinda Louise < (b) (6) EVANS, Roger < (b) (6) Dr VAN KERKHOVE, Maria
< (b) (6) BEN EMBAREK, Peter Karim < (b) (6) PERKINS, Mark < (b) (6)
SUBISSI, Lorenzo < (b) (6) CARTER, Lisa < (b) (6) PEREYASLOV, Dmitriy < (b) (6)
ALEXANDER, Nyka < (b) (6) KHARE, Shagun < (b) (6) ARCHER, Brett < (b) (6) ALLAN,
Maya < (b) (6) HAMBLION, Esther < (b) (6)
Subject: [WHO] For review | Working Group on naming SARS-CoV-2 variants

Dear colleagues,

I hope this message finds you well and thank you once again for your contributions during the variants naming discussions.

Attached is a draft manuscript outlining the proposed mechanism for labeling of SARS-CoV-2 Variants of Interest and Concern. We would very much appreciate your feedback on the manuscript. Please note that the actual labels or names for the variants will become available within the next couple of days.

Aside from your review of the manuscript, please let us know whether you are agreeable to be a co-author on this publication. If yes, please look into the clearance process required by your institution.

Finally, we have just published the working definitions for VOI and VOC (attached). Thank you to those of you who have provide their inputs.

We would appreciate your review and feedback by Wednesday, March 3, close of business.

Thank you,
Frank

<who sars-cov-2 voi voc nomenclature 02282021 Leo_Sue T.docx>

Labeling of SARS-CoV-2 Variants of Interest and Concern Conducive for Global Discourse

WHO Working Group on naming SARS-CoV-2 variants*

*(list all by alphabetical order)

[1]Affiliations

*Corresponding author: (WHO)

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has a linear, unsegmented, positive-sense, RNA genome. Like all viruses, SARS-CoV-2 continuously adapts to its changing environments via seemingly random genome mutations. The majority of these mutations ~~is~~ are lethal to the virus because they negatively affect its replication machinery or its interaction with host cells. Most of the remaining mutations confer neither advantage nor disadvantage to the virus. However, a small number of mutations become fixed over time~~, i.e., those that~~ because they provide a selective advantage for the virus, such as viral escape from the host immune system and medical countermeasures or increased fitness in terms of pathogenesis and transmissibility.

Commented [TS((1]: Suggest to add a reference?

Commented [EH2]: Many of the fixed mutations will be neutral.

The World Health Organization (WHO) COVID-19 Reference Laboratory Network[1] has been tracking SARS-CoV-2 mutations since the beginning of the pandemic and, in June 2020, established the WHO Virus Evolution Working Group (VEWG) to specifically assess new variants. WHO has also established a global risk monitoring framework to coordinate components of an international system for monitoring and assessing SARS-CoV-2 variants and their impact.

Specifically, this system is designed to collect, analyze and share data in order to identify critical priorities and triggers for decision-making; and to leverage and enhance existing technical networks and expert groups.

WHO has provided working definitions of variants of interest (VOIs) and variants of concern (VOCs).[2] They describe how VOIs and VOCs should be reported to WHO, and critical actions required by member states and by WHO ~~in order~~ to assess their impact on the epidemiology and severity of disease, and on performance of available diagnostics, therapeutics, vaccines as well as public health and social measures. At the time of writing, there are several VOIs and VOCs that are being tracked globally.[3]

Several nomenclature systems have been created to identify and track SARS-CoV-2 variants, and these systems vary in their scientific approach and scientific question. Unfortunately, the existence of several systems also inevitably leads to the same virus isolate being referred to by different names, requiring ever increasing expert knowledge to understand scientific publications and results. None of the existing nomenclatures meet the needs of health officials, the media, or the general public, who are focused on practical questions about the potential health impact of specific variants and need a ~~clearn~~ easy way to communicate about them across different disciplines.

Naming of SARS-CoV-2 variants is not trivial for several reasons: 1) Currently, there is no authority on VOI and VOC naming, thus different groups have designated the same variant with different names; 2) A name that includes the location where a VOI or VOC was first discovered may have negative consequences, such as stigmatization of places/countries or of people originating from these areas; and 3) Alphanumerical naming schemes have resulted in designations not conducive for media discourse and inevitable confusion; even the smallest

mistake (for instance, accidentally typing "1" instead of "2") in a numerical list provides misinformation.

To address this issue, the VEWG developed a specific SARS-CoV-2 labelling mechanism for VOIs and VOCs with the dedicated goal of creating novel, non-stigmatizing labels for global communication. To achieve this goal, the VEWG invited major groups that have published phylogenetic-based SARS-CoV-2 variant classification and nomenclature systems (GISAID, NextStrain and Pango) and experts in the field of virus research as subject matter experts to help frame the discussion and outcomes. Based on the input from all participants, the following was agreed:

1. GISAID, NextStrain, Pango and other classification and nomenclature systems each support specific specialist subcommunities and serve different purposes. However, because all of these systems are based on phylogeny and not on phenotype, none offers an obvious solution to VOI and VOC naming for easy communication. All provide individual variant designations that are confusing for political decision-makers as well as the public.
2. Consequently, all involved parties agreed to create a new, specific labelling mechanism for VOIs and VOCs only. All other SARS-CoV-2 variants which do not meet the WHO definitions for VOI or VOC are not labelled. The labelling mechanism is independent but can be cross-linked to the existing phylogenetics-based SARS-CoV-2 classification and nomenclature systems. When VOIs and VOCs are confirmed by WHO, institutions will receive a label for their variant from the VEWG. This label anchors the three different names within the existing nomenclature systems (GISAID, Nextstrain, and Pango).
3. Labels will be created by the VEWG using a programmed algorithm that takes existing words and extracts useful syllables. The algorithm will create novel but pronounceable

Commented [LP3]: Can we use other terms like:

"highly technical" or "too technical"

Commented [AR4R4]: Is the confusion stemming from the names themselves or the fact there are multiple names?

Commented [AR5]: Are these labels actually for variants even if they have independently arisen? For example, the B.1.1.7 lineage has had a number of additional mutations (such as E484K and L18F in spike) arise multiple times independently. B.1.1.7+E484K is considered a VOC by PHE. Under the new system are these all given the same VOI/VOC name? I.e., is a VOI/VOC defined by the mutational constellation or is it still phylogenetic in definition?

names that have no meaning but can be easily remembered. To the casual reader these labels will have no obvious associated meaning connected to SARS-CoV-2 or a geographical location, thereby reducing stigmatization.

4. The established labels of VOIs and VOCs, their links to existing phylogenetics-based SARS-CoV-2 classification and nomenclature systems, and their key scientific/medical characteristics will be published and updated continuously by WHO at www.who.int/xxx. It is recommended that journalists and all other interested parties visit this site frequently.

With this new mechanism in place, the VEWG is asking for a joint effort to no longer use the outdated, stigmatizing variant names.

An example of the VEWG-supported VOC nomenclature, i.e., excerpts from webpage content, is shown in Figure 1.

Commented [LP6]: VEWG is encourage others to use this system for easy communication. But, there is a need of some clarifications here:

1.This sentence somewhat implies GISAID, NextStrain and Pango are generating names like this, which is not the case.
2. The existing 3 nomenclature systems are important to specialists. The newly proposed system is not intend to interfere scientific research, but provide a platform for easy communications.

Commented [TS((7]: No figure is attached. In the figure will an example of a hypothesized VOI or VOC name be given to show the name theme structure?

Acknowledgements

We thank xxx.

This work was supported by xxx.

The views and conclusions contained in this document are those of the authors and should not be interpreted as necessarily representing the official policies, either expressed or implied, of xxx, or of the institutions and companies affiliated with the authors.

Competing interests

The authors declare no competing financial interests.

92 **Figure legends**

93 **Figure 1. New public SARS-CoV-2 VOI and VOC nomenclature. a**) Examples of newly coined
94 names for global discourse along with their scientific designations in three different classification
95 systems based on phylogenetics: GISAID, NextStrain, and Pango. A continuously updated list of
96 names can be found at www.who.int/xxx. **b**) Graphical depiction of available scientific
97 information characterizing an exemplary VOC as outline for every VOC at www.who.int/xxx.

[1] WHO reference laboratories providing confirmatory testing for COVID-19 at https://www.who.int/publications/m/item/who-reference-laboratories-providing-confirmatory-testing-for-covid-19

[2] WHO COVID-19 Weekly Epidemiological Update, 25 February 2021, Special edition: Proposed working definitions of SARS-CoV-2 Variants of Interest and Variants of Concern.

[3] Coronavirus disease (COVID-19) Weekly Epidemiological Update and Weekly Operational Update at https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 26 Feb 2021 21:34:25 +0000
To: Plowright, Raina; Alison Peel
Cc: Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: RE: Tentative: HeV variant and RNA plates discussion

I'll send one

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

-----Original Message-----
From: Plowright, Raina < (b) (6)
Sent: Friday, February 26, 2021 2:31 PM
To: Alison Peel < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F]
< (b) (6)
Subject: Re: Tentative: HeV variant and RNA plates discussion

do we have a zoom link?

> On Feb 21, 2021, at 4:57 PM, Alison Peel < (b) (6) wrote:
>
> Agenda:
> - decisions on screening for novel variant (how many, what samples)
> - affect of thawing plates for this work on RNA for multi viral work in Australia
> - how does this fit with AVL/VTM investigations?
> - plans for shipment of plates to Australia - what needs to happen.

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 26 Feb 2021 21:30:44 +0000
To: Alison Peel; Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: RE: HeV variant and RNA plates discussion

Do we have a zoom link for this one?

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

-----Original Appointment-----
From: Alison Peel <(b) (6)
Sent: Tuesday, February 23, 2021 4:33 PM
To: Munster, Vincent (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: HeV variant and RNA plates discussion
When: Saturday, February 27, 2021 7:30 AM-8:30 AM (UTC+10:00) Brisbane.
Where:

Agenda:
- decisions on screening for novel variant (how many, what samples)
- affect of thawing plates for this work on RNA for multi viral work in Australia
- how does this fit with AVL/VTM investigations?
- plans for shipment of plates to Australia - what needs to happen.

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 26 Feb 2021 03:02:57 +0000
To: Edward Annand; John-Sebastian Eden; Alison Peel; Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina; (b) (6)
Subject: RE: Hendra-variant primers

Perfect, we'll order the primers on this end, the gblocks sounds cool.

Kwe, setting-up an ARCTIC protocol might not be a bad idea for Hendra from our end (we use an optimized vircapseq, essentially a probe based enrichment), especially with some of the high CT-value samples.

Pretty cool!

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

From: Edward Annand <(b) (6)
Sent: Thursday, February 25, 2021 7:24 PM
To: John-Sebastian Eden <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6) (b) (6)
Subject: Re: Hendra-variant primers

Thanks JS – this is great ☺

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

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 25 February 2021 at 20:40
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Alison Peel (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6) Edward Annand <(b) (6) (b) (6) <(b) (6)
Subject: Re: Hendra-variant primers

Hey Vincent,

Yes but it actually hasn't arrived yet. I went through IDT first but they cancelled the order because of US export controls and it being a high risk pathogen… Funny because in the same order I had another one which was a similar design but an Ebola gene. Anyways, I found another company who would make it. Should be here early next week. If you have a look at the spreadsheet it has our primers, cDNA synthesis, qPCR and gblock design. For now, I've been using cDNA from our horse case as a positive control.

When I have the gblocks, we will optimise the assay as a duplex for the reference and variant Hendra via FAM & HEX reporters.

Then, I also have some slightly outer reverse primers on hand though not tested. If there were sensitivity issues, I was going to play with a limited cycle semi-nested version of the assay.

Then, then, I have an ARTIC-like protocol (1kb amplicons) for WGS that we've run. The sequencing is scheduled for tomorrow, so I can let you know how that goes too. I wanted something to easily sequence any cases that might pop-up again.

J-S

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

Room O.6.23 | 176 Hawkesbury Road | PO Box 412 | Westmead NSW 2145 Australia
(b) (6) | T (b) (6) | M (b) (6)
westmeadinstitute.org.au | Follow us on Facebook | Watch us on YouTube

---

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Thursday, 25 February 2021 at 2:10 am
To: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6) John-Sebastian Eden <(b) (6)
Subject: RE: Hendra-variant primers

Sounds good, JS did you design a run-off transcript as positive control as well?

Cheers,

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

From: Alison Peel <[redacted]>
Sent: Tuesday, February 23, 2021 7:44 PM
To: Kwe Claude, Yinda (NIH/NIAID) [F] <[redacted]>; Munster, Vincent (NIH/NIAID) [E] <[redacted]>; Plowright, Raina <[redacted]>; John-Sebastian Eden <[redacted]>
Subject: Hendra-variant primers

Kwe and Vincent – just talking with JS and they've already designed primers that distinguish between the two variants (pick up one variant and exclude the other)

It would be great to use the same primer set across studies if possible.
JS – I'm not sure if each of these has previously been shared and gotten lost in the email chains, but would you mind please re-sharing?
Thanks
Ali

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 25 Feb 2021 22:21:06 +0000
To: Edward Annand
Cc: Breed, Andrew; Alison Peel; Plowright, Raina; John-Sebastian Eden; (b) (6) Broder, Chris (USU-DoD); Peter Reid; Navneet Dhand; philip.britton; Wong, William; (b) (6)
Subject: RE: Strict Confidence - Updated HeV M assays for priority testing and reporting to Australian Animal and Human Health Sectors.

Thanks Ed,

Fully understood. All updates will be communicated throughout this email chain,

Kind regards,

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

From: Edward Annand <(b) (6)
Sent: Wednesday, February 24, 2021 5:06 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Breed, Andrew <(b) (6) Alison Peel <(b) (6) Plowright, Raina <(b) (6) John-Sebastian Eden <(b) (6) (b) (6) Broder, Chris (USU-DoD) <(b) (6) Peter Reid <(b) (6) Navneet Dhand <(b) (6) philip.britton <(b) (6) Wong, William <(b) (6) (b) (6)
Subject: Re: Strict Confidence - Updated HeV M assays for priority testing and reporting to Australian Animal and Human Health Sectors.

Edited email (Redcliff replaces Redlands)

Dear Vincent, (Vincent Munster NIH/NIAD)

We sent the attached update on our Horses As Sentinels research's most significant findings that you have been made aware of less specifically previously via your collaboration with our research collaboration led by Ali Peel and Raina Plowright (CC'd).

We understand your research group have Qld CVO Allison Crook CC'd (and inferred Australian CVO) approval to test for HeV as part of Ali Peel's ARC DECRA led research in Flying fox Samples obtained in Qld.

We understand that this includes your having extracted RNA extracts from optimal samples from flying foxes in Redcliff and Gympie colonies ready to test that are of particular interest to our Horses as Sentinels research as well as to the interpretation of our findings by state and national biosecurity.

Ali has let me know that she has identified most suitable cohorts to test based on our interest in these colonies and spillover dynamics.

Please proceed in testing the most-appropriate selection of your samples (guided by Ali) in a prioritised collaborative extension of the Horses as Sentinels research (within your current resources and time line limitations) with our updated HeV-variant PCR detection approach shared with you via this National Update as well as with any further PCR approaches that that our collaborative research team feel is most appropriate and share with you also by scientific collaboration.

As you know Chris Broder has supported both of our research groups in our serology approaches that run in parallel to both the bat and horse molecular research testing (and our human samples) and has afforded our nation urgent reassurance of expected vaccine and human monoclonal antibody efficacy to the new variant. Comparing molecular and serological results for this cohort will be of similar interest and as such please include Chris when informing of these priority findings.

Please report the findings of this prioritised testing to this email chain that includes the Horses as Sentinels research leadership, Andrew Breed and William Wong of DAWE and Allison Crook (Qld CVO), after initial interpretation with our collaborative research team by similar 'in confidence' CVO update to best support the priory responses to our finding.

Please share only the information required for your laboratory approvals with key persons regarding this variant and please let at least Ali, Raina and Chris know who these are. Please understand these precautions relate to aspects of sensitivity that we hold as highly important but that are beyond our research teams influence and require time, including local stakeholder notifications.

Please communicate any significant updates back to this email chain.

Huge gratitude in advance,

Ed

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

From: Edward Annand <(b) (6)
Date: Thursday, 25 February 2021 at 10:30
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Breed, Andrew <(b) (6) Alison Peel <(b) (6) Plowright, Raina <(b) (6) John-Sebastian Eden <(b) (6) (b) (6) < (b) (6) Broder, Christopher <(b) (6) Peter Reid <(b) (6) Navneet Dhand <(b) (6) philip.britton <(b) (6) Wong, William <(b) (6) (b) (6) <(b) (6)
Subject: Strict Confidence - Updated HeV M assays for priority testing and reporting to Australian Animal and Human Health Sectors.

Dear Vincent, (Vincent Munster NIH/NIAD)

We sent the attached update on our Horses As Sentinels research's most significant findings that you have been made aware of less specifically previously via your collaboration with our research collaboration led by Ali Peel and Raina Plowright (CC'd).

We understand your research group have Qld CVO Allison Crook CC'd (and inferred Australian CVO) approval to test for HeV as part of Ali Peel's ARC DECRA led research in Flying fox Samples obtained in Qld.

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Please report the findings of this prioritised testing to this email chain that includes the Horses as Sentinels research leadership, Andrew Breed and William Wong of DAWE and Allison Crook (Qld CVO),

after initial interpretation with our collaborative research team by similar 'in confidence' CVO update to best support the priory responses to our finding.

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Please communicate any significant updates back to this email chain.

Huge gratitude in advance,

Ed

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 23 Feb 2021 14:26:36 +0000
To: Laing, Eric
Cc: Broder, Chris (USU-DoD); De wit, Emmie (NIH/NIAID) [E]
Subject: RE: Variant serum samples

We should have hamster sera in a couple of weeks,

WA1
D614G
SA
UK

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

From: Laing, Eric <(b) (6)
Sent: Monday, February 22, 2021 7:50 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Broder, Chris (USU-DoD) <(b) (6) De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Subject: Re: Variant serum samples

Of the 2 available sera on BEI resources, neither are from variant infections. What's the timeline for hamster challenges? We can work-up an RBD-multiplex and qualify a serum dilution with post-Wash1 vaccinated serum samples in the meantime.

Then change the secondary to anti-hamster IgG for model validation.

- 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 Mon, Feb 22, 2021 at 11:33 AM Laing, Eric <(b) (6) wrote:
I agree about proof of concept - multiplex RBD differentiation of variant induced antibodies. I'll look for hamster secondaries and also see if BEI has any variant infected convalescent human sera.

On Mon, Feb 22, 2021 at 9:38 AM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
Yeah, typically sars-cov-2 is very transient in NHPs so everything happened between day 1-6 (focused at shedding and pathogenesis).

For the hamsters, it would be a potentially good proof of principle, as we will be getting reinfection sera as well (e.g. WA1 primary infection and SA secondary infection). With the current situation with WA1 vaccines, D614G, 20C-CA, SA and UK circulating the reinfection serology gets interesting (or very complicated). That said, you do need to work around your secondary Ab

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

From: Broder, Christopher <(b) (6)
Sent: Monday, February 22, 2021 7:32 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Laing, Eric <(b) (6) De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Subject: Re: Variant serum samples

hey. thats too bad.. Focused in really early innate responses?

Although we have not done that many rodents, and would work the
assay now is set up using goat anti-human IgG cross-absorbed biotin-conjugated

chris

On Mon, Feb 22, 2021 at 9:23 AM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
The problem is that we don't take the NHPs out that long (only did this for the first experiment). Now they all get necropsied at day 6.

That said, we will have hamster sera for D614G, UK and SA variants soon, so let me know if that would be useful.

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

From: Laing, Eric <(b) (6)
Sent: Sunday, February 21, 2021 7:23 PM
To: Broder, Chris (USU-DoD) <(b) (6) De wit, Emmie (NIH/NIAID) [E] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Variant serum samples

Hey Emmie and Vincent,

We're going to start testing variant sera reactivity differentiation in a RBD multiplex strategy. While we wait for genomic confirmation of human variant infections, do you happen to have any experimental variant challenged NHP serum samples that we could use to get a head-start on RBD multiplex qualification?

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)

--
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: (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

--

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: Sat, 20 Feb 2021 15:14:22 +0000
To: Edward Annand; Alison Peel; Plowright, Raina; Hector Aguilar-Carreno
Cc: Broder, Chris (USU-DoD); John-Sebastian Eden; Ina Smith; Peter Reid
Subject: RE: In confidence

Same on this end, our screening primers likely don't pick up this novel variant. We have updated the primers and ordered them (thanks JS!) and run some screens on samples we have previously tested for Hendra-1

Will keep you updated!

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

From: Edward Annand <(b) (6)
Sent: Friday, February 19, 2021 6:16 PM
To: Alison Peel <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Plowright, Raina <(b) (6) Hector Aguilar-Carreno <(b) (6)
Cc: Broder, Chris (USU-DoD) <(b) (6) John-Sebastian Eden
<(b) (6) Ina Smith <(b) (6) Peter Reid <(b) (6)
Subject: Re: In confidence

Just one more thing for the bat team - JS had identified issues in some of the primers - not the ones Ina or he designed but those used in the past in screening FFs. We need to share the updated versions with you. We will mention this to some extent in government letter/email in relation to your urgent screening and in justification for Re screening Amy Burroughs Geelong study cohort in time also. (We request this aspect of Amy samples be funded by fed gov)

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From: Edward Annand <(b) (6)
Sent: Saturday, February 20, 2021 12:07:03 PM
To: Alison Peel <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Plowright, Raina <(b) (6) Hector Aguilar-Carreno <(b) (6)
Cc: Broder, Christopher <(b) (6) John-Sebastian Eden
<(b) (6) Ina Smith <(b) (6) Peter Reid <(b) (6)
Subject: Re: In confidence

Thanks Ali and for everyone understanding - the politics are as usual complicated - we are trying to ensure best rapid scientific interpretation. Linking the new strain to GHFF seems of rapid importance to our vet perspectives and to public health. Ensuring the current vaccine in horses, that being developed in humans and the currently available and effective mAB 102.4 are effective against the variant we describe is the other urgent imperative. I am making this clear to the CVOs and we expect their full

support if we can ensure to them appropriate confidentiality of sensitive info, direct reporting and preprint notification. Thanks everyone for understanding. We are building on the long term trust of our nations leaders in Chris Broder. His generosity and upstanding ethics have saved lives here already. We see it as logical that the US extensions of the rapid scientific work relating to the horses as sentinels findings be in close collaboration, communication and scientific trust. We are really excited to be working in this effective team and feel that Ali, Raina and Vincent are best placed for rapid scientific consideration of the GHFF and the variant. Hector, great to have your contribution in collaboration also with Chris's team on the aspects relating to the F and G :) we will update this email chain with the proposed wording of the urgent US extensions of the work for the letter we are preparing this weekend. Cheers Ed

Get Outlook for iOS

From: Alison Peel <(b) (6)
Sent: Saturday, February 20, 2021 10:49:58 AM
To: Munster, Vincent (NIH/NIAID) [E] (b) (6) Plowright, Raina <(b) (6) Hector Aguilar-Carreno <(b) (6)
Cc: Edward Annand <(b) (6) Broder, Christopher <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6) Peter Reid <(b) (6)
Subject: In confidence

Hi Raina, Vincent, Hector, and all.

Ed – please add anyone in if I've missed anyone.

I think everyone here is aware of the Hendra-like virus findings by Ed, J-S and Ina, and the potentially high significance of the current results and those that will arise in coming days and weeks. They are working very hard at the moment to ensure that all, and only, the appropriate people are aware of these findings, and to determine its link to grey-headed flying foxes. This is just a flag to emphasise the confidential nature of these findings at the moment and the imperative not to share the information outside of this group.

Ed and the team is trying to gain the CVO support for the urgent extension research including screening of suitable bat samples in proximity to the spillover and also for the G-P work by Hector and his team as an extension of the protein characterisation by Chris, Eric and Spencer and their team.

Ed – please follow up with any other points you wanted to raise.

Cheers

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

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

Pronouns: she/her

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.

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 20 Feb 2021 14:41:26 +0000
To: (b) (6) Schountz, Tony
Cc: Wang Linfa; Patrick Woo; Susanna Lau; epstein; Prof.Dr. Martin Schwemmle; Richard Yanagihara; zlshi; Plowright, Raina
Subject: RE: Bat infectious diseases symposium, 2022

Same here Tony,

Looking forward to a fun conference!

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

From: (b) (6) < (b) (6)
Sent: Friday, February 19, 2021 11:52 PM
To: Schountz, Tony < (b) (6)
Cc: Wang Linfa < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Patrick Woo < (b) (6) Susanna Lau < (b) (6) epstein < (b) (6) Prof.Dr. Martin Schwemmle < (b) (6) Richard Yanagihara < (b) (6) zlshi < (b) (6) Plowright, Raina < (b) (6)
Subject: Re: Bat infectious diseases symposium, 2022

Hi, Tony,

Thanks for your effort for continuing this symposium. I am sure it will be more attractive than ever next year. Also, I am happy to serve on the committee.

Best wishes,
Peng Zhou, PhD, Professor,
Wuhan Institute of Virology, CAS
PI, Bat Viruses Infection and Immunity Group

peng.zhou

邮箱：(b) (6)

On 02/20/2021 05:26, Schountz,Tony wrote:

Hi Everyone,

We were hoping to host the 3rd bat infectious diseases symposium this summer in Fort Collins; however, because COVID is expected to still be an issue here and the vaccine roll-out has been slow, we must postpone it until 2022. The date is 24 July (Sunday evening only for a reception) to 27 July (Wednesday), 2022.

The reason for this email is that I am submitting an R13 conference grant proposal to NIH to provide a few thousand dollars of funding to subsidize the symposium, and one expectation of the reviewers for R13 proposals is an advisory committee. So, if you are willing and able to serve on the committee, I would be greatly appreciative. The work for you will mostly involve reviewing abstracts to choose talks (instead of posters). The last meeting we had about 70 abstracts submitted and we had just enough that requested posters that we did not have to choose talks. I am optimistic that it will be similar this time, so that should limit the amount of work for you. Of course, you wouldn't get all abstracts, but instead perhaps 10 to 12 to review to help decide which ones are worthy of talks. One caveat, of course, is that with the COVID pandemic there will probably be greater interest in the symposium, particularly for coronaviruses. I have attached a graph that shows the number of PubMed references for "bats AND viruses" and as you can see 2020 was a remarkable year - most of the increase was in the last half of the year. I expect 2021 will be even larger!

Although your attendance at the symposium is not required to serve on the advisory committee, if you do attend we will cover your hotel and registration fees as members of the advisory committee. If you do attend, I would like each of you to give a talk if you are willing. The symposium will be held in our newly-renovated conference center on our campus.

Thanks very much for your consideration and if you have questions, please let me know.

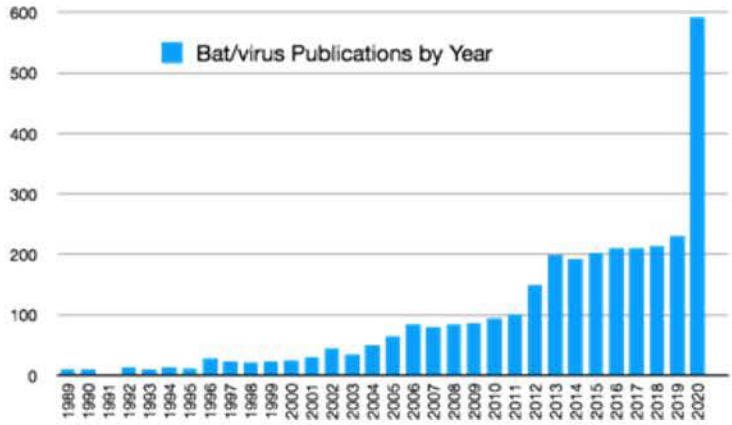
Tony

—

Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692

(b) (6)

(b) (6)


Bat/virus Publications by Year
600
500
400
300
200
100
0
1989
1990
1991
1992
1993
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1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 17 Feb 2021 16:05:19 +0000
To: Plowright, Raina
Subject: FW: Pan CoV vaccines

Trying to put a bit more visibility to our work within PREEMPT/NSF,

He is a great guy to talk to (from Science)

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

-----Original Message-----
From: Jon Cohen <(b) (6)
Sent: Wednesday, February 17, 2021 8:18 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: Re: Pan CoV vaccines

Where can I go to best observe this in the field with you? Fabulous.

> On Feb 17, 2021, at 7:08 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
>
> [EXTERNAL EMAIL]
>
> Lol, bit of a jack-of-all traits.
>
> This is what we are trying to do in a really nice large framework, working from fieldwork, pathogen detection and discovery, functional analyses and countermeasure design
>
>
https://nam12.safelinks.protection.outlook.com/?url=https%3A%2F%2Fbatonehealth.org%2F&data=04%7C01%7Cjcohen%40aaas.org%7Cfca1c0851eac4c03097c08d8d355fb84%7C2eebd8ff9ed140f0a15638e5dfb3bc56%7C0%7C0%7C637491713543988720%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=b2d2Xz35Qtm8JCR%2F7v2rn3yHs2bSNcX1J1T5xte66Dw%3D&reserved=0
>
> we were mainly focusing at henipaviruses for now, and now adding coronaviruses as well. We use Hendra in Australia really as a model to see changes in dietary stress, fruiting and flowering patters and anthropological changes like forest fires) would increase spillover events. Using this info, we are then trying to overlap this with field sites in Bangladesh (Nipah), Madagascar, Ghana and Congo.
>
> I've cc-ed Raina Plowright, who is really an outstanding disease ecologist and can really explain everything about the Australia system.
>
> Cheers,
>
> Vincent Munster, PhD
> Chief Virus Ecology Section
> Rocky Mountain Laboratories
> NIAID/NIH
>

> -----Original Message-----
> From: Jon Cohen <(b) (6)
> Sent: Wednesday, February 17, 2021 7:39 AM
> To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
> Subject: Re: Pan CoV vaccines
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>> <Munsternejmp1807691.pdf>
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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 17 Feb 2021 16:04:32 +0000
To: Jon Cohen
Cc: Plowright, Raina
Subject: RE: Pan CoV vaccines

Oz might be a good option as a very well developed natural host-spillover system using decades of different layers of data from pathogen detection, natural populations to satellite telemetry and spillover to horses, liked to full genome data of the detected Hendra viruses. This system is really well developed in Australia and we are trying to model the different sites based on the data coming out of those studies. Congo would be a good additional site to see how we are translating some of the information into more remote sites.

For Congo (RoC, Brazzaville), we are now working with the MoH and WCS to shore-up local SARs-coV-2 surveillance focused at the gorilla trackers to prevent spill-back into the western lowland gorillas in Congo. This largely entails setting-up local molecular diagnostics and quarantine program. At the moment we have a quarantine system in place.

Anyway lots to do,

Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories
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Sent: Wednesday, February 17, 2021 8:18 AM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Cc: Plowright, Raina < (b) (6)
Subject: Re: Pan CoV vaccines

Where can I go to best observe this in the field with you? Fabulous.

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https://nam12.safelinks.protection.outlook.com/?url=https%3A%2F%2Fbatonehealth.org%2F&data=04%7C01%7Cjcohen%40aaas.org%7Cfca1c0851eac4c03097c08d8d355fb84%7C2eebd8ff9ed140f0a15638e5dfb3bc56%7C0%7C0%7C637491713543988720%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=b2d2Xz35Qtm8JCR%2F7v2rn3yHs2bSNcX1J1T5xte66Dw%3D&reserved=0
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> I've cc-ed Raina Plowright, who is really an outstanding disease ecologist and can really explain everything about the Australia system.
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To: Jon Cohen; Plowright, Raina
Subject: RE: Pan CoV vaccines

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https://batonehealth.org/

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From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 17 Feb 2021 15:05:24 +0000
To: Alison Peel
Cc: Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: RE: Re-screening preempt urines for novel Hendra

Will try to get started on organizing the RNA, depending on what we still need to do (e.g. screen a part of the samples with the new primer set)

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

From: Alison Peel <(b) (6)
Sent: Tuesday, February 16, 2021 6:44 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Re-screening preempt urines for novel Hendra

Ok, thanks Vincent – can you name any afternoons that are better than others?
I'm available from 2/3pm on your Monday and Wednesday afternoons, or from 10am on the other afternoons

---

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Wednesday, 17 February 2021 at 11:30 am
To: Alison Peel <(b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Re-screening preempt urines for novel Hendra

Hi Ali,

Let's push it to next week, this week I'm absolutely swamped.

Cheers,

Vincent

On Feb 16, 2021, at 17:44, Alison Peel <(b) (6) wrote:

Hi Vincent, Kwe and Raina,

What do you think is the best way forward from here? Shall we discuss via email or zoom? I'm available:

- Now
- from 4pm Wednesday your time
- from 2pm Thursday your time

Primary future screening objectives from my perspective are to:

1. see whether we're missing Hendra detections in our samples, and then whether these are systematic (e.g. by species) and say anything about ecology and spillover risk
2. screen samples for broader viral community, using either multiplexed qPCR assays (developed with Ina for known rubulaviruses Menangle, Yeppoon, Grove, Alston etc) or consensus PCR w/ sequencing approach.

So, I think decisions to be made are

1. whether those two objectives can be combined with the one approach, or should remain separate
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I have funding for the broader viral community work. If it is sensible for the objectives to be combined under the same method, and that was to be done on already-extracted RNA (sent from RML to USyd) I'd have funding to screen a subset of samples but not all (at a first guess, maybe 40%, but would have to explore that in more detail with J-S).
Alternatively, I could approach CVOs for permission for the work to be done at RML, but I imagine that that isn't feasible from a capacity perspective anyway

Anyway, keen to hear your thoughts

Cheers

Ali

From: John-Sebastian Eden <(b) (6)
Date: Wednesday, 17 February 2021 at 9:38 am
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Alison Peel <(b) (6) Edward Annand <(b) (6) Plowright, Raina <(b) (6) Ina Smith <(b) (6)
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(b) (6) | T (b) (6) | M + (b) (6)
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<image001.png>

From: Kwe Claude, Yinda (NIH/NIAID) [F] < (b) (6)
Date: Wednesday, 17 February 2021 at 2:48 am
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Alison Peel < (b) (6) Edward Annand < (b) (6) John-Sebastian Eden < (b) (6) Plowright, Raina < (b) (6)
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Thanks

Kwe Claude Yinda, PhD
Postdoc Fellow
Virus Ecology Section, Laboratory of Virology
Rocky Mountain Laboratories, NIAID/NIH
903S 4th St. Hamilton, MT 59840
Email: (b) (6)
Tel: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 17 Feb 2021 14:42:05 +0000
To: Alison Peel; Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: RE: Re-screening preempt urines for novel Hendra

Would be good if we can have an idea how to address the geography – species question. I think we should try to screen a targeted set with the updated primerset (Kwe, can you order a run-off transcript positive control?)

I think if we can identify a selected set (e.g. 1000 samples or so), we can go ahead and rescreen these for the novel variant

Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories
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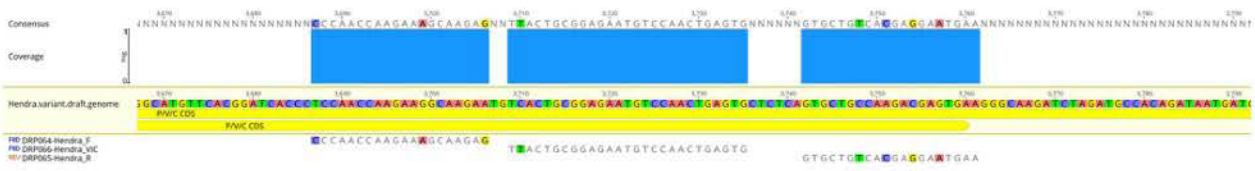

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To: John-Sebastian Eden; Kwe Claude, Yinda (NIH/NIAID) [F]; Alison Peel; Edward Annand; Plowright, Raina; Ina Smith
Subject: RE: Collaborator on a DP

Probably be good to get an update primer set as well,

Kwe, do you want the to run as a duplex and have different dyes? It would be good to be able to discriminate between the two variants in our screening.

Vincent Munster, PhD
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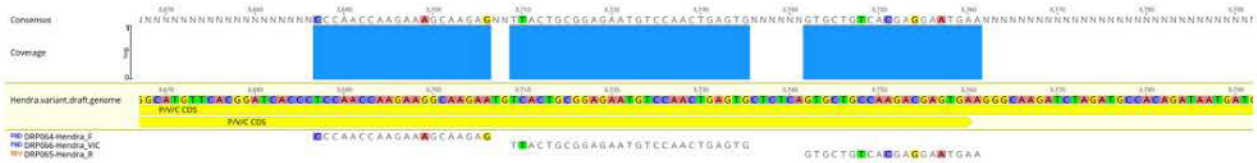

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DRP66-Hendra_VIC	VIC-TTACTGCGGAGAATGTCCAACTGAGTG-QSY

Thanks

Kwe Claude Yinda, PhD
Postdoc Fellow
Virus Ecology Section, Laboratory of Virology
Rocky Mountain Laboratories, NIAID/NIH
903S 4th St. Hamilton, MT 59840
Email: [redacted] (b) (6)
Tel: [redacted] (b) (6)

From: "Munster, Vincent (NIH/NIAID) [E]" <[redacted] (b) (6)
Date: Monday, February 15, 2021 at 5:19 PM
To: Alison Peel <[redacted] (b) (6) Edward Annand <[redacted] (b) (6) John-Sebastian Eden <[redacted] (b) (6) "Plowright, Raina" <[redacted] (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <[redacted] (b) (6)

Cc: Ina Smith <[redacted]
Subject: Re: Collaborator on a DP

Hi Kwe,

Can you send your Hendra screening primer-probe sequences to John-Sebastian? They want to check them with some of their assays,

Thanks,

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

From: Alison Peel <[redacted]
Date: Thursday, February 11, 2021 at 6:33 PM
To: Edward Annand <[redacted] John-Sebastian Eden <[redacted] "Plowright, Raina" <[redacted] "[redacted] <[redacted]
Cc: Ina Smith <[redacted]
Subject: Re: Collaborator on a DP

Hi All,
Looks like everyone is available at that time. I've added a zoom link to the calendar invite, and here it is below
Looking forward to chatting then!
Cheers
Ali

PREEMPT is inviting you to a scheduled Zoom meeting.

Topic: Australia CoV results meeting
Time: Feb 16, 2021 09:00 AM Brisbane

Join Zoom Meeting
https://us02web.zoom.us/j/[redacted]?pwd=aUlFRUJDTUJKU2hEcVpManZjU0lqZz09

Meeting ID: [redacted]
Passcode: [redacted]
One tap mobile
+12532158782,[redacted] US (Tacoma)
+13017158592,[redacted] US (Washington DC)

Dial by your location
+1 253 215 8782 US (Tacoma)
+1 301 715 8592 US (Washington DC)
+1 312 626 6799 US (Chicago)
+1 346 248 7799 US (Houston)
+1 646 558 8656 US (New York)
+1 669 900 9128 US (San Jose)
Meeting ID: (b) (6)
Passcode: (b) (6)
Find your local number: https://us02web.zoom.us/u/kbl3d4elMv

From: Edward Annand <(b) (6)
Date: Thursday, 11 February 2021 at 5:00 pm
To: John-Sebastian Eden <(b) (6) Plowright, Raina <(b) (6) Alison Peel <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Superb JS!

Vincent the other significant finding in our parallel horse testing so far is most closely related to HeV and caused indistinguishable disease. This finding is following sensitive and important notification and consideration by relevant Gov depts and national reference lab personnel and isolation is being attempted at ACDP. We have shared the sequence with the state lab to allow them to prepare to use the adapted qPCR that we develop and with Chris's UHS Lab (who already contributed to the finding directly by our using their proteins in the serology assays on the same samples) to allow them to begin preparing protein production and antibody binding assessment.

We would like to discuss your proposed Genotype to Phenotype analyses for this.

Of course JS and his team at WIMR (Beth and Rachel) stand 'ready to go' in screening the bat samples already extracted for Paramyxoviruses including this novel one by the same approach combining PanPCR and RNA seq.

I have mentioned sharing the sequence with you and with this project and hope it might be possible in strict confidence within the month.

Please keep the horse findings in strictest confidence.

Looking forward to a lot of very interesting analyses and collaboration to come! ☺

Cheers

Ed

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

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 13:36
To: Plowright, Raina <(b) (6) Alison Peel <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Ina Smith <(b) (6) Edward Annand <(b) (6)
Subject: Re: Collaborator on a DP

Raina – It looks like about 17% (36/210 pools). We found multiple viruses in a few pools too, so at some point we will need to work out some estimated prevalence. Those times are fine for me.

Ali – From a quick NJ tree, I think the sequence is close to cluster 2d.ii. I'm running a proper one now with it and the horse one we found. More soon.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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---

From: Plowright, Raina (b) (6)
Date: Thursday, 11 February 2021 at 1:19 pm
To: Alison Peel <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6) Edward Annand <(b) (6)
Subject: Re: Collaborator on a DP

This is so exciting!

J-S, what proportion of the fecal samples were positive? I assume these were the pooled samples?

Yes I'd love to talk about this.

I can do do the following times next week, if I have a few days notice (all in Sydney time):

- Tuesday AM: any time after 10am
- Wednesday AM: 7am-9am, any time after 10am
- Thursday aM: any time after 9.30am
- Friday am: any time after 9.00am

On Feb 10, 2021, at 7:01 PM, Alison Peel <(b) (6)> wrote:

Hi Raina and Vincent,

Are you free for a meeting to discuss initial CoV results with J-S/Ed/Ina one afternoon your time next week?
The detections in cluster 2b.v cluster with PREDICT_CoV-67, which is from the same species in Sulawesi, collected in 2013. (though there is debate about the Australian individuals being a different subspecies, so this is super-interesting)

<image001.png>

Ed also has some horse results that may be relevant. Lots exciting to discuss.

J-S The sequences from Craig Smith and Diana Prada's papers would also be great to include. See phylogeny in attached paper.

Cheers

Ali

From: John-Sebastian Eden <(b) (6)>
Date: Thursday, 11 February 2021 at 11:59 am
To: Alison Peel <(b) (6)> Edward Annand <(b) (6)> Ina Smith <(b) (6)>
Subject: RE: Collaborator on a DP

Wow, cool. It'll be good to get more sequence still or at least make sure the trees are the best they can be. I build this first one from just blasting and pulling what was returned. I might need to scour GenBank to ensure everything relevant is there.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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---

From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:55 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Thanks both. No, the PREDICT_CoV-67 is from the same species – in Sulawesi, collected in 2013!
<image002.png>

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:50 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: RE: Collaborator on a DP

Early mornings are okay for me. Maybe 730am onwards. Any day should be okay if you want to check in with Raina etc.

They likely the same group/variant. It's a little hard to say from the short, relatively conserved region we sequenced from the PCR. I think the PREDICT ones were from different bat genera but the MG256393_Bat coronavirus isolate BtCoV/B55440/Pte_lyl/CB1-THA/Apr12 one is from lyles flying fox in Thailand. So, matching some of that diversity makes sense. I can take representatives from the clusters and get more data etc. So, maybe discuss next steps for this work next week too?

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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---

From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:43 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Oooh, so many questions already!! Quickly though – do you think the ones clustering with the PREDICT sequences in cluster 2d.v are the same virus (/different variants?) as the PREDICT detections?

From: Alison Peel <(b) (6)
Date: Thursday, 11 February 2021 at 11:41 am
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

WOW!!!!!!!!!!!!!!!!!!

Absolutely!! I'm pretty flexible next week. Let me know when best suits. If it's first thing in the morning your time, then Raina may be able to join and I'm sure she'd be interested! Maybe Vincent too?

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:36 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

No worries. I was surprised a bit by your lack of apparent excitement in the findings =)

Basically, across the three plates there were plenty of CoV, and mostly Beta 2d. It's not the tidiest tree. I'm still working on the summary with tables for the hits to each pool etc but for now just wanted to share.

We should zoom next week. Would that work?

J-S

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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---

From: Alison Peel <(b) (6)
Date: Thursday, 11 February 2021 at 12:31 pm
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Hi J-S,
Our uni had an issue with emails yesterday and have notified me that an email sent by you in this thread was inadvertently filtered as spam and deleted. Can you please re-send?
Thanks
Ali

From: Alison Peel <(b) (6)
Date: Wednesday, 10 February 2021 at 1:30 pm
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Hi Ed,
Cool. Our final internal deadline is in about a week or so. For collaborators, I don't need any additional information except permission to list your name
Will be exciting to hear results!
Great to hear re: Geelong Ed. I keep putting off advertising for some PhD students, but hopefully will do so soon, and hope to include ACDP in at least one (and Ina – as previously discussed pre-COVID!)

Cheers

Ali

From: Edward Annand <(b) (6)
Date: Wednesday, 10 February 2021 at 1:12 pm
To: Alison Peel <(b) (6) John-Sebastian Eden <(b) (6) Ina

Smith <(b) (6)
Subject: Re: Collaborator on a DP

Sounds wonderful Ali – when is the deadline?

JS is super close in sharing preliminary results from your cohort. You may be able to refer to the success of our work together in this regard while adhering to sensitivities of the more detailed info of course.

Eddie not directly involved in our work with JS and JS has set up a separate lab based in the WIMR but of-course JS collaborates with him closely and likely shares supervision with him still on some grad students. JS will be best placed to advise you on what's best RE his association with the funding application.

I'll be in Geelong from the second half of tthis year and hope to continue my CSIRO affiliation from there. Working in with ACDP is probably a good idea and there are other who we have worked with from their who might be well suited such as Kim Blasdell who has done viral work in rats in SE Asia.

Cheers

Ed

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

From: Alison Peel <(b) (6)
Date: Wednesday, 10 February 2021 at 14:02
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Collaborator on a DP

Hi Ed, J-S and Ina,

I've recently been invited to join an ARC DP application that would utilise some of our CoV data. It's being led by GU palaeoecologist Julien Louys, with CIs including Paul Oliver (Queensland Museum/Griffith - biogeographer), Gilbert Price (UQ, palaeontologist) and Sue Hand (UNSW - palaeontologist). I've come on fairly late in the piece.
The DP aims to investigate bat and rat colonisation histories of Australia from fossil records and dating, and also look at estimating colonisation dates from improved resolution and dating in bat/rat phylogenies – all that is obviously outside of my expertise, but it will involve some fieldwork looking for bat fossils in Australia and Timor. The viral component is fairly minor, but comes in to try and see if bat

viruses (henipaviruses, coronaviruses) in Australia are more closely related by geography or bat phylogeny, and whether phylogenetic splits match that of their hosts. Overall, the stated aim is to provide information on how Australia's natural barriers to colonisation influence risk of zoonotic viral incursions in the future, or how susceptible Australia's endemic wildlife might be to novel viruses circulating in human populations.
Anyway, as I only came on board a week or two ago (after our internal deadline) and the application was well developed, I haven't asked about adding additional CIs, but it would be great to list you as collaborators if you'd be happy to? If funded, there's a bit of funding for further CoV screening in there (P. scapulatus in Australia and other Pteropus in Timor). Let me know if you're happy for me to list you as a collaborator (And J-S, is Eddie involved too? Would I list him?)

Cheers

Ali
<CoV.RdRp.Aligned.phyml.edited.tree.pdf><Peel 2020 Coronaviruses in Australian bats.pdf>

From: Plowright, Raina
Sent: Wed, 17 Feb 2021 03:28:13 +0000
To: Alison Peel
Cc: Munster, Vincent (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: Re: Re-screening preempt urines for novel Hendra

I can do most afternoons, have a few things on 1-2pm MT but can work around them. Monday is harder.

On Feb 16, 2021, at 6:44 PM, Alison Peel <(b) (6) wrote:

Ok, thanks Vincent – can you name any afternoons that are better than others?
I'm available from 2/3pm on your Monday and Wednesday afternoons, or from 10am on the other afternoons

---

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Wednesday, 17 February 2021 at 11:30 am
To: Alison Peel <(b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Re-screening preempt urines for novel Hendra

Hi Ali,

Let's push it to next week, this week I'm absolutely swamped.

Cheers,

Vincent

On Feb 16, 2021, at 17:44, Alison Peel <(b) (6) wrote:

Hi Vincent, Kwe and Raina,

What do you think is the best way forward from here? Shall we discuss via email or zoom? I'm available:

- Now
- from 4pm Wednesday your time
- from 2pm Thursday your time

Primary future screening objectives from my perspective are to:

1. see whether we're missing Hendra detections in our samples, and then whether these are systematic (e.g. by species) and say anything about ecology and spillover risk

2. screen samples for broader viral community, using either multiplexed qPCR assays (developed with Ina for known rubulaviruses Menangle, Yeppoon, Grove, Alston etc) or consensus PCR w/ sequencing approach.

So, I think decisions to be made are

1. whether those two objectives can be combined with the one approach, or should remain separate
2. where the work could be done/funded

I have funding for the broader viral community work. If it is sensible for the objectives to be combined under the same method, and that was to be done on already-extracted RNA (sent from RML to USyd) I'd have funding to screen a subset of samples but not all (at a first guess, maybe 40%, but would have to explore that in more detail with J-S).
Alternatively, I could approach CVOs for permission for the work to be done at RML, but I imagine that that isn't feasible from a capacity perspective anyway

Anyway, keen to hear your thoughts

Cheers

Ali

From: John-Sebastian Eden <(b) (6)
Date: Wednesday, 17 February 2021 at 9:38 am
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Alison Peel <(b) (6) Edward Annand <(b) (6) Plowright, Raina <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Thanks Kwe.

I've mapped the primers onto our new strain. I would say there are more than enough mis-matches for the assay to not pick it up.

I've got redesigned assays that target M and P but maybe you prefer updating your assay? I strongly agree with comments yesterday that the urine are they key samples.

J-S

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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<image001.png>

From: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Date: Wednesday, 17 February 2021 at 2:48 am
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Alison Peel <(b) (6), Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Plowright, Raina <(b) (6)
Cc: Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Hi John-Sabastian,

Here are the primers and probes for the HeV screening.

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DRP065-Hendra_R	TTCATTCCTCGTGACAGCAC
DRP66-Hendra_VIC	VIC-TTACTGCGGAGAATGTCCAACTGAGTG-QSY

Thanks

Kwe Claude Yinda, PhD
Postdoc Fellow
Virus Ecology Section, Laboratory of Virology
Rocky Mountain Laboratories, NIAID/NIH
903S 4th St. Hamilton, MT 59840
Email: (b) (6)
Tel: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 17 Feb 2021 01:30:10 +0000
To: Alison Peel
Cc: Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: Re: Re-screening preempt urines for novel Hendra
Attachments: image001.png

Hi Ali,

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Cheers,

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On Feb 16, 2021, at 17:44, Alison Peel <[redacted] (b) (6)> wrote:

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Anyway, keen to hear your thoughts

Cheers

Ali

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Date: Wednesday, 17 February 2021 at 9:38 am
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Alison Peel <(b) (6) Edward Annand <(b) (6) Plowright, Raina <(b) (6) Ina Smith <(b) (6)
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J-S

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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<image001.png>

From: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Date: Wednesday, 17 February 2021 at 2:48 am
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Alison Peel <(b) (6) Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Plowright, Raina <(b) (6)
Cc: Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

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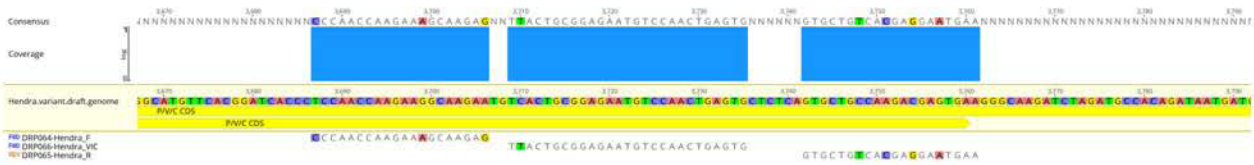
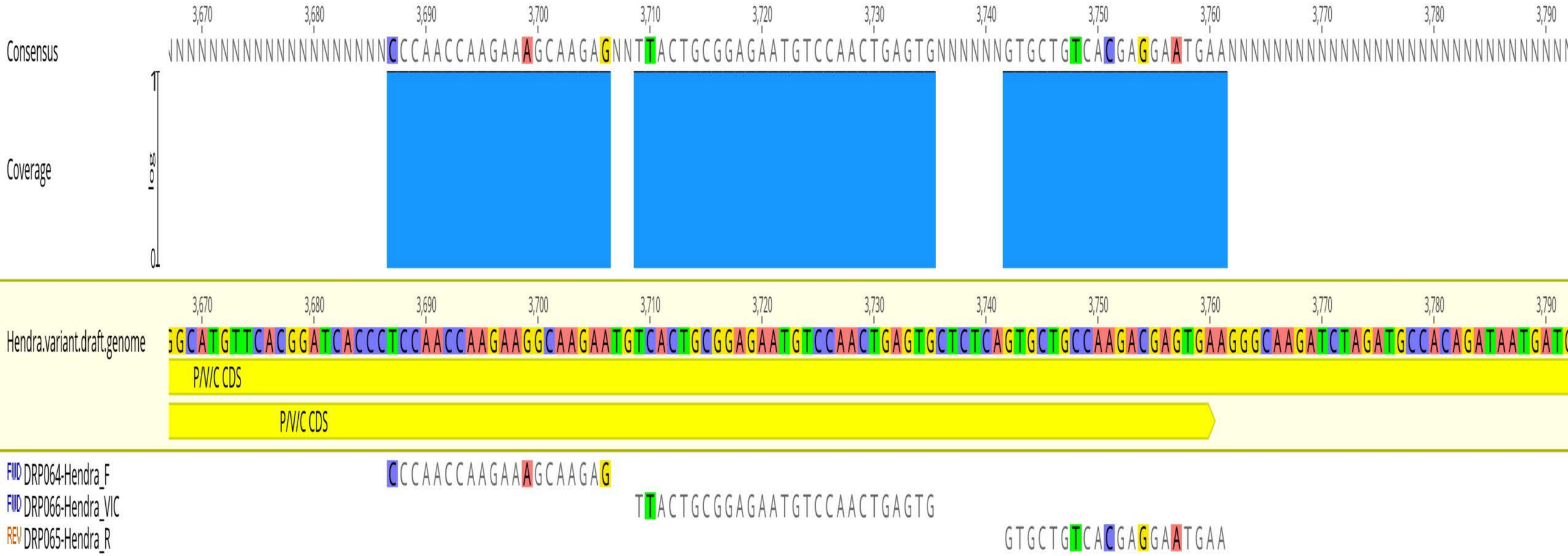
DRP065-Hendra_R	TTCATTCCTCGTGACAGCAC
DRP66-Hendra_VIC	VIC-TTACTGCGGAGAATGTCCAACTGAGTG-QSY

Thanks

Kwe Claude Yinda, PhD
Postdoc Fellow
Virus Ecology Section, Laboratory of Virology
Rocky Mountain Laboratories, NIAID/NIH
903S 4th St. Hamilton, MT 59840
Email: (b) (6)
Tel: (b) (6)




Consensus
Coverage
log
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3,680
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3,720
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3,740
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3,760
3,770
3,780
3,790
Hendra.variant.draft.genome
P/V/C CDS
P/V/C CDS
FWD DRP064-Hendra_F
FWD DRP066-Hendra_VIC
REV DRP065-Hendra_R

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 16 Feb 2021 21:07:37 +0000
To: Plowright, Raina; Hector Aguilar-Carreno
Cc: Jamie Lloyd-Smith; Peter J. Hudson; LaTrielle, Sara; Barbara Han
Subject: RE: CLosed-door mtg tomorrow: (b) (6)

Agreed, unless you can read this kind of figures it's not too important

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

From: Plowright, Raina <(b) (6)
Sent: Tuesday, February 16, 2021 1:52 PM
To: Hector Aguilar-Carreno <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Peter J. Hudson <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) LaTrielle, Sara <(b) (6) Barbara Han <(b) (6)
Subject: Re: CLosed-door mtg tomorrow: (b) (6)

thanks Hector, if the other one works (SARS, but who can really tell! hmmm you probably can tell!) we can stick to that.

On Feb 16, 2021, at 1:45 PM, Hector Aguilar-Carreno <(b) (6) wrote:

Hi Raina,

Sorry for my delayed response. That image works for me. I don't think at this level of resolution it really matters which protein is shown. If you want it to be NiV-G ephrinB2, you can use this one I generated for one of our PLoS Pathogens articles. However, I think the one you had served an equal purpose, so maybe the simpler the better? So basically the one you have totally works just fine.

I made the slide so that you can remove all the blue arrows and the stalk and still be useful.

Hope this helps, and sorry again for the delay,

Hector

Hector Aguilar-Carreno
Associate Professor
Microbiology and Immunology

College of Veterinary Medicine
Cornell University
Office: (b) (6)

From: Plowright, Raina <(b) (6)
Sent: Tuesday, February 16, 2021 3:36 PM
To: Jamie Lloyd-Smith <(b) (6)
Cc: Peter J. Hudson <(b) (6); Hector Aguilar-Carreno <(b) (6); Munster, Vincent (NIH/NIAID) [E] (b) (6); LaTrielle, Sara (b) (6); Barbara Han <(b) (6)
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<DARPA summary graphic V2 - .pptx>

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Attachments: 2021Raina BatProjectOverview R2.pdf

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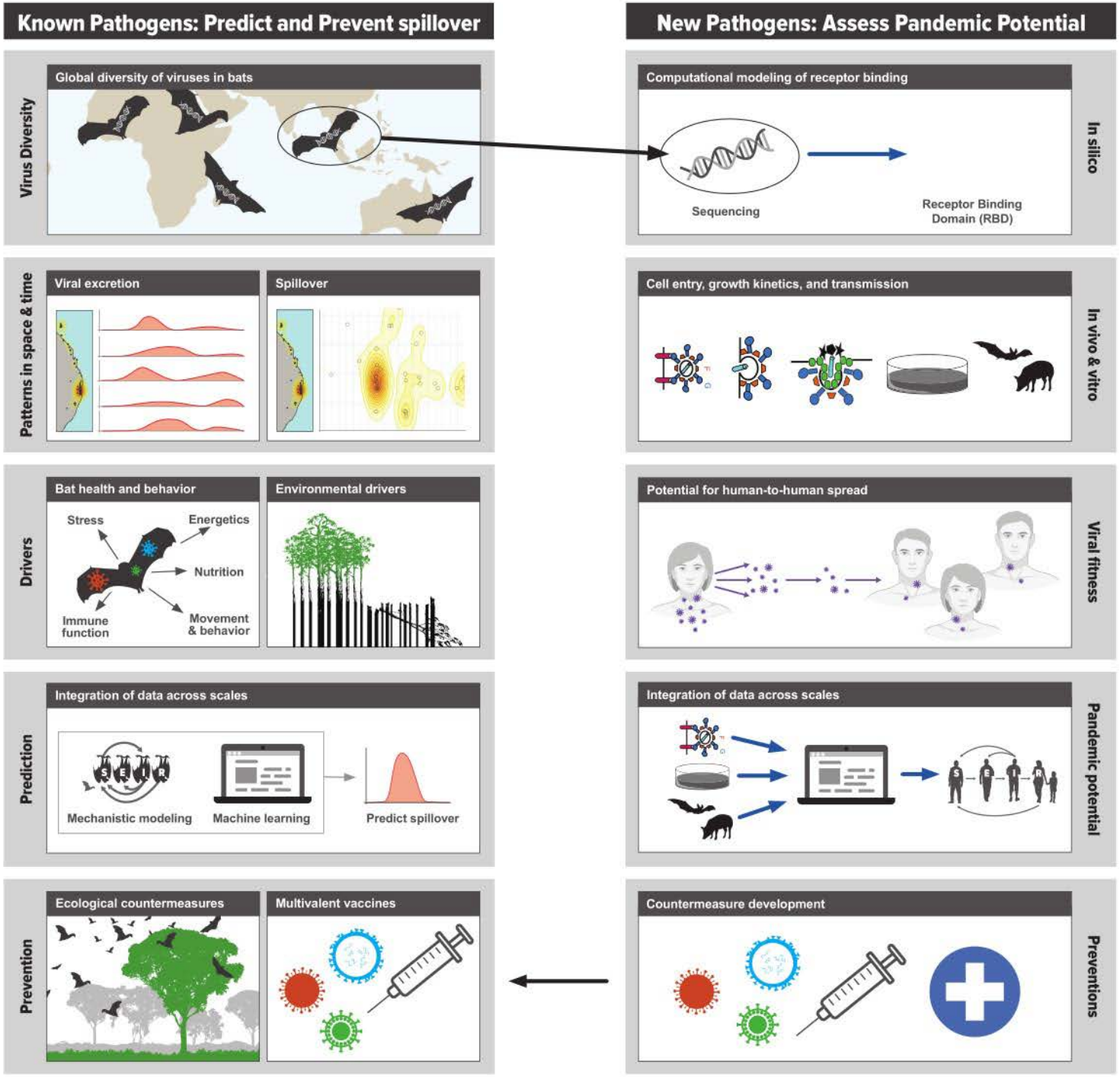
Known Pathogens: Predict and Prevent spillover
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Virus Diversity
Global diversity of viruses in bats
Computational modeling of receptor binding
Sequencing
Receptor Binding Domain (RBD)
In silico
Patterns in space & time
Viral excretion
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In vivo & vitro
Drivers
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Ecological countermeasures
Multivalent vaccines
Countermeasure development
Preventions

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Sent: Tue, 16 Feb 2021 15:48:05 +0000
To: Kwe Claude, Yinda (NIH/NIAID) [F]; Alison Peel; Edward Annand; John-Sebastian Eden; Plowright, Raina
Cc: Ina Smith
Subject: RE: Collaborator on a DP

Thanks Kwe!

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Hi John-Sabastian,

Here are the primers and probes for the HeV screening.

Name	Sequence (5'->3'
DRP064- Hendra_F	CCCAACCAAGAAAGCAAGAG
DRP065-Hendra_R	TTCATTCCTCGTGACAGCAC
DRP66-Hendra_VIC	VIC-TTACTGCGGAGAATGTCCAACTGAGTG-QSY

Thanks

Kwe Claude Yinda, PhD
Postdoc Fellow
Virus Ecology Section, Laboratory of Virology
Rocky Mountain Laboratories, NIAID/NIH
903S 4th St. Hamilton, MT 59840
Email: (b) (6)
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From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Monday, February 15, 2021 at 5:19 PM

To: Alison Peel <(b) (6)> Edward Annand <(b) (6)> John-Sebastian Eden <(b) (6)> "Plowright, Raina" <(b) (6)> "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6)>
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Hi Kwe,

Can you send your Hendra screening primer-probe sequences to John-Sebastian? They want to check them with some of their assays,

Thanks,

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Hi All,
Looks like everyone is available at that time. I've added a zoom link to the calendar invite, and here it is below
Looking forward to chatting then!
Cheers
Ali

PREEMPT is inviting you to a scheduled Zoom meeting.

Topic: Australia CoV results meeting
Time: Feb 16, 2021 09:00 AM Brisbane

Join Zoom Meeting
https://us02web.zoom.us/j/(b) (6)pwd=aUlFRUJDTUJKU2hEcVpManZjU0lqZz09

Meeting ID: (b) (6)

Passcode: (b) (6)
One tap mobile
+12532158782,(b) (6) US (Tacoma)
+13017158592,(b) (6) US (Washington DC)

Dial by your location
+1 253 215 8782 US (Tacoma)
+1 301 715 8592 US (Washington DC)
+1 312 626 6799 US (Chicago)
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Superb JS!

Vincent the other significant finding in our parallel horse testing so far is most closely related to HeV and caused indistinguishable disease. This finding is following sensitive and important notification and consideration by relevant Gov depts and national reference lab personnel and isolation is being attempted at ACDP. We have shared the sequence with the state lab to allow them to prepare to use the adapted qPCR that we develop and with Chris's UHS Lab (who already contributed to the finding directly by our using their proteins in the serology assays on the same samples) to allow them to begin preparing protein production and antibody binding assessment.

We would like to discuss your proposed Genotype to Phenotype analyses for this.

Of course JS and his team at WIMR (Beth and Rachel) stand 'ready to go' in screening the bat samples already extracted for Paramyxoviruses including this novel one by the same approach combining PanPCR and RNA seq.

I have mentioned sharing the sequence with you and with this project and hope it might be possible in strict confidence within the month.

Please keep the horse findings in strictest confidence.

Looking forward to a lot of very interesting analyses and collaboration to come! ☺

Cheers

Ed

Ed Annand
BVSc(Hons) MANZCVS (Equine Surgery) & (Epidemiology) CertAVP (Equine Stud Medicine) PgCertVPS MRCVS
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Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Ina Smith (b) (6) Edward Annand <(b) (6)
Subject: Re: Collaborator on a DP

Raina – It looks like about 17% (36/210 pools). We found multiple viruses in a few pools too, so at some point we will need to work out some estimated prevalence. Those times are fine for me.

Ali – From a quick NJ tree, I think the sequence is close to cluster 2d.ii. I'm running a proper one now with it and the horse one we found. More soon.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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---

From: Plowright, Raina (b) (6)
Date: Thursday, 11 February 2021 at 1:19 pm
To: Alison Peel <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) John-Sebastian Eden

< (b) (6) Ina Smith < (b) (6) Edward Annand
< (b) (6)
Subject: Re: Collaborator on a DP

This is so exciting!

J-S, what proportion of the fecal samples were positive? I assume these were the pooled samples?

Yes I'd love to talk about this.

I can do do the following times next week, if I have a few days notice (all in Sydney time):

- Tuesday AM: any time after 10am
- Wednesday AM: 7am-9am, any time after 10am
- Thursday aM: any time after 9.30am
- Friday am: any time after 9.00am

On Feb 10, 2021, at 7:01 PM, Alison Peel < (b) (6) wrote:

Hi Raina and Vincent,

Are you free for a meeting to discuss initial CoV results with J-S/Ed/Ina one afternoon your time next week?
The detections in cluster 2b.v cluster with PREDICT_CoV-67, which is from the same species in Sulawesi, collected in 2013. (though there is debate about the Australian individuals being a different subspecies, so this is super-interesting)

<image001.png>

Ed also has some horse results that may be relevant. Lots exciting to discuss.

J-S The sequences from Craig Smith and Diana Prada's papers would also be great to include. See phylogeny in attached paper.

Cheers

Ali

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:59 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: RE: Collaborator on a DP

Wow, cool. It'll be good to get more sequence still or at least make sure the trees are the best they can be. I build this first one from just blasting and pulling what was returned. I might need to scour GenBank to ensure everything relevant is there.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:55 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Thanks both. No, the PREDICT_CoV-67 is from the same species – in Sulawesi, collected in 2013!
<image002.png>

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:50 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: RE: Collaborator on a DP

Early mornings are okay for me. Maybe 730am onwards. Any day should be okay if you want to check in with Raina etc.

They likely the same group/variant. It's a little hard to say from the short, relatively conserved region we sequenced from the PCR. I think the PREDICT ones were from different bat genera but the MG256393_Bat coronavirus isolate BtCoV/B55440/Pte_lyl/CB1-THA/Apr12 one is from lyles flying fox in Thailand. So, matching some of that diversity makes sense. I can take representatives

from the clusters and get more data etc. So, maybe discuss next steps for this work next week too?

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:43 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Oooh, so many questions already!! Quickly though – do you think the ones clustering with the PREDICT sequences in cluster 2d.v are the same virus (/different variants?) as the PREDICT detections?

From: Alison Peel <(b) (6)
Date: Thursday, 11 February 2021 at 11:41 am
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

WOW!!!!!!!!!!!!!!!!!!

Absolutely!! I'm pretty flexible next week. Let me know when best suits. If it's first thing in the morning your time, then Raina may be able to join and I'm sure she'd be interested! Maybe Vincent too?

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:36 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

No worries. I was surprised a bit by your lack of apparent excitement in the findings =)

Basically, across the three plates there were plenty of CoV, and mostly Beta 2d. It's not the tidiest tree. I'm still working on the summary with tables for the hits to each pool etc but for now just wanted to share.

We should zoom next week. Would that work?

J-S

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Alison Peel (b) (6)
Date: Thursday, 11 February 2021 at 12:31 pm
To: Edward Annand < (b) (6) John-Sebastian Eden
< (b) (6) Ina Smith < (b) (6)
Subject: Re: Collaborator on a DP

Hi J-S,
Our uni had an issue with emails yesterday and have notified me that an email sent by you in this thread was inadvertently filtered as spam and deleted. Can you please re-send?
Thanks
Ali

From: Alison Peel < (b) (6)
Date: Wednesday, 10 February 2021 at 1:30 pm
To: Edward Annand < (b) (6) John-Sebastian Eden
< (b) (6) Ina Smith < (b) (6)
Subject: Re: Collaborator on a DP

Hi Ed,
Cool. Our final internal deadline is in about a week or so. For collaborators, I don't need any additional information except permission to list your name
Will be exciting to hear results!
Great to hear re: Geelong Ed. I keep putting off advertising for some PhD students, but hopefully will do so soon, and hope to include ACDP in at least one (and Ina – as previously discussed pre-COVID!)

Cheers

Ali

From: Edward Annand <(b) (6)
Date: Wednesday, 10 February 2021 at 1:12 pm
To: Alison Peel <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Sounds wonderful Ali – when is the deadline?

JS is super close in sharing preliminary results from your cohort. You may be able to refer to the success of our work together in this regard while adhering to sensitivities of the more detailed info of course.

Eddie not directly involved in our work with JS and JS has set up a separate lab based in the WIMR but of-course JS collaborates with him closely and likely shares supervision with him still on some grad students. JS will be best placed to advise you on what's best RE his association with the funding application.

I'll be in Geelong from the second half of tthis year and hope to continue my CSIRO affiliation from there. Working in with ACDP is probably a good idea and there are other who we have worked with from their who might be well suited such as Kim Blasdell who has done viral work in rats in SE Asia.

Cheers

Ed

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

From: Alison Peel <(b) (6)
Date: Wednesday, 10 February 2021 at 14:02
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Collaborator on a DP

Hi Ed, J-S and Ina,

I've recently been invited to join an ARC DP application that would utilise some of our CoV data. It's being led by GU palaeoecologist Julien Louys, with CIs including Paul Oliver (Queensland

Museum/Griffith - biogeographer), Gilbert Price (UQ, palaeontologist) and Sue Hand (UNSW - palaeontologist). I've come on fairly late in the piece.
The DP aims to investigate bat and rat colonisation histories of Australia from fossil records and dating, and also look at estimating colonisation dates from improved resolution and dating in bat/rat phylogenies – all that is obviously outside of my expertise, but it will involve some fieldwork looking for bat fossils in Australia and Timor. The viral component is fairly minor, but comes in to try and see if bat viruses (henipaviruses, coronaviruses) in Australia are more closely related by geography or bat phylogeny, and whether phylogenetic splits match that of their hosts. Overall, the stated aim is to provide information on how Australia's natural barriers to colonisation influence risk of zoonotic viral incursions in the future, or how susceptible Australia's endemic wildlife might be to novel viruses circulating in human populations.
Anyway, as I only came on board a week or two ago (after our internal deadline) and the application was well developed, I haven't asked about adding additional CIs, but it would be great to list you as collaborators if you'd be happy to? If funded, there's a bit of funding for further CoV screening in there (P. scapulatus in Australia and other Pteropus in Timor). Let me know if you're happy for me to list you as a collaborator (And J-S, is Eddie involved too? Would I list him?)

Cheers

Ali
<CoV.RdRp.Aligned.phyml.edited.tree.pdf><Peel 2020 Coronaviruses in Australian bats.pdf>

From: Plowright, Raina
Sent: Sun, 14 Feb 2021 23:13:33 +0000
To: Tamika Lunn
Cc: Munster, Vincent (NIH/NIAID) [E]; Hoegh, Andrew; Alison Peel; Jamie Lloyd-Smith; Olivier Restif; Hamish McCallum
Subject: Re: Spatio-temporal Hendra virus manuscript

A lot of really great stuff in this ms from Mike Minna's group. At a really quick skim — look at the neat violin plots & inverting y axis for ct value. Also makes me wonder if it we could simulate SEIR (and SILI) dynamics accounting for viral loads at different parts of the infectious period to explore likelihood of finding only high Ct values outside of spillover periods if low-level endemic dynamics (how likely to get the data we see given different assumptions about infectious periods and Ct dynamics, if Ct is truly related to days post infection in bats).

Another implication of low Cts associated with spillover that we can mention in the ms is that low-Se tests may be most appropriate for screening reservoir hosts for spillover risk… not logistically intensive and expensive PCR requiring insane sample handling, biosafety, and shipping etc.

Raina

On Nov 19, 2020, at 7:20 PM, Tamika Lunn <(b) (6)> wrote:

Hi all,

I think we should tentatively push ahead with meeting on the 24th at 4pm (Bozeman time). I'll send through a calendar invite and Zoom link shortly.

I'll make sure to record the session for anyone that isn't able to attend, and will aim to give more advanced notice next time!

Thanks!
Tamika

From: Tamika Lunn <(b) (6)>
Sent: Thursday, November 19, 2020 10:09 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)> Plowright, Raina <(b) (6)> Hoegh, Andrew <(b) (6)>
Cc: Alison Peel <(b) (6)> Jamie Lloyd-Smith <(b) (6)> Olivier Restif <(b) (6)> Hamish McCallum <(b) (6)>
Subject: Re: Spatio-temporal Hendra virus manuscript

Thanks everyone,

There isn't a time on Monday that suits everyone - so far Tuesday 24th at 1pm or 4pm (Bozeman time) is the earliest time that works in the Doodle Poll. Olivier, Vincent and Kwe would either of those work for you? (that's 8pm or 11pm in London, and 6am or 9am in Brisbane).

Thanks,
Tamika

From: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Sent: Thursday, November 19, 2020 2:11 AM
To: Plowright, Raina (b) (6); Hoegh, Andrew < (b) (6)
Cc: Alison Peel < (b) (6) Jamie Lloyd-Smith < (b) (6) Olivier Restif < (b) (6) Tamika Lunn < (b) (6) Hamish McCallum < (b) (6)
Subject: RE: Spatio-temporal Hendra virus manuscript

Monday works from my end

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

From: Plowright, Raina < (b) (6)
Sent: Tuesday, November 17, 2020 8:56 PM
To: Hoegh, Andrew < (b) (6)
Cc: Alison Peel < (b) (6) Jamie Lloyd-Smith < (b) (6) Olivier Restif < (b) (6) Tamika Lunn < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Hamish McCallum < (b) (6)
Subject: Re: Spatio-temporal Hendra virus manuscript

Monday or Tuesday next week could work (this week is not possible). Wednesday-Sunday is Thanksgiving holiday. After thanksgiving (>Sunday 29) is much more flexible.

On Nov 17, 2020, at 8:47 PM, Hoegh, Andrew < (b) (6) wrote:

Hi All,

I had originally just replied to Tamika, but will extend the discussion here. I'm excited to think about the spatiotemporal modeling and could find a little time for a meeting in the next week. I have 2 dissertation defenses on Friday, but I'd be fairly available Thursday, Monday, Tuesday.

As Raina mentioned, with our adjusted calendar at Montana State, final exams (and all the associated fun) will take place in the lead up to Thanksgiving. So my time is a bit limited in the next week, but I'll plan to focus my attention on part 2 (methods) and part 3 (ideas for formal analyses).

Andy

On Nov 17, 2020, at 7:39 PM, Alison Peel <[redacted] (b) (6) wrote:

Thanks Jamie!

Tamika - while I'm looking at it again, I'm going to make a couple of further comments here on the new parts of the analyses/explorations that I haven't commented on yet, so that others can also contribute to the discussion

Re defining a pulse
- I think the method needs to take into account the magnitude of the prevalence at that point in time, but also relative to prevalence at points either side of it. i.e. that a pulse has a rise to a peak followed by a decline (to the original baseline?). In our dataset, there seems to be a mix of epidemic-like dynamics followed by apparent local fadeout at our sites (winter 2017) (Note for others: this is also demonstrated across several other sites that are not shown in Tamika's plots, because we stopped sampling from them part way through 2018). Also epidemic like-dynamics (winter 2018) that are followed by endemic-like dynamics (Oct 2018 onwards). With our sampling frequency, I'm not sure whether it's appropriate to attempt to define a pulse during that endemic-like period - though I'd love to hear from others on this, and formal approaches to this.
- I can't remember the details of how David Paez defined pulses (possibly as an output of the wavelet analyses? Might need to dig into the supp info). I also did a quick search for papers that attempt to define pulses, or differentiate epidemic from endemic dynamics and found some which may be helpful for ideas: eg. this, this , this and possibly also this paper - which includes an interesting plot in Fig 1 that combines prevalence with pathogen load.
- Also Olivier - I wondered whether Emma had explored this kind of space with her syndromic surveillance work? i.e. answering the question "how do we know when an outbreak is starting?" (assuming some level of normal baseline detection). The first link I provided in the point above also gets at this.
- Saying all that, given Tamika's short timeline til submission, I think a pragmatic approach may be required for the short term for her thesis submission, but if there are ideas for more detailed analyses prior to manuscript submission, then that would still be good to discuss.

Re: Frequency distribution of Ct values per month and whether it is informative about stage in pulse in our system.
- I arranged your viral load plots in a matrix of year and month to more easily see if there were any discernible patterns over time (attached). I think our data are insufficient to see this, but yep, I'd be interested to hear if anyone else who has a student who may be interested in modelling this (with pooling)

Cheers

Ali

On Wed, 18 Nov 2020 at 12:02, Jamie Lloyd-Smith <[redacted] (b) (6) wrote:
Hi Tamika, hi Ali (hi everyone)!

Thanks for sharing this. I'm happy to help out if I can. I will look over the document but agree that a Zoom call would probably be a productive/efficient way to get the creative juices flowing. I have some flexibility later this week, a little bit early next week (but Thanksgiving etc will intervene, as all childcare will cease).

Cheers,
Jamie

On Tue, Nov 17, 2020 at 5:25 PM Alison Peel <(b) (6) wrote:
Thanks Raina and Olivier,
Can you suggest a day (or couple of options) when a zoom meeting might be possible with your current schedule? Hopefully we can find a time that works for all/most
As Tamika mentioned, I think one of the main components that we'd like to seek input on is the best spatiotemporal analytical approaches, and I sense that this might be productive as a discussion rather than back and forth via emails. It would be great to lock in a time sooner than later, even if it is after your busy period.
Thanks!
Ali

On Wed, 18 Nov 2020 at 09:41, Plowright, Raina (b) (6) wrote:
Thanks Tamika,
So appreciate this collaborative approach to this paper. I will dig into this after a short delay to get through the final week of teaching/grading/exam writing…
raina

On Nov 17, 2020, at 1:57 AM, Olivier Restif <(b) (6) wrote:

Thanks Tamika and well done for taking the lead. I'll send you some comments next week.

Best wishes,

Olivier

On 17 Nov 2020, at 08:48, Tamika Lunn <(b) (6) wrote:

Hi all,

I'm emailing with an update on the spatio-temporal Hendra virus manuscript. I've taken on lead author of this paper again, but building predominantly from initial ideas and analyses developed by Ali, and code from both Wyatt and Ali.

I wanted to reach out to invite your feedback on these initial analyses and plans. In particular, we've come up with some ideas for formal analyses, but I would love to have a collective discussion about the best approach, and what other ideas people have. It would also be great

to hear people's thoughts on what we've included to try and differentiate this paper from Field et al 2015, and whether there is anything else people would like to see in the paper (or not see in the paper).

A reminder that this is intended to be an inclusive paper that recognizes the broad contributions from many people to these data and the CNH/PREEMPT data. Its primary aim is to create a foundation that introduces the study and the dataset, upon which to base other associated papers from CNH/PREEMPT.

So, what I've attached is:

An initial paper plan that outlines 1) a possible introduction structure, 2) our methods, 3) ideas for formal analyses, and 4) possible key take-away results and proposed main figures/tables.

An RMarkdown with all of our data visuals so far. This contains a lot of information so don't feel that you need to look through this thoroughly.

I've also started a google doc (link here) reviewing 'what we think we know about Hendra dynamics and spillover risk'. I was initially thinking this could be an SI for this paper, but Ali has suggested that it could be useful being worked into a separate manuscript. Please feel free to add to this (or use it if it's a useful reference point!)

I'm on a tight deadline for my thesis, so it would be great to hear back from people by the middle to end of next week (~25th-27th November). If people are interested/free I could schedule a zoom for this time to discuss ideas, otherwise I'd be happy for comments via email! Please also let me know if there is anyone key that I've missed from this initial email.

Thanks in advance!
Tamika
<20201112_HeV structural plan.docx><PREEMPT-data-checking_V6.html>

--
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

<Ct distribution by month_landscape.pdf>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 13 Feb 2021 16:44:32 +0000
To: Bushmaker, Trenton (NIH/NIAID) [E]; Plowright, Raina
Cc: Kwe Claude, Yinda (NIH/NIAID) [F]; Adney, Danielle (NIH/NIAID) [F]; Holbrook, Myndi (NIH/NIAID) [C]
Subject: RE: Goldberg drum - WA1, UK, and SA variants

I probably would. . One think you don't want in the stock is the furin deletion site.

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Friday, February 12, 2021 1:42 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Do you think I should sequence the UK stock?

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Friday, February 12, 2021 12:27 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) Plowright, Raina <(b) (6)
Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Perfect, fingers crossed

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

From: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Sent: Friday, February 12, 2021 12:24 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)

Cc: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6) Holbrook, Myndi (NIH/NIAID) [C] <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Vincent,
I started the UKvariant stock today. I will check it Tuesday and Wednesday for harvest.

For next week:

1. (3) runs of South African variant at timepoints 0 and 3 hrs.
2. Start titrations of these three runs on Friday with Danielle.
3. Harvest UKvariant and start titrations Friday.
4. Check Jeremiah's fungal samples and bring them out in Trizol for sequencing.

Let me know if you have questions.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Wednesday, February 10, 2021 2:53 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Sorry I will not have time the remainder of this week but I will try for the short week, next week.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Wednesday, February 10, 2021 2:35 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi Trent,

Just to make sure that analyses is a critical part of your thesis. For the WA runs you did you should try to get PCR data this week?

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

From: Trenton Bushmaker <(b) (6)
Date: Wednesday, February 10, 2021 at 2:22 PM
To: (b) (6)' <(b) (6) "Kwe Claude, Yinda (NIH/NIAID)

[F]" <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Sounds good. As you and me already discussed Kwe will be helping me with the PCR on Quant, data analysis, and maybe a little bit on the paper section. Once I get more data for SA variant titrations on Feb. 24th I will involve Kwe. He has enough irons in the fire for now. PCR samples will be pulled twice during these experiments: approximately the first week of March (around when Kwe can help me) and later in the week of March 23rd .

The request for the later timepoint is coming from UCLA so they should provide the data, graphs, and discussion points to back up the request.

Let me know if you have more questions.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Wednesday, February 10, 2021 12:14 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) van Doremalen, Neeltje (NIH/NIAID) [E] <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hey, Trent make sure you are doing some analyses on your own data as well and not only farm it out to UCLA. I want to see the correlation between the PCR data (as discussed previously) and the infectious data.

Bob, Neeltje and Kwe can give you some pointers how to analyze the data in graphpad, but I do want to see some analyses from our end, preferably in real-time

As discussed, the correlation between PCR results and infectious titers should be there and I expect to see little difference in genome copies now between 0 and 180, but you need to analyze this data and show this,

Cheers,

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, February 9, 2021 5:01 PM
To: Dylan H. Morris <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)

Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

What is your estimate for 8 hours? Somewhere between 10^0.75- 10^1? I would be more comfortable around 10^1 – 10^1.25 in case we see a drop.

8 hours can be done but Jamie will owe me tickets to a NHL game jk.

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Tuesday, February 9, 2021 4:55 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Got it. Based on our back-of-the-envelope calculations, the best option in that case might be 8 hours. Would that potentially be an option? We can also do a bit more modeling. 9 could work too, but might be a little long.

On Feb 9, 2021, at 5:31 PM, Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:

Dylan,
It looks like all inoculum (WA1, SA, & UK) will be ~1 X10^6. The WA1 was 1.7 x 10^6.

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Tuesday, February 9, 2021 3:07 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Jamie Lloyd-Smith
<(b) (6) Amandine Gamble <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

If we can go high enough, 12 hours is viable, and then we'll get a clearer estimate of the half-life. Otherwise we can do 9.

On Feb 9, 2021, at 5:02 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

In this case, would it be the highest of the lowest? Or WA1 as a standalone?

Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories

NIAID/NIH

From: Dylan H. Morris <(b) (6)
Sent: Tuesday, February 9, 2021 2:59 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

How high do you reckon you can get the WA1 inoculum? That'll determine 9 versus 12.

On Feb 9, 2021, at 4:51 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Sounds good, fingers crossed. Pretty sure we're still one of the only US labs with these viruses

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, February 9, 2021 2:46 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Dylan H. Morris <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hello crew,
I would like to figure out this extended timepoint (either 9 or 12) by the end of this week if we can? Just need some time to prep.

Plan for now…
Stocks:

- UKvairant- Start 2/12, titrations-2/19, Readout- 2/24

Runs:

- Feb.14-20 - 3x runs of SAvariant at T0,3hr
- Feb. 21-27 - 3x runs of WA1 at T0, 9 or 12hr - this is the timepoint we need to figure out?
- Feb. 28-Mar.6 - 3x runs of UKvariant at T0,3hr
- Mar. 7-13 - 3x runs of SAvariant at T0,??hr
- Mar. 14-10 - 3x runs of UKvariant at T0,??hr

Titrations and readout

- SAvariant at T0,3hr – 2/19, readout 2/24
- WA1 at T0, ??hr – 2/26, readout 3/3
- UKvariant at T0,3hr – 3/5, readout 3/10

- SAvariant at T0,??hr – 3/12, readout 3/17
- UKvariant at T0,??hr – 3/19, readout 3/24

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Monday, February 8, 2021 11:53 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)> Dylan H. Morris <(b) (6)>
Cc: Jamie Lloyd-Smith <(b) (6)> Amandine Gamble <(b) (6)>
Subject: RE: Goldberg drum - WA1, UK, and SA variants

It takes ~1 ½ hours to get the Timepoint 0. It will take the 1 – 1 ½ for the finial timepoint.

As Vincent said 15 hr point is not doable. 6 hour will take some work to do but not preferred. 9 and 12 can be done.

It is looking like our UK strain will be ~ 10^5 for the starting inoculum. Can you run the model with this number for which timepoint you want?

South African will be higher(~10^7) so we should be good on that. Start with the same dilution as we did for the WA1. We will probably start with the SA strain and see if we can increase the inoculum titer for the UK.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Sent: Saturday, February 6, 2021 8:25 AM
To: Dylan H. Morris <(b) (6)> Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)>
Cc: Jamie Lloyd-Smith <(b) (6)> Amandine Gamble <(b) (6)>
Subject: RE: Goldberg drum - WA1, UK, and SA variants

With a bit of planning every point might be doable, other than the 15 hour one

Trent: ho long exactly does it take you to start a run?

e.g. prep at 8, start run at 9 am? Sample at 9pm?

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

From: Dylan H. Morris <(b) (6)
Sent: Friday, February 5, 2021 8:24 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

I think 18h is probably too long given the T=0h measurements. I think we'd dip below the LOD. And I'm especially concerned given what you said about smaller initial virus concentrations for the new variant.

Which of the following intervals would be most practical given your protocols in 4?

A) T=0h, T=6h
B) T=0h, T=9h
C) T=0h, T=12h
D) T=0h, T=15h

Something else?

On Feb 5, 2021, at 4:47 PM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Dylan/Amandine,
Thank you again for the quick turnaround for the graphs. It was a big hit today in the presentation I think!

So we need to discuss the later timepoint. What do you think would be a good timepoint? 18hrs?

-Trent

From: Dylan H. Morris <(b) (6)
Sent: Thursday, February 4, 2021 8:41 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Amandine Gamble
<(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Here are some quick figures. Half-life looks to be 1 to 2 hours.

On Feb 4, 2021, at 1:27 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

I think at the moment anything goes

Vincent Munster, PhD

Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 11:18 AM
To: Dylan H. Morris <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Good idea Vincent.

-Trent

From: Dylan Morris <(b) (6)
Date: Thursday, February 4, 2021 at 11:15 AM
To: Vincent Munster <(b) (6)
Cc: Trenton Bushmaker <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Could do a virological micropub? Or does that have to be genetics?

Or just a skinny preprint to which we can add B.1.351 when ready.

On Feb 4, 2021, at 1:11 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

I think we should be able to run the UK variant very soon, we should probably see if that alone would already be good to get a preprint out or at least some communication in the public domain while we work on getting the SA variant plugged in?

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 11:09 AM
To: Dylan H. Morris <(b) (6) Amandine Gamble <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Dylan/Amandine,

Here is the temp and RH for the first (3) run of WA1 at timepoints 0 and 180 minutes.

-Trent

From: Dylan Morris <(b) (6)
Date: Thursday, February 4, 2021 at 10:50 AM
To: Vincent Munster <(b) (6)
Cc: Trenton Bushmaker <(b) (6) Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Agreed. Data looks clean; congrats and thanks, Trent! I think we'll get a decent read out here on the half-life, and a good idea of how long to go for the longer run.

On Feb 4, 2021, at 12:48 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Looked pretty solid by eyeballing the data

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 10:42 AM
To: Dylan H. Morris <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6)
Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thank you! Let me know if you have questions.

-Trent

From: Dylan Morris <(b) (6)
Date: Thursday, February 4, 2021 at 10:41 AM
To: Trenton Bushmaker <(b) (6)
Cc: Jamie Lloyd-Smith <(b) (6) Amandine Gamble <(b) (6) Vincent Munster <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Excellent. Thanks, Trent! Will get right on this.

On Feb 4, 2021, at 12:39 PM, Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:

Hey crew,
Here is the excel file with the first (3) runs for WA1 at timepoints 0 and 180 minutes. Let me know what you think we should do for the extended timepoint after run through the model.

Dylan/Amadine- As we discussed I would like to include this in my talk tomorrow @ 1pm MT but just let me know if you can't make timeline.

I will get a better idea what the starting inoculum titers will be for the UK and South African variants the middle of next week. Estimate is that we will have to be starting with a lower titer. I will update you when I find out more.

I will start to grow those up at the end of next week. My schedule looks like you should have some data again around the first week of March.

Thank you everyone.

-Trent

From: Trenton Bushmaker <(b) (6)
Date: Wednesday, February 3, 2021 at 1:03 PM
To: Vincent Munster <(b) (6)
Cc: "Plowright, Raina" (b) (6), "Adney, Danielle (NIH/NIAID) [F]" <(b) (6) "Holbrook, Myndi (NIH/NIAID) [C]" <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Vincent,
Here is the titration data for the first (3) runs of WA1 variant at timepoints 0 or 180 mins. I will send UCLA the excel file once you approve here today.

-Trent

From: Trenton Bushmaker <(b) (6)
Date: Wednesday, January 27, 2021 at 3:44 PM
To: Vincent Munster <(b) (6)
Cc: "Plowright, Raina" (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Vincent,
Updates the on the project:

1. For people helping on the project- Myndi will do the cells-TMEPRESS for titrations plates and the stocks. Danielle and me will do titrations. Kwe will help me with the quant qRT-PCR analysis and some paper writing. Dylan will work on the decay with me and paper writing. Let me know if you are ok with this?

2. For your email attached- For the aerosol stocks I think you already know the issues with the UK stock but the stock is only growing to 10^4 for the BEI isolate from California. Brand, Neeltje, and Myndi already know I need minimum of 120ml of stock of the highest stock. HOWEVER, if we get the South African (SA) variant grown up before the UK is figured out I will start with it.

I'm still projecting to be done with this project by the end of February.

Bob is in charge of the surface stability(according to Kwe) but let me know how you would like to proceed with it.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 7:07 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Maybe ask in todays meeting: just lay-out the tasks and we can see who signs-up?

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

From: Trenton Bushmaker <(b) (6)
Date: Monday, January 11, 2021 at 2:04 PM
To: "(b) (6) <(b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Vincent,
I'm looking at personnel to help me with this experiment. I'm thinking Myndi to grow stocks because she will be doing it anyways in BSL3. Vicky and Myndi to maintain cells for titrations and do plates(Monday passage, Thursday plate for Friday titrations). Danielle to help me with titrations(Fridays) and reading plates(Wednesdays/Thursdays).

Danielle and Vicky I would like to have involved because it will free up the senior group for other experiments.

Let me know if you agree with this.

Looks like at Goldberg runs on Monday, Thursday, and Friday. Titrations on Friday afternoon. Might have to do a few weekend days to accomidnate for Cara's schedule and school.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Friday, January 8, 2021 11:56 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Dylan H. Morris <(b) (6)
Cc: Plowright, Raina (b) (6)
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hey guys,

Please do understand the technical limitation of the set-up in a high containment laboratory. I favor shorter experiments, which will allow us to more rapidly determine whether there are differences between the isolates.
Given that the transmission window is likely under 3 hours, I'm not particularly in favor making these experiments longer in duration than absolutely necessary. Anything over a 3 hour window will have massive implication on the way we conduct experiments.

My main priority is not running a model, but a providing good comparison between the different strains, which should be done in under 3 hours. A limited analyses as was done in the NEJM should be sufficient (I'm not against running a model, but human resources are extremely limited and I think it would be best to have an experimental design which would get us the best result with the least effort). Also this data is urgent, and I don't want to have any delays with getting this data out.

Of note, you don't "lose" 2 logs during the spray, that's just the experimental system (from collision to collection), this is fixed for every experiment so no difference is expected there between variants (or viruses)

As discussed this week, at the moment no isolates are in yet (again, try to understand that this is a massive undertaking and is a process of several weeks), but titers are expected in the WA1 range

Cheers,

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 7, 2021 8:14 PM
To: Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Dylan H. Morris <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thank you for the quick reply, I like the points you made. I have some time tomorrow in BSL4 from 9-2pm to think and reply, thanks crew.

-Trent

From: "Amandine Gamble" <(b) (6)
Date: Thursday, January 7, 2021 at 7:01:22 PM
To: "Jamie Lloyd-Smith" <(b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]" <(b) (6) "Dylan H. Morris" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi everyone,

Thanks Trent for all the info and your work on those new strains (among other things!). I only have two minor thoughts following up on Jamie's e-mail:

- As Jamie noted, the longer we wait before taking the second time point, the more precise our estimate of decay rate / half-life will be (as long as we are still above the LOD), so I would also be tempted to target 4 or 5h rather than 3h based on the data we had for the NEJM paper and the fact that you are now using a more sensitive titration protocol (if we understood well), however that obviously depends on the starting dose (the intercept on the graph Jamie put) so, my question is: **do you have any idea of the stock concentrations for the new variants**, and whether we have any reason to expect more loss during spraying? It looks from the NEJM paper that we lose around 2 log10 during spraying with WA1 (and SARS-CoV-1). I guess you all already thought about this, but just writing down in case (there are lots of things to think about!). Also, if you already have an idea on the stock concentration, Dylan can run some analyses on mock data (as mentioned by Jamie) accounting for this, the loss at spraying and potential decay rates, as pointed by Jamie.

- The second point can be discussed after you got the data as it is only about formatting. I see from the raw data attached to one of the e-mails (the scan of the hand-written data) that some wells are blank, although in the Excel file we received, all the wells were classified as + or -. I assume that you did not collect data from those blank wells because you could assume they were all positive (based on higher dilutions being positive) or negative (based on lower dilutions being negative), right? Dylan can correct me, but I think his model would run perfectly on the raw data, even if they are "incomplete". In other words, I think we can let the model do what you were already doing when you complete the blank wells so there is no need for you to do this. So in the future, **we are happy to work on the raw data (i.e., with +, - and blanks [that you can note "NA" so we know it is not just a forgotten well]), rather the completed version (with only + and -)**. You can even just send us a scan of your data and we can generate the Excel file if you prefere.

With all this, I also with you all the best for 2021 =)

Amandine

Le jeu. 7 janv. 2021 à 16:53, Jamie Lloyd-Smith < (b) (6) a écrit :
Hi Trent, hi everyone (also copying in Amandine since she's the one on our side with most experience with the raw data),

Great to hear this -- a few quick responses.
- 22/65 makes sense to me
- great to add the SA strain!
- I hope we are planning to collect new data on the WA1 strain, not reuse the NEJM data. There were enough differences in design with the original experiments that I think it would be MUCH stronger science to study all three strains using the same design (updated to avoid some of the challenges of the first round). (Actually from your comment about 'another 9 days' to add a timepoint, i.e. 3 viruses times 3 replicates, I think we're on the same page here.)
- I think the 5% decline in RH due to settling should be OK, if it's basically consistent across the viruses. We can think about whether to account for it in the modelling... my instinct is that we can leave it out of the model unless it differs significantly across replicates and viruses.
- Great to hear about T=0. That's especially crucial if we're just doing the one later time-point.
- Regarding the timing of the later timepoint, I was surprised by your statement, since my memory from the NEJM paper was that the above-LOD detections would have continued well beyond 3 hours. i.e. look at the plots:

<image001.png>
The SARS-CoV-2 data (red) started at a lower titer, but given the slopes it looks like there'd still be useful super-LOD data out to 5 and probably 6 hours. The SARS-CoV-1 data (blue) show the same slope with a higher intercept, and look like they'd stay above LOD out to 6 hours and beyond. Looking at the raw well data, the difference in + counts across time points isn't so striking, i.e. it's not like we're losing a dilution per hour - which makes sense, given the estimated half-life of ~3 hrs. Also if I'm not mistaken, Neetlje or Vincent mentioned that you guys have changed protocols (spin inoculation and different cell line) to get higher sensitivity in culture.
Bottom line: again, it will depend on the titers achievable at T=0, but unless I'm misreading things badly I think there would be value in extending that later timepoint. I know there are complexities about how long you can spend in BSL4, etc, but I'm just talking about the raw information content.

Dylan, Amandine, any further/other thoughts? Dylan, do you want to do a quick analysis with mock data (and reasonable noise) to think about the power we'd have to distinguish differences among variants using this design (i.e. 3 replicates of a single uninterrupted decay window)? And how that might change if we stretch the window to longer time periods? Or if we need more information to get better estimates, do we do as well by adding a 4th replicate at the long time point, rather than adding intermediate time points? (nothing magic about intermediate time points, except for prettier decay graphs. one replicate at 5h might be equivalent to 2 at 2h, in terms of information gained)

cheers,
Jamie

On Thu, Jan 7, 2021 at 3:51 PM Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) wrote:
Jamie/Dylan,
First, I have added the pervious email so we can all stay on the same page(UK variant shams).

Next, I have talked with Vincent today but would like your input. For a quick paper, I think we should do condition at 22C @ 65%RH – hospital setting. Is everyone ok with this? This was the same setting as we had in the NEJM paper.

Third, we will do the UK variant (VOC), South African (SA) variants, and the original NEJM paper Washington (WA1) for the comparison.

Four, will a 5% percent decrease over 3 hours of the relative humidity cause issues with anything? This happens when nothing is pulled out of the drum, it just happens because of the time frame of 3 hours with the deposition. It should be ok for this decay model(linear regression) correct? I just want to confirm.

Lastly and most important, we will "for sure" have a timepoint at 0 minutes to check for the start values. However, we need to discuss the last timepoint. The LOD for ourtitrations with our cell culture seems to happen between 180-240 mins, so I would stick with the 180 minute timepoint (titrations attached- "2019-nCoV titrations goldberg drum.jpeg"). Do you agree with this? It would give you two points at timepoint 0 and 180 minutes.

I will collect (4) qRT-PCR per timepoint 0 and (4) more during the later timepoint.

How does this sound? Think about the later timepoint. Each run is a day of work in BSL4 and 10ml of virus. If in addition you want to collect at a middle timepoint this will adding another 9 days of BSL4 work, that will have to be spread out over 3 weeks. We can also think about a later timepoint. The titrations will be useless but qRT-PCR might be interesting. I think this will be usefully for a later experiment because we want to get this out quickly.

-Trent

--
James O. Lloyd-Smith

Professor
Department of Ecology & Evolutionary Biology
Department of Biomathematics

University of California, Los Angeles
610 Charles E Young Dr South
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Phone: (b) (6)

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Office: 4135 Terasaki Life Sciences Building

Lab: 4000 Terasaki Life Sciences Building

<2020-03-24 Raw data - 22C @ 65%RH- WA1, UK, & SA.xlsx>

From: Plowright, Raina
Sent: Fri, 12 Feb 2021 02:10:08 +0000
To: Edward Annand
Cc: John-Sebastian Eden; Alison Peel; Munster, Vincent (NIH/NIAID) [E]; Ina Smith
Subject: Re: Collaborator on a DP

Ed, sorry, you may have to deal with my enthusiasm a little more here. Have you been able to examine the ecological angles? Species composition at nearest roost, timing and conditions around time of spillover, land use type and availability of flowering in the area at the time of spillover? We are happy to provide data/insights to help put this in a bigger ecological context if that is helpful.

On Feb 11, 2021, at 6:59 PM, Raina Plowright <[redacted] (b) (6) wrote:

Dear Ed,
This is an extraordinary development. I will certainly keep this in the strictest confidence. Ideally it would be good to put the new pathogen through the full G-P pipeline, including cell entry etc in pseudotyped assays. This is done in Hector Aguilar-Carreno's lab at Cornell. He is currently doing this for a new henipavirus that our team member discovered in Madagascar. Vincent has incredible capacity at NIH as well. If you can get an isolate, could you send it to Vincent? Maybe ACDP could do some of the experiments?
Let's discuss on the call on Monday.
Raina

On Feb 11, 2021, at 12:00 AM, Edward Annand <[redacted] (b) (6) wrote:

Superb JS!

Vincent the other significant finding in our parallel horse testing so far is most closely related to HeV and caused indistinguishable disease. This finding is following sensitive and important notification and consideration by relevant Gov depts and national reference lab personnel and isolation is being attempted at ACDP. We have shared the sequence with the state lab to allow them to prepare to use the adapted qPCR that we develop and with Chris's UHS Lab (who already contributed to the finding directly by our using their proteins in the serology assays on the same samples) to allow them to begin preparing protein production and antibody binding assessment.

We would like to discuss your proposed Genotype to Phenotype analyses for this.

Of course JS and his team at WIMR (Beth and Rachel) stand 'ready to go' in screening the bat samples already extracted for Paramyxoviruses including this novel one by the same approach combining PanPCR and RNA seq.

I have mentioned sharing the sequence with you and with this project and hope it might be possible in strict confidence within the month.

Please keep the horse findings in strictest confidence.

Looking forward to a lot of very interesting analyses and collaboration to come! ☺

Cheers

Ed

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

From: John-Sebastian Eden < (b) (6)
Date: Thursday, 11 February 2021 at 13:36
To: Plowright, Raina < (b) (6) Alison Peel < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Ina Smith < (b) (6) Edward Annand < (b) (6)
Subject: Re: Collaborator on a DP

Raina – It looks like about 17% (36/210 pools). We found multiple viruses in a few pools too, so at some point we will need to work out some estimated prevalence. Those times are fine for me.

Ali – From a quick NJ tree, I think the sequence is close to cluster 2d.ii. I'm running a proper one now with it and the horse one we found. More soon.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Plowright, Raina (b) (6)
Date: Thursday, 11 February 2021 at 1:19 pm
To: Alison Peel < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) John-Sebastian Eden < (b) (6) Ina Smith < (b) (6) Edward Annand

< (b) (6)
Subject: Re: Collaborator on a DP

This is so exciting!

J-S, what proportion of the fecal samples were positive? I assume these were the pooled samples?

Yes I'd love to talk about this.

I can do do the following times next week, if I have a few days notice (all in Sydney time):

- Tuesday AM: any time after 10am
- Wednesday AM: 7am-9am, any time after 10am
- Thursday aM: any time after 9.30am
- Friday am: any time after 9.00am

On Feb 10, 2021, at 7:01 PM, Alison Peel < (b) (6) wrote:

Hi Raina and Vincent,

Are you free for a meeting to discuss initial CoV results with J-S/Ed/Ina one afternoon your time next week?
The detections in cluster 2b.v cluster with PREDICT_CoV-67, which is from the same species in Sulawesi, collected in 2013. (though there is debate about the Australian individuals being a different subspecies, so this is super-interesting)

<image001.png>

Ed also has some horse results that may be relevant. Lots exciting to discuss.

J-S The sequences from Craig Smith and Diana Prada's papers would also be great to include. See phylogeny in attached paper.

Cheers

Ali

From: John-Sebastian Eden < (b) (6)
Date: Thursday, 11 February 2021 at 11:59 am
To: Alison Peel < (b) (6) Edward Annand < (b) (6) Ina Smith < (b) (6)
Subject: RE: Collaborator on a DP

Wow, cool. It'll be good to get more sequence still or at least make sure the trees are the best they can be. I build this first one from just blasting and pulling what was returned. I might need to scour GenBank to ensure everything relevant is there.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:55 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Thanks both. No, the PREDICT_CoV-67 is from the same species – in Sulawesi, collected in 2013!
<image002.png>

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:50 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: RE: Collaborator on a DP

Early mornings are okay for me. Maybe 730am onwards. Any day should be okay if you want to check in with Raina etc.

They likely the same group/variant. It's a little hard to say from the short, relatively conserved region we sequenced from the PCR. I think the PREDICT ones were from different bat genera but the MG256393_Bat coronavirus isolate BtCoV/B55440/Pte_lyl/CB1-THA/Apr12 one is from lyles flying fox in Thailand. So, matching some of that diversity makes sense. I can take representatives from the clusters and get more data etc. So, maybe discuss next steps for this work next week too?

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
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From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:43 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Oooh, so many questions already!! Quickly though – do you think the ones clustering with the PREDICT sequences in cluster 2d.v are the same virus (/different variants?) as the PREDICT detections?

From: Alison Peel <(b) (6)
Date: Thursday, 11 February 2021 at 11:41 am
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

WOW!!!!!!!!!!!!!!!!!!

Absolutely!! I'm pretty flexible next week. Let me know when best suits. If it's first thing in the morning your time, then Raina may be able to join and I'm sure she'd be interested! Maybe Vincent too?

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:36 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

No worries. I was surprised a bit by your lack of apparent excitement in the findings =)

Basically, across the three plates there were plenty of CoV, and mostly Beta 2d. It's not the tidiest tree. I'm still working on the summary with tables for the hits to each pool etc but for now just wanted to share.

We should zoom next week. Would that work?

J-S

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Alison Peel <(b) (6)
Date: Thursday, 11 February 2021 at 12:31 pm
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Hi J-S,
Our uni had an issue with emails yesterday and have notified me that an email sent by you in this thread was inadvertently filtered as spam and deleted. Can you please re-send?
Thanks
Ali

From: Alison Peel <(b) (6)
Date: Wednesday, 10 February 2021 at 1:30 pm
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Hi Ed,
Cool. Our final internal deadline is in about a week or so. For collaborators, I don't need any additional information except permission to list your name
Will be exciting to hear results!
Great to hear re: Geelong Ed. I keep putting off advertising for some PhD students, but hopefully will do so soon, and hope to include ACDP in at least one (and Ina – as previously discussed pre-COVID!)

Cheers

Ali

From: Edward Annand <(b) (6)
Date: Wednesday, 10 February 2021 at 1:12 pm
To: Alison Peel <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Sounds wonderful Ali – when is the deadline?

JS is super close in sharing preliminary results from your cohort. You may be able to refer to the success of our work together in this regard while adhering to sensitivities of the more detailed info of course.

Eddie not directly involved in our work with JS and JS has set up a separate lab based in the WIMR but of-course JS collaborates with him closely and likely shares supervision with him still on some grad

students. JS will be best placed to advise you on what's best RE his association with the funding application.

I'll be in Geelong from the second half of tthis year and hope to continue my CSIRO affiliation from there. Working in with ACDP is probably a good idea and there are other who we have worked with from their who might be well suited such as Kim Blasdell who has done viral work in rats in SE Asia.

Cheers

Ed

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

From: Alison Peel <(b) (6)
Date: Wednesday, 10 February 2021 at 14:02
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Collaborator on a DP

Hi Ed, J-S and Ina,

I've recently been invited to join an ARC DP application that would utilise some of our CoV data. It's being led by GU palaeoecologist Julien Louys, with CIs including Paul Oliver (Queensland Museum/Griffith - biogeographer), Gilbert Price (UQ, palaeontologist) and Sue Hand (UNSW - palaeontologist). I've come on fairly late in the piece.
The DP aims to investigate bat and rat colonisation histories of Australia from fossil records and dating, and also look at estimating colonisation dates from improved resolution and dating in bat/rat phylogenies – all that is obviously outside of my expertise, but it will involve some fieldwork looking for bat fossils in Australia and Timor. The viral component is fairly minor, but comes in to try and see if bat viruses (henipaviruses, coronaviruses) in Australia are more closely related by geography or bat phylogeny, and whether phylogenetic splits match that of their hosts. Overall, the stated aim is to provide information on how Australia's natural barriers to colonisation influence risk of zoonotic viral incursions in the future, or how susceptible Australia's endemic wildlife might be to novel viruses circulating in human populations.
Anyway, as I only came on board a week or two ago (after our internal deadline) and the application was well developed, I haven't asked about adding additional CIs, but it would be great to list you as collaborators if you'd be happy to? If funded, there's a bit of funding for further CoV screening in there (P. scapulatus in Australia and other Pteropus in Timor). Let me know if you're happy for me to list you as a collaborator (And J-S, is Eddie involved too? Would I list him?)

Cheers

Ali
<CoV.RdRp.Aligned.phyml.edited.tree.pdf><Peel 2020 Coronaviruses in Australian bats.pdf>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 11 Feb 2021 21:15:17 +0000
To: Laing, Eric; Timothy Burgess; Broder, Chris (USU-DoD); Simon Pollett; Simons, Mark; Agan, Brian (IDCRP); Stephanie Richard; Nusrat Epsi; Esposito, Dominic (NIH/NCI) [C]; Lanteri, Charlotte A LTC USARMY USUHS (USA); Guy Clifton; Mende, Katrin CTR USARMY MEDCOM BAMC (USA); David Tribble; Chung, Kevin; Merritt, Scott E CTR (USA); Caroline English; De wit, Emmie (NIH/NIAID) [E]; Emily Samuels; Si'Ana Coggins
Subject: RE: SARS-CoV-2 multiplex serology manuscript

Looks good, go ahead and fingers crossed!

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

From: Laing, Eric < (b) (6)
Sent: Tuesday, February 9, 2021 7:38 PM
To: Timothy Burgess < (b) (6) Broder, Chris (USU-DoD) < (b) (6) Simon Pollett < (b) (6) Simons, Mark < (b) (6) Agan, Brian (IDCRP) < (b) (6) Stephanie Richard < (b) (6) Nusrat Epsi < (b) (6) Esposito, Dominic (NIH/NCI) [C] < (b) (6) Lanteri, Charlotte A LTC USARMY USUHS (USA) < (b) (6) Guy Clifton < (b) (6) Mende, Katrin CTR USARMY MEDCOM BAMC (USA) < (b) (6) David Tribble < (b) (6) Chung, Kevin < (b) (6) Merritt, Scott E CTR (USA) < (b) (6) Caroline English < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) De wit, Emmie (NIH/NIAID) [E] < (b) (6) Emily Samuels < (b) (6) Si'Ana Coggins < (b) (6)
Subject: SARS-CoV-2 multiplex serology manuscript

Hi everyone,

The first submission of our multiplex serology manuscript to NatComm required major revisions. Major revisions were made including the validation of two additional antigen-based multiplex validations.

I'd like to submit this soon, so if you have suggestions, if possible, please try to return those to me by the end of the week.

Regards,
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)

From: Plowright, Raina
Sent: Thu, 11 Feb 2021 04:15:38 +0000
To: Jamie Lloyd-Smith
Cc: Peter Hudson; Munster, Vincent (NIH/NIAID) [E]; LaTrielle, Sara; Hector Aguilar-Carreno; Barbara Han
Subject: Re: CLosed-door mtg tomorrow: (b) (6)
Attachments: DARPA summary graphic V2.pptx

Here is overall summary graphic, V2.
Would like to have this to show to USAID etc.
Love ideas or edits mostly **on the g-p section**. You can leave comments on the graphics (I have a few on the LHS for the designer).
Not sure what visual to do for modeling at the bottom. Also, the arrows should probably come from every box to the modeling box.
Thanks
Raina

On Feb 3, 2021, at 1:05 PM, Jamie Lloyd-Smith <(b) (6)> wrote:

Looks great to me! Really ties the pieces together, including our new franken-bits for phase II.

I was going to offer the nice graphic Amandine made
<image.png>
but clearly you're better off with little stick figures for the big schematic you're planning.

cheers
j

On Wed, Feb 3, 2021 at 11:35 AM Plowright, Raina <(b) (6)> wrote:
Here is latest mock up.
<Screen Shot 2021-02-03 at 12.33.57 PM.png>
On Feb 3, 2021, at 12:26 PM, Raina Plowright <(b) (6)> wrote:

great for future projects. this figure is trying to describe the current project only.

On Feb 3, 2021, at 12:19 PM, Hudson, P <(b) (6)> wrote:

At the very top of the right hand column I would include something on immunology surveillance in parallel with sequencing –
Call it antiviral antibody profiling ?

P

Peter Hudson FRS
Willaman Professor of Biology
Adjunct Professor at Nelson Mandela African Institute – Arusha
A co-hire of The Huck institutes & The Institutes of Energy & The Environment
229C Millennium Science Complex
Penn State University
(O) (b) (6)
(C) (b) (6)

Websites:
Science: https://www.huck.psu.edu/people/peter-hudson
Photography: https://www.peterhudsonphotos.com
Conservation: http://www.pawstrails.com

Instagram: https://www.instagram.com/peter_hudson018/

Zoom: https://psu.zoom.us/my/peterhudson

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Wednesday, February 3, 2021 at 1:55 PM
To: Plowright, Raina <(b) (6)
Cc: LaTrielle, Sara <(b) (6) Hudson, P <(b) (6) Hector Aguilar-Carreno <(b) (6) Barbara Han <(b) (6) (b) (6) <(b) (6)
Subject: RE: CLosed-door mtg tomorrow: (b) (6)

I think conceptually its great, I would merge in next-gen technologies in addition to multivalent vaccines. E.g. provide a genetic library which can used in rapid scalable technologies like mRNA vaccines.

Btw, totally agree, for the h-to-h just use one of the figures Jamie has in his presentation?

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

From: Plowright, Raina <(b) (6)
Sent: Wednesday, February 3, 2021 11:49 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: LaTrielle, Sara <(b) (6) Peter J. Hudson <(b) (6) Hector Aguilar-Carreno <(b) (6) Barbara Han <(b) (6) (b) (6)
Subject: Re: CLosed-door mtg tomorrow: (b) (6)

I'm mocking up a visual to describe the overall project and would love some input on the G-P section. Can you look at the first slide here? I was hoping to do this for our talk but its more likely a longer term project!

—especially like to know: what visuals (e.g. for h2h, probably not kosher to have monkeys and hamsters on public places like our website), and what wording?

See hand drawn mockup on LH side. and second slide shows the overall graphic mock up. Love feedback on any and all of it of course.

On Feb 3, 2021, at 8:22 AM, Plowright, Raina (b) (6) wrote:

Please note, they just cancelled this meeting and will reschedule next week. Enjoy your extra hour today.
Think about any issues we may want to raise one-on-one with (b) (6) and team next week.
Best,
Raina

On Feb 2, 2021, at 1:00 PM, Munster, Vincent (NIH/NIAID) [E] (b) (6) wrote:

Yes, I can attend but haven't seen the invite,

Cheers,

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

From: LaTrielle, Sara < (b) (6)
Sent: Tuesday, February 2, 2021 9:43 AM
To: Plowright, Raina < (b) (6) Hudson, P < (b) (6) Hector Aguilar-Carreno < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Barbara

Han < (b) (6) (b) (6)
Subject: CLosed-door mtg tomorrow: (b) (6)

All,

Per previous emails, Raina/Pete kindly request your presence/participation during tomorrow's MSU's 'closed-door' session which I have just re-sent the invite for, forwarded from DARPA. Please rsvp to Raina/me so I know who will be attending.

Meeting time is 11am-12pm MST with these call-in details:

As previously mentioned, this is a rather informal meeting where we address their technical queries, solve any issues, discuss challenges, and/or look to the future. We can discuss Phase I and II here. Show our excitement- woot woot!

Raina will provide guidance on a few points we should 'hit on'.

Slack page for internal discussions/ before/during the call here
(b) (6)

Sara

--
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

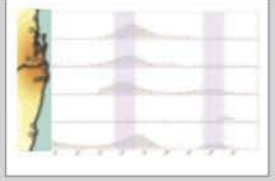
Predict and prevent spillover of known pathogens

Virus Diversity

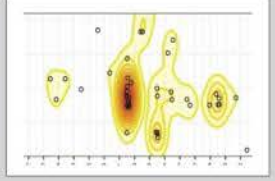
Global diversity of viruses in bats

Patterns in space & time

Viral excretion

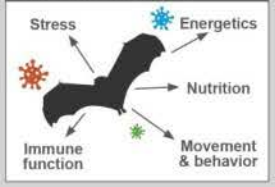


Spillover



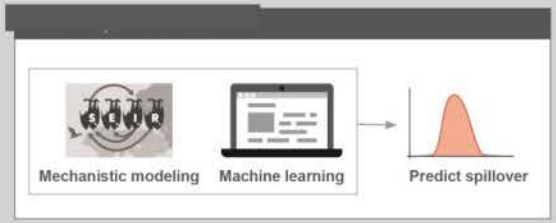
Drivers

Bat health and behavior



Environmental drivers

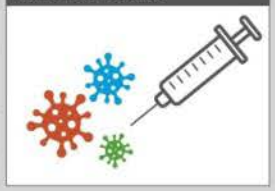
Prediction



Prevention

Ecological countermeasures

Multivalent vaccines

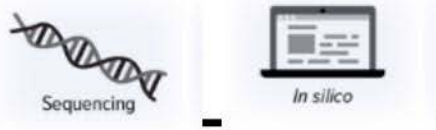


Field sequences

Assess pandemic potential of new pathogens

In silico

Computational modeling of human-receptor binding potential



In vitro

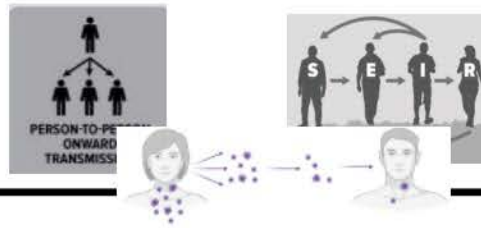
Cell entry and membrane fusion in vitro

In vivo

Growth kinetics and transmission in vivo

H2H transmission

Potential for human-to-human spread



Viral fitness in humans through integrative modeling

Countermeasure development

From: Plowright, Raina
Sent: Thu, 11 Feb 2021 02:40:52 +0000
To: John-Sebastian Eden
Cc: Alison Peel; Munster, Vincent (NIH/NIAID) [E]; Ina Smith; Edward Annand
Subject: Re: Collaborator on a DP

Oh my that is fabulous! Looking forward to seeing how those positive pools land over space and time (e.g., clustered into few times and places, or spread out), we can do this quickly after you send the data.

On Feb 10, 2021, at 7:36 PM, John-Sebastian Eden < (b) (6) wrote:

Raina – It looks like about 17% (36/210 pools). We found multiple viruses in a few pools too, so at some point we will need to work out some estimated prevalence. Those times are fine for me.

Ali – From a quick NJ tree, I think the sequence is close to cluster 2d.ii. I'm running a proper one now with it and the horse one we found. More soon.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Plowright, Raina (b) (6)
Date: Thursday, 11 February 2021 at 1:19 pm
To: Alison Peel < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) John-Sebastian Eden < (b) (6) Ina Smith < (b) (6) Edward Annand < (b) (6)
Subject: Re: Collaborator on a DP

This is so exciting!

J-S, what proportion of the fecal samples were positive? I assume these were the pooled samples?

Yes I'd love to talk about this.

I can do do the following times next week, if I have a few days notice (all in Sydney time):

- Tuesday AM: any time after 10am

- Wednesday AM: 7am-9am, any time after 10am
- Thursday aM: any time after 9.30am
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On Feb 10, 2021, at 7:01 PM, Alison Peel <(b) (6) wrote:

Hi Raina and Vincent,

Are you free for a meeting to discuss initial CoV results with J-S/Ed/Ina one afternoon your time next week?
The detections in cluster 2b.v cluster with PREDICT_CoV-67, which is from the same species in Sulawesi, collected in 2013. (though there is debate about the Australian individuals being a different subspecies, so this is super-interesting)

<image001.png>

Ed also has some horse results that may be relevant. Lots exciting to discuss.

J-S The sequences from Craig Smith and Diana Prada's papers would also be great to include. See phylogeny in attached paper.

Cheers

Ali

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:59 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: RE: Collaborator on a DP

Wow, cool. It'll be good to get more sequence still or at least make sure the trees are the best they can be. I build this first one from just blasting and pulling what was returned. I might need to scour GenBank to ensure everything relevant is there.

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:55 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Thanks both. No, the PREDICT_CoV-67 is from the same species – in Sulawesi, collected in 2013!
<image002.png>

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:50 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: RE: Collaborator on a DP

Early mornings are okay for me. Maybe 730am onwards. Any day should be okay if you want to check in with Raina etc.

They likely the same group/variant. It's a little hard to say from the short, relatively conserved region we sequenced from the PCR. I think the PREDICT ones were from different bat genera but the MG256393_Bat coronavirus isolate BtCoV/B55440/Pte_lyl/CB1-THA/Apr12 one is from lyles flying fox in Thailand. So, matching some of that diversity makes sense. I can take representatives from the clusters and get more data etc. So, maybe discuss next steps for this work next week too?

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

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From: Alison Peel <(b) (6)
Sent: Thursday, 11 February 2021 12:43 PM
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Oooh, so many questions already!! Quickly though – do you think the ones clustering with the PREDICT sequences in cluster 2d.v are the same virus (/different variants?) as the PREDICT detections?

From: Alison Peel <(b) (6)
Date: Thursday, 11 February 2021 at 11:41 am
To: John-Sebastian Eden <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

WOW!!!!!!!!!!!!!!!!!!

Absolutely!! I'm pretty flexible next week. Let me know when best suits. If it's first thing in the morning your time, then Raina may be able to join and I'm sure she'd be interested! Maybe Vincent too?

From: John-Sebastian Eden <(b) (6)
Date: Thursday, 11 February 2021 at 11:36 am
To: Alison Peel <(b) (6) Edward Annand <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

No worries. I was surprised a bit by your lack of apparent excitement in the findings =)

Basically, across the three plates there were plenty of CoV, and mostly Beta 2d. It's not the tidiest tree. I'm still working on the summary with tables for the hits to each pool etc but for now just wanted to share.

We should zoom next week. Would that work?

J-S

Dr John-Sebastian Eden
Research Scientist in Bioinformatics and Genomics, The Westmead Institute for Medical Research
Senior Research Fellow, The University of Sydney - Sydney Medical School

Room O.6.23 | 176 Hawkesbury Road | PO Box 412 | Westmead NSW 2145 Australia
(b) (6) | T (b) (6) | M (b) (6)
westmeadinstitute.org.au | Follow us on Facebook | Watch us on YouTube

---

From: Alison Peel <(b) (6)
Date: Thursday, 11 February 2021 at 12:31 pm
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Hi J-S,
Our uni had an issue with emails yesterday and have notified me that an email sent by you in this thread was inadvertently filtered as spam and deleted. Can you please re-send?
Thanks
Ali

From: Alison Peel <(b) (6)
Date: Wednesday, 10 February 2021 at 1:30 pm
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Hi Ed,
Cool. Our final internal deadline is in about a week or so. For collaborators, I don't need any additional information except permission to list your name
Will be exciting to hear results!
Great to hear re: Geelong Ed. I keep putting off advertising for some PhD students, but hopefully will do so soon, and hope to include ACDP in at least one (and Ina – as previously discussed pre-COVID!)

Cheers

Ali

From: Edward Annand (b) (6)
Date: Wednesday, 10 February 2021 at 1:12 pm
To: Alison Peel <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Re: Collaborator on a DP

Sounds wonderful Ali – when is the deadline?

JS is super close in sharing preliminary results from your cohort. You may be able to refer to the success of our work together in this regard while adhering to sensitivities of the more detailed info of course.

Eddie not directly involved in our work with JS and JS has set up a separate lab based in the WIMR but of-course JS collaborates with him closely and likely shares supervision with him still on some grad students. JS will be best placed to advise you on what's best RE his association with the funding application.

I'll be in Geelong from the second half of tthis year and hope to continue my CSIRO affiliation from there. Working in with ACDP is probably a good idea and there are other who we have worked with from their who might be well suited such as Kim Blasdell who has done viral work in rats in SE Asia.

Cheers

Ed

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

From: Alison Peel <(b) (6)
Date: Wednesday, 10 February 2021 at 14:02
To: Edward Annand <(b) (6) John-Sebastian Eden <(b) (6) Ina Smith <(b) (6)
Subject: Collaborator on a DP

Hi Ed, J-S and Ina,

I've recently been invited to join an ARC DP application that would utilise some of our CoV data. It's being led by GU palaeoecologist Julien Louys, with CIs including Paul Oliver (Queensland Museum/Griffith - biogeographer), Gilbert Price (UQ, palaeontologist) and Sue Hand (UNSW - palaeontologist). I've come on fairly late in the piece.
The DP aims to investigate bat and rat colonisation histories of Australia from fossil records and dating, and also look at estimating colonisation dates from improved resolution and dating in bat/rat phylogenies – all that is obviously outside of my expertise, but it will involve some fieldwork looking for bat fossils in Australia and Timor. The viral component is fairly minor, but comes in to try and see if bat viruses (henipaviruses, coronaviruses) in Australia are more closely related by geography or bat phylogeny, and whether phylogenetic splits match that of their hosts. Overall, the stated aim is to provide information on how Australia's natural barriers to colonisation influence risk of zoonotic viral incursions in the future, or how susceptible Australia's endemic wildlife might be to novel viruses circulating in human populations.
Anyway, as I only came on board a week or two ago (after our internal deadline) and the application was well developed, I haven't asked about adding additional CIs, but it would be great to list you as collaborators if you'd be happy to? If funded, there's a bit of funding for further CoV screening in there (P. scapulatus in Australia and other Pteropus in Timor). Let me know if you're happy for me to list you as a collaborator (And J-S, is Eddie involved too? Would I list him?)

Cheers

Ali
<CoV.RdRp.Aligned.phyml.edited.tree.pdf><Peel 2020 Coronaviruses in Australian bats.pdf>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 9 Feb 2021 23:26:14 +0000
To: Gay, Cyril; Feldmann, Heinrich (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Broder, Chris (USU-DoD); Ksiazek, Thomas (Galveston National Labortory-UT)
Subject: RE: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

Add Drs. Mike Holbrook and Jon Towner to the list of people contacted. Also reached out to Drs. Hensley and Cross,

Cheers,

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

From: Gay, Cyril <(b) (6)
Sent: Tuesday, February 9, 2021 12:05 PM
To: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) De wit, Emmie (NIH/NIAID) [E] <(b) (6) Broder, Chris (USU-DoD) <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Ksiazek, Thomas (Galveston National Labortory-UT) <(b) (6)
Subject: RE: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

Dear Colleagues,

Could we meet 30 minutes between 3 and 6 pm (EST) this Thursday, February 11th?

Please find attached our worksheet. We have identified 17 candidates, one is not eligible (not a U.S citizen), but only three have been contacted - Thank you Emmie!

Thank you for all your help and support.

Cyril

Cyril Gerard Gay, DVM, PhD
Senior National Program Leader
Animal Production and Protection
Agricultural Research Service
Tel: (b) (6); e-mail (b) (6)
Website: https://www.ars.usda.gov/

USDA United States Department of Agriculture
Agricultural Research Service

From: Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6)
Sent: Friday, February 5, 2021 6:05 PM
To: De wit, Emmie (NIH/NIAID) [E] <(b) (6) Gay, Cyril <(b) (6) Broder, Chris (USU-DoD) <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Ksiazek, Thomas (Galveston National Labortory-UT) <(b) (6)
Subject: RE: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

Just three more names.

From: De wit, Emmie (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, February 4, 2021 12:52 PM
To: Gay, Cyril <(b) (6) Broder, Chris (USU-DoD) <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Ksiazek, Thomas (Galveston National Labortory-UT) <(b) (6)
Subject: RE: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

A few additions

From: Gay, Cyril <(b) (6)
Sent: Thursday, February 4, 2021 11:54 AM
To: Broder, Chris (USU-DoD) (b) (6); De wit, Emmie (NIH/NIAID) [E] <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Ksiazek, Thomas (Galveston National Labortory-UT) <(b) (6)
Subject: RE: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

Dear Colleagues,

I started a work sheet with list of candidates - thanks Vincent for providing this initial list. Please add additional candidates and send it back to me. We need volunteers to contact these candidates – see Excel sheet.

I will have a meeting with those of you that are available this afternoon, and meet with the rest of you when you are ready. It may be good to have a group meeting once all the candidates are identified.

Thank you.

Cyril

From: Gay, Cyril
Sent: Wednesday, February 3, 2021 2:03 PM
To: Broder, Christopher <(b) (6) (b) (6) (b) (6); Munster, Vincent (NIH/NIAID) [E] <(b) (6) (b) (6)
Subject: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee
Importance: High

Dear colleagues,

Thank you so much for accepting to help ARS with this project. Unfortunately USDA-ARS provides very short timelines for filling positions – as you may have seen from the job announcement the deadline for applying for this position is March 1st, so we need to move quickly.

https://www.usajobs.gov/GetJob/ViewDetails/590498300

I will hold a 30 minutes zoom conference tomorrow Thursday at 3 pm (EST) to share with you what the responsibilities of an RL is at ARS, and in particular NBAF. I realize some of you may not be available on such short notice so I will reach out to you again on Monday if you can't make it but please let me know of a good time to call you.

We have three things to accomplish for this project:

1. Identify potential qualified candidates – please send me names, title, and affiliation of candidates and I will start a list.
2. I need you to contact the potential candidate and entice them to apply.
3. I need you to verify that they have submitted their application.

I will explain further when we talk. Here is the zoom link for our meeting tomorrow: https://www.zoomgov.com/j(b) (6)

Thank you!

Cyril

Cyril Gerard Gay, DVM, PhD
Senior National Program Leader
Animal Production and Protection
Agricultural Research Service
Tel: (b) (6); e-mail (b) (6)
Website: https://www.ars.usda.gov/
USDA United States Department of Agriculture
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From: Gay, Cyril
Sent: Thursday, January 28, 2021 6:08 PM
To: Broder, Christopher <(b) (6) Korch, George W. (CTR) <(b) (6) (b) (6) (b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee
Importance: High

Dear Chris, George, Emmie, Heinz, and Vincent,

I was wondering if you could help me recruiting candidates for the subject position at NBAF? Specifically, I've been asked to lead a search committee and I would like to invite you to be on the committee. We've had a hard time so far recruiting candidates for NBAF and we want to make sure the job announcement below will result in some good scientists with experience working in a BSK4 lab.

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The research at the ZEDRU at NBAF will involve studies on the pathogen-vector-host interrelationships of zoonotic and emerging BSL-4 diseases such as Crimean Congo Hemorrhagic Fever (CCHF) and Nipah Virus, and potentially other emerging or zoonotic diseases.

As you know, NBAF (National Agro and Biodefense Facility) is our $1.4 billion facility that will give USDA for the first time the ability to research BSL4 agents. I don't think serving on the committee will take much of your time. I anticipate 2-3 zoom meetings at the most and for you to contact directly the scientists we identify as potential candidates. Of course, some of you may want to apply as well, seriously!

If for some reason you can't help me on the search committee, could I ask you to at least send the announcement withing your BSL4 network? As you know, this is a select agent-regulated facility and the applicants must be U.S citizens and will have to obtain security clearance.

Thank you so much gentlemen for considering this request.

Cyril

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Sent: Tue, 9 Feb 2021 21:57:23 +0000
To: Feldmann, Heinrich (NIH/NIAID) [E]; Gay, Cyril; De wit, Emmie (NIH/NIAID) [E]; Broder, Chris (USU-DoD); Ksiazek, Thomas (Galveston National Labortory-UT)
Subject: RE: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

Same here

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

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Fine with me.

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Senior National Program Leader
Animal Production and Protection
Agricultural Research Service
Tel: (b) (6); e-mail (b) (6)
Website: https://www.ars.usda.gov/

From: Broder, Christopher
Sent: Mon, 8 Feb 2021 13:13:45 -0500
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Cara Brook; Hector Aguilar-Carreno; Laing, Eric; Amy Kistler; (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F]; Alison Peel; Plowright, Raina; Moushimi Amaya; Yan, Lianying
Subject: Re: Madagascar henipavirus

We just got the genes for F and G in. Moushimi will attempt a rCedV chimera, but Linda is also making sGtet and sF

When the first batch of proteins are available we will make PC rabbit sera for G.

Hector and I have been going back and forth on this. We would like to see some fusion data. MojV has been
a real weird one, as Benhur showed some time ago. Sofia had essentially the same data at that time as well
but she focused on characterizing the MojV G and F more, and expand those findings.

paper in review now, but I am waiting to see if we can get some nsEM on the new proteins in that paper.

Based on the tables, I am guessing there is good chance your new virus is going to be similar to the MojV issues.
But we hope not !

chris

On Mon, Feb 8, 2021 at 12:52 PM Munster, Vincent (NIH/NIAID) [E]
<(b) (6) wrote:

Easy one would be to make some control sera and run it through eric's Luminex again.

The phylogeny is still a bit complicated with the large bat paramyxo's as there are very little full genomes, and they are very divergent. One thing one could do look at the withing genus variation e.g. with the morbilliviruses and more phenotypic descriptions (like receptor usage). In the end phylogeny is always a moving field.

Cheers,

Vincent Munster, PhD

Chief Virus Ecology Section

Rocky Mountain Laboratories

NIAID/NIH

From: Cara Brook <(b) (6)>
Sent: Monday, February 8, 2021 10:44 AM
To: Hector Aguilar-Carreno <(b) (6)>; Laing, Eric <(b) (6)>; Broder, Chris (USU-DoD) <(b) (6)>
Cc: Amy Kistler <(b) (6)>; (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)>; Alison Peel <(b) (6)>; Plowright, Raina <(b) (6)>; Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Subject: Re: Madagascar henipavirus

Hi Hector,

Thanks so much for this reply. This is all very helpful. I am adding Chris Broder and Eric Laing into this email chain as well--Chris and Eric, apologies, as I should have listed you on the first one, but I am reattaching the trees listed below based on full genome, F, G, and L for the Madagascar henipavirus so you won't miss anything. See below for comments from Hector about F and G identity and whether we think this sequence is the same virus that you all detected in Luminex so many years ago.

A few points of follow-up:

1. We have new serum coming in to Berkeley soon from our 2018-2020 sampling--we are still fighting through Malagasy exports but the export has to be out of the country prior to April 16 and hopefully even sooner. The old serum samples (2013-2016 sampling) were collected in many aliquots, and there are some leftover. However, they are in Singapore currently with Linfa's group, and they were going to run VirScan on them before everyone's priorities shifted due to COVID. We clearly should have kept them here (sorry, Chris!) but so it goes. It is possible to get them back if really needed, but I think it

might make more sense to focus on the new ones, which have never been thawed or refrozen and see how they do on the Luminex panel in the months ahead.
2. I am also trying to add the original urine samples to this export because we are running out of RNA in experiments to fill the gap in the genome and because -- to Vincent's point -- this presents opportunities for virus isolation. I am not sure we will get these out before April 16 but I will try.
3. If Vincent or Kwe have thoughts on the L-gene divergence when vs. the substantial identity with F and G, I would love to hear them.

Thanks all! Excited to follow this mystery as it unfolds.

Cheers,
Cara

On Mon, Feb 8, 2021 at 3:28 AM Hector Aguilar-Carreno <[redacted] (b) (6) wrote:

Hi Cara,

I agree that this is all very exciting. Here are my thoughts, for what they are worth:

1. Our previous work shows that bats of this species are seropositive to both HeV and NiV F and G using Chris Broder's Luminex, with a minority of animals also seropositive to CedPV-G. The highest MFI observed for this species was to NiV-G with a seroprevalence of ~24%. From what you see of the F and G sequences, do you think this is the same virus we observed in the serology?

It is possible, but uncertain to assess one way or the other. Henipavirus G is typically more immunogenic that henipavirus F, so by definition you will likely find more serology corresponding to the Gs than to the Fs. In my opinion it will be difficult to assess whether the serology of these animals corresponds to this virus. However, if you still have sera, one thing we can do is test such sera for neutralizing antibodies against our pseudotyped virions that contain G and F from NiV, HeV, CedV, MojV, and MadV (this latter one we are setting up now). Luminex tell you Ab binding, whereas this tells you neutralizing antibodies, which may give you a larger clue.

2. In addition to Kwe's phylogeny, I also looked at the L-gene sequence of our virus and found it very divergent from the henipas. Are there F and G sequences available for these other paramyxos that it clusters with by L? I could not find any F or G for the accession numbers from Kwe's tree for on GenBank, but I wondered about the RML isolates.

I have no information on the comparison between G/F and L, but my guess is that this will highly depend on the portion of the L sequence that is used for comparison, as some portions will be more conserved than others. Vincent may have a greater insight here?

We hope to complete some of the fusion and receptor-binding studies with several cell lines. Depending on how this goes in the next month or so, we plan to engage in receptor identification. That will be exciting if we can determine it with a good level of certainty.

All the best,

Hector

Hector Aguilar-Carreno
Associate Professor
Microbiology and Immunology
College of Veterinary Medicine
Cornell University
Office: (b) (6)

From: Cara Brook < (b) (6)
Sent: Sunday, February 7, 2021 11:51 PM
To: Amy Kistler < (b) (6) (b) (6)
< (b) (6) Hector Aguilar-Carreno < (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] < (b) (6) Alison Peel < (b) (6)
Plowright, Raina < (b) (6) Munster, Vincent (NIH/NIAID) [E]
< (b) (6)
Subject: Madagascar henipavirus

Hi all,

I hope all is well with you! Great job to those who presented to DARPA last week--thanks, Ali, for summarizing the Madagascar data.

I wanted to check in re: Madagascar henipavirus since there seem to be a few divergent lines of research going on simultaneously, and I thought it would be helpful to synthesize the current state of the work. Attached here I've included a full genome phylogeny of paramyxoviruses as well as F and G protein phylogenies of the same set of paramyxos, all including the largest 12kb contig of our Madagascar virus, which clusters among the henipaviruses.

Kwe called last week about the other attached phylogeny here which is an L-gene phylogeny that shows the Madagascar virus clustering among these henipa-adjacent viruses, but this is based on only a ~400bp segment with no full genome reference sequences in the clade.

Hector also shared this table of F and G protein identity, which fits with the F, G, and full genome phylogenies attached here:

% G Protein Identity

	NiV	HeV	KumV	CedV	MadV	MojV
NiV	100	79	28	33	23	23
HeV	90	100	29	31	21	22
KumV	55	55	100	28	22	20
CedV	45	47	42	100	25	20
MadV	44	43	45	41	100	22
MojV	43	44	44	36	42	100

% F Protein Identity

Dr. Amy Kistler and Gloria Castaneda (cc'ed) at the Chan Zuckerberg Biohub are currently running a suite of amplification experiments on our remaining RNA to try to piece together the full genome of the virus. We have three contigs of, respectively, 12kb, 2kb, and 2kb and are trying to fill in the gaps, though it is possible that there are multiple paramyxos in the sample, which may complicate things.

I am not a henipavirus phylogeneticist by training, so I was wondering the following, mostly from Hector:

1. Our previous work shows that bats of this species are seropositive to both HeV and NiV F and G using Chris Broder's Luminex, with a minority of animals also seropositive to CedPV-G. The highest MFI observed for this species was to NiV-G with a

seroprevalence of ~24%. From what you see of the F and G sequences, do you think this is the same virus we observed in the serology?

2. In addition to Kwe's phylogeny, I also looked at the L-gene sequence of our virus and found it very divergent from the henipas. Are there F and G sequences available for these other paramyxos that it clusters with by L? I could not find any F or G for the accession numbers from Kwe's tree for on GenBank, but I wondered about the RML isolates.

Thanks much! All very exciting

Cheers,
Cara

--
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: (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: Plowright, Raina
Sent: Fri, 5 Feb 2021 21:45:09 +0000
To: Hudson, P; LaTrielle, Sara; Jamie Lloyd-Smith
Cc: Schountz, Tony; Hector Aguilar; Manuel Ruiz; Emily Gurley; Munster, Vincent (NIH/NIAID) [E]
Subject: Re: NEW TIMES Re: [External] - Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

That was surprisingly productive with Monica – she suggests that we put forward a P01 program proposal. She will introduce us to a relevant program officer.
And for Tracey Goldstein – they want us to give a webinar on our work and we may have an opportunity to shape PREDICT 2.

From: Hudson, P <(b) (6)
Date: Friday, February 5, 2021 at 1:43 PM
To: LaTrielle, Sara <sara.(b) (6) Plowright, Raina <(b) (6) Jamie Lloyd-Smith <(b) (6)
Cc: Schountz,Tony <(b) (6) Hector Aguilar <(b) (6) Manuel Ruiz <(b) (6) Emily Gurley <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: NEW TIMES Re: [External] - Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

Never thought that speed dating was like that – and not your fault Sara
They should respect people's time

P

Peter Hudson FRS
Willaman Professor of Biology
Adjunct Professor at Nelson Mandela African Institute – Arusha
A co-hire of The Huck institutes & The Institutes of Energy & The Environment
229C Millennium Science Complex
Penn State University
(O) (b) (6)
(C) (b) (6)

Websites:
Science: https://www.huck.psu.edu/people/peter-hudson
Photography: https://www.peterhudsonphotos.com
Conservation: http://www.pawstrails.com

Instagram: https://www.instagram.com/peter_hudson018/

Zoom: https://psu.zoom.us/my/peterhudson

From: LaTrielle, Sara <(b) (6)
Date: Friday, February 5, 2021 at 3:37 PM
To: Plowright, Raina <(b) (6) Jamie Lloyd-Smith <(b) (6)
Cc: Schountz,Tony <(b) (6) Hudson, P <(b) (6) Hector Aguilar <(b) (6) Manuel Ruiz <(b) (6) Emily Gurley <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: NEW TIMES Re: [External] - Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

It's like how one imagines 15 min 'speed dating' .... some show up on time and some don't. □ In all seriousness... sorry for the time changes. grrr

Speaking of- we just added another 'date' .... NIH/Monica at 4:15EST. (To thank her and check in with any possible opportunities at NIH).

From: Plowright, Raina <(b) (6)
Sent: Friday, February 5, 2021 1:33 PM
To: Jamie Lloyd-Smith <(b) (6) LaTrielle, Sara <(b) (6)
Cc: Schountz,Tony <(b) (6) Hudson, Peter John <(b) (6) Hector Aguilar <(b) (6) Manuel Ruiz <(b) (6) Emily Gurley <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: NEW TIMES Re: [External] - Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

Sorry Jamie. Specifically asked for the previous time bc of your schedule and others. It's a real shame. Reading Predict 2 now and there may be real opportunities for us there....if we want them!

From: Jamie Lloyd-Smith <(b) (6)
Date: Friday, February 5, 2021 at 1:24 PM
To: LaTrielle, Sara <(b) (6)
Cc: Schountz,Tony <(b) (6) Plowright, Raina <(b) (6) Hudson, Peter John <(b) (6) Hector Aguilar <(b) (6) Manuel Ruiz <(b) (6) Emily Gurley <(b) (6) Munster, Vincent (NIH/NIAID) [E]

<[redacted] (b) (6)
Subject: Re: NEW TIMES Re: [External] - Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

Same here. I'm now conflicted for the USAID mtg. :(

Let us know how it goes.

Jamie

On Fri, Feb 5, 2021 at 11:51 AM LaTrielle, Sara <[redacted] (b) (6) wrote:
Apologies- not sure why the times changed.

Whoever can make it works just fine- all good. Pete and Raina will be on both.

Sara

From: Schountz,Tony <[redacted] (b) (6)
Sent: Friday, February 5, 2021 12:44 PM
To: LaTrielle, Sara <[redacted] (b) (6)
Cc: Plowright, Raina <[redacted] (b) (6) Hudson, Peter John <[redacted] (b) (6) Jamie Lloyd-Smith <[redacted] (b) (6) Hector Aguilar <[redacted] (b) (6) Manuel Ruiz <[redacted] (b) (6) Emily Gurley <[redacted] (b) (6) Schountz,Tony <[redacted] (b) (6) Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Subject: Re: NEW TIMES Re: [External] - Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

Ugh. I had moved a previously scheduled meeting to this time so I could be on the call with Tracy and Rob. I cannot change it again, unfortunately.

—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
[redacted] (b) (6)
[redacted] (b) (6)

On Feb 5, 2021, at 12:22 PM, LaTrielle, Sara <[redacted] (b) (6) wrote:

All,

Amended (slightly) times to meet with transition partners:
FBI 3:45pm EST
USAID 4pm EST

Join the main call and they will give instructions then.

Sara

On Fri, Feb 5, 2021 at 11:10 AM LaTrielle, Sara <(b) (6) wrote:
Today: If you would like to join, please do.

These are very quick (15 mins) break-out sessions. I put a few of you in both meetings, as I see you on the ZOOM- but you are under no obligation to attend- they just needed names to put Zoom rooms together.

3:30pm EST USAID (Tracy Goldstein)
3:45pm EST FBI (Rob Bull)

*Manual- I will sign you up for both.

Best,
Sara

From: LaTrielle, Sara <(b) (6)
Sent: Thursday, February 4, 2021 4:05 PM
To: Renee Besanson <(b) (6) Plowright, Raina <(b) (6)
Cc: (b) (6); (b) (6); (b) (6); (b) (6); Peter J. Hudson <(b) (6)
Subject: Re: [External] - Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

Renee,

We don't have a full/complete tally just yet but thinking it will look like this for both: A few of these may be unavailable but for pre-grouping- best use this. Thanks!

USAID
Raina Plowright
Pete Hudson
Jamie Lloyd-Smith

Vincent Munster
Barbara Han
Hector Aguilar
Tony Schountz
Sara LaTrielle
Emily Gurley

Rob Bull/FBI
Raina Plowright
Pete Hudson
Emily Gurley
Barbara Han
Hector Aguilar
Tony Schountz
Sara LaTrielle

--
Dr. Barbara A. Han
Disease Ecologist
Cary Institute of Ecosystem Studies
Tel: (b) (6)
<Transition Partners Schedule_Feb. 5 (1).xlsx><ATPFile_CE6EEE48-3663-4393-AEBB-9A55F7C1723F.token>

--
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Phone: (b) (6)

https://www.eeb.ucla.edu/Faculty/lloydsmith/

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Lab: 4000 Terasaki Life Sciences Building

From: Plowright, Raina
Sent: Thu, 4 Feb 2021 18:31:18 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: LaTrielle, Sara
Subject: Re: Sign-up request: PREEMPT Transition Partners (one-on-one)

yep 1.30-2pm MT. I've requested that now.

On Feb 4, 2021, at 11:27 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

Should work too, again MT?
Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

From: Plowright, Raina <[redacted] (b) (6)
Sent: Thursday, February 4, 2021 11:16 AM
To: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)
Cc: LaTrielle, Sara <[redacted] (b) (6)
Subject: Re: Sign-up request: PREEMPT Transition Partners (one-on-one)
can u do 3.30-4pm

On Feb 4, 2021, at 11:08 AM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:
1:15 Mountain time? Can make that work, always happy to chat with Tracey
Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

From: Plowright, Raina <[redacted] (b) (6)
Sent: Thursday, February 4, 2021 11:04 AM
To: preempt <[redacted] (b) (6)
Cc: LaTrielle, Sara <[redacted] (b) (6)
Subject: Fwd: Sign-up request: PREEMPT Transition Partners (one-on-one)
Importance: High
I've signed us up to meet Rob Bull and the USAID folks. See times below. If you want to be on these calls but have a conflict, let Sara and I know asap.
Raina

Begin forwarded message:
From: Renee Besanson <[redacted] (b) (6)

Subject: Sign-up request: PREEMPT Transition Partners (one-on-one)
Date: February 4, 2021 at 10:40:57 AM MST
Cc: (b) (6) " (b) (6)
< (b) (6) (b) (6),
(b) (6), Renee Besanson < (b) (6)

Hello,

Are you interested in speaking with one of the Transition Partners tomorrow, for 10-15 minutes, during 3:15 pm – 4:45 pm time block? Please let me know who, from the Transition Partners below, you would like to meet with and if anyone else from your team should be included? Transition Partners available are:

FBI/NBFAC:
Robert Bull
Microsoft:
Ethan Jackson
USAID/Emerging Threats Division:
Padma Shetty and Tracey Goldstein
NGA:
Erik Scully and Tony Nguy-Robertson
More partners may be added as their schedules become available.

Your reply would be appreciated by 1:00 PM (EST) on February 5th but sooner is better.

Please let me know if you have any questions.

Thanks!

Renée A. Besanson
Senior Meeting Planner
Strategic Analysis, Inc.
Conference Services Division
(b) (6)

From: Plowright, Raina
Sent: Wed, 3 Feb 2021 21:15:40 +0000
To: Hector Aguilar-Carreno; Munster, Vincent (NIH/NIAID) [E]
Cc: (b) (6)
Subject: Re: Check slides on Box before 4.30pm ET, 2.30pm MT

I'll run the deck but I planned to reach out to you and Vincent and Jamie to see if you want to share for your section given its complexity. I'll email you all on a separate thread.

From: Hector Aguilar-Carreno <(b) (6)
Date: Wednesday, February 3, 2021 at 2:12 PM
To: Plowright, Raina <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: (b) (6) <(b) (6)
Subject: Re: Check slides on Box before 4.30pm ET, 2.30pm MT

Hi Raina,

This works for me.

Just curious if we will be all working from a single slide deck that you flip over, or if everyone will be showing their own slides from their computers. If course each has advantages and dissadvantages, but I wonder if we have decided one way or another.

Thank you!

Hector

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Wednesday, February 3, 2021 3:59 PM
To: Plowright, Raina <(b) (6)

Cc: (b) (6) <(b) (6)
Subject: Re: Check slides on Box before 4.30pm ET, 2.30pm MT

Works for me!

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

From: "Plowright, Raina" <(b) (6)
Reply-To: "Plowright, Raina" <(b) (6)
Date: Wednesday, February 3, 2021 at 1:51 PM
To: "Plowright, Raina" <(b) (6)
Cc: "(b) (6) <(b) (6)
Subject: Re: Check slides on Box before 4.30pm ET, 2.30pm MT

I just did a zoom check with the DARPA IT person and learned 2 really important things:

1. You must be **signed in to Zoom with a personal account so your full name shows in the waiting room.** They will only let you in if your name matches that on your registration. If you come in as 'PREEMPT' you wont get in.
2. They are **letting us share our screens**. So Although we have to send the talk today at COB EST, that is only a back up. They have already approved the talk and we can fiddle with slides for longer if needed.

I think it's best that I operate the slide deck, and you all tell me 'next slide'.

I've attached a screen grab of the timing. We must stick to our times, so I'll boot people off when they go over their time and I will try to give a 1 min warning so you can wrap up.

Raina

Presentation (75 min)

1. Raina intro — 2 min
2. Ali Field data collection — 15 min
3. Tony Immunology, metadata, and bat experiments — 5 min
4. Olivier mechanistic modeling — 10 min
5. G-P — 20 min
    1. Jamie Intro
    2. Hector G-P
    3. Jamie G-P modeling to transmission work
    4. Vincent SARS2 work
6. Hector HNV vaccination — 5 min
7. Peggy & Andy eco-countermeasure and models — 10 min
8. Barbara multiscale modeling — 5 min
9. Pete conclusion — 3 min

On Feb 3, 2021, at 1:10 PM, Plowright, Raina < (b) (6) wrote:

Hi everyone,
Can you check your slides in the Box folder > Research PREEMPT for PI's > Reporting > DARPA FEB 2021 ppt?
All slides should be in order now. I've gone through them in presentation mode to check for glitches and it looks good to me.
I'm still working on the intro and conclusion slides.
We will submit the slides at 4.30pm ET/ 2.30 MT.
Raina

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 3 Feb 2021 14:06:45 -0700
To: Cara Brook
Cc: Plowright, Raina; Kwe Claude, Yinda (NIH/NIAID) [F]; Louise Gibson; Alison Peel; LaTrielle, Sara; Olivier Restif; Emily Gurley; Clif McKee
Subject: Re: [EXT]: DARPA slides in box - Final checks and small updates in the morning by Cara and Kwe

Cool additional model system! Another potential fun step is make some pseudotypes with F and G and see if they enter human cells

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

From: Cara Brook <(b) (6)
Date: Wednesday, February 3, 2021 at 2:05 PM
To: "(b) (6) <(b) (6)
Cc: "Plowright, Raina" <(b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) Louise Gibson <(b) (6) Alison Peel <(b) (6) "LaTrielle, Sara" <(b) (6) Olivier Restif <(b) (6) Emily Gurley <egurley1@jhu.edu>, Clif McKee <(b) (6)
Subject: Re: [EXT]: DARPA slides in box - Final checks and small updates in the morning by Cara and Kwe

Mean 10% prevalence in urine samples, sometimes up to 20%.

Seroprevalence to Nipah-G in a different subset of samples (a few years ago) was also quite high (24%) which is why I assumed they were the same viruses... will send the F and G trees when I have them. Again, not for this presentation--I think we have plenty.

@ Raina, not sure if your last email was for me, but all slides are up-to-date. I manually edited #23 in the compiled deck this morning (it is perfect as is), and Kwe's new tree should be swapped in at #10.

On Wed, Feb 3, 2021 at 12:58 PM Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:
Its really cool though, any idea of the prevalence? Would be easy to generate a G-glycoprotein so you can do some Elisa's.

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

NIAID/NIH

From: "Plowright, Raina" <(b) (6)
Date: Wednesday, February 3, 2021 at 1:57 PM
To: Cara Brook <(b) (6)
Cc: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6)
"(b) (6) <(b) (6) Louise Gibson
<(b) (6) Alison Peel <(b) (6) "LaTrielle, Sara"
<(b) (6) Olivier Restif <(b) (6) Emily Gurley
<(b) (6) Clif McKee (b) (6)
Subject: Re: [EXT]: DARPA slides in box - Final checks and small updates in the morning by Cara and Kwe

Thanks for all your work on this.
Can you send me a single slide (or two, if it is two slides) and tell me which one to replace and if you want to change the order?

On Feb 3, 2021, at 1:52 PM, Cara Brook <(b) (6) wrote:

Hi all,

Just following up to say that my phylogeny is a full genome one, which has it clustering with the henipas, though as Kwe says none of the other paramyxos have full genomes and thus could not be included in mine. Kwe's tree is just L gene.

These won't be in the presentation, but I'm making some F and G trees this afternoon, and our primers just arrived to fill the gap for our full genome. So we should hopefully be able to figure out where it falls soon. If not a henipa, it begs the question why we have Nipah seropositives, so important to look at the F and G trees too!

Cara

On Wed, Feb 3, 2021 at 12:46 PM Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
wrote:
Hi Ali,

It was a little more work than I thought. Just to note with you that we may not want to call the novel Madagascan sequence as a henipa for now (I had a quick call with Cara regarding this). In my phylogenetic tree it showed that it is a distantly related paramyxovirus with about ~50% amino acid sequence similarity with henipas. I have updated the slide in the presentation to this effect. However, this is very important because it might be the only paramyxo in this clade that we have near full genome. I also have the phylogeny attached.

Thanks

Kwe

From: Cara Brook <(b) (6)
Date: Wednesday, February 3, 2021 at 11:11 AM
To: "Plowright, Raina" (b) (6)
Cc: Louise Gibson <(b) (6) Alison Peel <(b) (6) "LaTrielle, Sara" <(b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) Olivier Restif <(b) (6) Emily Gurley <(b) (6) Clif McKee (b) (6)
Subject: Re: [EXT]: DARPA slides in box - Final checks and small updates in the morning by Cara and Kwe

Just a note that I made some edits to the seasonal prevalence slide. Most up-to-date version of the ppt is now "DARPA Feb 2021 Field teams report - NEAR FINAL-Cara-edits.pptx"

So I think we are just waiting on the phylogeny at this point.

Best,
Cara

On Wed, Feb 3, 2021 at 8:37 AM Plowright, Raina (b) (6) wrote:
The slides look excellent. Thank you all and especially Ali.
I'll look for Kwe's new slide and will place that at the end of the presentation alongside within spp phylogeographic…. see screen grab.
I changed the subtitle on the first slide as the original title said 1 HNV but below said 2. So new title is sufficiently vague to allow adjustments.
Raina
<image001.png>

On Feb 3, 2021, at 8:59 AM, Louise Gibson <(b) (6) wrote:

Hi Ali,
Totally understand why you just use RMH only. It's much more targeted and more successful, however we run the PAR PCR because it does pick up a wider range of paramyxoviruses (and the odd gem) such as rubulavirsues that RMH doesn't.
Using RMH-PCR we have detected:

- In the captive bats 10 distinct viral sequences (1 which is novel and 2 which were detected 4 years previously). Showing a large diversity and evidence of viral persistence in a much smaller population size (approx. 150 bats) than what is known.
- In the wild bats (only two batches analysed so far) 6 distinct viral sequences detected (3 which are novel).

Kwe has all our sequences.
Cheers,
Louise

From: Alison Peel <(b) (6)
Sent: 03 February 2021 15:37
To: Plowright, Raina (b) (6); LaTrielle, Sara <(b) (6)
Cc: Cara Brook <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Olivier Restif <(b) (6) Louise Gibson <(b) (6) Emily Gurley <(b) (6) Clif McKee <(b) (6)
Subject: [EXT]: DARPA slides in box - Final checks and small updates in the morning by Cara and Kwe

Hi all,

The field team slides are in the Box folder: DARPA FEB 2021 ppt/Field team updates/DARPA Feb 2021 Field teams report - NEAR FINAL.pptx

Kwe is finalising a phylogeny that will include Cara's Madagascar henipavirus (and maybe some rubulaviruses) – to replace the phylogeny in slide 3.
Some formatting notes for this change:

Please delete the old phylogeny, replace with the new one then Arrange>Send to back, and ensure the purple star is in the correct positioning alongside Nipah/Hendra.

Please Change the colour of the Madagascar bullet point heading with the colour selector so that it matches whatever point is chosen for that sequence in the new phylogeny.

Hopefully Kwe should be able to get this done first thing in the morning (thank you!!), so that Raina can grab the updated slides well in advance of the deadline to send to DARPA (before 3pm MT).

For everyone else – I've pimped up a couple of plots to help with visual explanations (e.g slides 9 and 10), though the original plots are still off to the right of the visible area of the slide if you want to change them back. Please also correct anything drastically wrong, and let me and Raina know if so.

E.g. Louise/Kwe I'm still not 100% sure I've got the numbers of viral detections/novel viral detections correct for Ghana. I meant to go back through all your original slides, but I've run out of time. Kwe said "Unfortunately not all sequences from GHA can be represented in one tree because they were screened using two different PCRs (PAR-PCR or RMH-PCR), each of which target different parts of the L-gene. I have chosen to include only sequences identified with the RMH-PCR because in our hands, this PCR is more sensitive and should normally detect all that are positive by PAR-PCR and not the reverse." Can you please edit the numbers if what I've got is underselling your detections?

Thanks everyone!

Nothing like cutting it down to the wire…. Sorry Raina and Sara for the added stress!
Raina – happy to chat further in the morning my time re: refining the narrative if you want.

Cheers

Ali

From: Plowright, Raina
Sent: Wed, 3 Feb 2021 20:27:37 +0000
To: Jamie Lloyd-Smith
Cc: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Pictures

Just did a zooom test with DARPA and the IT person said WE ARE SHARING OUR OWN SCREENS!!! So we actually can take more time. But it would be nice to be done, so send me your new deck when you can.

On Feb 3, 2021, at 1:11 PM, Jamie Lloyd-Smith <(b) (6)> wrote:

Epic experiment!!

Re where to include, I think the best spot would be a second slide in Vincent's 'on-going and future work' section. Even just to show the picture and say big things are coming... it def does complement the points I'm ending on about dissecting the airborne route of transmission. Cool!

btw Raina I'm working on crunching down my slides... will send... it's a bugger to squeeze in all the overall framing + some substance into my 7-8 minutes.

j

On Wed, Feb 3, 2021 at 11:03 AM Plowright, Raina <(b) (6)> wrote:
OK, Jamie, let me know if you want me to add it to any particular slide, or as a separate slide. I agree, it really looks amazing.

On Feb 3, 2021, at 11:56 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6)> wrote:

It would drive home to h-to-h part

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

From: Plowright, Raina <(b) (6)>
Sent: Wednesday, February 3, 2021 11:53 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Cc: (b) (6)
Subject: Re: Pictures

wow thats impressive!
do you want me to insert this anywhere in the presentation?

On Feb 3, 2021, at 11:46 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6)> wrote:

Massive experiments outlined, not really DARPA (as they actually don't pay for anything), but we'll make them think it is ☺

These are the directional flow experiments with controlled airflow with distances ranging from ~10 cm, 1 ft and 6 ft

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

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Sent: Wednesday, February 3, 2021 11:43 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Subject: Pictures

<IMG_7944.JPG>

<IMG_7945.JPG>

--
James O. Lloyd-Smith

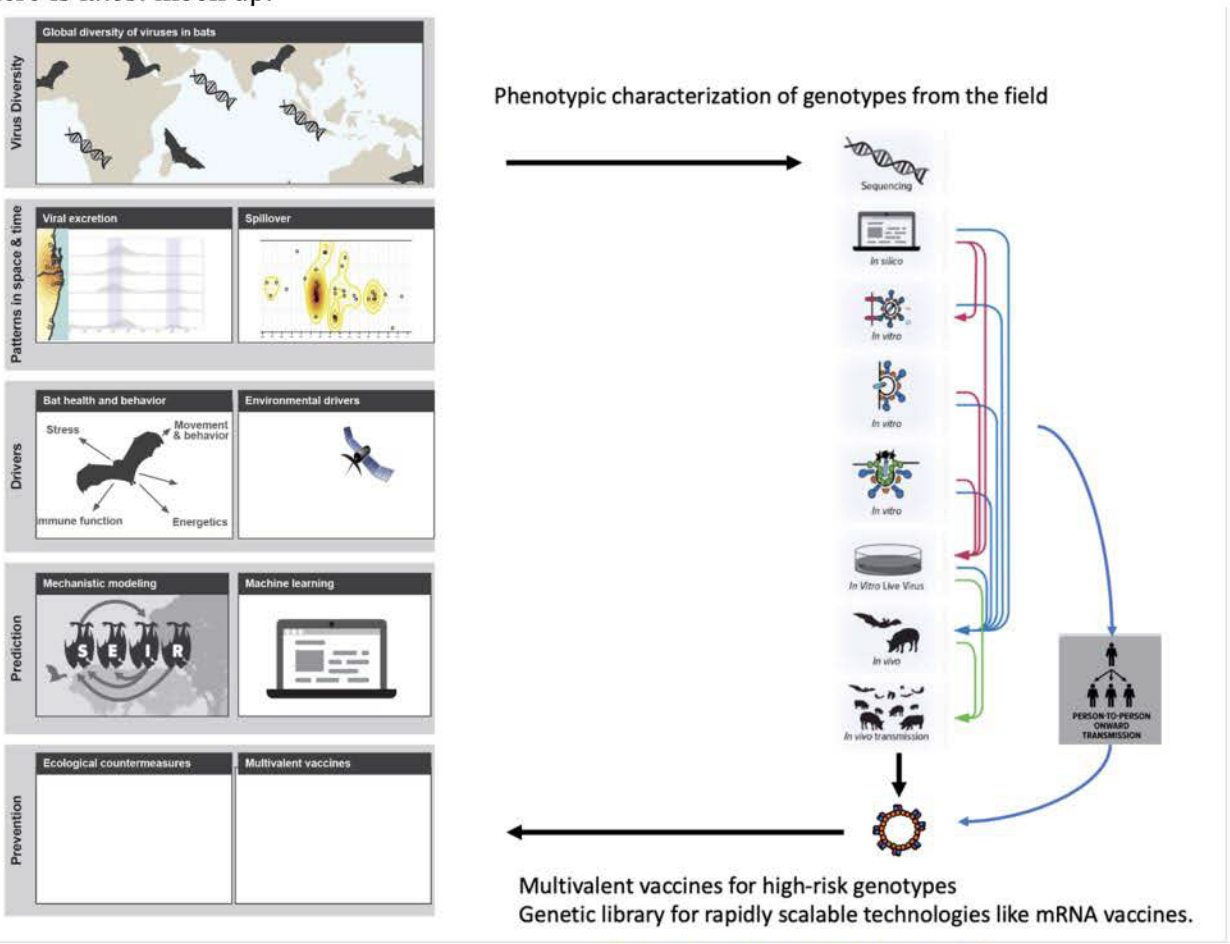
Professor
Department of Ecology & Evolutionary Biology
Department of Biomathematics
University of California, Los Angeles
610 Charles E Young Dr South
Box 723905
Los Angeles, CA 90095-7239

Phone: (b) (6)

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

From: Plowright, Raina
Sent: Wed, 3 Feb 2021 19:34:57 +0000
To: Peter J. Hudson
Cc: Munster, Vincent (NIH/NIAID) [E]; LaTrielle, Sara; Hector Aguilar-Carreno; Barbara Han; (b) (6)
Subject: Re: CLosed-door mtg tomorrow: (b) (6)

Here is latest mock up.



On Feb 3, 2021, at 12:26 PM, Raina Plowright < (b) (6) wrote:

great for future projects. this figure is trying to describe the current project only.

On Feb 3, 2021, at 12:19 PM, Hudson, P < (b) (6) wrote:

At the very top of the right hand column I would include something on immunology surveillance in parallel with sequencing –
Call it antiviral antibody profiling ?

P

Peter Hudson FRS
Willaman Professor of Biology
Adjunct Professor at Nelson Mandela African Institute – Arusha
A co-hire of The Huck institutes & The Institutes of Energy & The Environment
229C Millennium Science Complex
Penn State University
(O) (b) (6)
(C) (b) (6)

Websites:
Science: https://www.huck.psu.edu/people/peter-hudson
Photography: https://www.peterhudsonphotos.com
Conservation: http://www.pawstrails.com

Instagram: https://www.instagram.com/peter_hudson018/

Zoom: https://psu.zoom.us/my/peterhudson

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Wednesday, February 3, 2021 at 1:55 PM
To: Plowright, Raina <(b) (6)
Cc: LaTrielle, Sara <(b) (6) Hudson, P <(b) (6) Hector Aguilar-Carreno <(b) (6) Barbara Han <(b) (6) (b) (6) <(b) (6)
Subject: RE: CLosed-door mtg tomorrow: (b) (6)

I think conceptually its great, I would merge in next-gen technologies in addition to multivalent vaccines. E.g. provide a genetic library which can used in rapid scalable technologies like mRNA vaccines.

Btw, totally agree, for the h-to-h just use one of the figures Jamie has in his presentation?

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

From: Plowright, Raina <(b) (6)
Sent: Wednesday, February 3, 2021 11:49 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: LaTrielle, Sara <(b) (6) Peter J. Hudson <(b) (6) Hector Aguilar-Carreno <(b) (6) Barbara Han <(b) (6) (b) (6)
Subject: Re: CLosed-door mtg tomorrow: (b) (6)

I'm mocking up a visual to describe the overall project and would love some input on the G-P section. Can you look at the first slide here? I was hoping to do this for our talk but its more likely a longer term project!

—especially like to know: what visuals (e.g. for h2h, probably not kosher to have monkeys and hamsters on public places like our website), and what wording?

See hand drawn mockup on LH side. and second slide shows the overall graphic mock up. Love feedback on any and all of it of course.

On Feb 3, 2021, at 8:22 AM, Plowright, Raina (b) (6) wrote:

Please note, they just cancelled this meeting and will reschedule next week. Enjoy your extra hour today.
Think about any issues we may want to raise one-on-one with (b) (6) and team next week.
Best,
Raina

On Feb 2, 2021, at 1:00 PM, Munster, Vincent (NIH/NIAID) [E] (b) (6) wrote:

Yes, I can attend but haven't seen the invite,

Cheers,

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

From: LaTrielle, Sara < (b) (6)
Sent: Tuesday, February 2, 2021 9:43 AM
To: Plowright, Raina < (b) (6) Hudson, P < (b) (6) Hector Aguilar-Carreno < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Barbara

Han < (b) (6) (b) (6)
Subject: CLosed-door mtg tomorrow: (b) (6)

All,

Per previous emails, Raina/Pete kindly request your presence/participation during tomorrow's MSU's 'closed-door' session which I have just re-sent the invite for, forwarded from DARPA. Please rsvp to Raina/me so I know who will be attending.

Meeting time is 11am-12pm MST with these call-in details:

As previously mentioned, this is a rather informal meeting where we address their technical queries, solve any issues, discuss challenges, and/or look to the future. We can discuss Phase l and ll here. Show our excitement- woot woot!

Raina will provide guidance on a few points we should 'hit on'.

Slack page for internal discussions/ before/during the call here
(b) (6)

Sara

From: Plowright, Raina
Sent: Wed, 3 Feb 2021 18:48:43 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: LaTrielle, Sara; Peter J. Hudson; Hector Aguilar-Carreno; Barbara Han; (b) (6)
Subject: Re: CLosed-door mtg tomorrow: (b) (6)
Attachments: GP DARPA overview graphic.pptx

I'm mocking up a visual to describe the overall project and would love some input on the G-P section. Can you look at the first slide here? I was hoping to do this for our talk but its more likely a longer term project!

—especially like to know: what visuals (e.g. for h2h, probably not kosher to have monkeys and hamsters on public places like our website), and what wording?

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Think about any issues we may want to raise one-on-one with (b) (6) and team next week.
Best,
Raina

On Feb 2, 2021, at 1:00 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Yes, I can attend but haven't seen the invite,

Cheers,

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

From: LaTrielle, Sara <(b) (6)
Sent: Tuesday, February 2, 2021 9:43 AM
To: Plowright, Raina (b) (6); Hudson, P <(b) (6) Hector Aguilar-Carreno <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Barbara Han <(b) (6) (b) (6)
Subject: CLosed-door mtg tomorrow: (b) (6)

All,

Per previous emails, Raina/Pete kindly request your presence/participation during tomorrow's MSU's 'closed-door' session which I have just re-sent the invite for, forwarded from DARPA. Please rsvp to Raina/me so I know who will be attending.

Meeting time is 11am-12pm MST with these call-in details:

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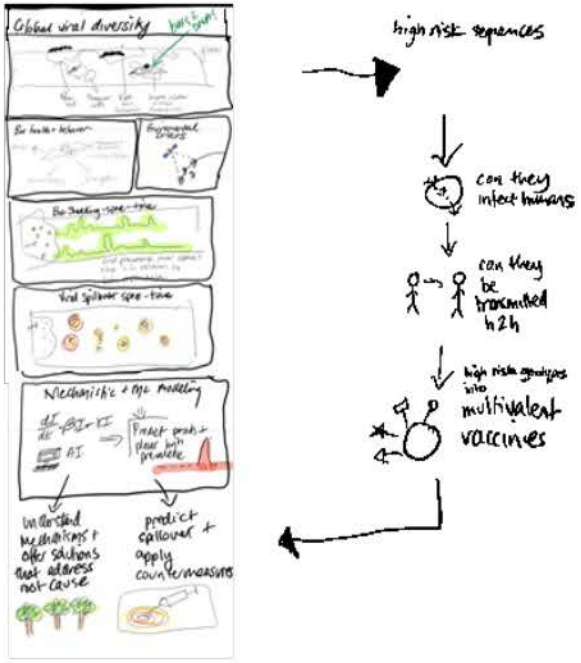
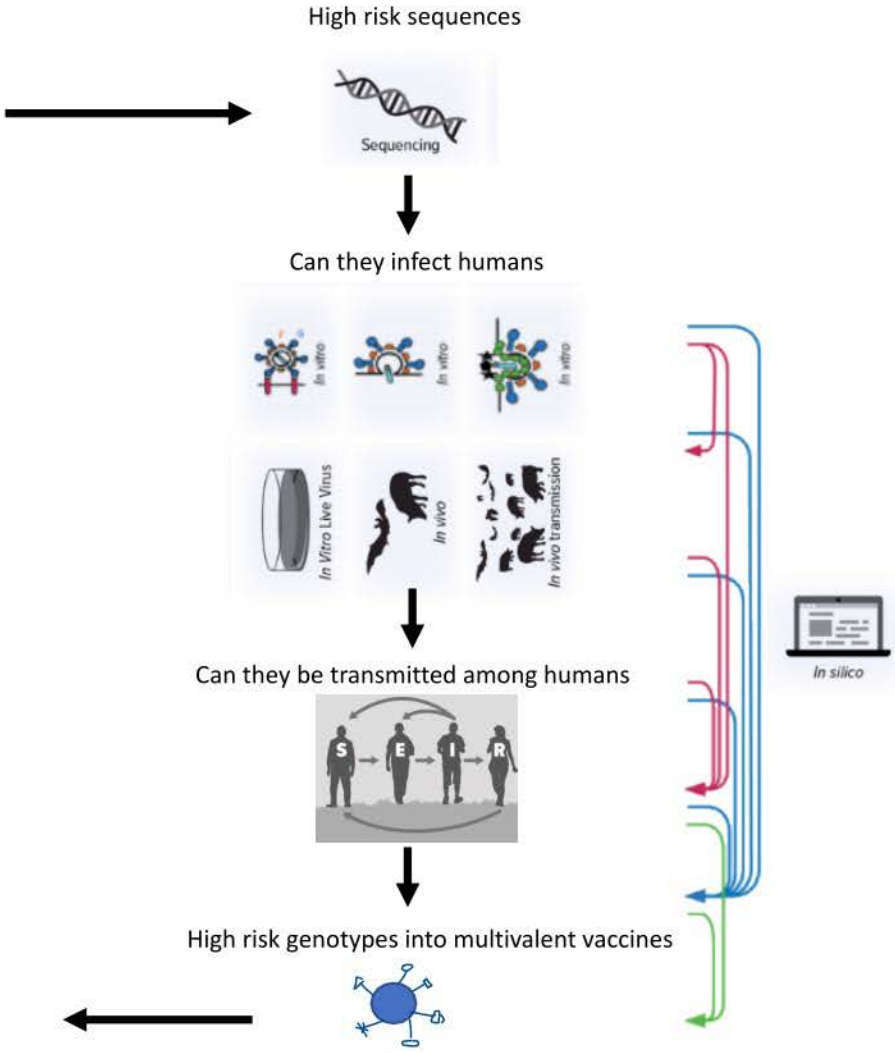
Raina will provide guidance on a few points we should 'hit on'.

Slack page for internal discussions/ before/during the call here
(b) (6)

Sara


Global viral diversity
high risk sequences
can they infect humans
can they be transmitted h2h
multivalent vaccines
predict spillover + apply counte/measures


High risk sequences
Sequencing
Can they infect humans
In vitro
In vitro
In vitro
In Vitro Live Virus
In vivo
In vivo transmission
Can they be transmitted among humans
S
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High risk genotypes into multivalent vaccines
In silico

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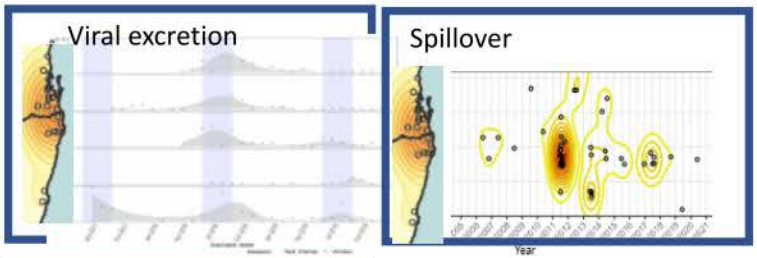
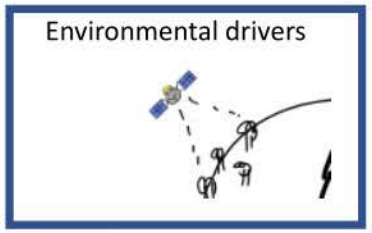
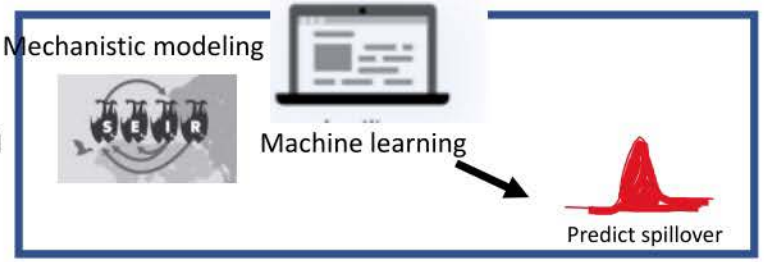
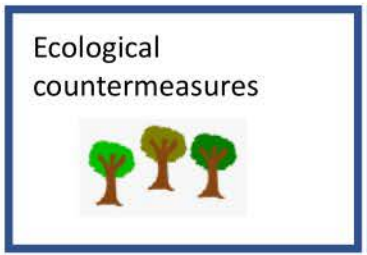
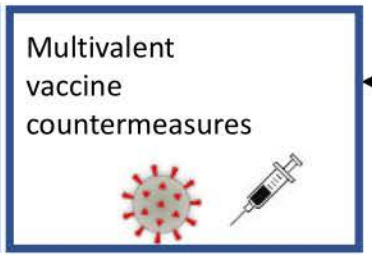
Global diversity of viruses in bats

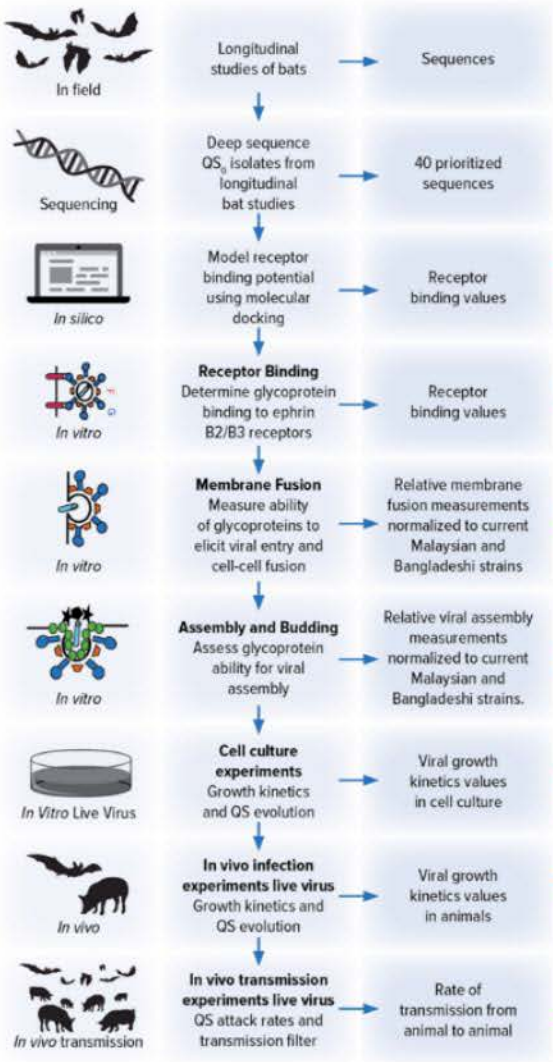




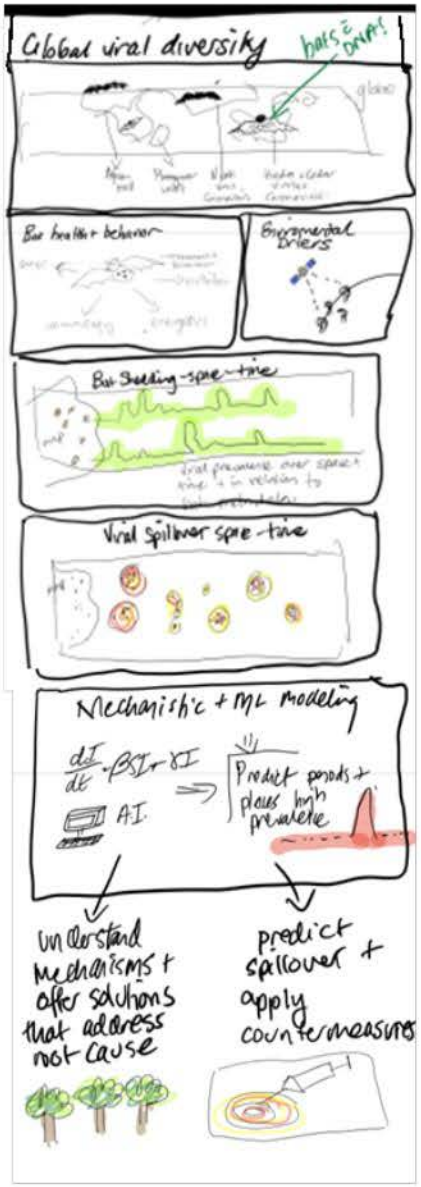


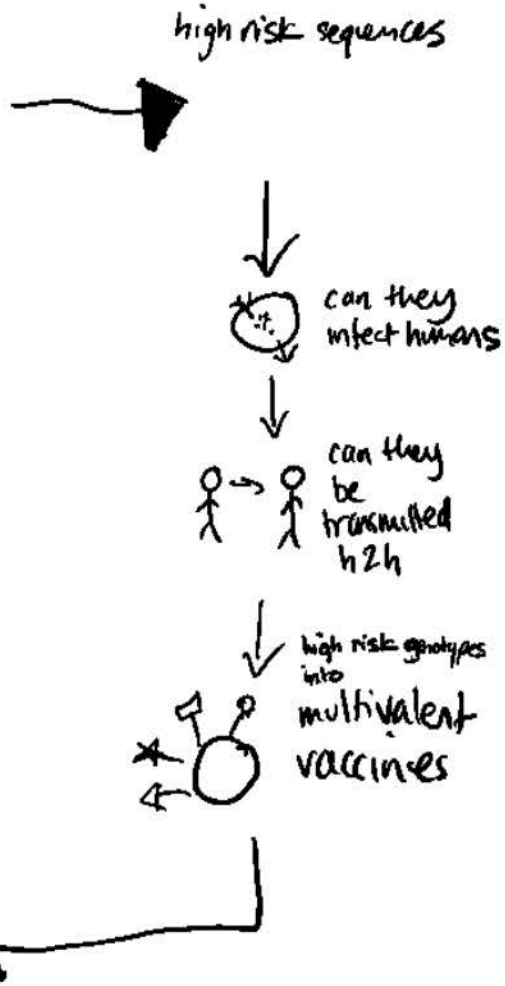






Multivalent vaccines


Global viral diversity
Bat health + behavior
Environmental Drivers
Bat Shedding - space - time
Viral spillover space - time
Mechanistic + ML modeling
AI
Predict periods + places high prevalence
understand mechanisms + offer solutions that address root cause
predict spillover + apply countermeasures


high risk sequences
can they infect humans
can they be transmitted h2h
high risk genotypes into multivalent vaccines

From: Plowright, Raina
Sent: Tue, 2 Feb 2021 20:09:56 +0000
To: Hector Aguilar-Carreno; LaTrielle, Sara; Munster, Vincent (NIH/NIAID) [E]; Jamie Lloyd-Smith
Cc: Sara LaTrielle
Subject: Re: Slides for DARPA PI meeting

Thanks. I replaced your slides in the presentation.

From: Hector Aguilar-Carreno < (b) (6)
Date: Tuesday, February 2, 2021 at 12:31 PM
To: LaTrielle, Sara < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Jamie Lloyd-Smith < (b) (6)
Cc: Plowright, Raina < (b) (6) Sara LaTrielle < (b) (6)
Subject: Re: Slides for DARPA PI meeting

Raina,

I made some modifications to several of my slides for the G-P part of the DARPA presentation, including but not limited to the order of some of the slides. Could you please replace the older ones for this set? Sorry for the last minute. We had a big snow storm this morning that slowed me down. I hope there is still time and it is easy enough to switch these slides.

Thank you very much in advance!!!!

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: LaTrielle, Sara < (b) (6)
Sent: Friday, January 29, 2021 1:23 PM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Jamie Lloyd-Smith < (b) (6) Hector Aguilar-Carreno < (b) (6)

Cc: Plowright, Raina <(b) (6) Sara LaTrielle <(b) (6)
Subject: Re: Slides for DARPA PI meeting

Thank you.

Sara LaTrielle

Program Manager
PREEMPT Project
Montana State University

(b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 28, 2021 1:41 PM
To: Jamie Lloyd-Smith <(b) (6) Hector Aguilar-Carreno <(b) (6)
Cc: Plowright, Raina <(b) (6) LaTrielle, Sara
<(b) (6) Sara LaTrielle <(b) (6)
Subject: RE: Slides for DARPA PI meeting

Added my slides to Jamie's

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

From: Jamie Lloyd-Smith <(b) (6)
Sent: Thursday, January 28, 2021 12:18 AM
To: Hector Aguilar-Carreno <(b) (6)
Cc: Plowright, Raina <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6) LaTrielle, Sara <(b) (6) Sara LaTrielle
<(b) (6)
Subject: Re: Slides for DARPA PI meeting

Hi everyone,

Here are my slides. There are a lot, but I plan to skim through the HNV ones very fast, and then there are a lot of multi-slide animations. Still, I will make cuts if I can't present in the ~8 minutes our team agreed on.

I didn't add in Hector's slides yet, because I wasn't sure exactly where he wants them. Vincent, I tried to tee up the experimental work at the end.

Hope this does the trick. I'll put in the Box folder as well. Sorry to be a bit late... our one precious part-time childcare helper had to quarantine all week (COVID case in her house) so it's been chaos. Again. Also the slides at the end are hot off the presses.

cheers,
Jamie

On Wed, Jan 27, 2021 at 8:39 PM Hector Aguilar-Carreno <(b) (6) wrote:
Thank you, Raina.

I sent the G-P part and the vaccine part separately, and that worked just fine.

Good night to all!

Hector

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Plowright, Raina <(b) (6)
Sent: Wednesday, January 27, 2021 11:30 PM
To: Hector Aguilar-Carreno <(b) (6) Jamie Lloyd-Smith <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) LaTrielle, Sara <(b) (6) Sara LaTrielle (b) (6)
Subject: Re: Slides for DARPA PI meeting

Also a Box folder in the PI area for slides (b) (6) if you are struggling with large files.

From: Hector Aguilar-Carreno <(b) (6)
Date: Wednesday, January 27, 2021 at 9:25 PM

To: Jamie Lloyd-Smith <(b) (6)>
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)> Plowright, Raina <(b) (6)> LaTrielle, Sara <(b) (6)> Sara LaTrielle <(b) (6)>
Subject: Re: Slides for DARPA PI meeting

Jamie and Vince,

Here are my slides for the G-P part.

Jamie, I could not send all the slides here (too big of a file), but if you don't mind to stitch my slides after your first couple of general G-P slides, that would be fantastic! I will separately send Raina and Sara my slides for the vaccine story towards the end of the overall presentation.

Thank you!

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Jamie Lloyd-Smith <(b) (6)>
Sent: Wednesday, January 27, 2021 3:34 AM
To: Hector Aguilar-Carreno <(b) (6)>
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Subject: Re: Slides for DARPA PI meeting

Hi guys,

Sounds broadly good. I haven't had a chance to look at it again yet, but will do something tomorrow.

cheers

jamie

On Tue, Jan 26, 2021 at 1:35 PM Hector Aguilar-Carreno <(b) (6)> wrote:

Sounds good to me, Vince.

We will send a few slides tomorrow.

I hope you are both well!

Hector

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Sent: Tuesday, January 26, 2021 4:29 PM
To: Hector Aguilar-Carreno <(b) (6)> Jamie Lloyd-Smith

<[redacted]>
Subject: RE: Slides for DARPA PI meeting

Slides look great, I can put some final slides in there with some human work – moving to evolution and new variants of interest into the transmission modeling and how this would relate to the countermeasures.

Sounds good?

Vincent Munster, PhD

Chief Virus Ecology Section

Rocky Mountain Laboratories

NIAID/NIH

From: Hector Aguilar-Carreno <[redacted]>
Sent: Tuesday, January 26, 2021 3:53 AM
To: Jamie Lloyd-Smith <[redacted]> Munster, Vincent (NIH/NIAID) [E] <[redacted]>
Subject: Re: Slides for DARPA PI meeting

Hi Jamie,

That sounds about right, and I can talk for just 5 minutes at the beginning, since I will have more time to talk about the multivalent HNV vaccines at the end. FYI, I will likely use a couple of the slides at the beginning of the deck you sent, then a couple of slides on HeV sequences and their G-P analysis, one on CedV, and one the new Madagascar virus. The problem is that we won't have all the data until Wed morning. But I think Wed is an MSU internal deadline, so we should be ok. The real deal is next week, so we have the rest of this week to finalize the slide deck.

Jamie, if I decide to pivot the idea to mention the coronaviruses on the vaccine side, I may use the dose curves from Amandine. However, I may stick to HNV. I will decide soon.

Best,

Hector

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Jamie Lloyd-Smith <(b) (6)>
Sent: Tuesday, January 26, 2021 4:25 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>; Hector Aguilar-Carreno <(b) (6)>
Subject: Slides for DARPA PI meeting

Hi guys,

So we're supposed to be coordinating for this PI review meeting, with our (draft) slides due on Wednesday. I've spoken briefly with each of you individually, but we need to coordinate. We've been asked to cover henipa G-to-P, then the shift to COVID, then the beginnings of transmission phenotyping work -- all in 20 minutes. I believe the grand plan is to have Hector speak, then me, then Vincent.

I have taken a quick first hack at some slides, starting from the slides used for the last PI meeting with some additions and cuts. See attached. These are very rough, obviously,

but I thought it would help you guys to see what I'm envisioning. I've added some quick thoughts in the Notes field of the powerpoint... basically I'm thinking that Hector can lead in with the empirical work on henipas, from sequence to lab virology. Then I pick up with the modeling framework, pivot to COVID, stability work, and our model for airborne transmission, then close out by circling back to the G-to-P framework*. Then Vincent brings it home with a bunch of CoV experimental data (*or maybe you want to do the loop back to G-to-P at the end?).

See what you think. As you'll see, I've got a lot of work to do to tighten things up, so still plenty of scope for revising the plan.

Hector, you're going to be talking about your vaccination work later in the presentation, I believe? Not sure if it's relevant, but you're welcome to use Amandine's dose-response plots if they'd be helpful there (though probably you're sticking with the HNV vaccines?).

Last thing, I guess we should decide on time targets for each of us... should we do 7 minutes each? Or Hector do you want to be quicker here, since you speak again later? Maybe 5, 8, 8? Let me know what you think, so I can start chopping accordingly.

cheers,

Jamie

---------- Forwarded message ---------
From: **LaTrielle, Sara** <(b) (6)
Date: Mon, Jan 25, 2021 at 6:16 AM
Subject: SLIDES DUE Jan 27th (Re: PREEMPT PI Monthly meeting (updated 2020)
To: Plowright, Raina <(b) (6) (b) (6)
<(b) (6) (b) (6) <(b) (6)
Barbara Han <(b) (6) Cara Brook <(b) (6) Colin

Ross Parrish < (b) (6) Emily Gurley (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno < (b) (6) (b) (6) < (b) (6) (b) (6) < (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6) Peggy Eby < (b) (6) Hudson, Peter John (b) (6), Schountz,Tony < (b) (6) (b) (6) < (b) (6) Hoegh, Andrew < (b) (6) Cara Brook < (b) (6)

All,

Slides are now due Wed **Jan 27th, -** to Raina/me due to DARPA needing all performer slides- as DARPA needs time to put these all through an internal review process. Please prioritize these slides over the quarterly report, due Friday, but there is wiggle room there to ensure the slides are to DARPA.

Please send asap, and better yet, upload to Box, per below. Thank you!

**Important documents in this Box folder.

Sara

From: LaTrielle, Sara < (b) (6)
Sent: Tuesday, January 12, 2021 10:13 AM
To: Plowright, Raina < (b) (6) (b) (6) < (b) (6) (b) (6) < (b) (6) Barbara Han < (b) (6) Cara Brook < (b) (6) Colin Ross Parrish < (b) (6) Emily Gurley (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno < (b) (6) (b) (6) < (b) (6) (b) (6) < (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6) Peggy Eby < (b) (6) Hudson, Peter John (b) (6); Schountz,Tony < (b) (6) (b) (6) < (b) (6) Hoegh, Andrew < (b) (6) Cara Brook < (b) (6)
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

All,

Please find the following important documents in this Box folder

1. DARPA slide template that needs to be used for the ppt, and
2. Raina's instructional slides (same as email below)
3. Recording of yesterday's PI Zoom mtg, for reference.

Please drop your slide in this Box folder by Jan 27th.

Thank you,

Sara

From: Plowright, Raina <(b) (6)
Sent: Monday, January 11, 2021 7:00 PM
To: LaTrielle, Sara <(b) (6) (b) (6)
<(b) (6) (b) (6) <(b) (6)
Barbara Han <(b) (6) Cara Brook <(b) (6) Colin
Ross Parrish <(b) (6) Emily Gurley <(b) (6) Hamish
McCallum <(b) (6) Hector Aguilar-Carreno
<(b) (6) (b) (6) <(b) (6)
(b) (6) <(b) (6) Nita Bharti <(b) (6) Olivier
Restif <(b) (6) Peggy Eby <(b) (6) Hudson, Peter John
<(b) (6) Schountz,Tony <(b) (6)
(b) (6) <(b) (6) Hoegh, Andrew
<(b) (6) Cara Brook <(b) (6)
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Hi Everyone,

Thanks for the productive call today.

Here is an updated version of the Phase I review outline. I incorporated the changes we discussed on the call and played with the timing to get us to 75 minutes. Use the proposed timing as a rough ball-park as we may adjust the scope of each section when we see the full slide deck.

Please send your slides to Sara by 27th January (2.5 weeks from now) and of course we will accept late-breaking data to be added to slides on the week of Feb 4th!

Raina

From: Plowright, Raina <(b) (6)
Date: Monday, January 11, 2021 at 12:37 PM
To: LaTrielle, Sara <(b) (6) (b) (6)
<(b) (6) (b) (6) <(b) (6)
Barbara Han <(b) (6) Cara Brook <(b) (6) Colin
Ross Parrish <(b) (6) Emily Gurley (b) (6), Hamish
McCallum <(b) (6) Hector Aguilar-Carreno
<(b) (6) (b) (6) <(b) (6)
(b) (6) <(b) (6) Nita Bharti <(b) (6) Olivier
Restif <(b) (6) Peggy Eby <(b) (6) Hudson, Peter John
(b) (6), Schountz,Tony (b) (6),
(b) (6) <(b) (6) Hoegh, Andrew
<(b) (6) Cara Brook <(b) (6)
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Hi Everyone,

Here is an outline for our Phase I Review presentation. Instructions are on the first pages. I've suggested a format and potential presenters and I'd like to make final decisions on the call today. Some of the headings are wonky bc DARPA have gone back to the original BAA and aligned our SOW with the original goals/language.

Also, prioritize analysis of phase I data that could be finalized by the deadline (at least a couple of days before Feb 4th) so we can include it in the final presentation. I'm thinking of the nutritional stress experiments in Artibeus bats, calibration of bioelectric

impedance, initial cortisol analyses, or whatever is feasible in less than a month. Think about what is most strategic and please work with your teams to prioritize these data.

Talk to you in 1.5 hours.

Raina

From: LaTrielle, Sara <(b) (6)
Date: Monday, January 11, 2021 at 10:48 AM
To: (b) (6) <(b) (6) (b) (6) <(b) (6) Barbara Han <(b) (6) Cara Brook <(b) (6) Colin Ross Parrish <(b) (6) Emily Gurley <(b) (6) Hamish McCallum <(b) (6) Hector Aguilar-Carreno <(b) (6) (b) (6) <(b) (6) (b) (6) <(b) (6) Nita Bharti <(b) (6) Olivier Restif <(b) (6) Peggy Eby <(b) (6) Hudson, Peter John <(b) (6) Plowright, Raina <(b) (6) Schountz,Tony <(b) (6) (b) (6) <(b) (6) Hoegh, Andrew <(b) (6) Cara Brook <(b) (6)
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Reminder for today's PI meeting 2-3pm MST. Thanks to the few who already informed me that they will not be able to attend.

Join Zoom Meeting

https://zoom.us/j/(b) (6)

*full call-in (dial) details below

agenda

From: LaTrielle, Sara
Sent: Monday, December 30, 2019 10:13 AM
To: (b) (6) < (b) (6)
(b) (6) < (b) (6) Barbara Han
< (b) (6) Cara Brook < (b) (6) Colin Ross
Parrish < (b) (6) Emily Gurley < (b) (6) Hamish
McCallum < (b) (6) Hector Aguilar-Carreno
< (b) (6) (b) (6) < (b) (6)
(b) (6) < (b) (6) Nita Bharti < (b) (6)
Olivier Restif < (b) (6) Peggy Eby < (b) (6)
Hudson, Peter John (b) (6); Plowright, Raina
< (b) (6) Schountz,Tony
(b) (6); (b) (6)
< (b) (6) Hoegh, Andrew < (b) (6).
Cc: (b) (6) < (b) (6).
Subject: PREEMPT PI Monthly meeting (updated 2020)
When: Monday, January 11, 2021 2:00 PM-3:00 PM.
Where: https://zoom.us/j/ (b) (6)

Due to a date conflict our PI meeting is shifting to a week later.

All,

Please use this calendar invite with zoom and agenda links for our regular monthly meetings.

agenda

Zoom here:

PREEMPT is inviting you to a scheduled Zoom meeting.

Topic: PREEMPT PI Monthly Mtg

Join Zoom Meeting

https://zoom.us/j/ (b) (6)

Meeting ID: (b) (6)

One tap mobile

+16699009128,, (b) (6) US (San Jose)

+16465588656,, (b) (6) US (New York)

Dial by your location

+1 669 900 9128 US (San Jose)

+1 646 558 8656 US (New York)

Meeting ID: (b) (6)

Find your local number: https://zoom.us/u/adzPR7PsUq

--

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

--

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Office: 4135 Terasaki Life Sciences Building
Lab: 4000 Terasaki Life Sciences Building

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 1 Feb 2021 21:52:44 +0000
To: Schountz,Tony; Avanzato, Victoria (NIH/NIAID) [F]
Subject: RE: weird results

Hi Vicky,

Do you have some Nipah G for Tony for a Elisa? He did some VLP vaccinations in his Artibeus bats under different levels of immunological pressure.

And maybe send your Elisa protocol just to be sure

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

From: Schountz,Tony <(b) (6)
Sent: Monday, February 1, 2021 2:45 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: weird results

Yes, Nipah G.
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Feb 1, 2021, at 2:44 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Is this Nipah G? we might have some

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

From: Schountz,Tony <(b) (6)
Sent: Monday, February 1, 2021 2:44 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Schountz, Tony <(b) (6)
Subject: Re: weird results

Yes, Luminex bead assay. If I had a suitable soluble antigen I'd do the ELISAs.

T.
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Feb 1, 2021, at 2:41 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Doesn't really trail off? More conventional Elisa would be better, did he do a Luminex of some sort?

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

From: Schountz,Tony <(b) (6)
Sent: Monday, February 1, 2021 2:34 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: weird results

I've attached the two slides that Hector and I came up with. He thinks it's statistically significant but didn't do the calculations (I haven't seen his raw data, just the graphs).

Yes, we have approval to do immunosuppression in Aj bats with Cedar virus and SARS-CoV-2, but it's difficult to get the work done because we're limited to one virus at a time in the bat BSL3 by our biosafety committee. Just finishing up an H18N11 experiment tomorrow, then we have a MERS-CoV experiment to do for Susan Weiss that will take 3 weeks.

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1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Feb 1, 2021, at 2:30 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

The slide was a bit hard to read, but the dex/methasone didn't work out to well either?

Cool exp to do with Nipah, once I finally have some time again!

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

From: Schountz,Tony <(b) (6)
Sent: Monday, February 1, 2021 2:27 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: weird results

No idea. Probably a question for Hector. We handled them just as he told us and he and I have discussed doing a hamster or mouse study to see what's going on.

Really unexpected, though.
—
Tony Schountz, PhD
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1685 Campus Delivery
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(b) (6)
(b) (6)

On Feb 1, 2021, at 2:25 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

VLP issue?

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 1 Feb 2021 21:51:01 +0000
To: Schountz,Tony
Subject: RE: weird results

Lol, drummer of the muppet show!

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

From: Schountz,Tony <(b) (6)
Sent: Monday, February 1, 2021 2:50 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: weird results

Wow, I didn't even recognize Colin. Nice hair!
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
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Fort Collins, CO 80523-1692
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NIAID/NIH

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

On Feb 1, 2021, at 2:25 PM, Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6) wrote:

VLP issue?

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 1 Feb 2021 21:42:06 +0000
To: Schountz,Tony
Subject: RE: weird results

From our end full force on SARS-coV-2 for now, so no bandwidth for anything else

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

From: Schountz,Tony <(b) (6)
Sent: Monday, February 1, 2021 2:34 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: weird results

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(b) (6)
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VLP issue?

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

From: Schountz,Tony
Sent: Mon, 1 Feb 2021 21:33:40 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: weird results
Attachments: DARPA template .pptx

I've attached the two slides that Hector and I came up with. He thinks it's statistically significant but didn't do the calculations (I haven't seen his raw data, just the graphs).

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NIAID/NIH

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To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
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(b) (6)
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VLP issue?

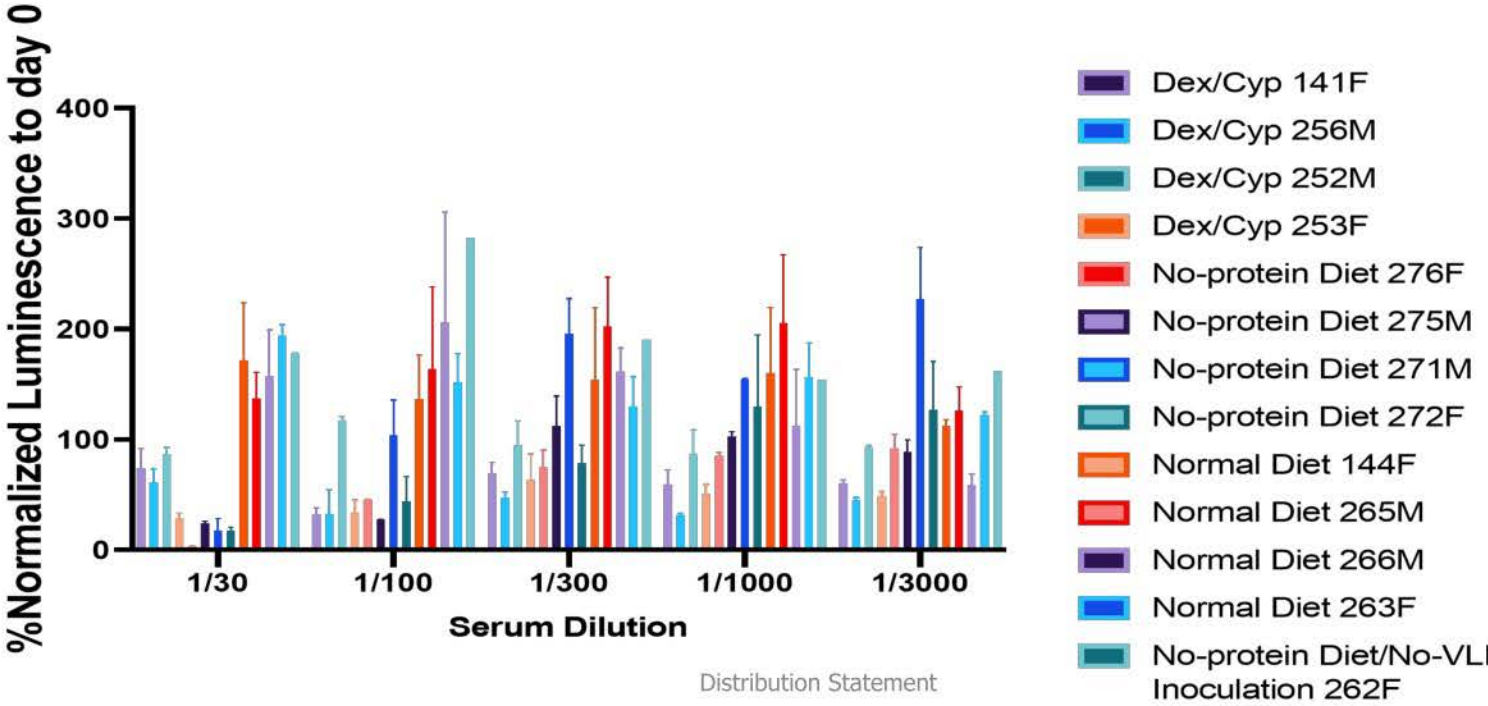
Vincent Munster, PhD
Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

Protein Deprivation and Bat Antibody Responses

- What is the role of protein in Jamaican fruit bat antibody responses?
  - Provide bats a low-protein diet (fresh fruit without protein supplement)
  - Immunize with a Nipah virus VLP
  - Collect sera 28 days later
  - Test sera for neutralization of Nipah FG VSV pseudotype virus
- Groups
  - Nominal diet, VLP immunization (control)
  - Nominal diet, dexamethasone and cyclophosphamide immunosuppression (control)
  - Low protein diet, VLP immunization
  - Low protein diet, no VLP immunization

Results

- Bats with low-protein diet had best antibody response – not what we expected!
- Why?
  - Perhaps protein deprivation compromises innate immunity, thus forcing a more robust adaptive response
  - For Jamaican fruit bats, high protein diet is a stressor
- Repeat with hamsters or mice to see if there are differences



From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 1 Feb 2021 15:16:06 +0000
To: (b) (6); Plowright, Raina
Cc: (b) (6);
Subject: RE: Follow up on performer accolades

Hi (b) (6),

For our award,, this comprises the complete COVID19 response of the lab, which included the work from DARPA. A small part of the workforce was DARPA funded (one post-doc), but the majority of the PREEMPT funds went still into Nipah / Hendra screening and full genome sequencing.

Of note, DARPA has been really hard to work with in terms of transfer of funds. I'm currently still waiting for my 2021 fiscal year allocation. Of note, as USG/NIH my lab is also subject to end-of-year policy, which means that the funds will still; need to be obligated before August. It is really not working well if my full year funds can only be accessed for ~ 6 months and I need to cover DARPA projects for a large amount by my own NIH funding. This is not sustainable.

Cheers,

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

-----Original Message-----
From: (b) (6)
Sent: Monday, February 1, 2021 7:46 AM
To: Plowright, Raina < (b) (6) Munster, Vincent (NIH/NIAID) [E]
< (b) (6)
Cc: (b) (6)
Subject: Follow up on performer accolades

Good morning Raina and Vincent,

We had a follow-up question about the performer accolades that you sent us last week. Were the following received for DARPA funded work?

Vincent's 2020 AAAS Golden Goose award, COVID-19 response And Emily Gurley's JHSPH Shikani/El Hibri prize for Innovation and Discovery for 2020 for work on pandemic response

Thank you,
(b) (6)

(b) (6)
SETA Support to DARPA BTO
Quantitative Scientific Solutions (QS-2)
(b) (6)
Office: (b) (6)
Work Mobile: (b) (6)

From: Broder, Christopher
Sent: Fri, 29 Jan 2021 11:09:55 -0500
Cc: Korch, George W. (CTR); De wit, Emmie (NIH/NIAID) [E]; Feldmann, Heinrich (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]
Subject: Re: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

Dear all,

Thanks so much for getting back to Cyril so quickly. He reached out to me yesterday and since it's not really my wheelhouse, I sent him all your contact info.

all best
Chris

On Thu, Jan 28, 2021 at 6:08 PM Gay, Cyril <(b) (6)> wrote:

Dear Chris, George, Emmie, Heinz, and Vincent,

I was wondering if you could help me recruiting candidates for the subject position at NBAF? Specifically, I've been asked to lead a search committee and I would like to invite you to be on the committee. We've had a hard time so far recruiting candidates for NBAF and we want to make sure the job announcement below will result in some good scientists with experience working in a BSK4 lab.

https://www.usajobs.gov/GetJob/ViewDetails/590498300

The research at the ZEDRU at NBAF will involve studies on the pathogen-vector-host interrelationships of zoonotic and emerging BSL-4 diseases such as Crimean Congo Hemorrhagic Fever (CCHF) and Nipah Virus, and potentially other emerging or zoonotic diseases.

As you know, NBAF (National Agro and Biodefense Facility) is our $1.4 billion facility that will give USDA for the first time the ability to research BSL4 agents. I don't think serving on the committee will take much of your time. I anticipate 2-3 zoom meetings at the most and for you to contact directly the scientists we identify as potential candidates. Of course, some of you may want to apply as well, seriously!

If for some reason you can't help me on the search committee, could I ask you to at least send the announcement withing your BSL4 network? As you know, this is a select agent-regulated facility and the applicants must be U.S citizens and will have to obtain security clearance.

Thank you so much gentlemen for considering this request.

Cyril

Cyril Gerard Gay, DVM, PhD

Senior National Program Leader

Animal Production and Protection

Agricultural Research Service

Tel: (b) (6); e-mail (b) (6)

Website: https://www.ars.usda.gov/

USDA United States Department of Agriculture
Agricultural Research Service

--
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: (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: Thu, 28 Jan 2021 23:13:09 +0000
To: Gay, Cyril; Broder, Chris (USU-DoD); Korch, George W. (CTR); De wit, Emmie (NIH/NIAID) [E]; Feldmann, Heinrich (NIH/NIAID) [E]
Subject: RE: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee

More than happy to help,

Cheers,

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

From: Gay, Cyril <(b) (6)
Sent: Thursday, January 28, 2021 4:08 PM
To: Broder, Chris (USU-DoD) <(b) (6) Korch, George W. (CTR) <(b) (6) De wit, Emmie (NIH/NIAID) [E] <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Research Leader (RL) Position for the NBAF BSL-4 Zoonotic and Emerging Disease Research unit (ZEDRU) - Search Committee
Importance: High

Dear Chris, George, Emmie, Heinz, and Vincent,

I was wondering if you could help me recruiting candidates for the subject position at NBAF? Specifically, I've been asked to lead a search committee and I would like to invite you to be on the committee. We've had a hard time so far recruiting candidates for NBAF and we want to make sure the job announcement below will result in some good scientists with experience working in a BSK4 lab.

https://www.usajobs.gov/GetJob/ViewDetails/590498300

The research at the ZEDRU at NBAF will involve studies on the pathogen-vector-host interrelationships of zoonotic and emerging BSL-4 diseases such as Crimean Congo Hemorrhagic Fever (CCHF) and Nipah Virus, and potentially other emerging or zoonotic diseases.

As you know, NBAF (National Agro and Biodefense Facility) is our $1.4 billion facility that will give USDA for the first time the ability to research BSL4 agents. I don't think serving on the committee will take much of your time. I anticipate 2-3 zoom meetings at the most and for you to contact directly the scientists we identify as potential candidates. Of course, some of you may want to apply as well, seriously!

If for some reason you can't help me on the search committee, could I ask you to at least send the announcement withing your BSL4 network? As you know, this is a select agent-regulated facility and the applicants must be U.S citizens and will have to obtain security clearance.

Thank you so much gentlemen for considering this request.

Cyril

Cyril Gerard Gay, DVM, PhD
Senior National Program Leader
Animal Production and Protection
Agricultural Research Service
Tel: (b) (6); e-mail (b) (6)
Website: https://www.ars.usda.gov/

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 28 Jan 2021 20:41:45 +0000
To: Jamie Lloyd-Smith; Hector Aguilar-Carreno
Cc: Plowright, Raina; LaTrielle, Sara; Sara LaTrielle
Subject: RE: Slides for DARPA PI meeting
Attachments: UCLA_DARPA_Phase1reportMunster.pptx

Added my slides to Jamie's

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

From: Jamie Lloyd-Smith < (b) (6)
Sent: Thursday, January 28, 2021 12:18 AM
To: Hector Aguilar-Carreno < (b) (6)
Cc: Plowright, Raina < (b) (6) Munster, Vincent (NIH/NIAID) [E]
< (b) (6) LaTrielle, Sara < (b) (6) Sara LaTrielle
< (b) (6)
Subject: Re: Slides for DARPA PI meeting

Hi everyone,

Here are my slides. There are a lot, but I plan to skim through the HNV ones very fast, and then there are a lot of multi-slide animations. Still, I will make cuts if I can't present in the ~8 minutes our team agreed on.

I didn't add in Hector's slides yet, because I wasn't sure exactly where he wants them. Vincent, I tried to tee up the experimental work at the end.

Hope this does the trick. I'll put in the Box folder as well. Sorry to be a bit late... our one precious part-time childcare helper had to quarantine all week (COVID case in her house) so it's been chaos. Again. Also the slides at the end are hot off the presses.

cheers,
Jamie

On Wed, Jan 27, 2021 at 8:39 PM Hector Aguilar-Carreno < (b) (6) wrote:
Thank you, Raina.

I sent the G-P part and the vaccine part separately, and that worked just fine.

Good night to all!

Hector

Hector Aguilar-Carreno
Associate Professor
Microbiology and Immunology
College of Veterinary Medicine
Cornell University
Office: (b) (6)

From: Plowright, Raina < (b) (6)
Sent: Wednesday, January 27, 2021 11:30 PM
To: Hector Aguilar-Carreno < (b) (6) Jamie Lloyd-Smith < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) LaTrielle, Sara < (b) (6) Sara LaTrielle < (b) (6)
Subject: Re: Slides for DARPA PI meeting

Also a Box folder in the PI area for slides (b) (6) if you are struggling with large files.

From: Hector Aguilar-Carreno < (b) (6)
Date: Wednesday, January 27, 2021 at 9:25 PM
To: Jamie Lloyd-Smith < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Plowright, Raina < (b) (6) LaTrielle, Sara < (b) (6) Sara LaTrielle < (b) (6)
Subject: Re: Slides for DARPA PI meeting

Jamie and Vince,

Here are my slides for the G-P part.

Jamie, I could not send all the slides here (too big of a file), but if you don't mind to stitch my slides after your first couple of general G-P slides, that would be fantastic! I will separately send Raina and Sara my slides for the vaccine story towards the end of the overall presentation.

Thank you!

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Jamie Lloyd-Smith <(b) (6)
Sent: Wednesday, January 27, 2021 3:34 AM
To: Hector Aguilar-Carreno <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Slides for DARPA PI meeting

Hi guys,

Sounds broadly good. I haven't had a chance to look at it again yet, but will do something tomorrow.

cheers

jamie

On Tue, Jan 26, 2021 at 1:35 PM Hector Aguilar-Carreno <(b) (6) wrote:

Sounds good to me, Vince.

We will send a few slides tomorrow.

I hope you are both well!

Hector

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Sent: Tuesday, January 26, 2021 4:29 PM
To: Hector Aguilar-Carreno <(b) (6)>; Jamie Lloyd-Smith <(b) (6)>
Subject: RE: Slides for DARPA PI meeting

Slides look great, I can put some final slides in there with some human work – moving to evolution and new variants of interest into the transmission modeling and how this would relate to the countermeasures.

Sounds good?

Vincent Munster, PhD

Chief Virus Ecology Section

Rocky Mountain Laboratories

NIAID/NIH

From: Hector Aguilar-Carreno <(b) (6)>
Sent: Tuesday, January 26, 2021 3:53 AM
To: Jamie Lloyd-Smith <(b) (6)>; Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Subject: Re: Slides for DARPA PI meeting

Hi Jamie,

That sounds about right, and I can talk for just 5 minutes at the beginning, since I will have more time to talk about the multivalent HNV vaccines at the end. FYI, I will likely use a couple of the slides at the beginning of the deck you sent, then a couple of slides on HeV sequences and their G-P analysis, one on CedV, and one the new Madagascar virus. The problem is that we won't have all the data until Wed morning. But I think Wed is an MSU internal deadline, so we should be ok. The real deal is next week, so we have the rest of this week to finalize the slide deck.

Jamie, if I decide to pivot the idea to mention the coronaviruses on the vaccine side, I may use the dose curves from Amandine. However, I may stick to HNV. I will decide soon.

Best,

Hector

Hector Aguilar-Carreno

Associate Professor

Microbiology and Immunology

College of Veterinary Medicine

Cornell University

Office: (b) (6)

From: Jamie Lloyd-Smith <(b) (6)>
Sent: Tuesday, January 26, 2021 4:25 AM

To: Munster, Vincent (NIH/NIAID) [E] <[redacted] (b) (6)> Hector Aguilar-Carreno <[redacted] (b) (6)>
Subject: Slides for DARPA PI meeting

Hi guys,

So we're supposed to be coordinating for this PI review meeting, with our (draft) slides due on Wednesday. I've spoken briefly with each of you individually, but we need to coordinate. We've been asked to cover henipa G-to-P, then the shift to COVID, then the beginnings of transmission phenotyping work -- all in 20 minutes. I believe the grand plan is to have Hector speak, then me, then Vincent.

I have taken a quick first hack at some slides, starting from the slides used for the last PI meeting with some additions and cuts. See attached. These are very rough, obviously, but I thought it would help you guys to see what I'm envisioning. I've added some quick thoughts in the Notes field of the powerpoint... basically I'm thinking that Hector can lead in with the empirical work on henipas, from sequence to lab virology. Then I pick up with the modeling framework, pivot to COVID, stability work, and our model for airborne transmission, then close out by circling back to the G-to-P framework*. Then Vincent brings it home with a bunch of CoV experimental data (*or maybe you want to do the loop back to G-to-P at the end?).

See what you think. As you'll see, I've got a lot of work to do to tighten things up, so still plenty of scope for revising the plan.

Hector, you're going to be talking about your vaccination work later in the presentation, I believe? Not sure if it's relevant, but you're welcome to use Amandine's dose-response plots if they'd be helpful there (though probably you're sticking with the HNV vaccines?).

Last thing, I guess we should decide on time targets for each of us... should we do 7 minutes each? Or Hector do you want to be quicker here, since you speak again later? Maybe 5, 8, 8? Let me know what you think, so I can start chopping accordingly.

cheers,

Jamie

---------- Forwarded message ---------
From: **LaTrielle, Sara** <(b) (6)
Date: Mon, Jan 25, 2021 at 6:16 AM
Subject: SLIDES DUE Jan 27th (Re: PREEMPT PI Monthly meeting (updated 2020)
To: Plowright, Raina <(b) (6) (b) (6)
<(b) (6) (b) (6) <(b) (6) Barbara Han
<(b) (6) Cara Brook <(b) (6) Colin Ross Parrish
<(b) (6) Emily Gurley <(b) (6) Hamish McCallum
<(b) (6) Hector Aguilar-Carreno <(b) (6)
(b) (6) <(b) (6) (b) (6)
<(b) (6) Nita Bharti <(b) (6) Olivier Restif <(b) (6)
Peggy Eby <(b) (6) Hudson, Peter John (b) (6), Schountz,Tony
<(b) (6) (b) (6) <(b) (6)
Hoegh, Andrew <(b) (6) Cara Brook <(b) (6).

All,

Slides are now due Wed **Jan 27th, -** to Raina/me due to DARPA needing all performer slides- as DARPA needs time to put these all through an internal review process. Please prioritize these slides over the quarterly report, due Friday, but there is wiggle room there to ensure the slides are to DARPA.

Please send asap, and better yet, upload to Box, per below. Thank you!

**Important documents in this Box folder.

Sara

From: LaTrielle, Sara <(b) (6)>
Sent: Tuesday, January 12, 2021 10:13 AM
To: Plowright, Raina <(b) (6)> <(b) (6)> <(b) (6)> <(b) (6)> Barbara Han <(b) (6)> Cara Brook <(b) (6)> Colin Ross Parrish <(b) (6)> Emily Gurley <(b) (6)>; Hamish McCallum <(b) (6)> Hector Aguilar-Carreno <(b) (6)> <(b) (6)> <(b) (6)> <(b) (6)> <(b) (6)> Nita Bharti <(b) (6)> Olivier Restif <(b) (6)> Peggy Eby <(b) (6)> Hudson, Peter John <(b) (6)> Schountz,Tony <(b) (6)> <(b) (6)> <(b) (6)> Hoegh, Andrew <(b) (6)> Cara Brook <(b) (6)>
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

All,

Please find the following important documents in this Box folder

1. DARPA slide template that needs to be used for the ppt, and
2. Raina's instructional slides (same as email below)
3. Recording of yesterday's PI Zoom mtg, for reference.

Please drop your slide in this Box folder by Jan 27th.

Thank you,

Sara

From: Plowright, Raina <(b) (6)>
Sent: Monday, January 11, 2021 7:00 PM
To: LaTrielle, Sara <(b) (6)> <(b) (6)> <(b) (6)> <(b) (6)> Barbara Han <(b) (6)> Cara Brook <(b) (6)> Colin Ross Parrish <(b) (6)> Emily Gurley <(b) (6)> Hamish McCallum

< (b) (6) Hector Aguilar-Carreno < (b) (6)
(b) (6) < (b) (6) (b) (6)
< (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6)
Peggy Eby < (b) (6) Hudson, Peter John < (b) (6) Schountz,Tony
(b) (6) (b) (6) < (b) (6)
Hoegh, Andrew < (b) (6) Cara Brook < (b) (6).
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Hi Everyone,

Thanks for the productive call today.

Here is an updated version of the Phase I review outline. I incorporated the changes we discussed on the call and played with the timing to get us to 75 minutes. Use the proposed timing as a rough ball-park as we may adjust the scope of each section when we see the full slide deck.

Please send your slides to Sara by 27th January (2.5 weeks from now) and of course we will accept late-breaking data to be added to slides on the week of Feb 4th!

Raina

From: Plowright, Raina < (b) (6).
Date: Monday, January 11, 2021 at 12:37 PM
To: LaTrielle, Sara < (b) (6) (b) (6)
< (b) (6) (b) (6) < (b) (6) Barbara Han
< (b) (6) Cara Brook < (b) (6) Colin Ross Parrish
< (b) (6) Emily Gurley < (b) (6) Hamish McCallum
< (b) (6) Hector Aguilar-Carreno < (b) (6)
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< (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6)
Peggy Eby < (b) (6) Hudson, Peter John (b) (6), Schountz,Tony
< (b) (6) (b) (6) < (b) (6)
Hoegh, Andrew < (b) (6) Cara Brook < (b) (6).
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Hi Everyone,

Here is an outline for our Phase I Review presentation. Instructions are on the first pages. I've suggested a format and potential presenters and I'd like to make final decisions on the call today. Some of the headings are wonky bc DARPA have gone back to the original BAA and aligned our SOW with the original goals/language.

Also, prioritize analysis of phase I data that could be finalized by the deadline (at least a couple of days before Feb 4th) so we can include it in the final presentation. I'm thinking of the nutritional stress experiments in Artibeus bats, calibration of bioelectric impedance, initial cortisol analyses, or whatever is feasible in less than a month. Think about what is most strategic and please work with your teams to prioritize these data.

Talk to you in 1.5 hours.

Raina

From: LaTrielle, Sara <(b) (6)>
Date: Monday, January 11, 2021 at 10:48 AM
To: (b) (6) <(b) (6)> (b) (6) <(b) (6)> Barbara Han <(b) (6)> Cara Brook <(b) (6)> Colin Ross Parrish <(b) (6)> Emily Gurley <(b) (6)> Hamish McCallum <(b) (6)> Hector Aguilar-Carreno (b) (6), (b) (6) <(b) (6)> (b) (6) <(b) (6)> Nita Bharti <(b) (6)> Olivier Restif <(b) (6)> Peggy Eby <(b) (6)> Hudson, Peter John <(b) (6)> Plowright, Raina <(b) (6)> Schountz,Tony (b) (6), (b) (6) <(b) (6)> Hoegh, Andrew <(b) (6)> Cara Brook <(b) (6)>
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Reminder for today's PI meeting 2-3pm MST. Thanks to the few who already informed me that they will not be able to attend.

Join Zoom Meeting

https://zoom.us/j/(b) (6)

*full call-in (dial) details below

agenda

From: LaTrielle, Sara
Sent: Monday, December 30, 2019 10:13 AM
To: (b) (6) < (b) (6) (b) (6) < (b) (6) Barbara Han < (b) (6) Cara Brook < (b) (6) Colin Ross Parrish < (b) (6) Emily Gurley < (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno (b) (6) (b) (6) (b) (6); (b) (6) < (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6) Peggy Eby < (b) (6) Hudson, Peter John (b) (6) Plowright, Raina < (b) (6) Schountz,Tony < (b) (6) (b) (6) < (b) (6) Hoegh, Andrew < (b) (6).
Cc: (b) (6) < (b) (6).
Subject: PREEMPT PI Monthly meeting (updated 2020)
When: Monday, January 11, 2021 2:00 PM-3:00 PM.
Where: https://zoom.us/j/ (b) (6)

Due to a date conflict our PI meeting is shifting to a week later.

All,

Please use this calendar invite with zoom and agenda links for our regular monthly meetings.

agenda

Zoom here:

PREEMPT is inviting you to a scheduled Zoom meeting.

Topic: PREEMPT PI Monthly Mtg

Join Zoom Meeting

https://zoom.us/j/ (b) (6)

Meeting ID: (b) (6)

One tap mobile

+16699009128,, (b) (6) (San Jose)

+16465588656,, (b) (6) (New York)

Dial by your location

+1 669 900 9128 US (San Jose)

+1 646 558 8656 US (New York)

Meeting ID: (b) (6)

Find your local number: https://zoom.us/u/adzPR7PsUq

--

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

Department of Ecology & Evolutionary Biology

Department of Biomathematics

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610 Charles E Young Dr South

Box 723905

Los Angeles, CA 90095-7239

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--

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

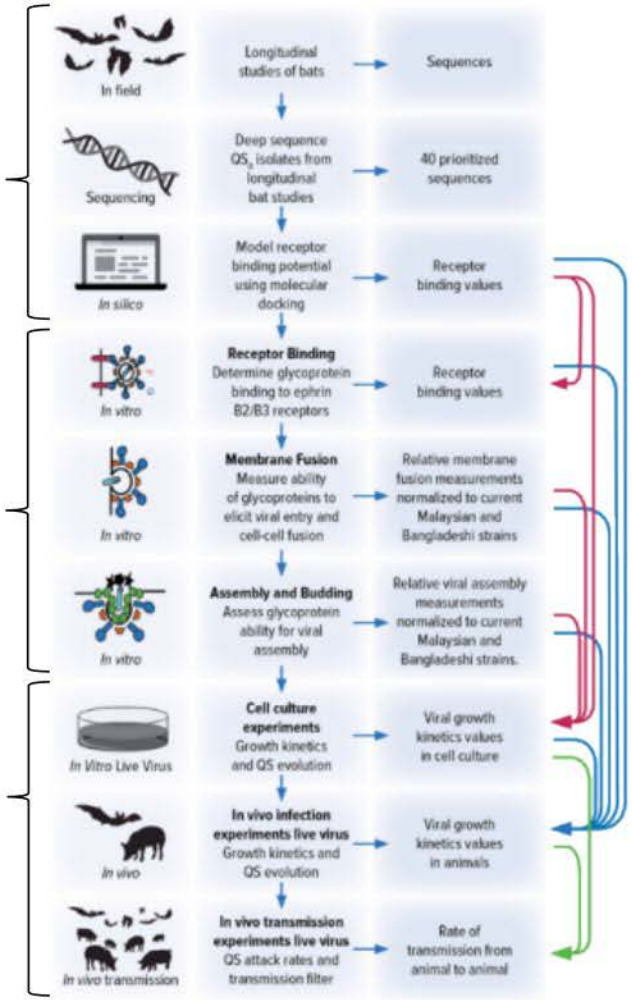
The genotype-trait-phenotype model for predicting spillover risks

Using models and computation to link virology to spillover and transmission risk.

Genotype

Virologic traits

Risk phenotypes

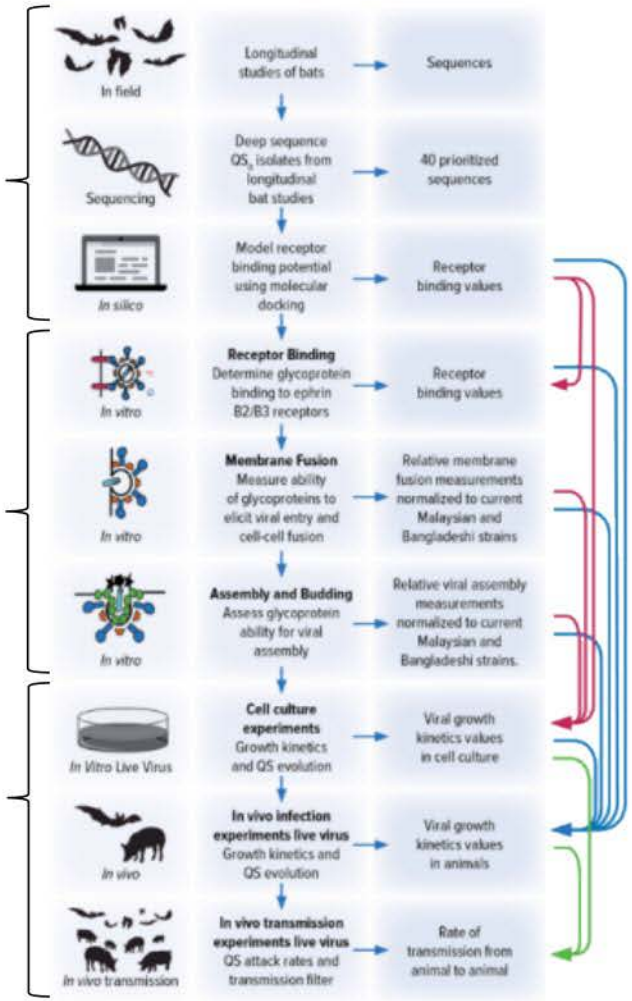


The genotype-trait-phenotype model for predicting spillover risks

Field isolates and sequences, lab mutants → Genotype

Receptor affinity, cell entry, budding…
(Constructs; e.g., VLP, pseudotyped viruses ; **BSL2**) → Virologic traits

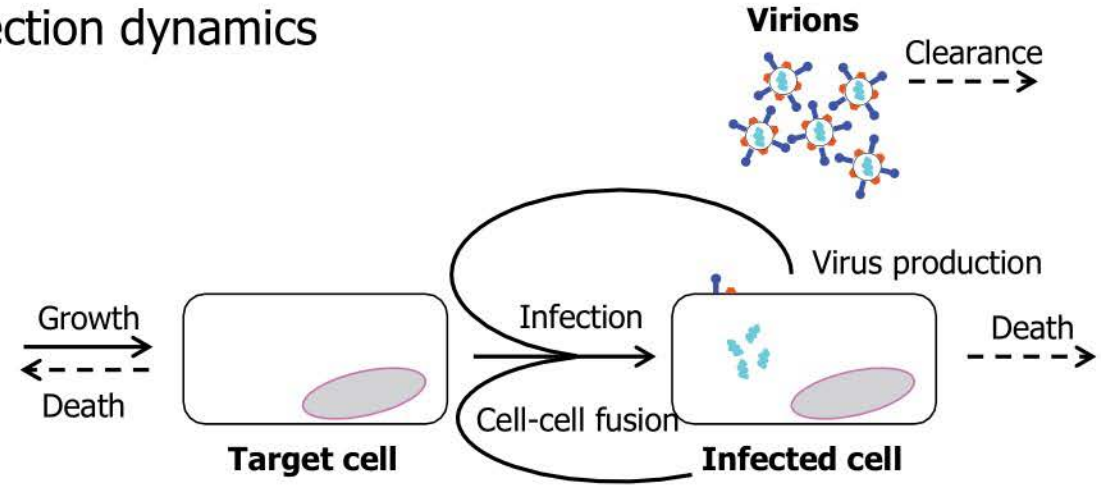
Viral fitness
(Live viruses; **BSL4**) → Risk phenotypes



- Hector's slides here, I think?

Genotype-to-phenotype mapping: within-host mechanistic models

Virus-cell infection dynamics



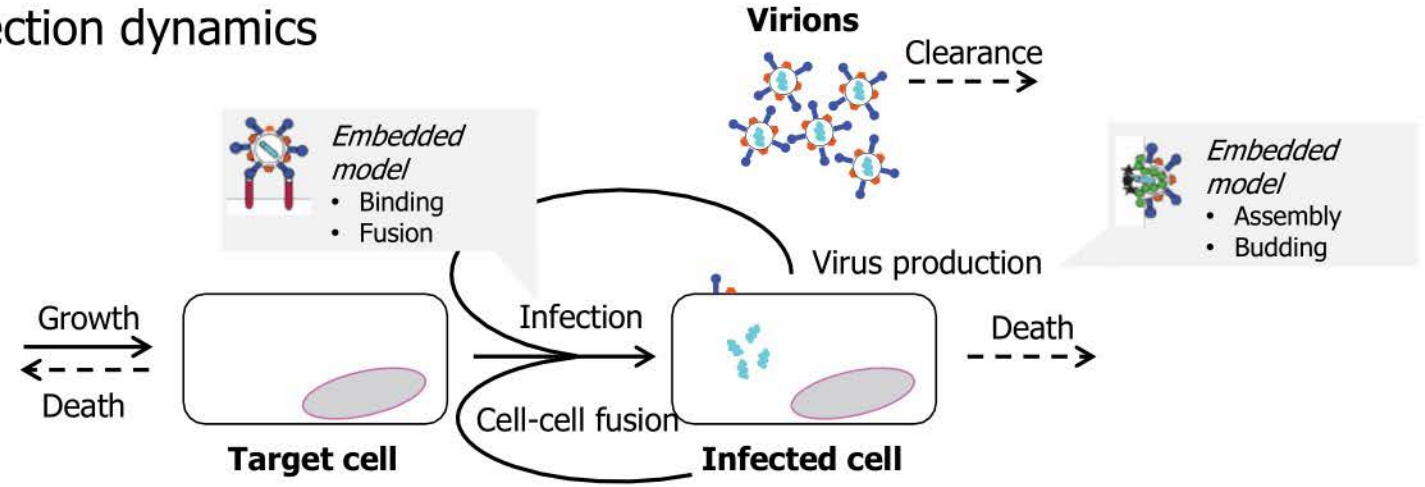
Goal:

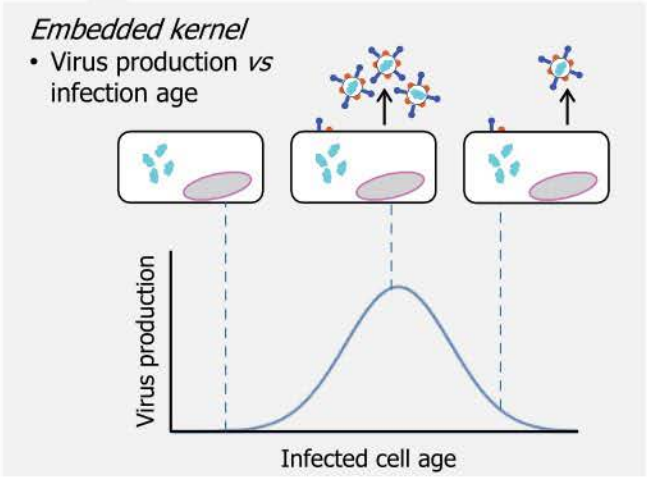
Develop mechanistic model linking molecular traits and interactions to viral fitness and pathogenicity.

→ Platform for screening novel viruses.

Genotype-to-phenotype mapping: within-host mechanistic models

Virus-cell infection dynamics





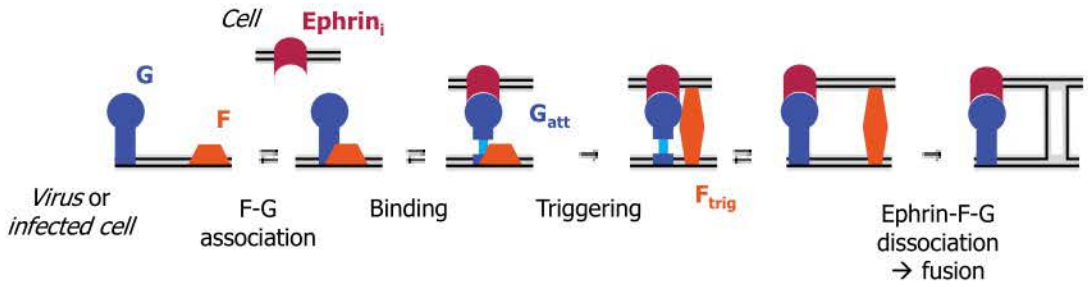
Goal:

Develop mechanistic model linking molecular traits and interactions to viral fitness and pathogenicity.

→ Platform for screening novel viruses.

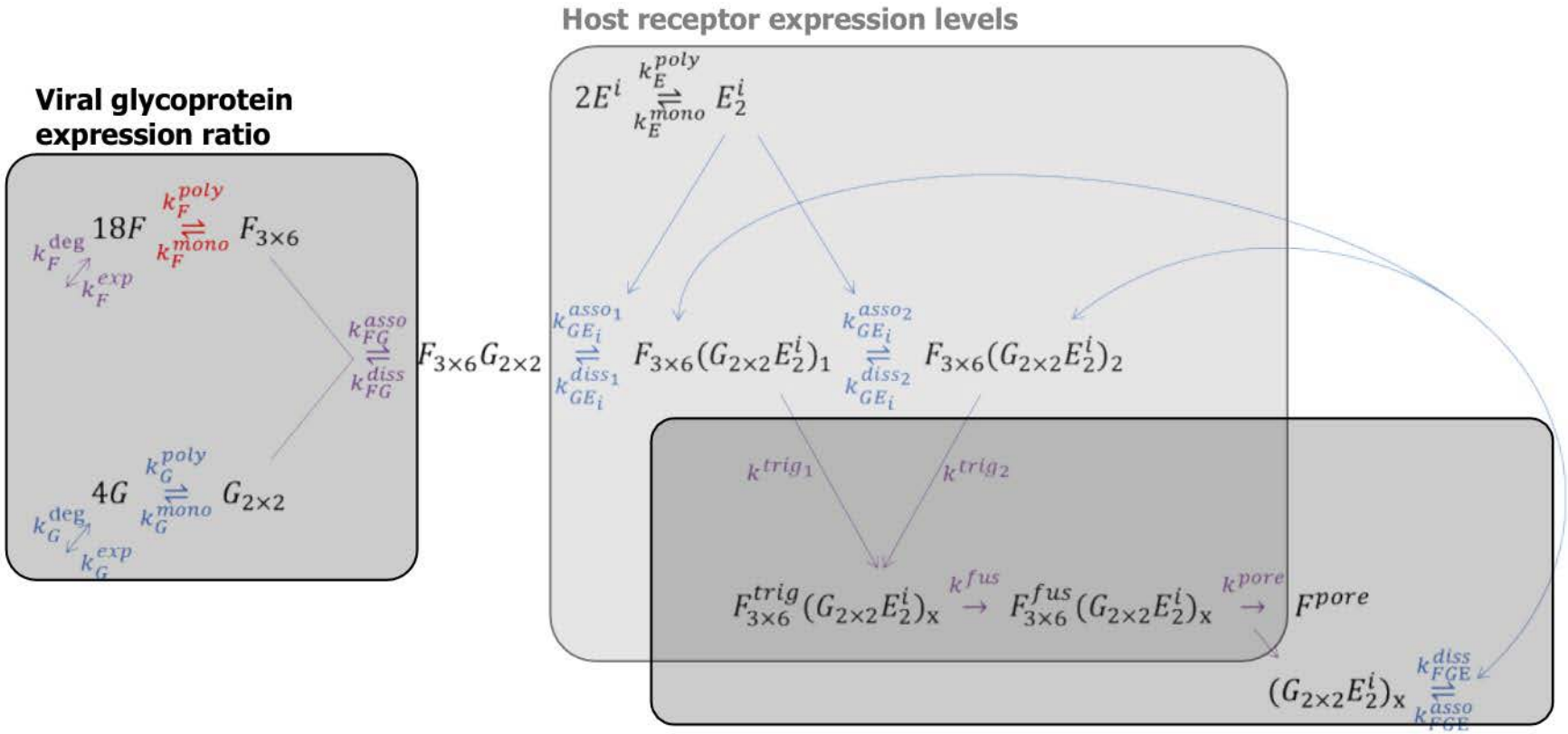
Genotype-to-phenotype mapping: within-host mechanistic models

- Embedded mechanistic model of the membrane fusion cascade



Genotype-to-phenotype mapping: within-host mechanistic models

- Embedded mechanistic model of the membrane fusion cascade



Viral chimeras → Parameter identifiability

Parameter impacted by F genotype

Parameter impacted by G genotype

Parameter impacted by F and G genotypes

F = matured F (F_1F_2 heterodimer)
F_{18} = F hexamer of trimers
G = mature G
$G_{2\times2}$ = G tetramer
E_i = ephrin i, with $i \in [A_2, A_5, B_1, B_2, B_3]$
FG = complex of F and G polymers
$F(GE_i)_j$ = complex of F and G polymers binding to j ephrin i

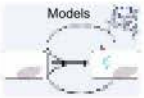
Henipavirus genotype-to-phenotype work – Summary

- Field teams collecting viruses & sequences at field sites around the world, generating hundreds of virus-positive samples and discovery of at least one novel henipavirus.

- Sequences being assessed for genotypic variation at sites involved in receptor binding, fusion & viral entry, for new and old henipaviruses.

- Assays in BSL2 laboratory – measuring viral traits of binding, fusion and entry – designed to interface with modeling to predict spillover risk, virulence.

- Assays in BSL4 laboratory – measuring viral fitness in cell culture & bat infections – enable modeling to assess role of viral traits in risk phenotypes



- Establishing integrated lab and modeling platform – a tool to estimate and predict spillover risk of known and newly discovered viruses.

Henipavirus genotype-to-phenotype work – Summary

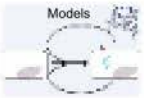
- Field teams collecting viruses & sequences at field sites around the world, generating hundreds of virus-positive samples and discovery of at least one novel henipavirus.

- Sequences being assessed for genotypic variation at sites involved in receptor binding, fusion & viral entry, for new and old henipaviruses.

- Assays in BSL2 la… g, fusion and entry – designed to int… spillover risk, virulence.

- Assays in BSL4 la… ulture & bat infections – enab… viral traits in risk phenotypes

- Establishing inte… o estimate and predict spillover … discovered viruses.



Interrupted by COVID-19 pandemic

Interrupted by COVID-19 pandemic

Interrupted by COVID-19 pandemic

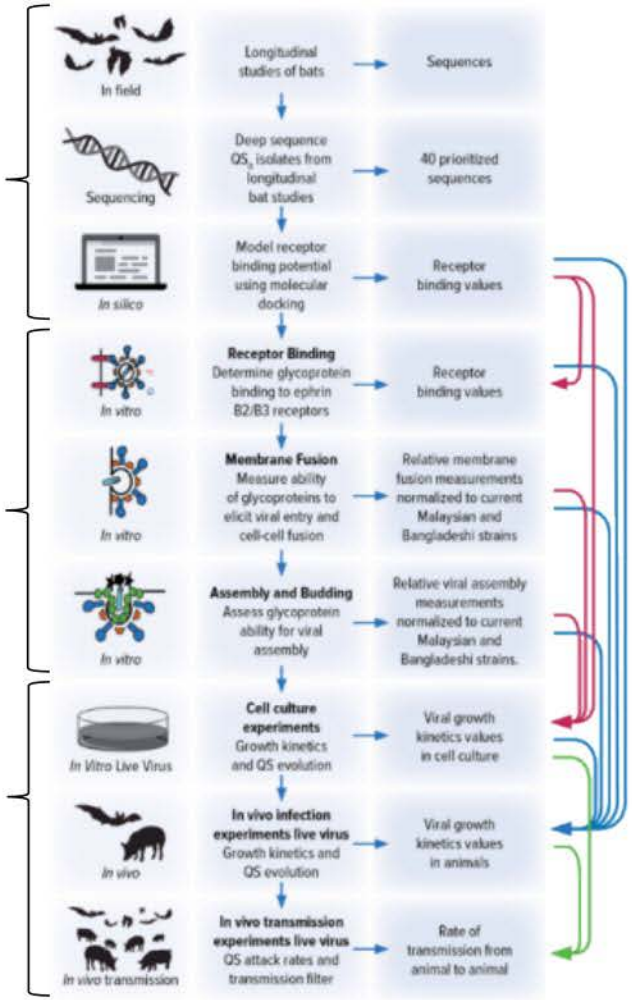
Pivot to COVID-19 pandemic response

Leverage collaborations and framework to study COVID-19 by linking virologic traits to transmission risks

Genotype

Virologic traits

Risk phenotypes



COVID-19 – From virologic traits to transmission risk

How long can SARS-CoV-2 remain infectious in the environment?

→ Determines infection risk from fomite and airborne exposure

Overarching goal: **rapid assessment of SARS-CoV-2 transmission routes**

COVID-19 – From virologic traits to transmission risk

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The NEW ENGLAND JOURNAL of MEDICINE

Aerosol and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1

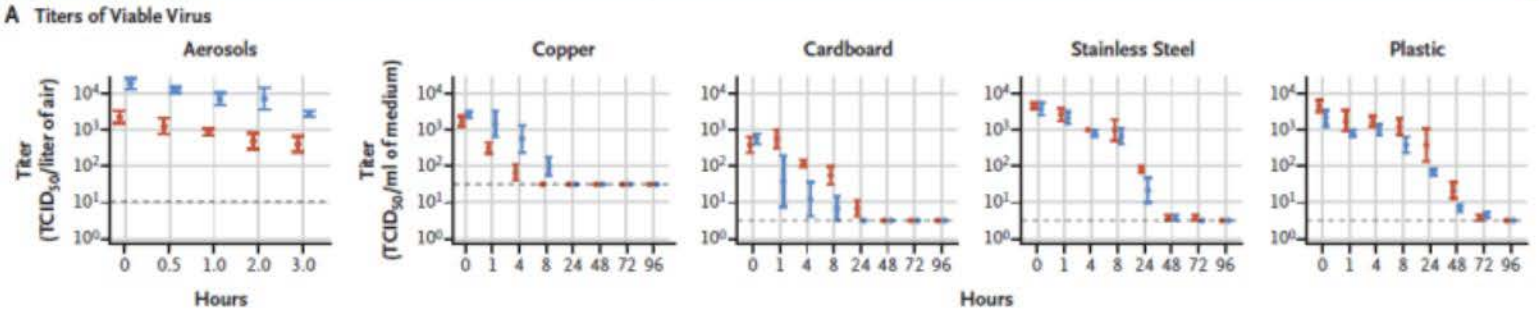

Neeltje van Doremalen *Vincent Munster*

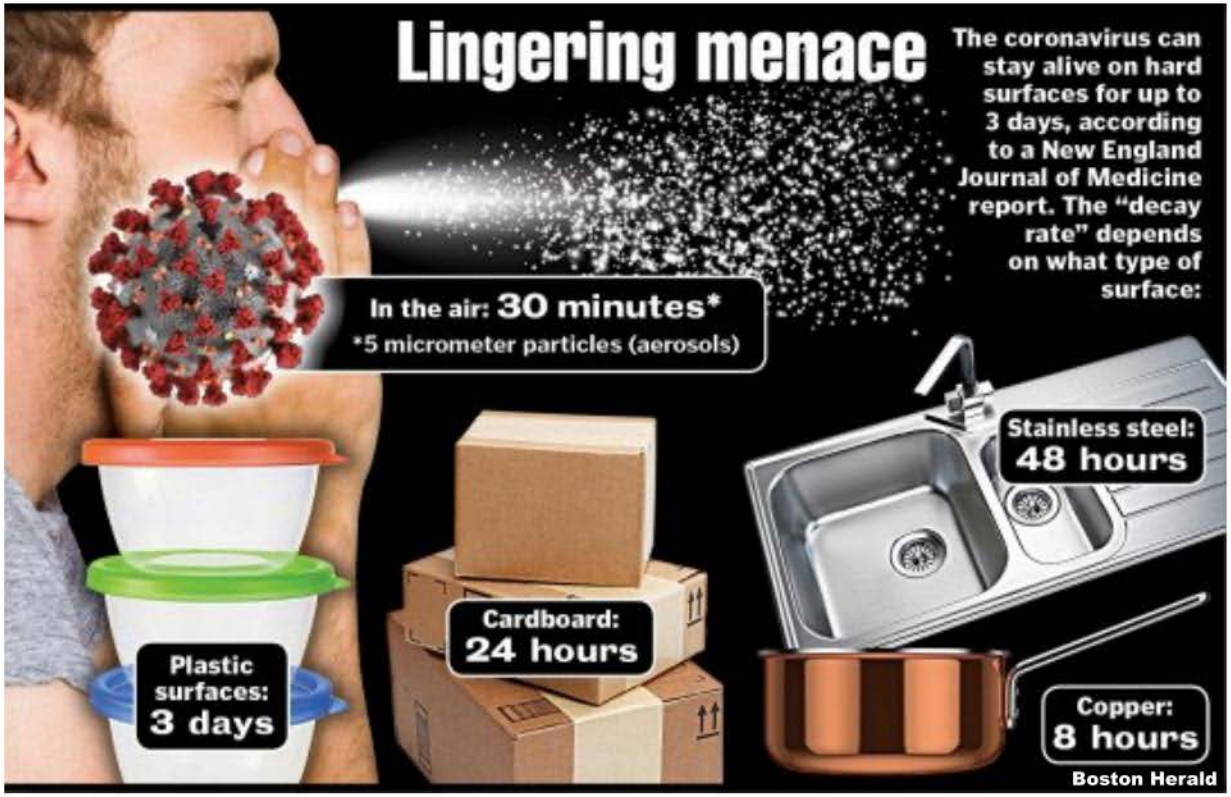

Dylan Morris *Amandine Gamble*

Van Doremalen et al. 2020, *NEJM*

COVID-19 – From virologic traits to transmission risk

Raw data





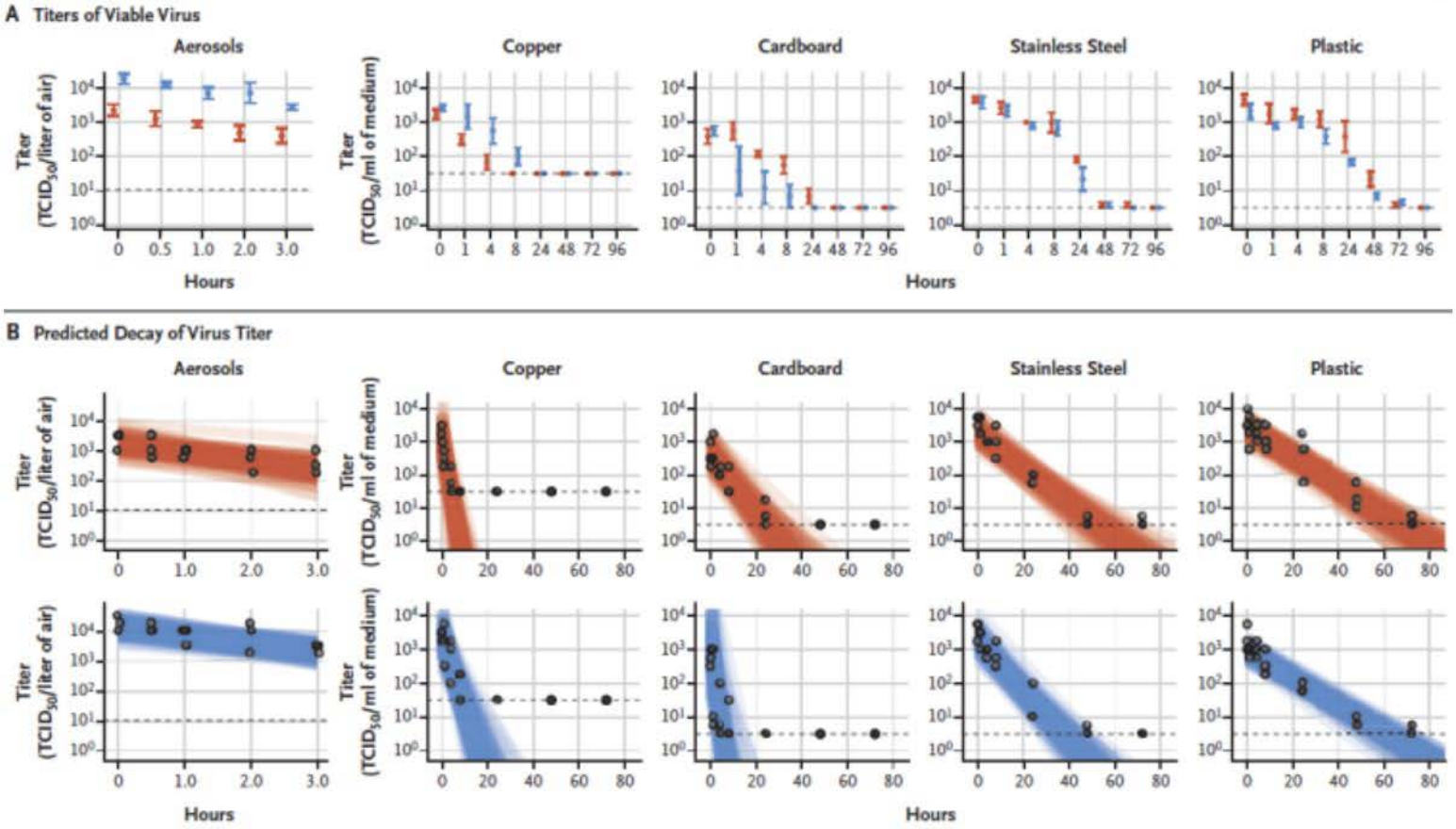
- SARS-CoV-2
- SARS-CoV-1

Van Doremalen et al. 2020, *NEJM*

COVID-19 – From virologic traits to transmission risk

Raw data

Decay rate



- Bayesian modeling of the data to estimate the decay rate…
  … which enabled us to estimate the half-life in each environment

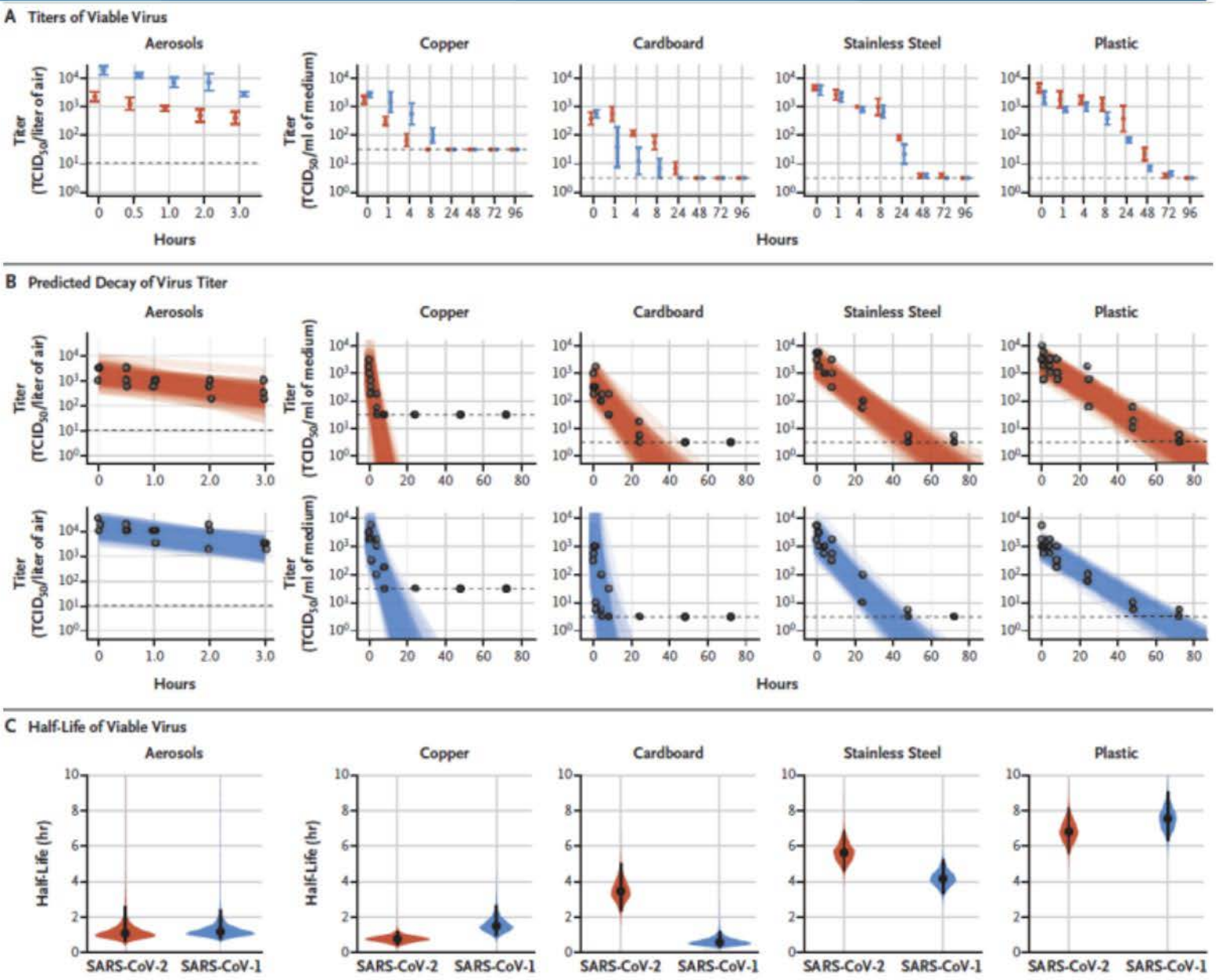
Van Doremalen et al. 2020, *NEJM*

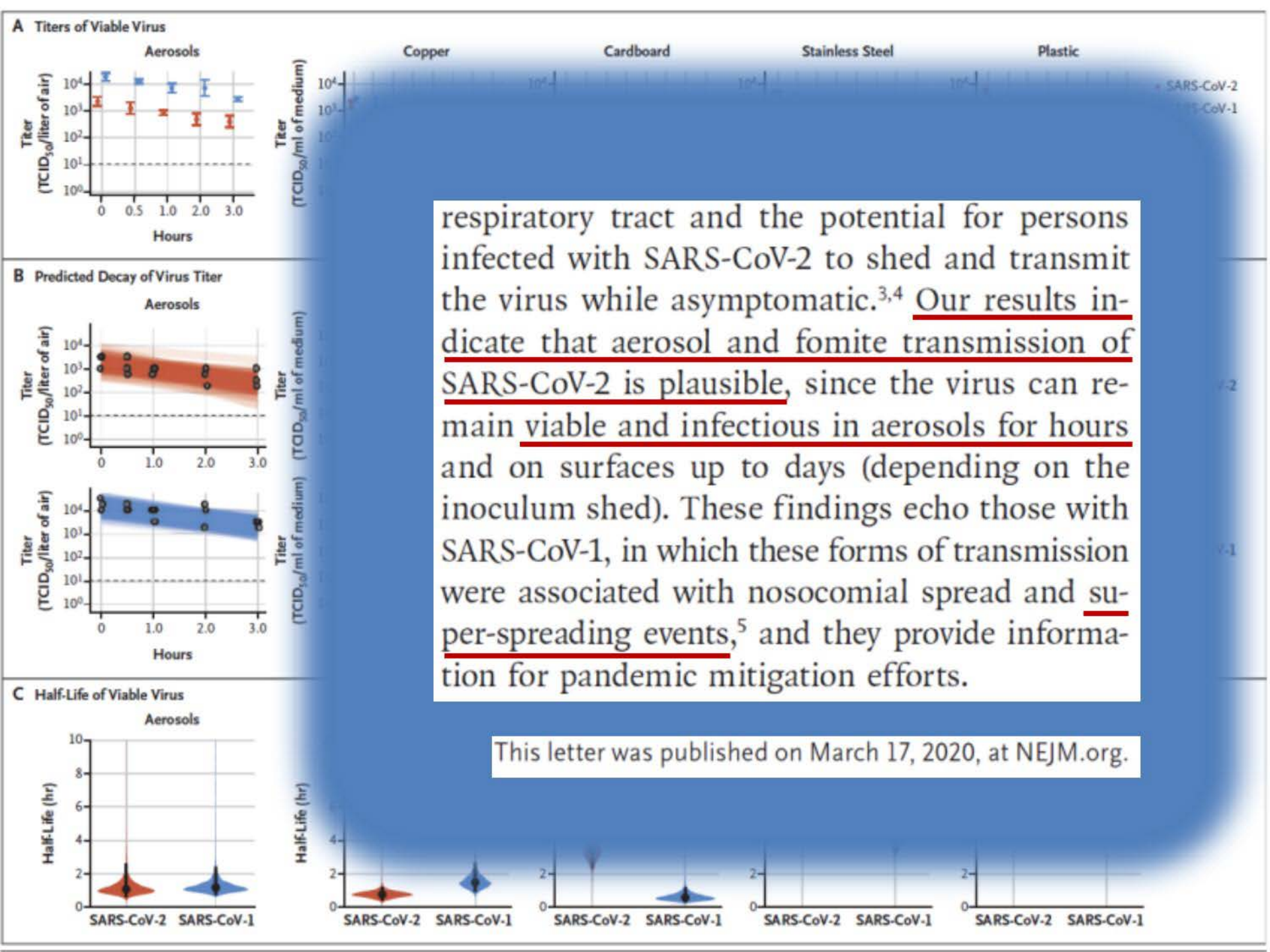
COVID-19 – From virologic traits to transmission risk

Raw data

Decay rate

Half-life





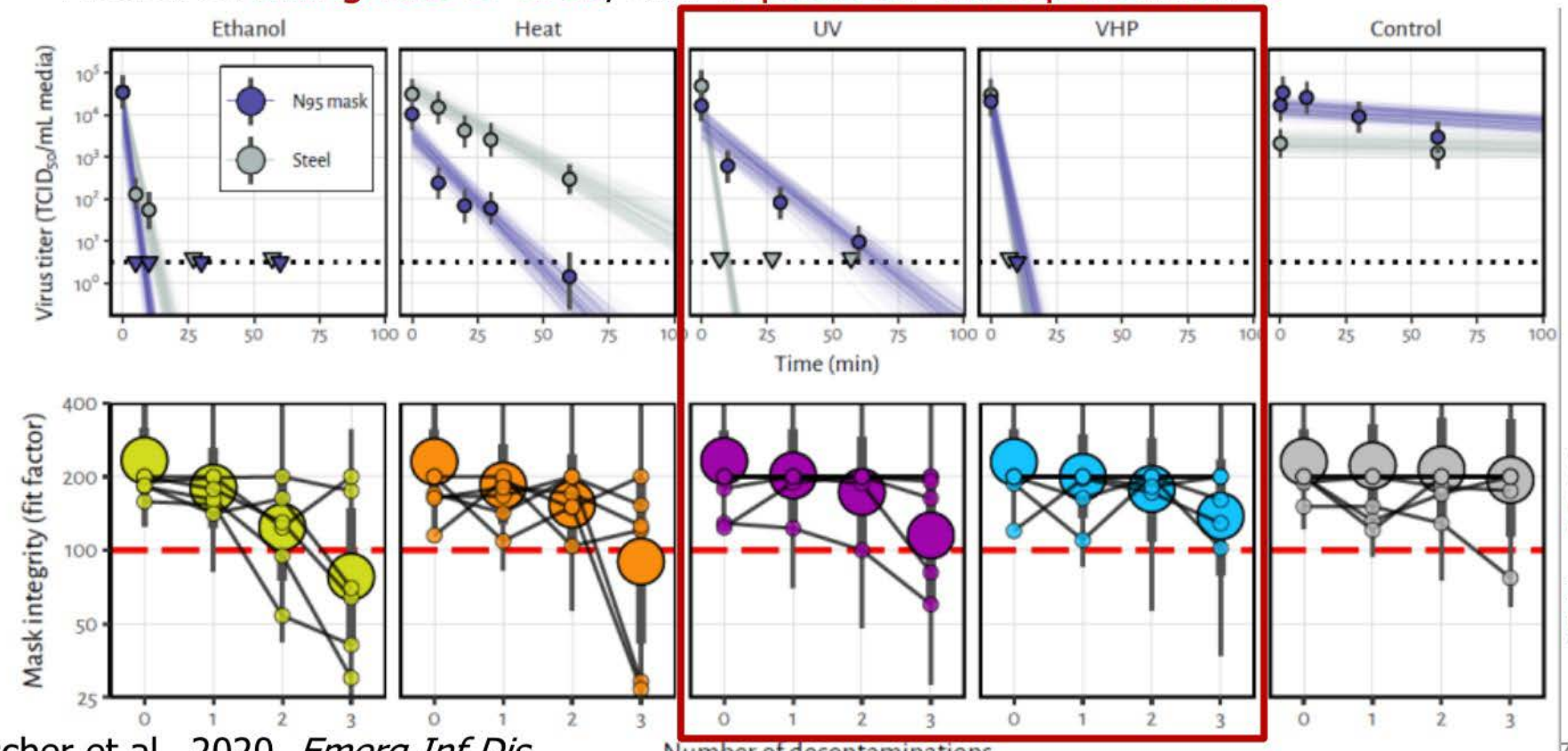
respiratory tract and the potential for persons infected with SARS-CoV-2 to shed and transmit the virus while asymptomatic.[3,4] Our results indicate that aerosol and fomite transmission of SARS-CoV-2 is plausible, since the virus can remain viable and infectious in aerosols for hours and on surfaces up to days (depending on the inoculum shed). These findings echo those with SARS-CoV-1, in which these forms of transmission were associated with nosocomial spread and super-spreading events,[5] and they provide information for pandemic mitigation efforts.

This letter was published on March 17, 2020, at NEJM.org.

Aside: Applications to pandemic mitigation

PPE is essential, but scarce! Can N95 masks be reused safely?

- Tested four methods for decontamination and reuse of N95 masks
  - Heat, UV-C radiation, ethanol, vaporized hydrogen peroxide
- Measured killing rate of virus, and impacts on mask performance



Fischer et al., 2020, *Emerg Inf Dis*

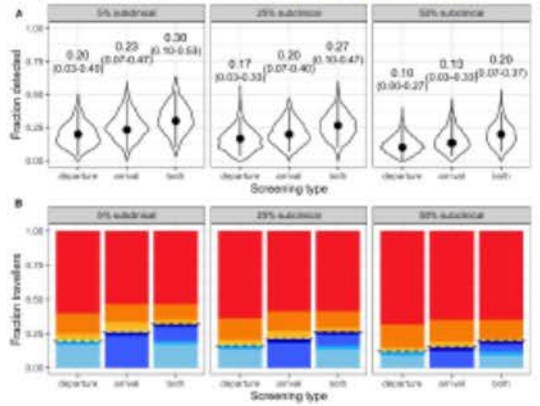
Aside: Applications to pandemic mitigation

eLIFE

Estimated effectiveness of symptom and risk screening to prevent the spread of COVID-19

Katelyn Gostic[1]*, Ana CR Gomez[2], Riley O Mummah[2], Adam J Kucharski[3], James O Lloyd-Smith[2,4]*

- Mathematical model integrating all host-level factors.
  - → Symptom and risk screening will **detect less than half** of infected people, maybe as few as **1 in 10.**



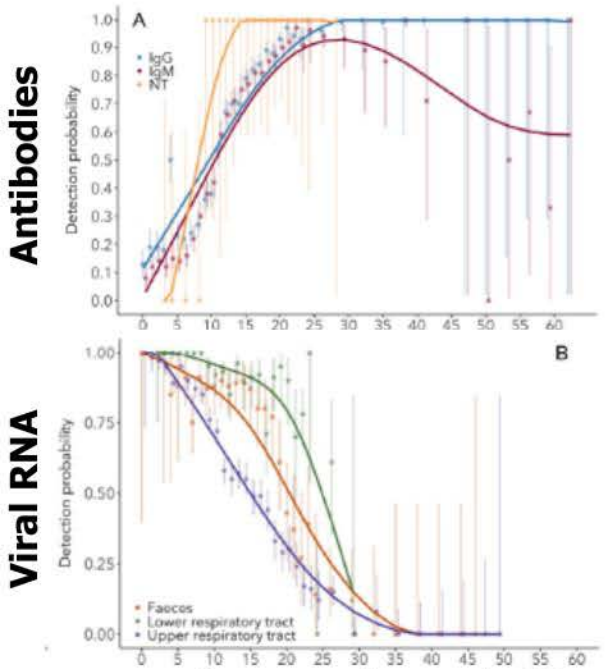
Gostic et al., 2020, *eLife*

eLIFE

Quantifying antibody kinetics and RNA detection during early-phase SARS-CoV-2 infection by time since symptom onset

Benny Borremans[1,2,3]*, Amandine Gamble[1], KC Prager[1], Sarah K Helman[1], Abby M McClain[4], Caitlin Cox[1], Van Savage[1,5], James O Lloyd-Smith[1]

- Quantitative meta-analysis of early data
  - → Time-course of **antibody and RNA detectability**, accounting for assay, target and severity.
  - → Guide use and interpretation of **testing** for clinical and epidemiological purposes.



Borremans et al., 2020, *eLife*

Virologic traits: Environmental effects on SARS-CoV-2 stability

Temperature and humidity can shape seasonality and transmission risk of respiratory viruses.

→ How would SARS-CoV-2 respond?

Experiments: measure surface stability of SARS-CoV-2 across 3 temperatures and 3 humidities.

10 °C 22 °C 27 °C	×	40% 65% relative humidity 85%

Modeling: to extract maximum insight from precious data, and generalize across settings and viruses.



Dylan Morris *Kwe Claude Yinda* *Amandine Gamble*

Morris, Yinda*, Gamble* et al., bioRxiv*

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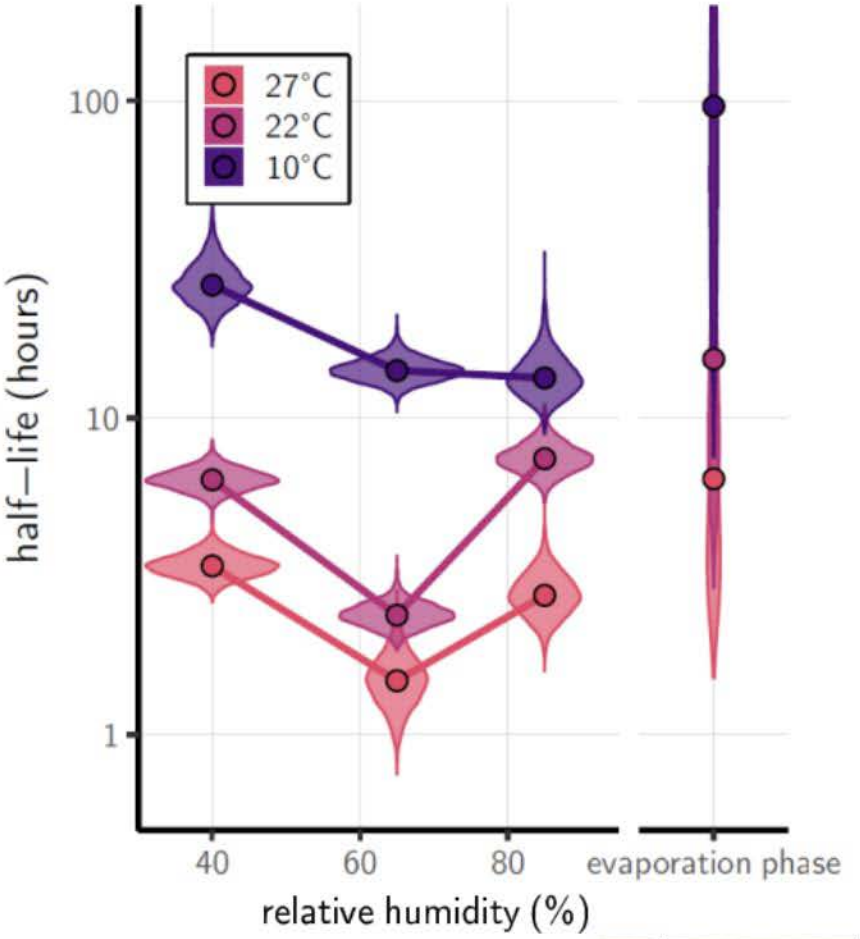



Dylan Morris


Kwe Claude Yinda


Amandine Gamble

Morris, Yinda*, Gamble* et al., bioRxiv*

Mechanistic model for temperature and humidity effects

Premise:

Inactivation is a chemical reaction, governed by physics and chemistry

Temperature dependence driven by Arrhenius kinetics.

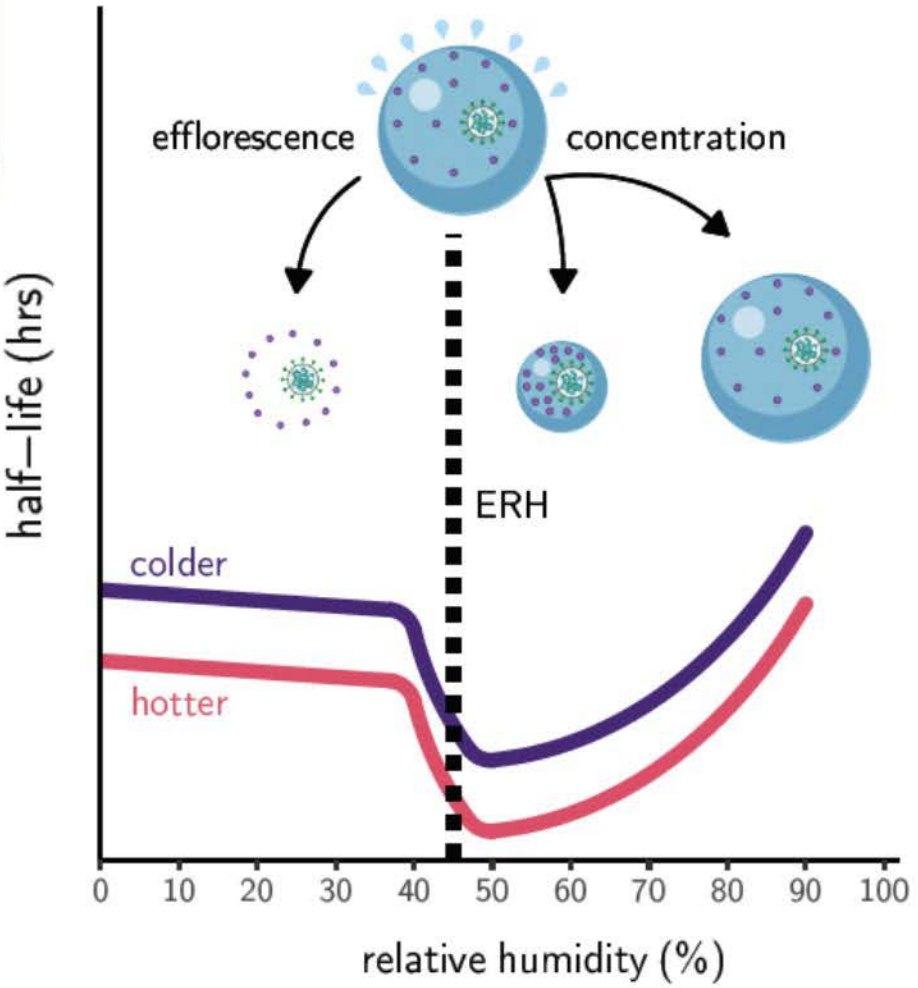
Humidity dependence has two distinct regimes, divided by the efflorescence relative humidity (ERH).

Below the ERH: crystal

$$k_{\text{eff}} = A_{\text{eff}} \exp\left(-\frac{E^a_{\text{eff}}}{RT}\right)$$

Above the ERH: solution

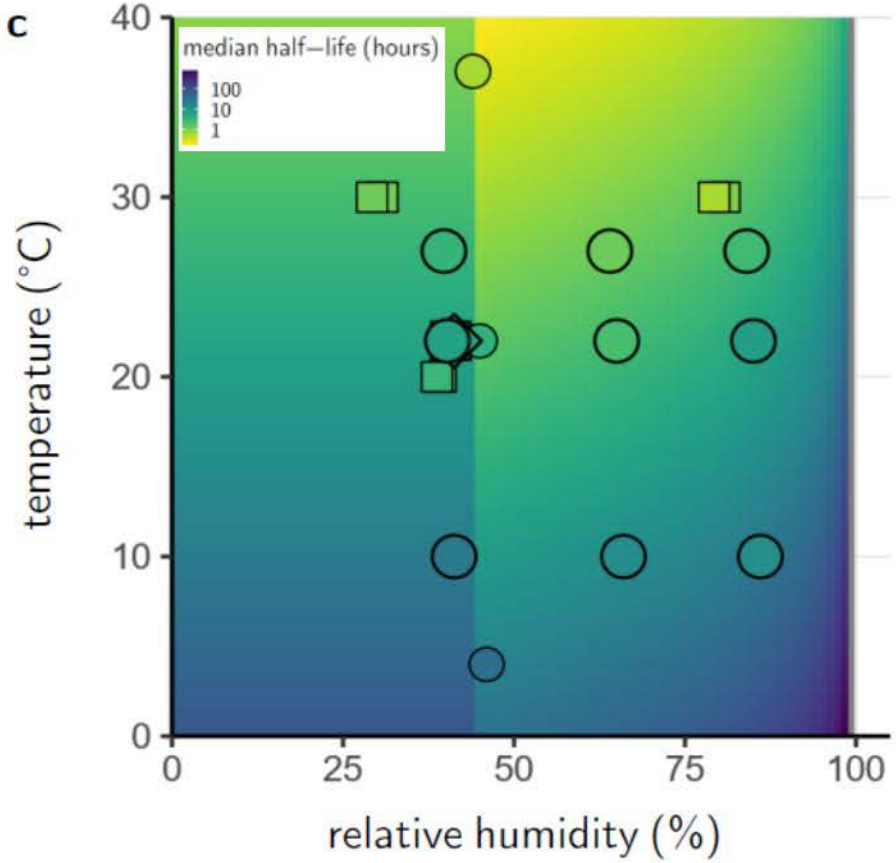
$$k_{\text{sol}} = \frac{[S_{\text{eq}}]}{[S_0]} A_{\text{sol}} \exp\left(-\frac{E^a_{\text{sol}}}{RT}\right)$$

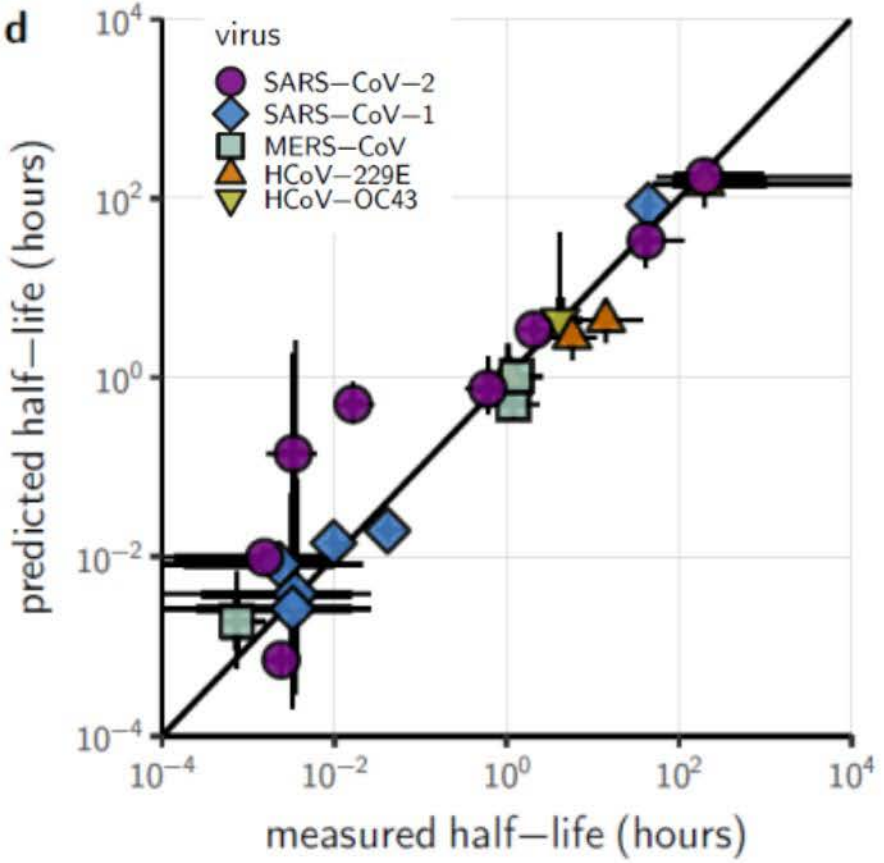


Morris, Yinda*, Gamble* et al., bioRxiv*

Predicting stability across settings and viruses

Mechanistic model predicts stability accurately, including data from other studies, unmeasured conditions of T and RH, and data from other coronaviruses.





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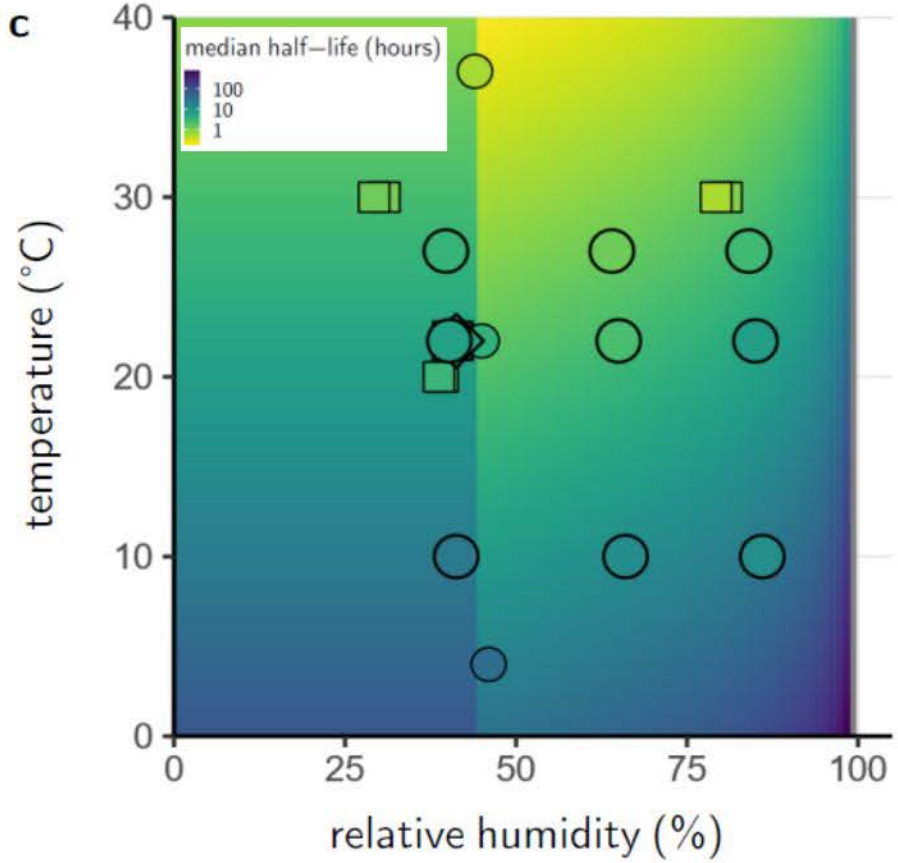
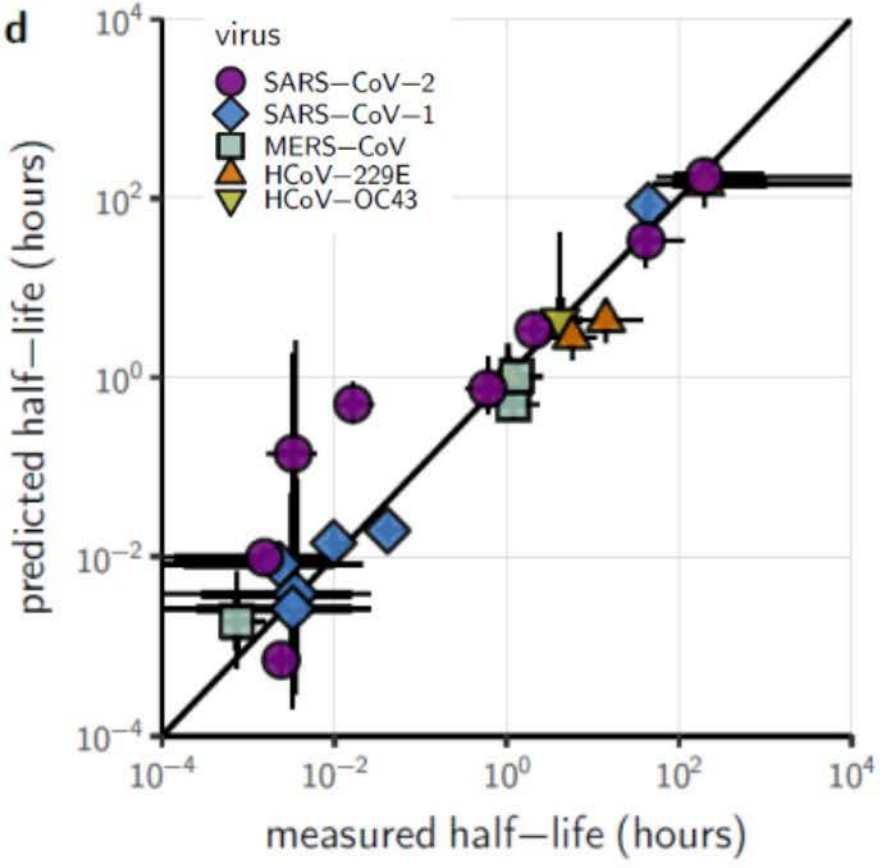




→ Temperature and humidity have strong effects on SARS-CoV-2 stability.

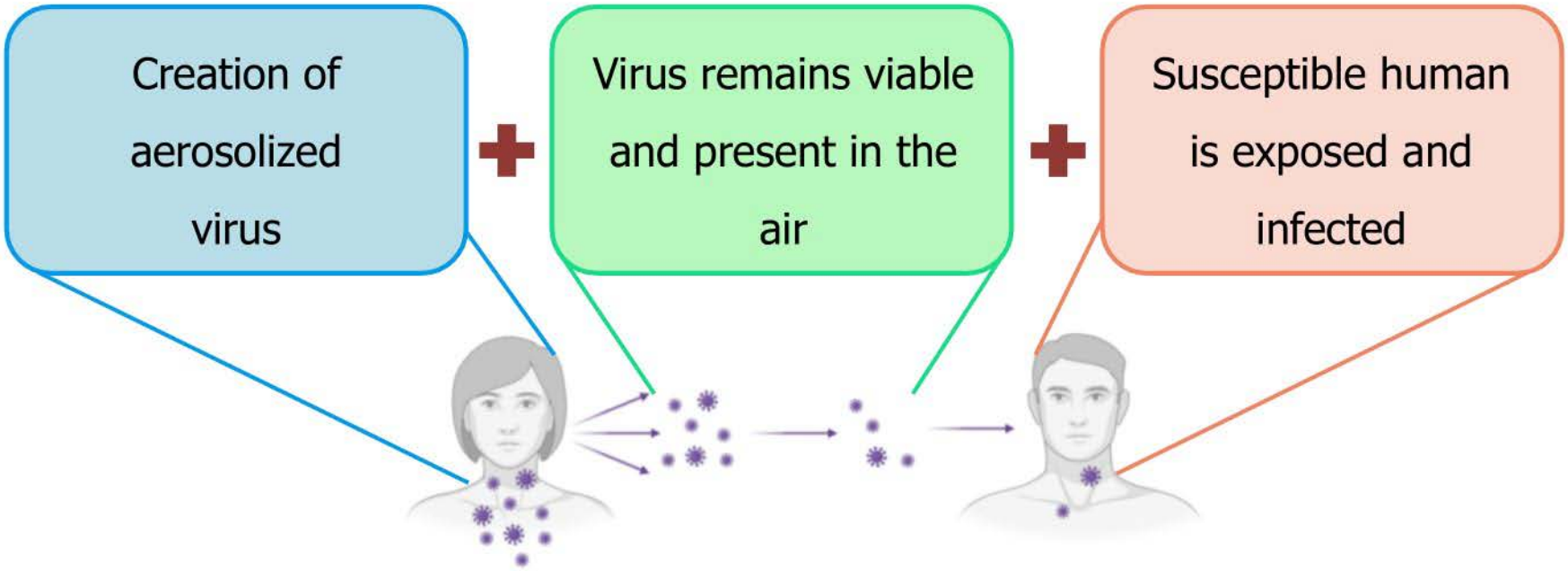
Predictive, mechanistic model → extrapolate to **new viruses**, new conditions.

From virologic traits to transmission risk

Modeling virological data to estimate transmission risk

Case study: aerosol infection

- For an airborne infection event, you need three processes to occur



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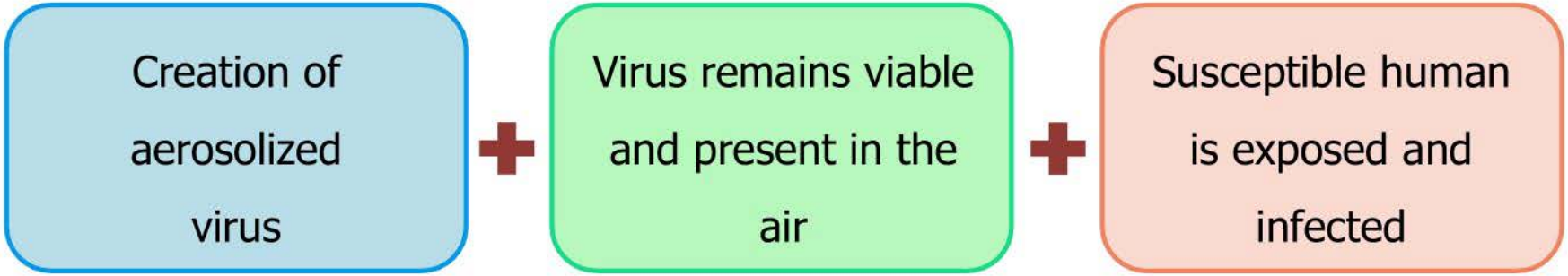
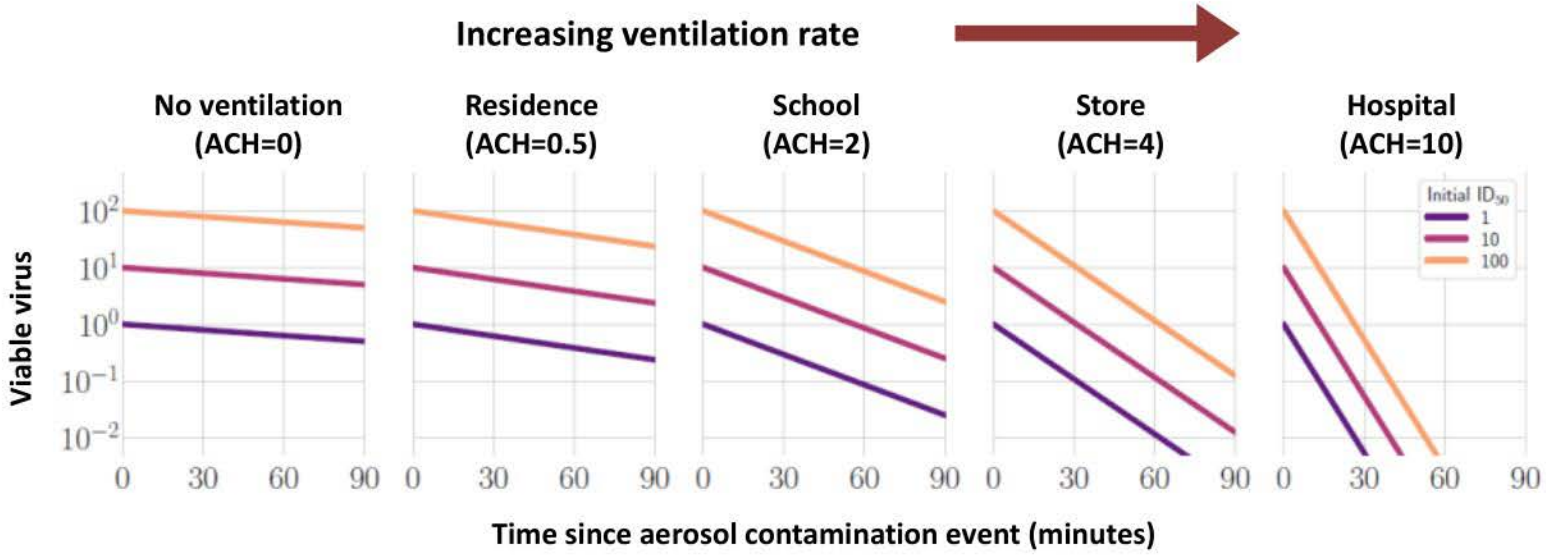


- Built mathematical model to integrate known factors
  Virus decay rate, aerosol physics, particle size distributions, dose-response theory
- Renormalized to ID_{50} units to compartmentalize the unknowns
  Aerosolization rates, infectious dose

→ Modeling tool to estimate infection risk using viral trait data

From virologic traits to transmission risk

- Modeled three exposure scenarios: **low-risk**, **medium-risk**, **high-risk** events



From virologic traits to transmission risk

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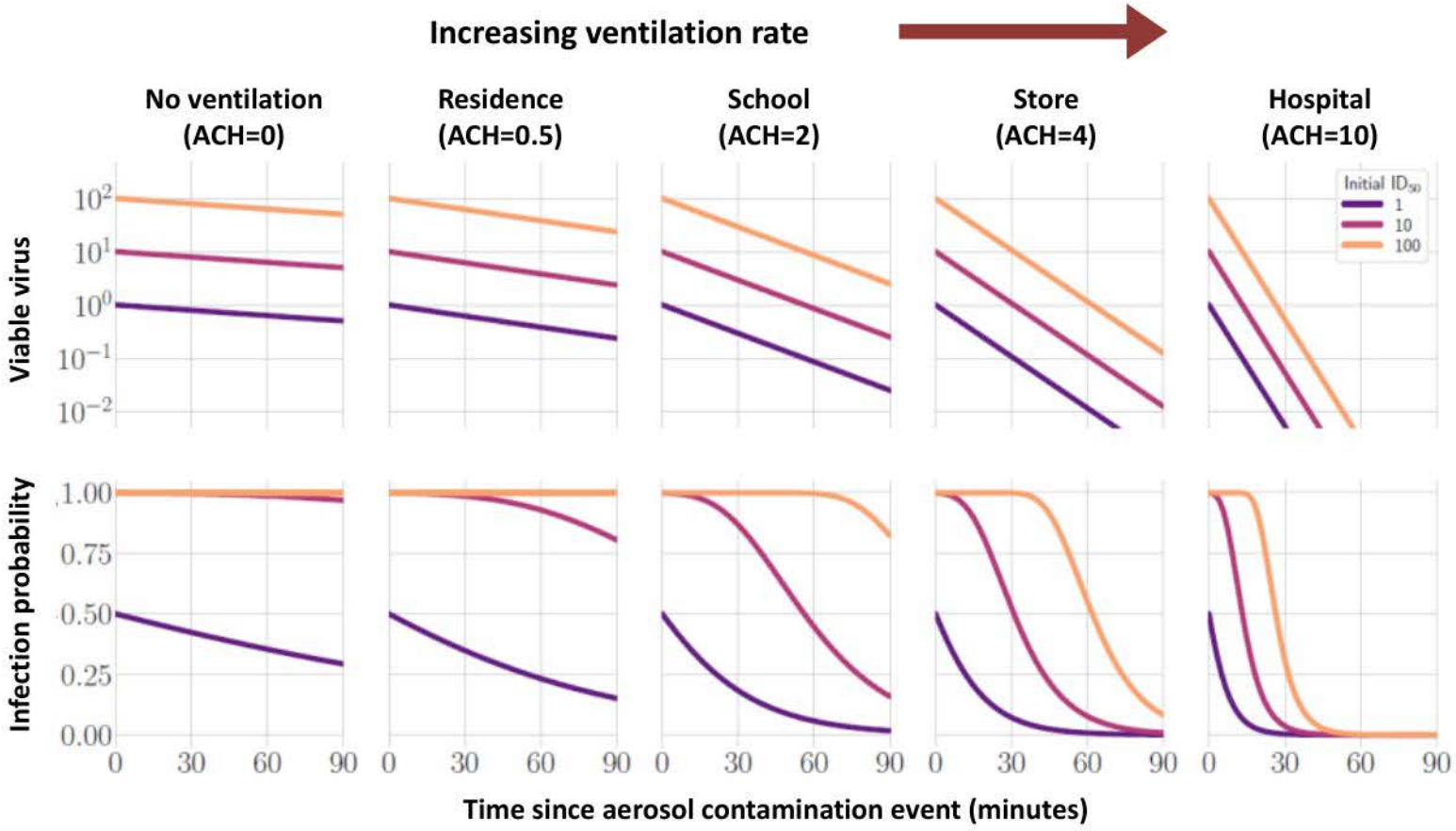


→ **Ventilation is the most important factor** in reducing airborne risk

No ventilation → risk lasts for hours

High-ventilation hospital settings → risk lasts 10s of minutes

New variants and increased transmissibility

How is **increased transmissibility** driven by (measurable) **changes in viral traits?**

New variants: viral traits and increased transmissibility

The Lancet

New variant of SARS-CoV-2 in UK causes surge of COVID-19

BBC

Covid-19: New variant 'raises R number by up to 0.7'

The Mutated Virus Is a Ticking Time Bomb

The New York Times

New California Variant May Be Driving Virus Surge There, Study Suggests

How is **increased transmissibility** driven by (measurable) **changes in viral traits?**

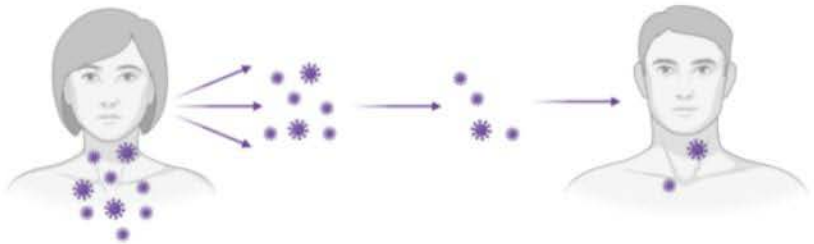
Creation of aerosolized virus

+

Virus remains viable and present in the air

+

Susceptible human is exposed and infected



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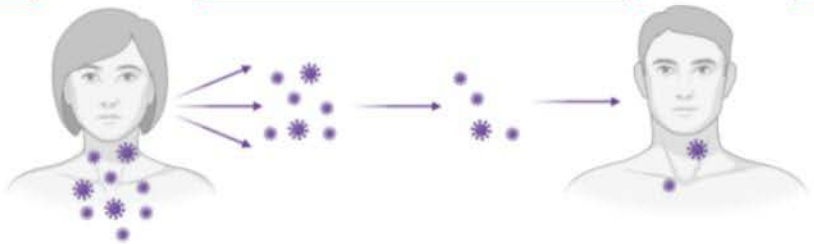
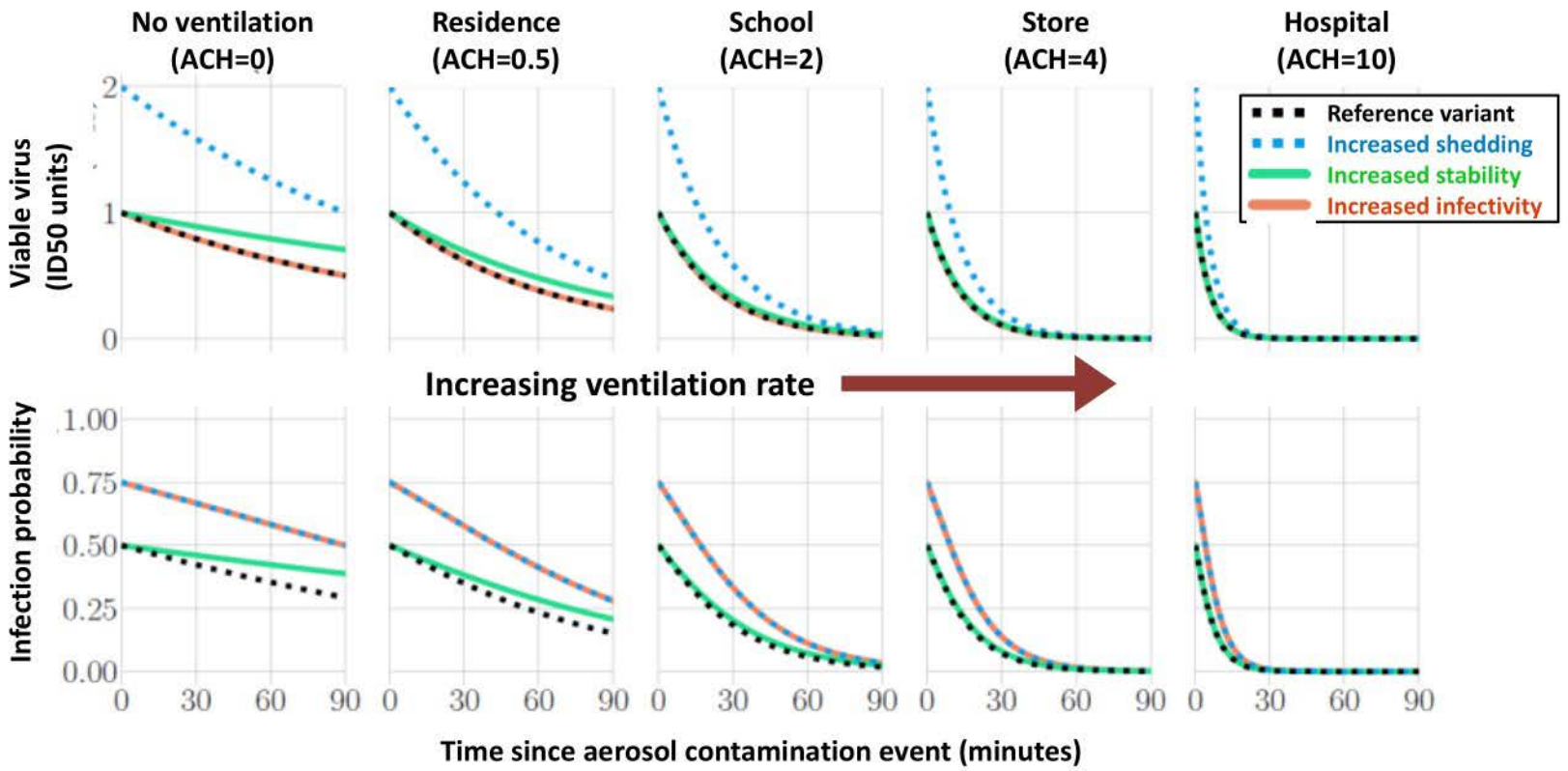
How is **increased transmissibility** driven by (measurable) **changes in viral traits?**

Creation of aerosolized virus	+	Virus remains viable and present in the air	+	Susceptible human is exposed and infected
Increased shedding		Increased stability		Increased infectivity



Effects of two-fold change in each viral trait

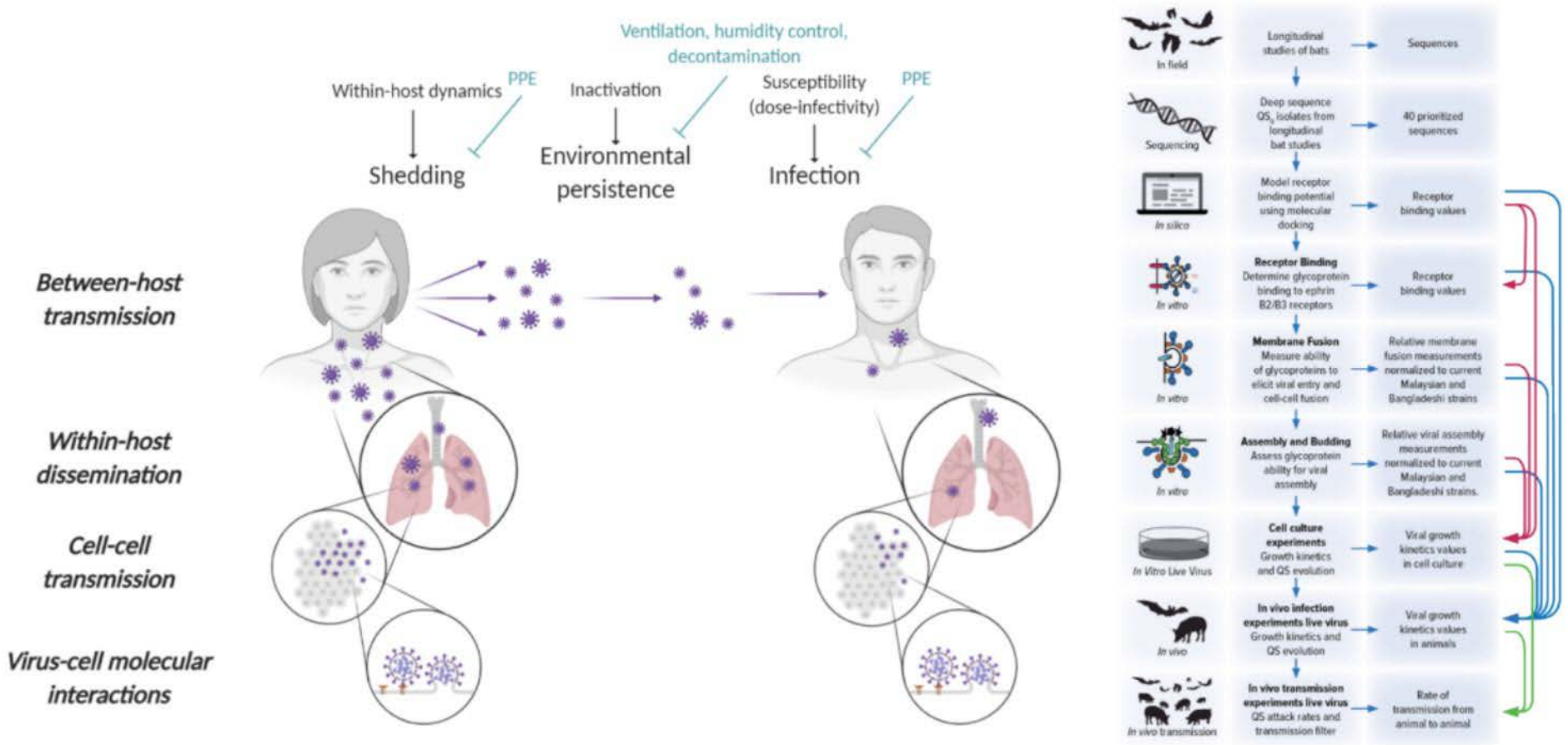


Effect of increased **stability** on risk is easily nullified by ventilation.
Increased **shedding** or infectivity have stronger, more pervasive effects.

Higher **shedding** boosts **contamination** levels most, but its impact on **infection risk** is identical to increased infectivity.

But interventions (**PPE**, **contact reduction**) will have differential efficacy.

From virologic traits to transmission risk



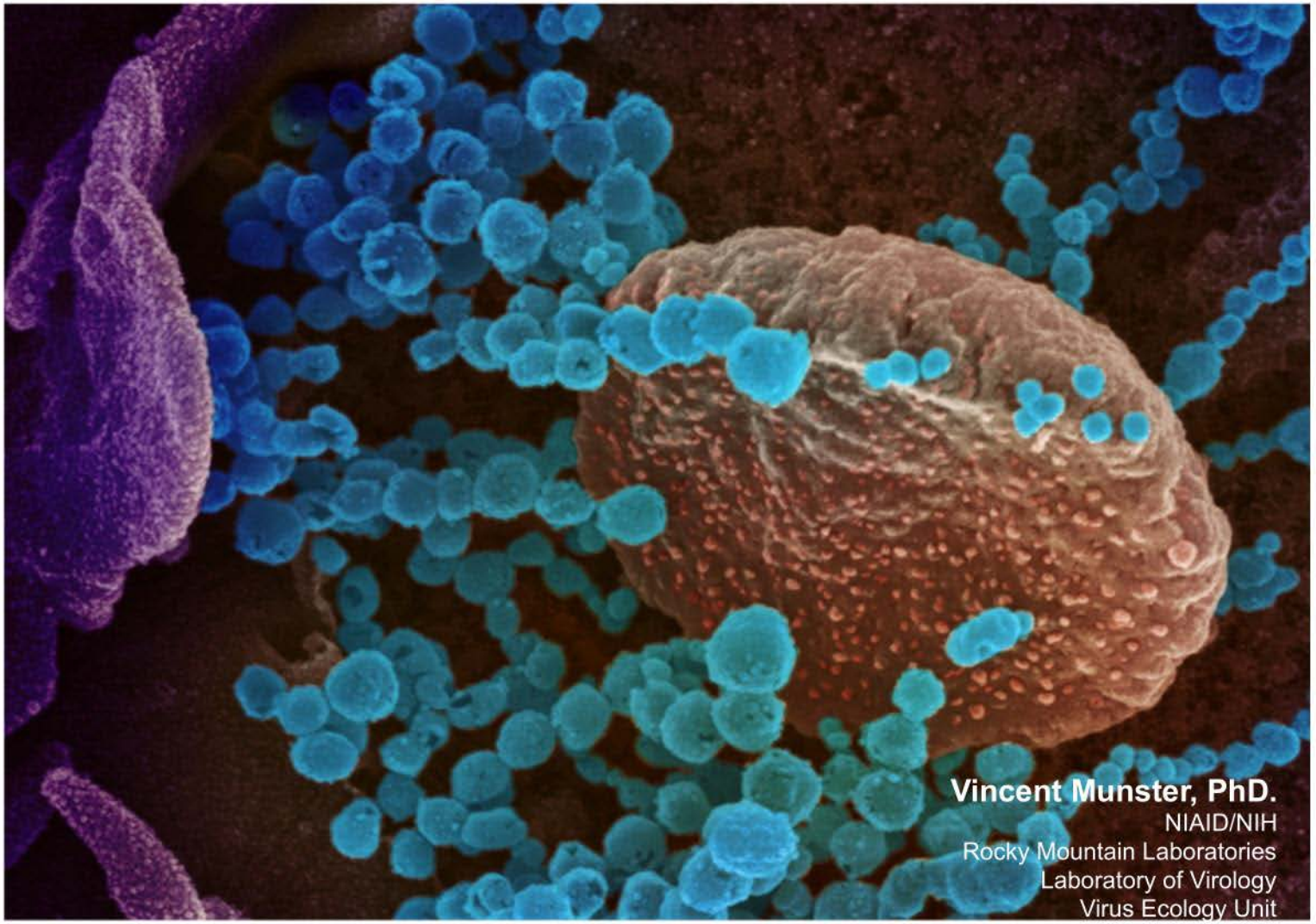
An integrated and iterative program

of experiments and modeling

→ Predict transmission phenotype (route, efficiency and mitigation)

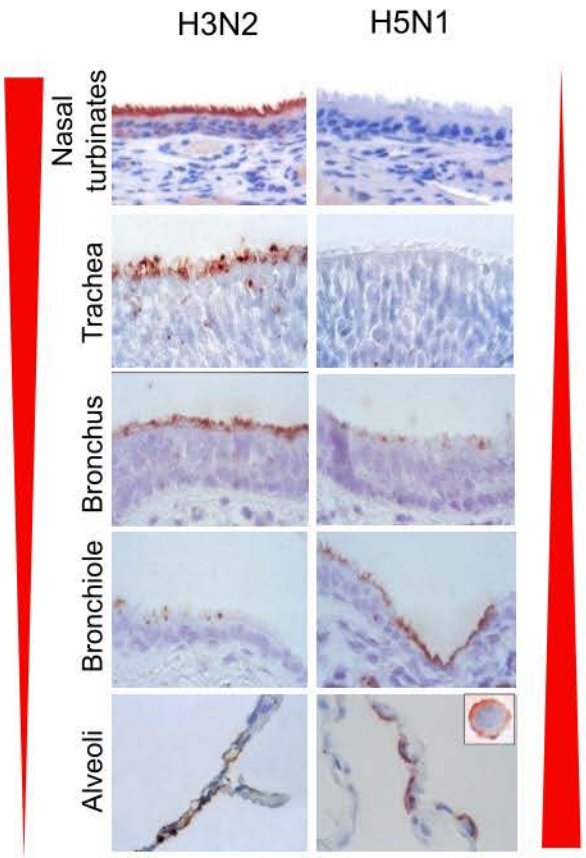
from measurable viral traits

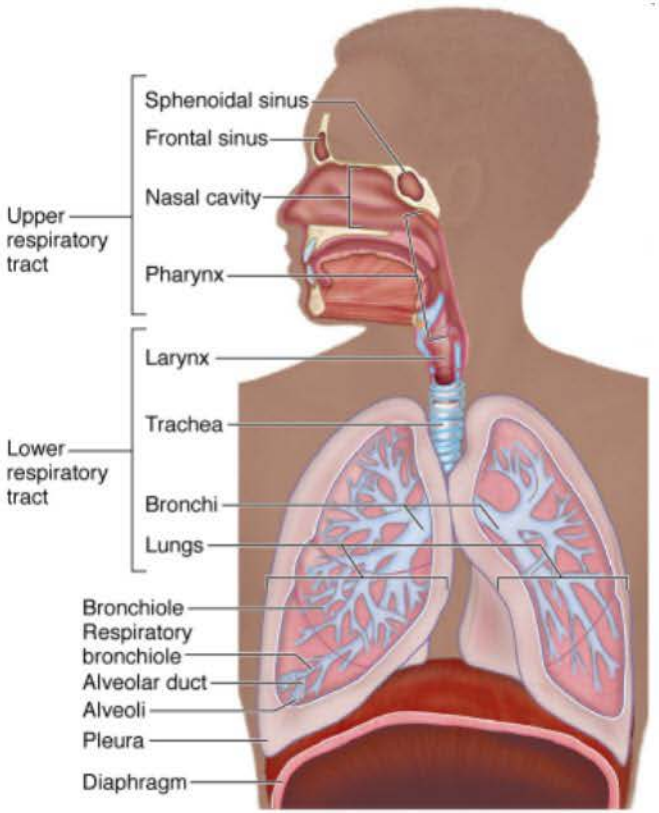
From virologic traits to transmission risk: SARS-CoV-2

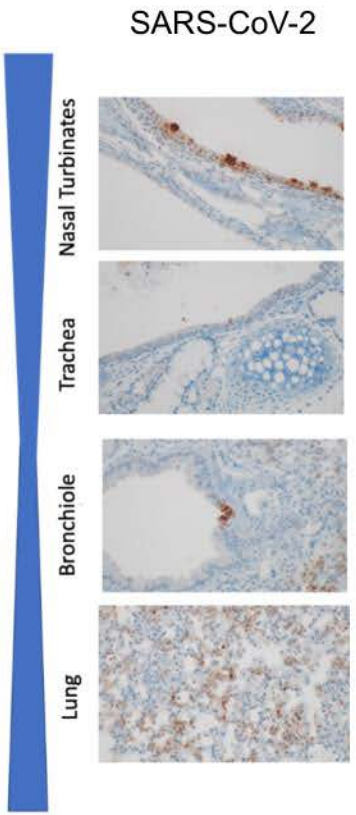


Influenza A virus

- Virus ecology, host factors, receptor distribution-

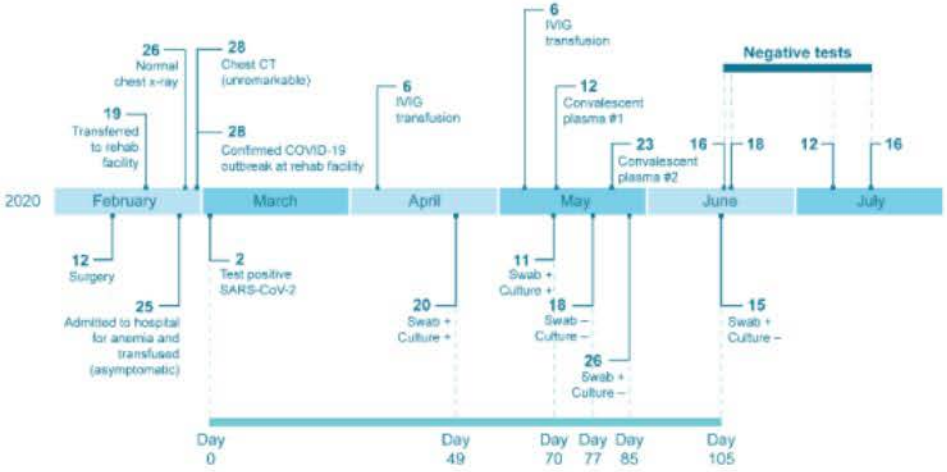


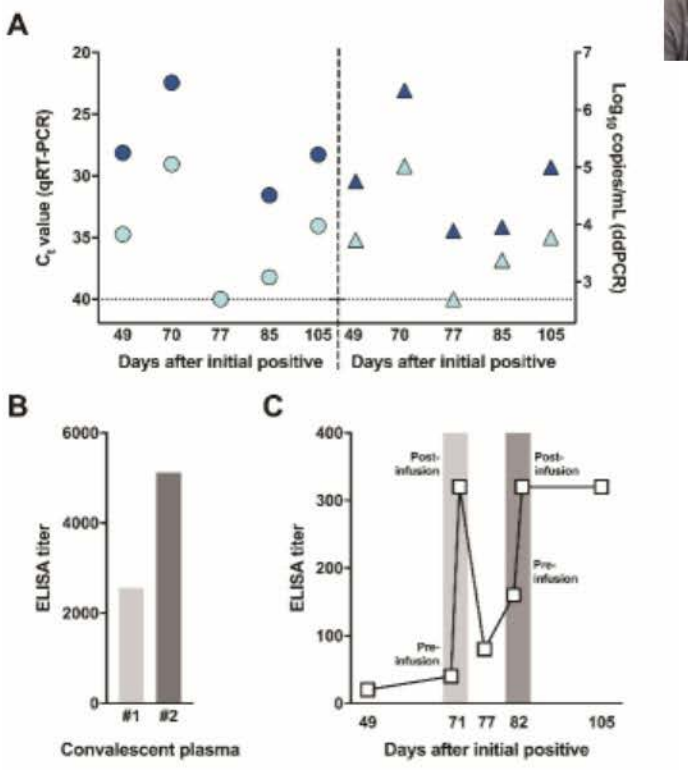




Van Riel, Munster, Science 2006
Munster, de Wit, Science 2009
Munster, Nature 2020

Case Study: Prolonged infectious SARS-CoV-2 shedding from an asymptomatic immunocompromised cancer patient





(Avanzato et al., Cell 2020)

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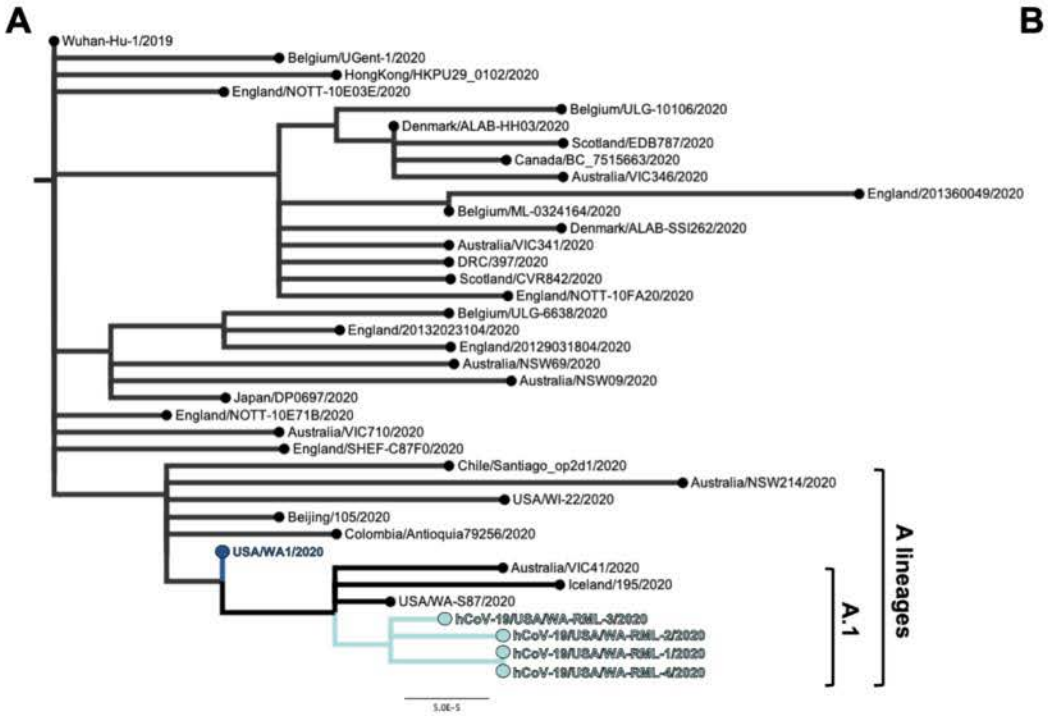
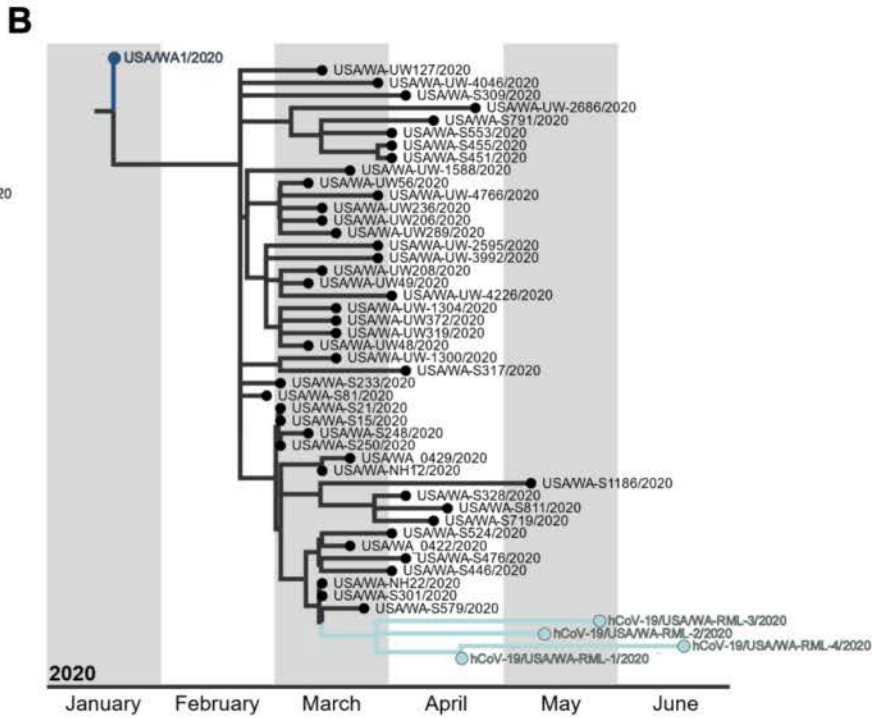
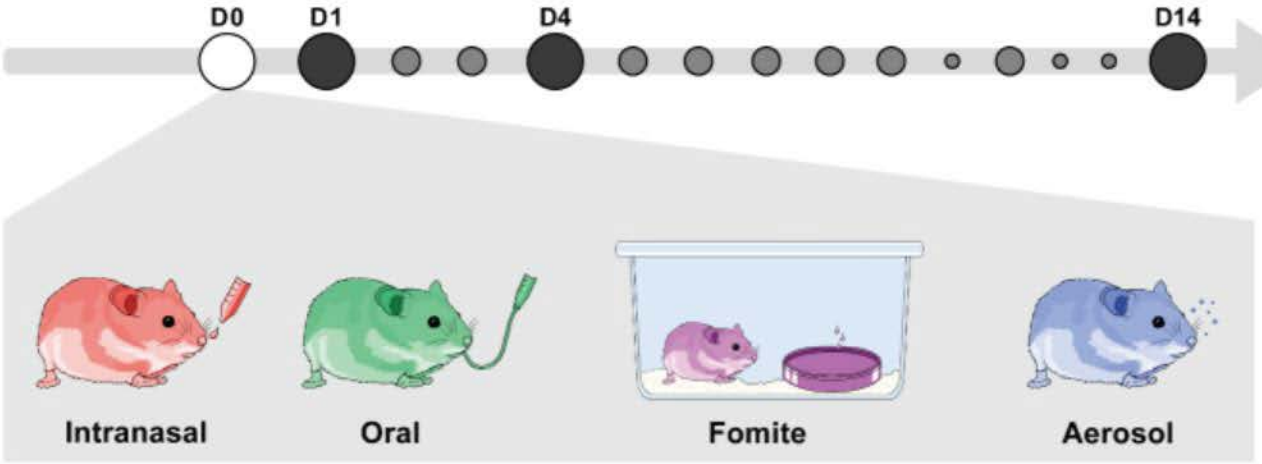




(Avanzato et al., Cell 2020)

- Experimental transmission-

(1) Primary routes of exposure

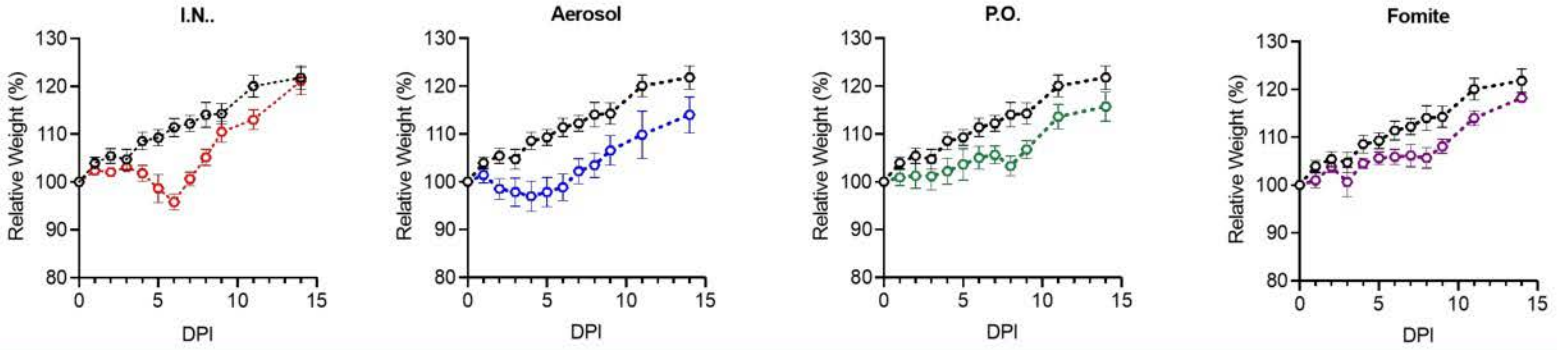


- Infection with $8x10^4$ SARS-CoV-2
- Serial necropsies
- Oropharyngeal and rectal sampling

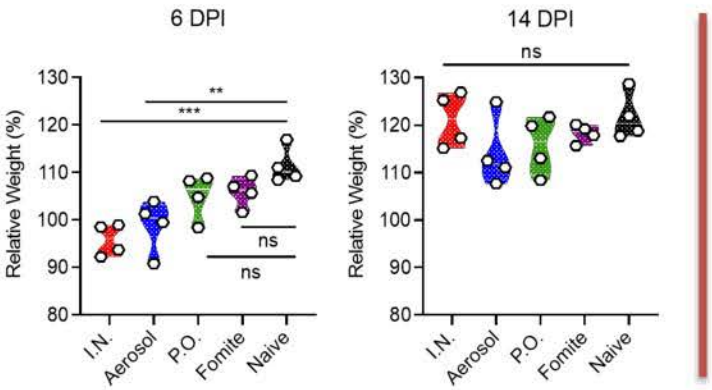
(Port et al., https://www.biorxiv.org/content/10.1101/2020.12.28.424565v1)

Primary Routes of Exposure: Disease Manifestation

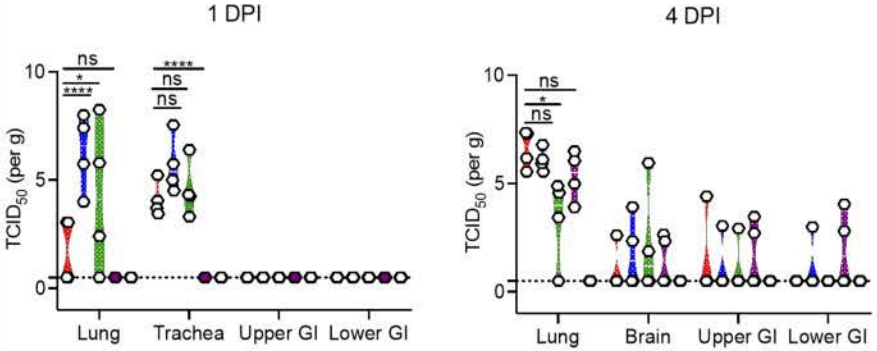
a.



b.



c.



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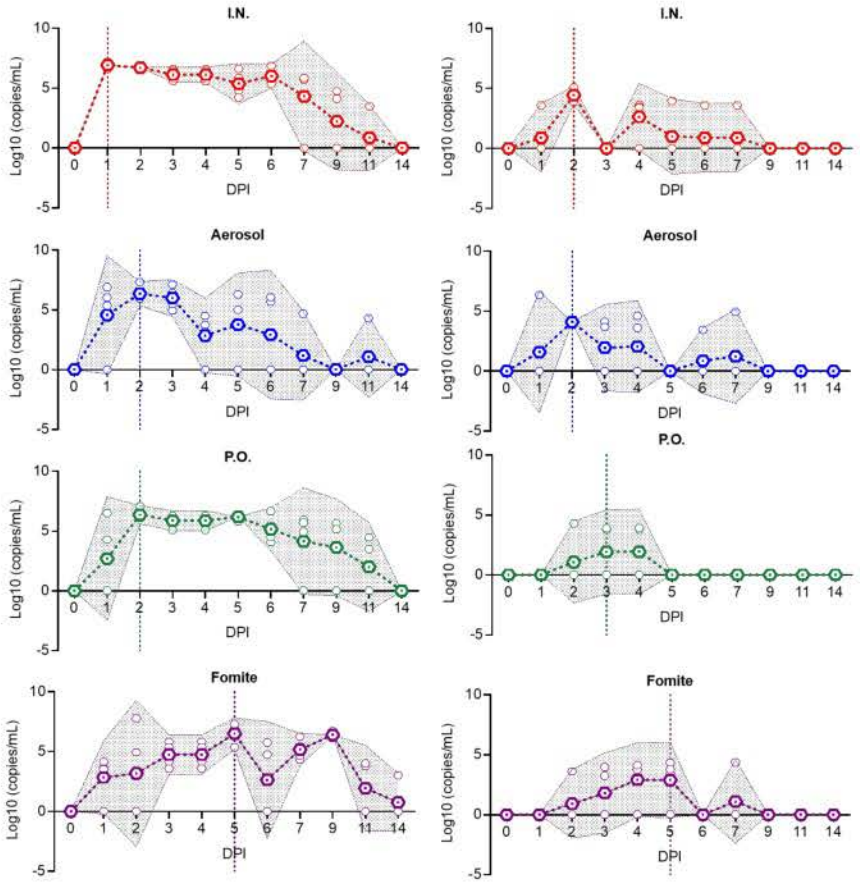
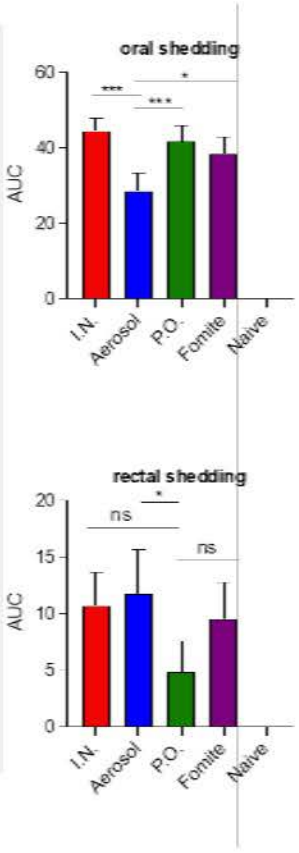
Primary Routes of Exposure: Shedding-profile

a. Oropharyngeal Rectal



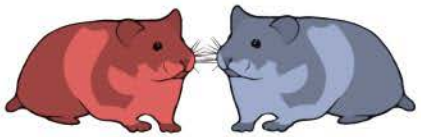
b.



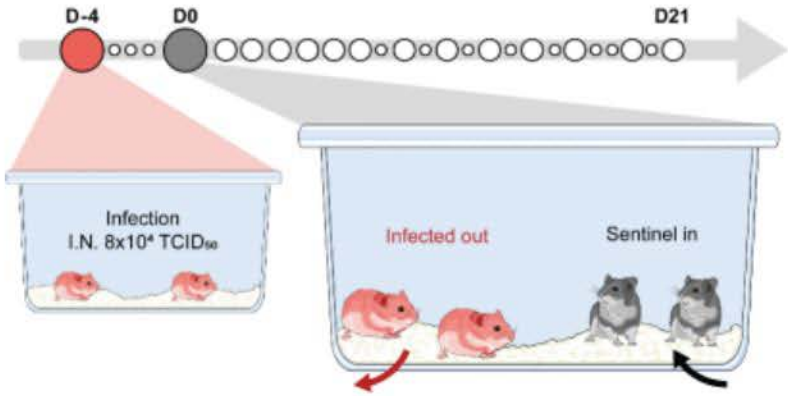
(Port et al., https://www.biorxiv.org/content/10.1101/2020.12.28.424565v1)

Hamster-to-Hamster Transmission

(2)
Hamster-to-
Hamster transmission

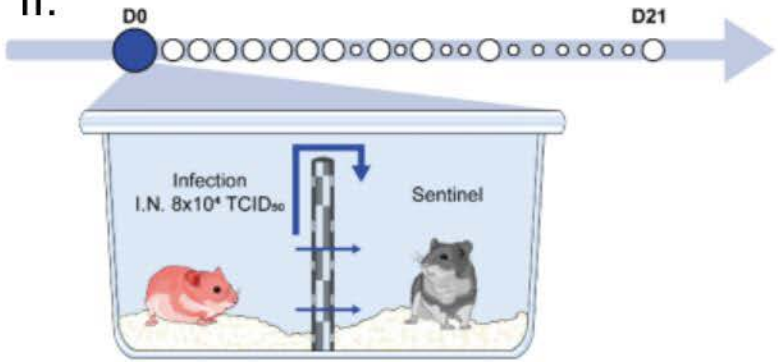


I.



- Infection with $8x10^4$ SARS-CoV-2
- Hamster exchange
- Oral sampling

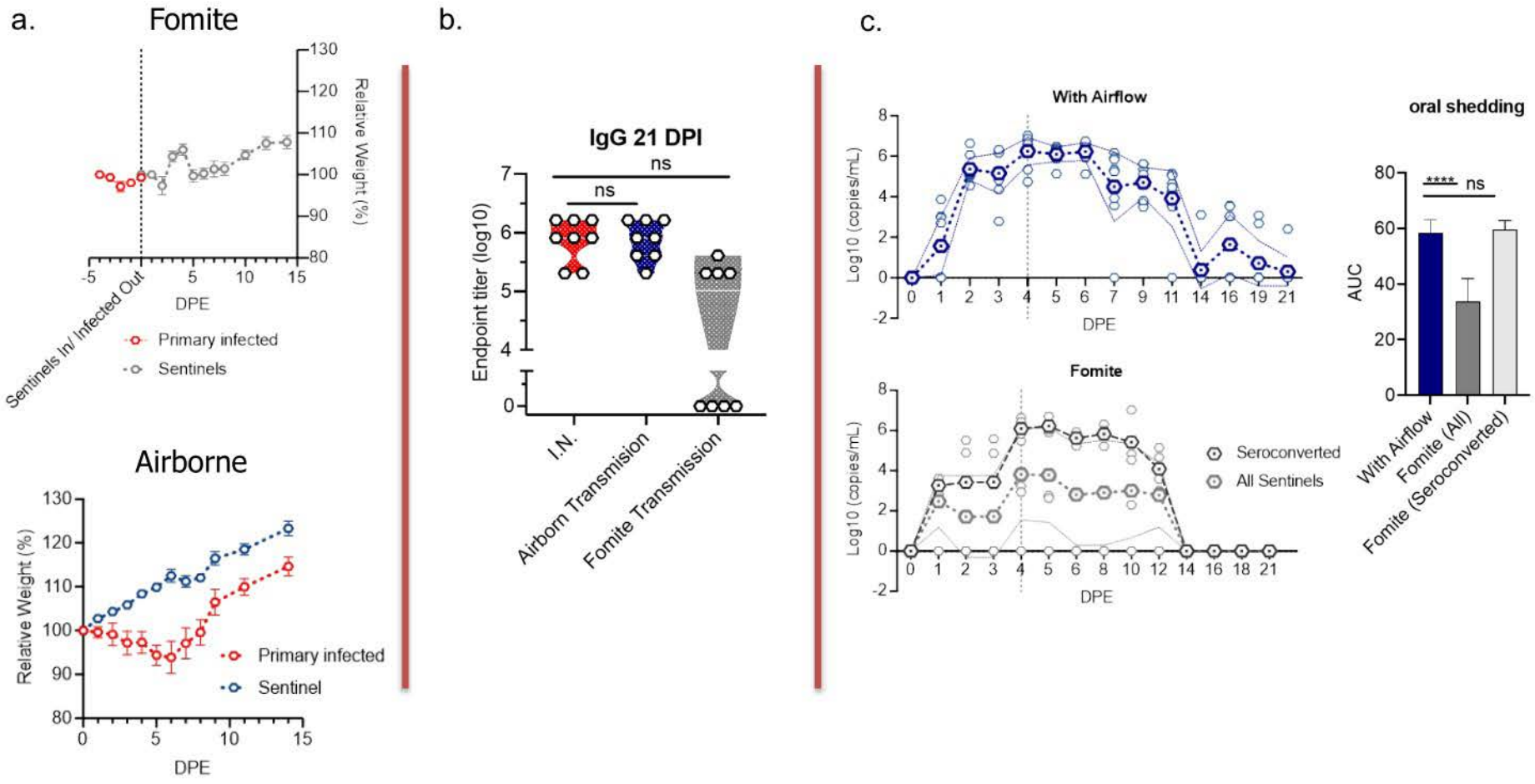
II.



- Infection with $8x10^4$ SARS-CoV-2 and start co-housing
- Oral sampling

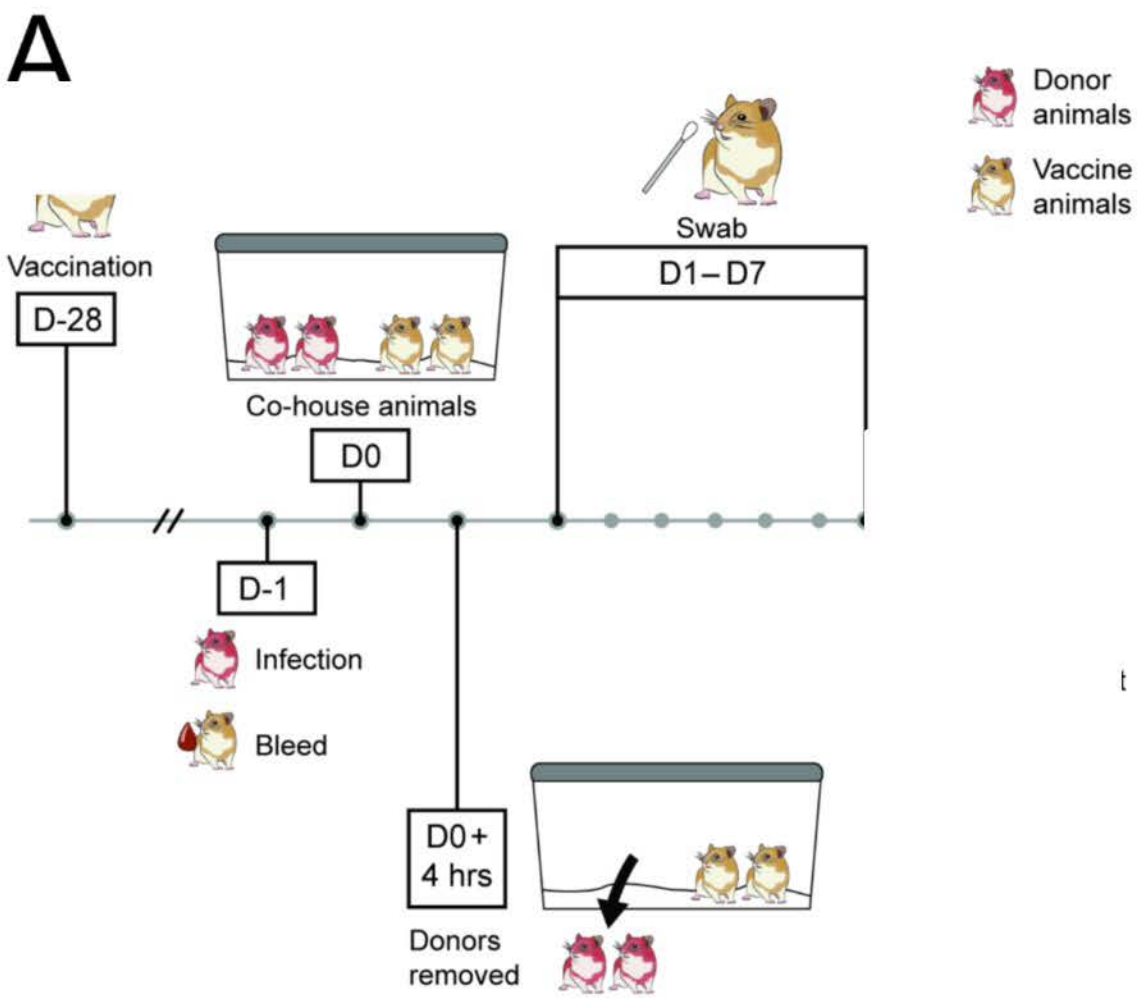
(Port et al., https://www.biorxiv.org/content/10.1101/2020.12.28.424565v1)

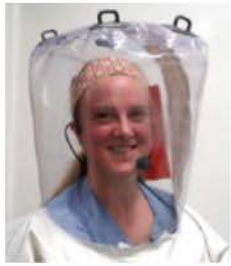
Hamster-to-Hamster Transmission: Disease Manifestation



(Port et al., https://www.biorxiv.org/content/10.1101/2020.12.28.424565v1)

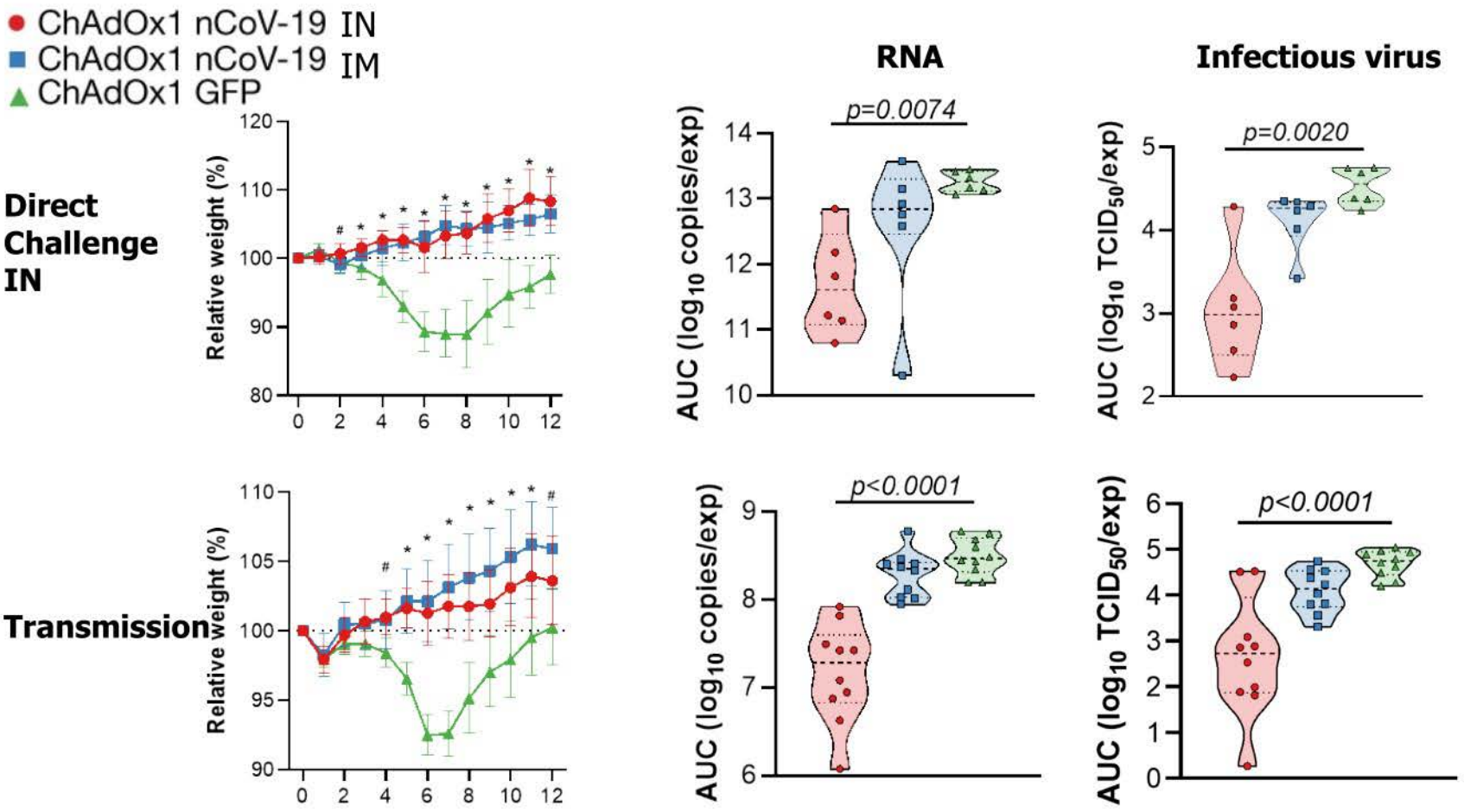
AZD1222: assessment intranasal vaccination



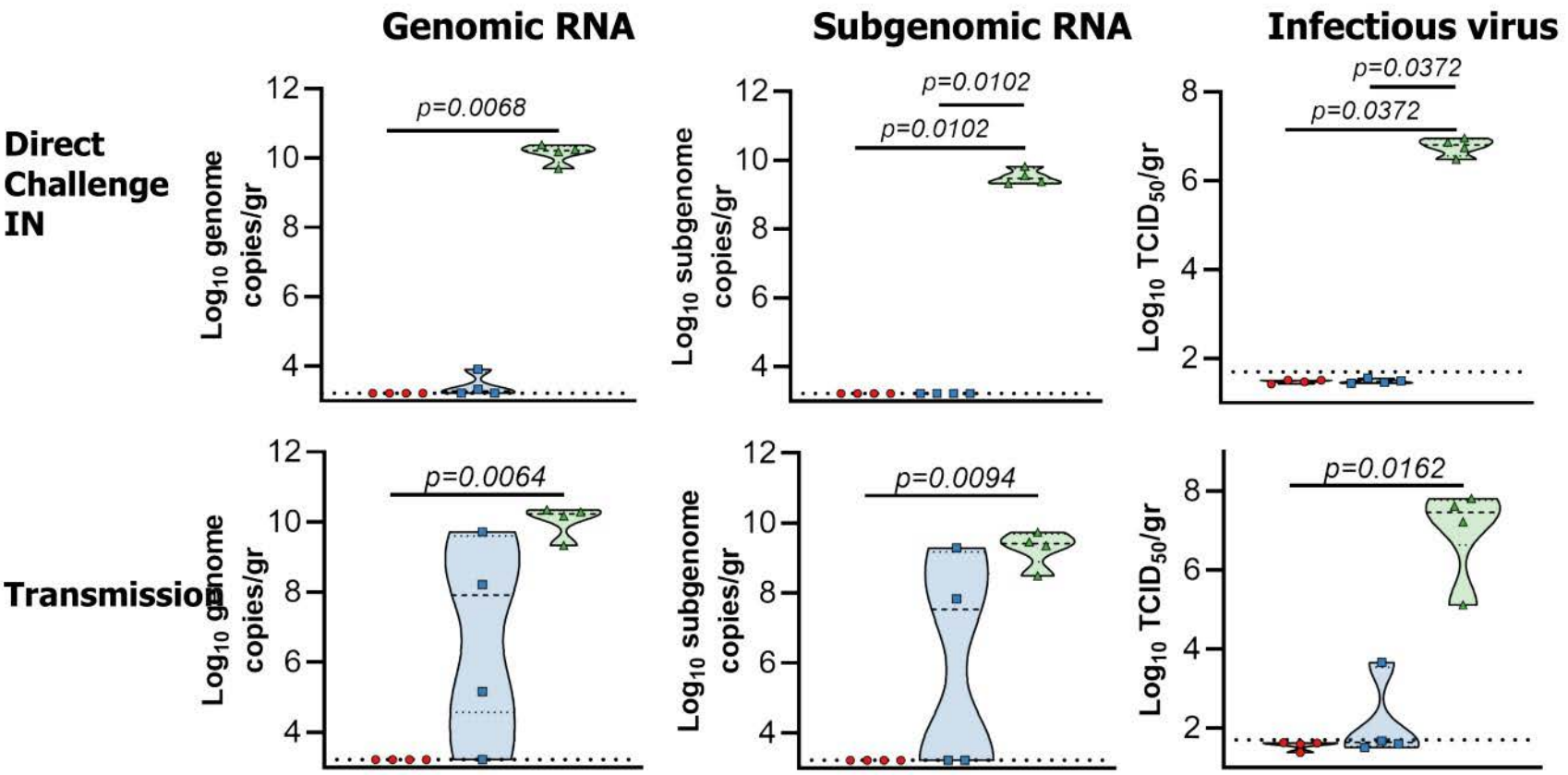


Preprint – BioRXiv, van Doremalen, 2021

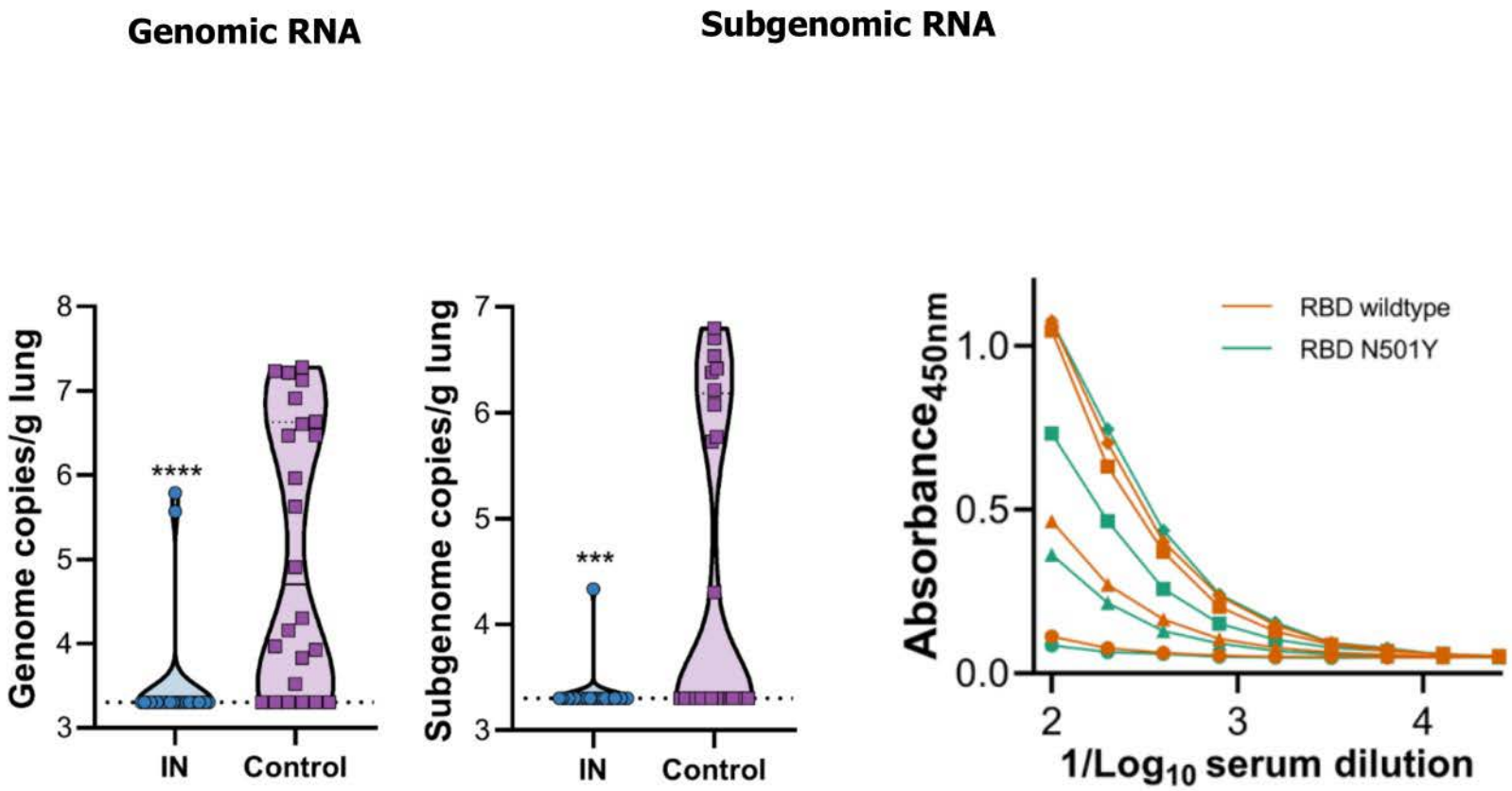
Shedding is reduced, particularly in intranasal vaccine group



Intranasal vaccination fully protects lower respiratory tract



Reduced amount of viral RNA in lung tissue (7 DPI)

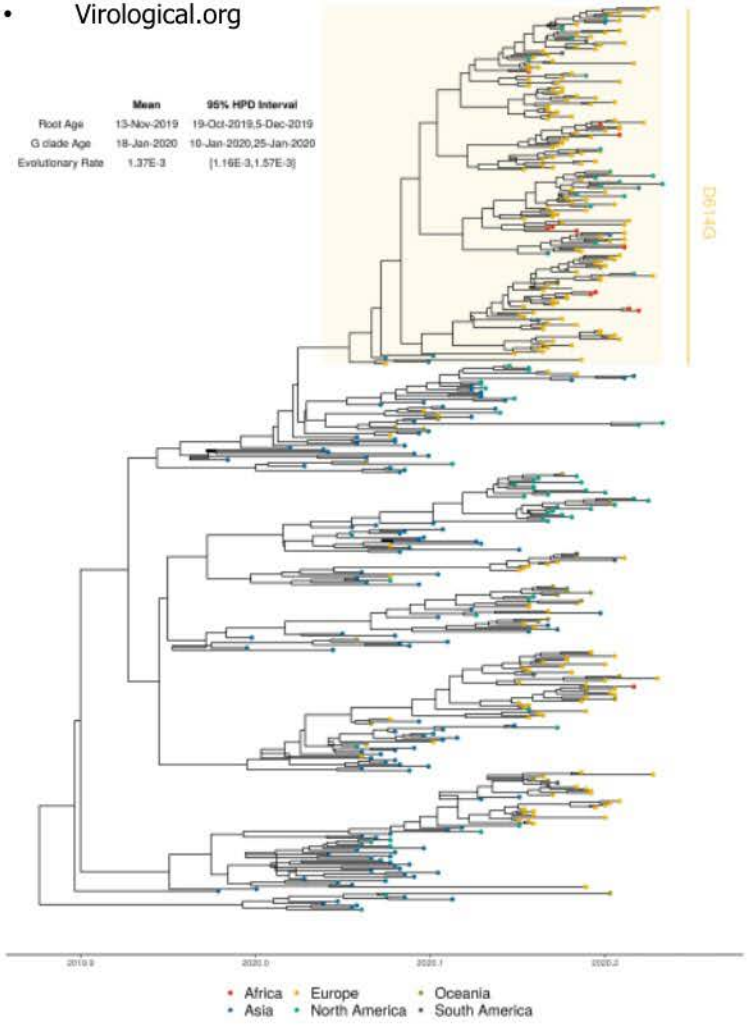


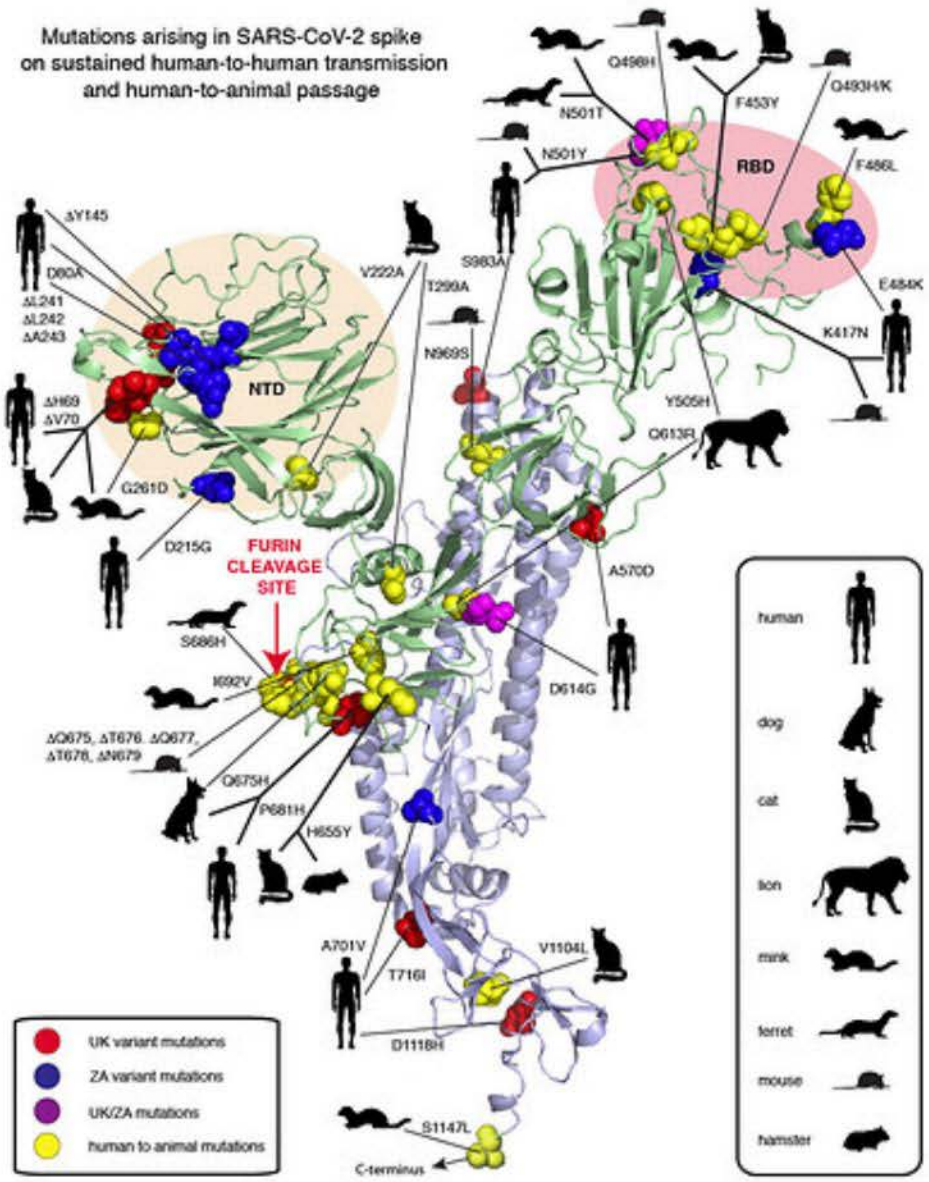
Preprint – BioRXiv, van Doremalen, 2021

Ongoing and future work

Assessment of genotypic and phenotypic characterization of SARS-CoV-2 (pathogenicity, transmissibility and antigenicity)

- Virological.org





Isabel et al., scientific reports & Garry, virological.org

From: Plowright, Raina
Sent: Thu, 28 Jan 2021 17:04:04 +0000
To: Zeitouni, Nathalie (contr-bto); Munster, Vincent (NIH/NIAID) [E]; Barbara Han; Peter Hudson; Hector Aguilar-Carreno
Cc: (b) (6); Skinner, Anna (contr-sto); Nilles, John "Mike" (contr-bto); Cunningham, Adam (contr-bto); Kumar, Srikanta (contr-i2o)
Subject: Re: Showcasing performer accolades

Daniel J. Becker[+], Gregory F. Albery, Maureen K. Kessler[*], Tamika Lunn[*], Caylee A. Falvo[*], Gábor Á. Czirják, Lynn B. Martin, **Raina K. Plowright**. Macroimmunology: the drivers and consequences of spatial patterns in wildlife immune defense. *2020. Journal of Animal Ecology* doi.org/10.1111/1365-2656.13166 [PDF]. ***Awarded the 2020 Sidnie Manton Award from British Ecological Society**

Vincent Munster:
2020 AAAS Golden Goose award, COVID-19 response
2020 NIAID Merit award, COVID-19 response

Kwe/Julia/Trent:
NIAID Merit award, COVID-19 response
Aerosol and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1 – published 4th in Altmetric top 100

Tamika:
Griffith University PhD Writing Scholarship

Emily:
won the JHSPH Shikani/El Hibri prize for Innovation and Discovery for 2020 for my work on pandemic response.

Jamie:
NEJM paper was in some top 5 most influential COVID papers compiled by Nature Index.

Many papers published! See reports. Or ask for a list.

From: (b) (6)
Date: Wednesday, January 27, 2021 at 12:43 PM
To: Plowright, Raina < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Barbara Han < (b) (6) Peter Hudson <pjh1 (b) (6) Hector Aguilar-Carreno < (b) (6)
Cc: (b) (6), (b) (6) < (b) (6) (b) (6), (b) (6), (b) (6)

(b) (6)

Subject: Showcasing performer accolades

Hello Raina and team,
We have received a short turnaround request from DARPA Director's Office, to highlight examples of performers who have received accolades for their DARPA research over the past year or so, including best papers, first prizes, etc. We would love to showcase the great work that your group is doing by highlighting your achievements in this timeframe.
Could please provide us with a list of any best papers, first prizes/awards or other accolades you have received, by mid-day tomorrow?
Thank you,
Nathalie

(b) (6)
SETA Support to DARPA BTO
Quantitative Scientific Solutions (QS-2)
(b) (6)
Office: (b) (6)
Work Mobile: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 27 Jan 2021 20:43:20 +0000
To: Plowright, Raina
Subject: RE: Showcasing performer accolades

Here is another one:

https://www.altmetric.com/top100/2020/

place 4 with thee combined RML/UCLA paper

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

From: Plowright, Raina <(b) (6)
Sent: Wednesday, January 27, 2021 12:50 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Showcasing performer accolades

Thanks! And huge congratulations. So glad you are being recognized for this work.

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Wednesday, January 27, 2021 at 12:49 PM
To: Plowright, Raina <(b) (6)
Subject: RE: Showcasing performer accolades

Me:

2020	AAAS Golden Goose award, COVID-19 response
2020	NIAID Merit award, COVID-19 response

Kwe/Julia/Trent: NIAID Merit award, COVID-19 response

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

From: Plowright, Raina <(b) (6)
Sent: Wednesday, January 27, 2021 12:45 PM
To: (b) (6)
Subject: FW: Showcasing performer accolades

Can you send list of prizes, awards for good papers? Due tomorrow midday EST.
Send to me bc Sara is working extremely hard on budgets right now.

From: (b) (6)
Date: Wednesday, January 27, 2021 at 12:43 PM
To: Plowright, Raina <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6) Barbara Han <(b) (6) Peter Hudson
<(b) (6) Hector Aguilar-Carreno <(b) (6)
Cc: (b) (6), (b) (6)
<(b) (6) (b) (6),
(b) (6), (b) (6)
(b) (6)
Subject: Showcasing performer accolades

Hello Raina and team,
We have received a short turnaround request from DARPA Director's Office, to highlight examples of performers who have received accolades for their DARPA research over the past year or so, including best papers, first prizes, etc. We would love to showcase the great work that your group is doing by highlighting your achievements in this timeframe.
Could please provide us with a list of any best papers, first prizes/awards or other accolades you have received, by mid-day tomorrow?
Thank you,
(b) (6)

(b) (6)
SETA Support to DARPA BTO
Quantitative Scientific Solutions (QS-2)
(b) (6)
Office: (b) (6)
Work Mobile: (b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 26 Jan 2021 16:11:23 +0000
To: Degrace, Marciela (NIH/NIAID) [E]; Van bakel, Harm; malik; Alessandro Sette
Cc: (b) (6) Jason McLellan; (b) (6) (b) (6) (b) (6) (b) (6) Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; (b) (6) Julie McElrath; (b) (6) (b) (6) (b) (6) Matthew Frieman; (b) (6) Baric, Ralph; Richard Webby; Adolfo García-Sastre; Andrew B. Ward; Ali Ellebedy; (b) (6) (b) (6) (b) (6) Aubree Gordon; stanley-perlman@uiowa.edu; AlessandroSette; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; Seder, Robert (NIH/VRC) [E]; Koup, Richard (NIH/VRC) [E]; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]
Subject: RE: Discussing SARS-CoV2 Variant Testing with NIAID

Beats a 4 o'clock am WHO call □

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

From: Degrace, Marciela (NIH/NIAID) [E] < (b) (6)
Sent: Tuesday, January 26, 2021 9:10 AM
To: Van bakel, Harm < (b) (6) malik < (b) (6) Alessandro Sette < (b) (6)
Cc: (b) (6) Jason McLellan < (b) (6) (b) (6) (b) (6) (b) (6) (b) (6) Suthar, Mehul < (b) (6) Pei yong. Shi < (b) (6) McDermott, Adrian (NIH/VRC) [E] < (b) (6) Florian Krammer < (b) (6) (b) (6) Julie McElrath < (b) (6) (b) (6) (b) (6) (b) (6) Matthew Frieman < (b) (6) (b) (6) Baric, Ralph < (b) (6) Richard Webby < (b) (6) Adolfo García-Sastre < (b) (6) Andrew B. Ward < (b) (6) Ali Ellebedy < (b) (6) (b) (6) (b) (6) (b) (6) Aubree Gordon < (b) (6) stanley-perlman@uiowa.edu; AlessandroSette < (b) (6) Post, Diane (NIH/NIAID) [E] < (b) (6) Stemmy, Erik (NIH/NIAID) [E] < (b) (6) Lampley, Rebecca (NIH/NIAID) [C] < (b) (6) Eakin, Ann (NIH/NIAID) [E] < (b) (6) Brown, Liliana (NIH/NIAID) [E] < (b) (6) Seder, Robert (NIH/VRC) [E] < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6) Koup, Richard (NIH/VRC) [E] < (b) (6) Graham, Barney (NIH/VRC) [E] < (b) (6) Schmaljohn, Connie (NIH/NIAID) [E] < (b) (6) Ghedin, Elodie (NIH/NIAID) [E] < (b) (6) Roberts, Chris (NIH/NIAID) [E] < (b) (6) Embry, Alan

(NIH/NIAID) [E] <(b) (6)
Subject: RE: Discussing SARS-CoV2 Variant Testing with NIAID

Hi everyone,

Based on the feedback I've received, we are going to leave this meeting at **8am ET Thursday the 28th.** I realize this isn't convenient for everyone, but I hope you can make it. We'll discuss a time that is better for a regular meeting on Thursday's call, especially for those of you on the west coast and in Asia.

Thank you all, and looking forward to speaking!

Marciela DeGrace Ph.D.
Program Officer, Centers of Excellence for Influenza Research and Surveillance (CEIRS)
NIH/NIAID/DMID/RDB
Phone: 240-627-3460

From: Van bakel, Harm <(b) (6)
Sent: Tuesday, January 26, 2021 8:58 AM
To: Degrace, Marciela (NIH/NIAID) [E] <(b) (6) malik <(b) (6) Alessandro Sette <(b) (6)
Cc: (b) (6) Jason McLellan (b) (6); (b) (6) (b) (6) (b) (6) (b) (6) Suthar, Mehul (b) (6); Pei yong. Shi <(b) (6) McDermott, Adrian (NIH/VRC) [E] <(b) (6) Florian Krammer <(b) (6) (b) (6) (b) (6) Julie McElrath (b) (6); (b) (6) (b) (6) (b) (6) (b) (6) (b) (6) Matthew Frieman <(b) (6) (b) (6) (b) (6) Baric, Ralph <(b) (6) Richard Webby <(b) (6) Adolfo García-Sastre <(b) (6) Andrew B. Ward <(b) (6) (b) (6) Ali Ellebedy <(b) (6) (b) (6) (b) (6) (b) (6); (b) (6) Aubree Gordon <(b) (6) (b) (6) AlessandroSette <(b) (6) Post, Diane (NIH/NIAID) [E] <(b) (6) Stemmy, Erik (NIH/NIAID) [E] <(b) (6) Lampley, Rebecca (NIH/NIAID) [C] <(b) (6) Eakin, Ann (NIH/NIAID) [E] <(b) (6) Brown, Liliana (NIH/NIAID) [E] <(b) (6)
Subject: Re: Discussing SARS-CoV2 Variant Testing with NIAID

Either of those times works for me.

Best,
Harm

On 1/25/21 8:34 PM, Degrace, Marciela (NIH/NIAID) [E] wrote:

Thanks, Malik. Looking at schedules here at NIAID, the only other time I see that might work this week would be **Friday January 29th at 9:30 ET.**

If that's better for the group, I'm happy to move the meeting. Please email me if you have preferences one way or another, and I will make any changes by tomorrow.

Thank you!

Marciela DeGrace Ph.D.
Program Officer, Centers of Excellence for Influenza Research and Surveillance (CEIRS)
NIH/NIAID/DMID/RDB
Phone: (b) (6)

From: malik < (b) (6)
Sent: Monday, January 25, 2021 8:12 PM
To: Alessandro Sette < (b) (6) Degrace, Marciela (NIH/NIAID) [E] < (b) (6)
Cc: (b) (6) Jason McLellan < (b) (6) (b) (6) (b) (6) (b) (6) (b) (6) Suthar, Mehul < (b) (6) Pei yong. Shi < (b) (6) McDermott, Adrian (NIH/VRC) [E] < (b) (6) Florian Krammer < (b) (6) (b) (6) (b) (6) Julie McElrath < (b) (6) (b) (6) (b) (6) (b) (6) (b) (6) Matthew Frieman < (b) (6) (b) (6) (b) (6) Baric, Ralph < (b) (6) Richard Webby < (b) (6) Adolfo García-Sastre < (b) (6) Andrew B. Ward < (b) (6) (b) (6) Ali Ellebedy < (b) (6) (b) (6) (b) (6) (b) (6) (b) (6) Aubree Gordon < (b) (6) (b) (6) AlessandroSette < (b) (6) (b) (6) Post, Diane (NIH/NIAID) [E] < (b) (6) Stemmy, Erik (NIH/NIAID) [E] < (b) (6) Lampley, Rebecca (NIH/NIAID) [C] < (b) (6) Eakin, Ann (NIH/NIAID) [E] < (b) (6) Brown, Liliana (NIH/NIAID) [E] < (b) (6)
Subject: Re: Discussing SARS-CoV2 Variant Testing with NIAID

As I am one possibly affected by a later time, like to let you know that I am OK with a later time. In fact, better, as I have another meeting clashing at proposed time.

Maik

From: Alessandro Sette < (b) (6)
Sent: Tuesday, January 26, 2021 5:43
To: Degrace, Marciela (NIH/NIAID) [E]
Cc: (b) (6) Jason McLellan; (b) (6) (b) (6) (b) (6)

(b) (6) Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; (b) (6) (b) (6) Julie McElrath; (b) (6) (b) (6) (b) (6) (b) (6) (b) (6) Matthew Frieman; (b) (6) (b) (6) Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik; Andrew B. Ward; (b) (6) Ali Ellebedy; (b) (6) (b) (6) (b) (6) (b) (6) Aubree Gordon; (b) (6) (b) (6); AlessandroSette; (b) (6) Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]
Subject: Re: Discussing SARS-CoV2 Variant Testing with NIAID

Hi Marciela,
a 8am ET time corresponds to 5am for people on the west coast. Can we find a later time to accommodate different time zones?

On Mon, Jan 25, 2021 at 1:37 PM Degrace, Marciela (NIH/NIAID) [E]
<(b) (6) wrote:
Good afternoon,

My name is Marciela DeGrace and I am a Program Officer in the Respiratory Diseases Branch at NIAID. As you know, SARS-CoV-2 variants associated with increased transmission and antigenic change have begun to emerge. We'd like to start a discussion a small group of researchers with the expertise and tools to characterize these variants to share research results in real-time. While this will start as information-sharing, our hope is to gradually operationalize a group to work together to characterize variants in the future.

We'd like to set up an initial discussion **for this Thursday January 28th at 8am ET.** I realize this time may not work for everyone, but I hope you will attend if you can. We'll discuss the goals and scope we have in mind and try to set a regular meeting time. We're trying to keep the group to a manageable size right now, so please don't forward the meeting invitation at this time.

Please let me know if you have any questions, and we look forward to speaking to you this Thursday.

Best,

Marciela DeGrace Ph.D.
Program Officer, Centers of Excellence for Influenza Research and Surveillance (CEIRS)
NIH/NIAID/DMID/RDB
Phone: (b) (6)

--

Alessandro Sette, Dr. Biol. Sci.
Professor and Member
La Jolla Institute for Immunology, Division of Vaccine Discovery
Center for Infectious Disease and Vaccine Research
Center for Autoimmunity and Inflammation
University of California, School of Medicine
9420 Athena Circle
La Jolla, California USA
Tel: (b) (6)
Fax: 858-752-6987
Email: (b) (6)
Web: http://www.liai.org/pages/faculty-sette

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 25 Jan 2021 04:28:22 -0700
To: Plowright, Raina
Subject: Re: IMPORTANT- Add/drop class

Hi Raina,

I'm know you are aware that (b) (6). My main worry is that he will not be able to finish his agreed upon thesis work as soon as he moves over to a different lab.

Obviously, this is largely his responsibility but I wanted to put it on your radar.

Cheers,

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

From: "Plowright, Raina" <(b) (6)
Date: Tuesday, January 19, 2021 at 9:48 AM
To: Trenton Bushmaker <(b) (6)
Cc: '(b) (6) <(b) (6)
Subject: Re: IMPORTANT- Add/drop class

Hi Trent,
Happy to talk through this but I think there is no doubt that you should drop STAT. this is a really tough time and keeping ourselves afloat, and sanity intact, has to be priority, especially with a young family. I'm around tomorrow before 11am MT and feel free to call anytime 9.15am-11am.
Raina

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Date: Monday, January 18, 2021 at 10:35 PM
To: Plowright, Raina <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: IMPORTANT- Add/drop class

Raina,
Would you have some time on Tuesday to talk about dropping STAT 411 and adding these (3) credits to my thesis credits? I would still like to stay in my journal club (b) (6) and do seminar credits. This would keep me full time at 6 credits. This will also put me at a total of my 7 of 10 thesis credit requirements. I don't think this will hurt my timeline of graduation the end of next fall. Just want to discuss this with you.

Reasoning is my household is feeling the extra pressure with the added variant project, RIP session coming up, thesis, kids being at home, and the stress of my (b) (6) working at the hospital lab with the pandemic. I have bitten off more than I can chew at the moment. I need to choose my family over the stress of this STAT 411 class and I don't think it will hurt my timeline.

Send me a text message tomorrow when you have time.

(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sat, 23 Jan 2021 15:20:17 +0000
To: Schountz,Tony; Luke Hamel
Subject: RE: 10X Genomics instrument

No, the library prep is done in 4, and then taken out

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

-----Original Message-----
From: Schountz,Tony <(b) (6)
Sent: Saturday, January 23, 2021 7:48 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: 10X Genomics instrument

Hi Vinnie, I'm trying to understand how the single cell RNA-Seq was done in your paper:

https://stm.sciencemag.org/content/scitransmed/early/2021/01/06/scitranslmed.abe8146.full.pdf

Is the 10X Genomics instrument in the BSL-4? I see the libraries are made, then another extraction before egress from the BSL-4, but it's not clear to me if the 10X instrument is what is used to make the libraries (in the BSL-4).

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases Department of Microbiology, Immunology and Pathology College of Veterinary Medicine Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 21 Jan 2021 19:05:25 +0000
To: Plowright, Raina; Bushmaker, Trenton (NIH/NIAID) [E]; Alison Peel; Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: RE: Results

Sounds good

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

From: Plowright, Raina <(b) (6)
Sent: Thursday, January 21, 2021 11:57 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Re: Results

Great, and note we are talking about NEXT WEEK Thursday.

> **From:** Munster, Vincent (NIH/NIAID) [E] <(b) (6)
> **Date:** Thursday, January 21, 2021 at 11:26 AM
> **To:** Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6) Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
> **Subject:** RE: Results
>
> We'll keep you posted
>
> Vincent Munster, PhD
> Chief Virus Ecology Section
> Rocky Mountain Laboratories
> NIAID/NIH
>
> ---
>
> **From:** Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
> **Sent:** Thursday, January 21, 2021 11:07 AM
> **To:** Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6) Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
> **Subject:** Re: Results
>
> Ok just go ahead and I will get a update from Kwe or I will listen in while at the appointment.

-Trent

From: Vincent Munster <(b) (6)
Date: Thursday, January 21, 2021 at 11:05 AM
To: Trenton Bushmaker <(b) (6) "Plowright, Raina" <(b) (6) Alison Peel <(b) (6) Yinda Kwe <(b) (6)
Subject: RE: Results

Won't work from my end, I have a IBC at 1 and an OWS at 3

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 21, 2021 11:04 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina (b) (6); Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Subject: Re: Results

Any chance we can do 1-2pm or after 3:15? I have a doctor's appointment 2-3pm. No worries if not, I can get an update from Kwe.

-Trent

From: Vincent Munster <(b) (6)
Date: Thursday, January 21, 2021 at 10:54 AM
To: "Plowright, Raina" (b) (6) Alison Peel <(b) (6) Yinda Kwe <(b) (6) Trenton Bushmaker <(b) (6)
Subject: RE: Results

Would bee able to do 2,

Its good to realize that the VTM will be a dilution. I assume that the AVL had directly urine out into it, whereas in the VTM it is diluted. It would be good if you guys compile a complete list of the AVL CT values and see whether there is a difference there. I would expect to see at least a 2-4 CT difference (with AVL having the lower CTs).

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

From: Plowright, Raina <(b) (6)
Sent: Thursday, January 21, 2021 9:09 AM
To: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Results

Hi Ali,
This is extremely concerning. I could talk Thursday afternoon at a time that works for Australia. Kwe, Vincent, Trent, could you talk after 2pm MT Thursday?
Raina

From: Alison Peel <(b) (6)
Date: Wednesday, January 20, 2021 at 10:27 PM
To: Plowright, Raina <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Results

Sorry - I meant to attach this spreadsheet.

From: Alison Peel <(b) (6)
Sent: 21 January 2021 15:05
To: Plowright, Raina <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Results

Thanks Raina - it will be handy once the results are in the database.
A quick look indicates that only 3/100 of the previously tested HeV samples (AVL samples) are also positive in VTM:

ARCLU012_VTM_u_59_1_
ARCLU010_VTM_u_4_1_
ARCUR001_VTM_u_61_1_

About 30% of the retest samples were Ct <32 in the AVL samples, so I would have thought that a lot more of the retested VTM samples would be positive. I think it would be good to have a call to talk through these results before we interpret the rest of the results in too much detail.

Can we arrange a time sometime next week?

Thanks again Kwe for the massive efforts to get through these.

Thanks
Ali

From: Plowright, Raina <(b) (6)
Sent: 21 January 2021 11:07
To: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: Results

That's an amazing turn around. Thank you Kwe, Trent, and Vincent! I've sent the data to Wyatt to get a quick visualization. Clunes looks red hot!

From: Alison Peel <(b) (6)
Date: Wednesday, January 20, 2021 at 5:24 PM
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina (b) (6)
Subject: Re: Results

Wow, what a powerhorse Kwe! Well done!

I'm not at my computer to look at the results fully, but does the 171 include the 100 positive samples we sent for retesting?

Can't wait to look in more detail!

From: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Sent: Thursday, January 21, 2021 10:00:54 AM
To: Alison Peel <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina (b) (6)
Subject: Results

Dear all,

We have been busy screening the samples.
This time we screened 2592 samples with 171 HeV and 57 CedV positives.

Interestingly, 37 samples had ct less than 30 and 4 of them less than ct 25. Hopefully we get some isolates from these. The results is attached.

Thanks

Kwe

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 19 Jan 2021 22:22:12 +0000
To: Schountz,Tony; Eric Laing
Subject: RE: Other documents
Attachments: RML Facilities.docx

Here it is

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

From: Schountz,Tony <(b) (6)
Sent: Tuesday, January 19, 2021 2:49 PM
To: Eric Laing <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Other documents

Vinnie, do you have **Facilities and Resources**, and **Equipment** documents for NIH submissions? I seem to recall we took a hit on the summary statement for the R01 that we sent in last year because these were not in the submission. I have your biosketch.

Eric, I need your **Biosketch**, **Facilities and Resources**, and **Equipment** documents.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

The Laboratory of Virology (LV) is located in the Integrated Research Facility (IRF) on the campus of Rocky Mountain Laboratories (RML) in Hamilton, Montana. RML houses several Laboratories of the NIAID Division of Intramural Research (DIR). All LV laboratory space is located in the IRF.

LV has presently been assigned 6140 sq.-ft. of BSL2 laboratory space. These labs are equipped with all necessary items that are needed to perform classic virology, basic immunology and advanced molecular biology/virology. Larger equipment includes: freezers, refrigerators, $C0_2$-incubators, class II biosafety cabinets, PCR thermocyclers, LightCycler, SmartCycler, ultracentrifuge, high speed centrifuge, microcentrifuges, FACS, electrophoreses equipment for protein and nucleic acid work, power supplies, spectrophotometer, ELISA reader, plate washer, light microscopes, fluorescence microscopes, and a confocal microscope.

The IRF houses "state-of-the-art" BSL-4 laboratory and animal space which is maintained by the Director of NIAID DIR as Director's Reserve. The IRF houses approximately 3500 square feet (SF) of BSL-4/BSL-3 lab space (flexible space). The BSL-4 lab is equipped with all necessary items needed to perform classic virology, basic immunology and molecular biology. The equipment includes: freezers, refrigerators, $C0_2$-incubators, class II biosafety cabinets, ultracentrifuge, high speed centrifuge, low speed centrifuges, microcentrifuges, ELISA reader, plate washer, microscopes, fluorescence microscope and computers.

The Rocky Mountain Veterinary Branch (RMVB) at RML has BSL-2 animal space of approximately 12,255 sq.-ft., which can house species such as mice, rats, guinea pigs, hamsters, bats, rabbits and nonhuman primates. The BSL-2 animal space is in a dedicated facility near the IRF. RMVB is led by Dr. D. Gardner, DVM, PhD, and is staffed by Board Certified clinical veterinarians, veterinary pathologists and well-trained animal care staff. RMVB provides the entire RML staff, including LV, with service on all levels of animal handling and care and procedures such as blood sampling, infections, necropsies, and euthanasia. Complete histopathology services are provided, including immunohistochemistry and in situ hybridization. All animal facilities at RML are fully accredited by AAALAC.

In addition, the IRF contains approximately 3000 sq.-ft. of animal space in high containment (ABSL-4/ABSL-3 – flexible space). This space is equipped for handling caged animals including bats, ferret, rodent and nonhuman primates (cynomolgus and rhesus macaques) species as well as smaller livestock animals such as pigs, goats and sheep. RMVB staff provides animal care and handling support. Procedures on animals are performed by fully trained personnel of LV or RMVB.

From: Plowright, Raina
Sent: Tue, 19 Jan 2021 20:22:10 +0000
To: (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E]; Peter Hudson; (b) (6); Barbara Han
Subject: Re: spillback-- can you weigh in on this please (MSU folks)

I'm teaching right now, so skim reading but I think you need to have Barbara on this chain. I've ccd her.

Sent from my iPhone

> On Jan 19, 2021, at 1:13 PM, (b) (6) wrote:
>
> Hi Raina, Pete, Vincent
> We received further comments from our Front Office on the DSD bullet we submitted (attached):
>
> 1) When you say, "Now validated against existing and emerging evidence..." What evidence are you validating against?
>
> 2) When you talk about "...identifying spillback risk mitigation plans in COVID-19 hotspots for DoD and public health decision makers." How are/will you get this info to these groups?
>
> We would greatly appreciate your input on addressing these comments, especially on any plans you have (or envision) for transferring that information to public health decision makers (e.g. sharing of outcomes of your analysis directly with public health agencies, MOA/MOU in place for data transfer...).
>
> We have drafted a response to comment #1, please feel free to edit, supplement or concur.
> 1) Particular species predicted to have high reservoir potential based on the MSU binding affinity and amino acid compatibility models have been validated against lab and field evidence. Susceptibility of deer mice (Peromyscus maniculatus) to SARS-CoV-2, predicted by ACE-2 receptor modeling, was confirmed by experimental evidence of infection and transmission in lab colonies of deer mice (Griffin et al., 2020). Predicted susceptibility of captive or domesticated animals was confirmed by field evidence from documented instances of human-to-animal transmission in tigers (USDA, 2020), mink (Oreshkova et al., 2020), cats (Zhang et al., 2020), and dogs (Sit et al., 2020).
>
> I would be happy to discuss this over a quick call if needed.
>
> Thank you
> (b) (6)
>
>
> (b) (6)
> SETA Support to DARPA BTO
> Quantitative Scientific Solutions (QS-2)
> (b) (6)
> Office: (b) (6)
> Work Mobile: (b) (6)
>
>
>
> -----Original Message-----
> From: (b) (6)
> Sent: Tuesday, January 12, 2021 2:58 PM
> To: Plowright, Raina < (b) (6) Munster, Vincent (NIH/NIAID) [E]
< (b) (6) Peter Hudson < (b) (6)

> Cc: (b) (6)
> Subject: RE: spillback-- can you weigh in on this please (MSU folks)
>
> Thanks all!
>
> -----Original Message-----
> From: Plowright, Raina < (b) (6)
> Sent: Tuesday, January 12, 2021 2:50 PM
> To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) (b) (6)
Peter Hudson <pjh (b) (6)
> Cc: (b) (6)
> Subject: Re: spillback-- can you weigh in on this please (MSU folks)
>
> Hi (b) (6)
>
> Vincent said it all. There is a conversation ongoing about potential for animals to be reservoirs (and vessels for viral evolution) for humans.
>
> It is a big concern.
>
> Raina
>
>
>
> From: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
> Date: Tuesday, January 12, 2021 at 11:42 AM
> To: (b) (6), Plowright, Raina < (b) (6) Peter Hudson
(b) (6)
> Cc: (b) (6)
> Subject: RE: spillback-- can you weigh in on this please (MSU folks)
>
> Hi (b) (6)
>
> That's indeed one of the bigger question surrounding the potential of other species getting infected and establishing a additional reservoir (besides humans) .Its smtg we are actively exploring within this group.
>
> I'm currently looking at mink infections and within host-evolution, and together with Tony Schountz, looking at deer mice which appear to be susceptible as well. Using population data, combined with experimental infection we are hoping to tease out what the risk for this. The "alternative" reservoirs could be an independent source of virus evolution and spill back.
>
> Another thing to put on your radar, within OWS (and WHO) large effort undergoing at the moment of the characterization of the UK, SA and Brazil variants. We will do stability and transmission studies and feed them into the genotype-to-phenotype pipeline (as it was designed for). Let me know whether you want to be part of a direct data share group (so typically the data is disseminated withing OWS, HHS and WHO.
>
> Most recent genotype-to-phenotype work from my group:
>
>
hxxxps://nam10.safelinks.protection.outlook.com/?url=https%3A%2F%2Fxxx.biorxiv.org%2Fcontent%2F10.1101%2F2020.12.28.424565v1&data=04%7C01%7Craina.plowright%40montana.edu%7C1184210cd9cd41cdedc008d8b729c5e8%7C324aa97a03a644fc91e43846fbced113%7C0%7C0%7C637460737332623961%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=u3xwXHga%2BluwhG7Rw%2BzqhohTSpvQaGprwT5vqrz5el0%3D&reserved=0
>
>

hxxxps://nam10.safelinks.protection.outlook.com/?url=https%3A%2F%2Fxxx.biorxiv.org%2Fcontent%2F10.1101%2F2021.01.09.426058v1&data=04%7C01%7Craina.plowright%40montana.edu%7C1184210cd9cd41cdedc008d8b729c5e8%7C324aa97a03a644fc91e43846fbced113%7C0%7C0%7C637460737332623961%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=rKy%2B0tOcu98G5kZM2XV5PY%2FLhd0A29PgUVYudMvzcuQ%3D&reserved=0
>
> Cheers,
>
>
> Vincent Munster, PhD
> Chief Virus Ecology Section
> Rocky Mountain Laboratories
> NIAID/NIH
>
> -----Original Message-----
> From: (b) (6)
> Sent: Tuesday, January 12, 2021 11:18 AM
> To: Plowright, Raina < (b) (6) Peter Hudson (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
> Cc: (b) (6)
> Subject: spillback-- can you weigh in on this please (MSU folks)
>
> Hi Raina, Pete, Vincent -
>
> Yesterday we submitted a DSD bullet (attached) and we have some comments from our Front Office as such:
>
> -----
> I think I am missing one quick point on "spillback". Yesterday actually in the news there were reports of Gorilla's at the San Diego Zoo (I think it was this zoo) testing positive for COVID-19 after a keeper had also tested positive. The point they made in the article was that the gorilla population was already at risk without the introduction of a new virus in the population. (Also important) But the part that they did not touch on and I think may be missing here is the risk of spillback. So what if there is spillover to other species (closely related or not) and spillback? Let me know if I am talking apples and oranges here.
>
> Also, are there talks of implementing such mitigation strategies yet or is it too soon?
> -----
>
> From my (b) (6) perspective, gorillas would be at risk of diseases from humans, so I suspect that is what they mean. Would be great to get your input on this above and the mitigation potential, as well.
>
> Thanks!
> (b) (6)
>
> <2021 01_11_DSD Weekly Update_PREEMPT_ (b) (6) update to address KD's questions.docx>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 18 Jan 2021 22:12:16 +0000
To: Schountz, Tony
Subject: Re: Sorter in your BSL4

Yes we can do single cell in 4,

Cite Speranza's science trans med

> On Jan 18, 2021, at 14:35, Schountz,Tony < (b) (6) wrote:
>
> Vinnie, Lin-fa wants to do single cell RNA Seq for Nipah. Do you have a sorter in the BSL4 that can sort GFP- or mCherry-expressing cells? If not, it looks like paraformaldehyde fixation can be used for RNA extraction but non-fixed would be better.
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Center for Vector-borne Infectious Diseases
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
> 200 West Lake Street
> 1685 Campus Delivery
> Fort Collins, CO 80523-1692
> (b) (6)
> (b) (6)
>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 18 Jan 2021 16:37:01 +0000
To: van Doremalen, Neeltje (NIH/NIAID) [E]; Bushmaker, Trenton (NIH/NIAID) [E]; Adney, Danielle (NIH/NIAID) [F]; Schountz, Tony
Subject: bat caging

Hi guys,

Can you source some pictures of our bat caging to share with Tony? The ones we used for the Rousettus?

Thanks,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 15 Jan 2021 20:59:33 +0000
To: Jon Epstein
Cc: Schountz, Tony; Sarah Munro
Subject: RE: request for letter of support for R24
Attachments: LOS CM Final.pdf

Approved and signed,

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

From: Jon Epstein <(b) (6)
Sent: Wednesday, January 13, 2021 3:48 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Schountz, Tony <(b) (6) Sarah Munro <(b) (6)
Subject: request for letter of support for R24

Hey Vincent,
We'll need a letter of support from you for the NIH R24 proposal. I've attached a draft, modified from the last one you wrote. Could you please edit and return signed?
Will we need a letter of approval from Steven Holland, like last time, for partnership? You'll be listed as a CO-I and an institutional partner in this, since we'll be doing experimental infections at RML with you.

We'll need these letters by Jan 18, if possible. Many thanks, in advance!

Cheers,
Jon

PS, please also send an updated biosketch.

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

(b) (6) (direct)
(b) (6) (mobile)

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

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Unit

Dr. Jonathan Epstein
Vice President for Science and Outreach EcoHealth Alliance
460 W 34th St. 17th Floor New York, NY 10001 USA

Subject: Letter of Collaboration on "Establishment of Bat Colonies for the Study of Bat-borne Zoonotic Viruses"

Dear Jon and Tony,

I am pleased to serve as a collaborator on your R24 proposal entitled "Establishment of Bat Colonies for the Study of Bat-borne Zoonotic Viruses." The Virus Ecology Unit at the Rocky Mountain Laboratories enthusiastically supports this project proposal and collaboration with EcoHealth Alliance and Colorado State University to improve our understanding of bat-borne viral zoonoses like SARS-CoV-2 and Nipah virus. As you know, we have been collaborating with EcoHealth Alliance and CSU for more than 15 years under several research and surveillance projects to study emerging zoonotic viruses, and this proposed project is one that I have personally been involved with since its inception. There is no greater indicator of the pressing need for bat models to study natural host-virus relationships than the current COVID-19 pandemic, which is most likely due to the emergence of a bat-origin coronavirus. There are currently no bat models available in the United States that are naturally associated with either SARS-related coronaviruses or henipaviruses – both of which are WHO and NIH priority pathogens for research. I enthusiastically support this work which will help create a desperately needed resource that will help in our efforts to prevent future pandemics.

We agreed to participate in activities that will help establish breeding colonies of *Pteropus medius* and *Rhinolophus* bat species at CSU, and that will strengthen capacity in Bangladesh to generate and work with reagents, assays, and any other data or products developed through the collaborative study of bat immunology, viral pathogenesis, and host tolerance as the result of this project. As a partner in this study, we will make our resources available to achieve its aims. My group at the Rocky Mountain Laboratories (RML), Division of Intramural Research (DIR), NIAID, NIH, will perform critical experiments in high and maximum containment, for generation and validation of cell lines, reagents, diagnostic assays and other outputs that can be used by the broader research community. We will perform all related work on infectious material and assist with study design, data interpretation, and publication.

We, Drs Port, Adney and Munster, will contribute approximately (b) (6) of our effort to this project, subject to availability of time and resources. Please note that this collaboration is part of my official duties as a federal employee at NIAID, NIH, and no funds from the grant will be used in intramural research, neither will I accept any form of remuneration, whether in the form of salary, honoraria, or travel expenses. I will provide scientific input (and mentoring) but will not have any duties associated with programmatic stewardship, which will be performed by the collaborators through a NIAID extramural program officer. Further, in accordance with NIAID's mission to promote and facilitate biomedical research and the dissemination of new knowledge, we would supply requested research materials and technical expertise not only to you, but also to other interested and qualified parties for research purposes.

903 S. 4th St., Hamilton, MT 59840
Phone: (b) (6)
Fax: 406-375-9620
Email: (b) (6)

Approval for this collaboration has been granted by the DIR Director, Dr. Steven M. Holland.

(b) (6)

Vincent Munster, Ph.D.
Chief, Virus Ecology Unit
Laboratory of Virology
Rocky Mountain Laboratories
National Institute of Allergy and Infectious Diseases
National Institutes of Health

Karyl S. Barron -S

Digitally signed by Karyl S. Barron -S
Date: 2021.01.15 15:06:40 -05'00'

Steven M. Holland, M.D.
Director, Division of Intramural Research
National Institute of Allergy and Infectious Diseases
National Institutes of Health

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 15 Jan 2021 16:13:17 +0000
To: Jon Epstein
Cc: Schountz, Tony; Sarah Munro
Subject: RE: request for letter of support for R24

Routed for signatures

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

From: Jon Epstein <(b) (6)
Sent: Wednesday, January 13, 2021 3:48 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Schountz, Tony <(b) (6) Sarah Munro <(b) (6)
Subject: request for letter of support for R24

Hey Vincent,
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Will we need a letter of approval from Steven Holland, like last time, for partnership? You'll be listed as a CO-I and an institutional partner in this, since we'll be doing experimental infections at RML with you.

We'll need these letters by Jan 18, if possible. Many thanks, in advance!

Cheers,
Jon

PS, please also send an updated biosketch.

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
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web: ecohealthalliance.org
Twitter: @epsteinjon
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Schountz,Tony
Sent: Fri, 15 Jan 2021 15:25:48 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Subject: Re: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Hjelle's were *P. maniculatus rufinus*. Ours are *P. maniculatus nebraskensis*. His were captured at the Sevilleta National Wildlife refuge (New Mexico), whereas ours are from Whitewater, Colorado (central-western Colorado). Do you want to mix subspecies?

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: Friday, January 15, 2021 8:03 AM
To: Schountz,Tony <(b) (6)
Subject: RE: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Think so, might be worthwhile to ship a couple of breeding pairs to restart here

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

From: Schountz,Tony <(b) (6)
Sent: Friday, January 15, 2021 8:02 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

I'm pretty sure white-footed deer mice are susceptible. Their ACE2 is nearly identical. We've tested 3 subspeices of P. manic, plus P. californicus and P. polionotis, and all 5 are susceptible.

It's peculiar that your P manics aren't doing well. Those are from Brian Hjelle, right?

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: Friday, January 15, 2021 7:38 AM
To: Schountz,Tony < (b) (6)
Subject: FW: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Apparently our maniculatis colony is not doing well, did you try the leucopus?

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

From: Smith, Brian (NIH/NIAID) [C] < (b) (6)
Sent: Thursday, January 14, 2021 7:19 PM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Subject: Re: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

We have two deer mouse colonies:
White footed deer mouse - peromyscus leucopus. The colony is doing well

Prairie deer mouse - peromyscus maniculatus. This colony is struggling with low numbers and none available for use.
Which are you looking for?

Sent from my iPhone

On Jan 14, 2021, at 4:00 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:

Thanks Brian,

Will plan accordingly. Btw, do you know what the status of the deer mouse colony is?

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

From: "Smith, Brian (NIH/NIAID) [C]" <(b) (6)
Date: Tuesday, January 12, 2021 at 3:38 PM
To: "(b) (6) <(b) (6)
Subject: RE: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Hello Vincent,
If you give me a good heads up when you need K18+ mice (how many, sex, age, and start date of study) – I can get breeders ready to potentially produce enough with our in-house colony that you can decrease potentially how many you have to order.
Brian

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 2:04 PM
To: Peterson, Melissa (NIH/NIAID) [E] <(b) (6) Haddock, Elaine (NIH/NIAID) [E] <(b) (6) Weidow, Amanda (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML RMVB BCSS <(b) (6) LaCasse, Rachel (NIH/NIAID) [E] <(b) (6) Taggart, Brian (NIH/NIAID) [E] <(b) (6)
Subject: RE: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Thanks Melissa!

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

From: Peterson, Melissa (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 1:49 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Haddock, Elaine (NIH/NIAID) [E] <(b) (6) Weidow, Amanda (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML RMVB BCSS <(b) (6) LaCasse, Rachel (NIH/NIAID) [E] <(b) (6) Taggart, Brian (NIH/NIAID) [E] <(b) (6)
Subject: rad a272210852 AND 10853 PLACED RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Hi all,
Two orders have been placed and tied for age match and same date delivery to Bldg 28 ABSL4 on 1/20. Order A272210852 for 15 Male Hemizygous K18 mice age 4-8wks and order A272210853 for 15 Female Hemizygous K18 age 4-8wks have been billed against protocol #2020-019-E COVID CAN 8044367.
Thanks,
Melissa

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 1:12 PM
To: Haddock, Elaine (NIH/NIAID) [E] <(b) (6) Peterson, Melissa (NIH/NIAID) [E] <(b) (6) Weidow, Amanda (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML RMVB BCSS <(b) (6) LaCasse, Rachel (NIH/NIAID) [E] <(b) (6)
Subject: RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Hi guys,

It should be 2020-019-E, so that might explain the confusion

we have had these mice on this protocol before from Jax, next week would be great!

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

From: Haddock, Elaine (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 11:58 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Peterson, Melissa (NIH/NIAID) [E] <(b) (6) Weidow, Amanda (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML RMVB BCSS <(b) (6) LaCasse, Rachel (NIH/NIAID) [E] <(b) (6)
Subject: RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Vincent, what about Melissa's other questions:

1. Delivery next week or 1/27
2. Has Jackson been added as a vendor, protocol number, etc.

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 11:43 AM
To: Peterson, Melissa (NIH/NIAID) [E] <(b) (6) Weidow, Amanda (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML RMVB BCSS <(b) (6) LaCasse, Rachel (NIH/NIAID) [E] <(b) (6) Haddock, Elaine (NIH/NIAID) [E] <(b) (6)
Subject: RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Older than 4 weeks

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

From: Peterson, Melissa (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 11:41 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Weidow, Amanda (NIH/NIAID) [E] (b) (6)
Cc: NIAID RML RMVB BCSS <(b) (6) LaCasse, Rachel (NIH/NIAID) [E] <(b) (6) Haddock, Elaine (NIH/NIAID) [E] <(b) (6)
Subject: RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Hi Vincent,

What sex and age range would you like me to order? Delivery requested for next week or delivery 1/27? Also, I did not see an addenda under #2019-020-E that added Jackson as a vendor or the B6.Cg-Tg(K18-Ace2)2Prlmn/J specific strain, only variations of CC and RIX mice? 2019-020-E is an Ebola study, so wondering if the protocol number referenced is incorrect? Is there an addenda that has not been added or did I miss it?

Thank you,
Melissa

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 11:06 AM
To: Weidow, Amanda (NIH/NIAID) [E] <(b) (6) Peterson, Melissa (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML RMVB BCSS (b) (6)
Subject: RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

Hi Melissa,

Can you order us 30 of the K18 mice (or from within RML breeding).

They need to go on protocol 2019-020E

They can go on the COVID-CAN for my group

Let me know if you need any further information,

Thanks!

Vincent Munster, PhD

Chief Virus Ecology Section
Rocky Mountain Laboratories
NIAID/NIH

From: Weidow, Amanda (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 8:02 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML RMVB BCSS <(b) (6)
Subject: RE: FW 1/18/21: Munster MCL request 2019-020E, 30 mice

No Problem, Shane will house 6 cages of 5 mice and place 24 colored tags into the mice☺
They will be placed into suite A, room 163.

Thanks,
Weidow

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Tuesday, January 12, 2021 6:57 AM
To: Weidow, Amanda (NIH/NIAID) [E] <(b) (6)
Subject: Re: FW 1/18/21: Munster MCL request

Yes that would be great! Can you use the color tags on the mice?

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

From: Amanda Weidow <(b) (6)
Date: Monday, January 11, 2021 at 2:39 PM
To: (b) (6) <(b) (6)
Subject: FW: FW 1/18/21: Munster MCL request

Hello Vincent,

Would you like your animals tagged in the 6 cages of HACE 2 mice?

Thanks,
Amanda

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Monday, January 11, 2021 2:11 PM
To: Jones, Michael (NIH/NIAID) [E] <(b) (6)
Cc: NIAID RML MCL Leads <(b) (6) van Doremalen, Neeltje (NIH/NIAID) [E]

(b) (6) Schulz, Jonathan (NIH/NIAID) [F] <(b) (6)
Subject: Re: FW 1/18/21: Munster MCL request

Thanks Mike!

On Jan 11, 2021, at 13:53, Jones, Michael (NIH/NIAID) [E] <(b) (6) wrote:

Vincent- We discussed your animal request a week early because next Monday is a holiday. That being said your animal request is now approved by the MCL!

-Mike

From: Jones, Michael (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 7, 2021 11:55 AM
To: NIAID RML MCL Leads <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) van Doremalen, Neeltje (NIH/NIAID) [E] <(b) (6) Schulz, Jonathan (NIH/NIAID) [F] <(b) (6)
Subject: FW 1/18/21: Munster MCL request

Vincent,
This will be discussed on 01/18/21

Thanks
-Mike

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 7, 2021 9:36 AM
To: Jones, Michael (NIH/NIAID) [E] <(b) (6)
Cc: Shupert, W. Lesley (NIH/NIAID) [E] <(b) (6) Feldmann, Ricki (NIH/NIAID) [C] <(b) (6) Feldmann, Heinrich (NIH/NIAID) [E] <(b) (6) Haddock, Elaine (NIH/NIAID) [E] <(b) (6) van Doremalen, Neeltje (NIH/NIAID) [E] (b) (6); Schulz, Jonathan (NIH/NIAID) [F] <(b) (6)
Subject: MCL request

Hi Mike,

Please find attached a MCL request for a short study with 30 K18 mice to be conducted in BSL4. Let me know if you need anything else from my end to schedule this,

Regards,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 12 Jan 2021 18:45:10 +0000
To: Benson, Evelyn; Bushmaker, Trenton (NIH/NIAID) [E]; Callison, Julie (NIH/NIAID) [E]; Shupert, W. Lesley (NIH/NIAID) [E]; Menk, Kay (NIH/NIAID) [E]; Manuel Ruiz; Maureen Kessler
Cc: Plowright, Raina
Subject: RE: ETOH and fecal samples- Sample shipment.

Great work,

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

From: Benson, Evelyn < (b) (6)
Sent: Tuesday, January 12, 2021 11:03 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) Callison, Julie (NIH/NIAID) [E] < (b) (6) Shupert, W. Lesley (NIH/NIAID) [E] < (b) (6) Menk, Kay (NIH/NIAID) [E] < (b) (6) Manuel Ruiz < (b) (6) Maureen Kessler < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Plowright, Raina < (b) (6)
Subject: Re: ETOH and fecal samples- Sample shipment.

Hello all,

Samples have arrived and are in the DARPA -80C freezer. I put the 22 boxes on the second shelf from the top.

Thanks everyone for all your efforts to get these shipped.

Best,

Evelyn

From: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6)
Sent: Thursday, December 31, 2020 9:09 AM
To: Callison, Julie (NIH/NIAID) [E] <callisonj@niaid.nih.gov>; Shupert, W. Lesley (NIH/NIAID) [E] < (b) (6) Menk, Kay (NIH/NIAID) [E] < (b) (6) Benson, Evelyn < (b) (6) Manuel Ruiz < (b) (6) Maureen Kessler < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Plowright, Raina < (b) (6)
Subject: RE: ETOH and fecal samples- Sample shipment.

Just to update everyone because we will have some people still gone next week(January 4th). We will send this shipment out on the week of January 11th.

We will also have an increase to 564 samples for this shipment but they all will be ETOH killed field samples.

Thank you everyone for the help!

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Wednesday, December 30, 2020 3:07 PM
To: Callison, Julie (NIH/NIAID) [E] < (b) (6) Shupert, W. Lesley (NIH/NIAID) [E] < (b) (6) Menk, Kay (NIH/NIAID) [E] < (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Benson, Evelyn < (b) (6) Manuel Ruiz < (b) (6) Maureen Kessler < (b) (6) Plowright, Raina < (b) (6)
Subject: RE: ETOH and fecal samples- Sample shipment.

Julie/Les,
I would like to send 164 samples of ETOH killed field samples(non-COVID) next week Wednesday (1/6/2021) to Bozeman, they will be on dry ice.

We have sent these same type of samples on late November of 2020.

Here is the address:

Attn: Evelyn or Monica

Montana State University

MBI/Health Sciences Building

Apple Lab

2155 Analysis Drive

Bozeman, MT 59718

Mobile: (b) (6)

Email: (b) (6)

Let me know if you have any issues.

-Trent

From: Callison, Julie (NIH/NIAID) [E] <(b) (6)
Sent: Wednesday, November 18, 2020 11:40 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Shupert, W. Lesley (NIH/NIAID) [E] <(b) (6) Menk, Kay (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: RE: ETOH and fecal samples- Sample shipment.

Hey Trent,

Les got it all packed up and it's on the way!

Here is the label with the tracking info, and you and Evelyn are on the Fed Ex alert emails.

Thanks!
Julie

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Friday, November 13, 2020 5:04 PM
To: Shupert, W. Lesley (NIH/NIAID) [E] <(b) (6) Callison, Julie (NIH/NIAID) [E] (b) (6); Menk, Kay (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: FW: ETOH and fecal samples- Sample shipment.

Hello,
I would like to send some irradiated and ETOH killed field samples next week Tuesday (11/17) to Bozeman. It will be 264 samples on dry ice.

We have sent these same type of samples in August of this year.

Here is the address:

Attn: Evelyn or Monica

Montana State University

MBI/Health Sciences Building

Apple Lab

2155 Analysis Drive

Bozeman, MT 59718

Mobile: (b) (6)

Email: (b) (6)

Let me know if you have any issues.

-Trent

From: Plowright, Raina <(b) (6)
Sent: Friday, November 13, 2020 4:52 PM
To: Manuel Ruiz <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: ETOH and fecal samples

Thank you Trent!!

From: Manuel Ruiz <(b) (6)
Date: Friday, November 13, 2020 at 4:10 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Cc: Plowright, Raina <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: ETOH and fecal samples

Hi Trent,

Thank you. I'll check with Devin about the samples in box AUS_165. Most likely, their location wasn't updated in the inventory.

Details for shipment:

Attn: Evelyn or Monica

Montana State University

MBI/Health Sciences Building

Apple Lab

2155 Analysis Drive

Bozeman, MT

59718

Thank you, once again, Trent and Vincent!,

Have a good weekend!

Manuel

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

On Fri, Nov 13, 2020 at 3:49 PM Bushmaker, Trenton (NIH/NIAID) [E] (b) (6) wrote:
Manuel,
(15) irradiated serum samples from "Serum_RML_MSU_20201113 (002)" should be sent out Tuesday. Yellow samples had questionable writing that was unreadable because the marker was smudged.I took a educated guess. Red ones should be ok.

(249 of 344) samples of the EtOH samples from "ETOH_f_r_RML_to_MSU_20201020" will be sent out Tuesday in addition. Samples from AUS_165 were already sent out to you in 8/10/2020. Please confirm everything is ok with these samples.

Please send me the shipping address, phone, and email like we always do.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Sent: Monday, October 26, 2020 10:14 PM
To: Manuel Ruiz <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: Re: ETOH and fecal samples

Hey,
I talked with Vincent about these samples(including RNAP and serum) and he wasn't very keen on me working on them right now. However, now that you have a shorten list I will revisit the conversation with him. Issue is now is just catching up with him. I will try later this week after the class presentation is submitted on Thursday. Could you check up with me early next week or on the Monday meeting? Thanks lots of balls in the air.

-Trent

From: Manuel Ruiz <(b) (6)
Date: Tuesday, October 20, 2020 at 5:48 PM
To: Trenton Bushmaker <(b) (6)
Cc: "Plowright, Raina" <(b) (6)
Subject: ETOH and fecal samples

Hi Trent,

Following up our call, attached is the list of samples in ETOH that we would like to move to MSU (file "ETOH_f_r_RML_to_MSU_20201020.csv"). It includes 344 samples in total. Most boxes only have these samples (a couple of exceptions), and I think they don't need any treatment at RML, so moving them would release some space in your freezers.

The second file attached ("NB_F_RML_to_MSU_20201020.csv") includes the samples for Maureen that would need to be aliquoted for her cortisol analysis (following previous protocol). It would be great to have an estimate from you about when these last samples could be shipped to MSU (Maybe we could split it so not to overload you and have some samples for Maureen to analyse?).

About the samples for Maureen's diet analyses for which we need to send DNA to Australia (~100 samples). I have a question and two potential plans that would be relevant only if the first question is a yes. Question: Is RML shipping DNA to Australia at some point this year? If so, plans for those 100 samples for Maureen could be: a) Ship them to MSU (inactivated) for DNA extraction, and then we could ship the DNA extracts back to RML to include it in the shipment to Australia or b) do the extractions at RML and include the DNA in the shipment to Australia. I am not sure whether paperwork might be required for plan "a".

I think we can leave the serum and RNAP samples out of the discussion at this stage, since they are a bit lower in priority in comparison to the samples detailed above.

Thanks once again for your work in this Trent! It is greatly appreciated!

Manuel

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

Error! Filename not specified.

Error! Filename not specified.

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Tue, 12 Jan 2021 18:42:08 +0000
To: (b) (6); Plowright, Raina; Peter Hudson
Cc: (b) (6)
Subject: RE: spillback-- can you weigh in on this please (MSU folks)

Hi (b) (6)

That's indeed one of the bigger question surrounding the potential of other species getting infected and establishing a additional reservoir (besides humans) .Its smtg we are actively exploring within this group.

I'm currently looking at mink infections and within host-evolution, and together with Tony Schountz, looking at deer mice which appear to be susceptible as well. Using population data, combined with experimental infection we are hoping to tease out what the risk for this. The "alternative" reservoirs could be an independent source of virus evolution and spill back.

Another thing to put on your radar, within OWS (and WHO) large effort undergoing at the moment of the characterization of the UK, SA and Brazil variants. We will do stability and transmission studies and feed them into the genotype-to-phenotype pipeline (as it was designed for). Let me know whether you want to be part of a direct data share group (so typically the data is disseminated withing OWS, HHS and WHO.

Most recent genotype-to-phenotype work from my group:

https://www.biorxiv.org/content/10.1101/2020.12.28.424565v1

https://www.biorxiv.org/content/10.1101/2021.01.09.426058v1

Cheers,

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

-----Original Message-----
From: (b) (6)
Sent: Tuesday, January 12, 2021 11:18 AM
To: Plowright, Raina < (b) (6) Peter Hudson (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Cc: (b) (6)
Subject: spillback-- can you weigh in on this please (MSU folks)

Hi Raina, Pete, Vincent -

Yesterday we submitted a DSD bullet (attached) and we have some comments from our Front Office as such:

I think I am missing one quick point on "spillback". Yesterday actually in the news there were reports of Gorilla's at the San Diego Zoo (I think it was this zoo) testing positive for COVID-19 after a keeper had also tested positive. The point they made in the article was that the gorilla population was already at risk without the introduction of a new virus in the population. (Also important) But the part that they did not touch on and I think may be missing here is the risk of spillback. So what if there is spillover to other species (closely related or not) and spillback? Let me

know if I am talking apples and oranges here.

Also, are there talks of implementing such mitigation strategies yet or is it too soon?

From my (b) (6) perspective, gorillas would be at risk of diseases from humans, so I suspect that is what they mean. Would be great to get your input on this above and the mitigation potential, as well.

Thanks!
(b) (6)

From: Schountz,Tony
Sent: Tue, 12 Jan 2021 14:46:28 +0000
To: Eric Laing; Wang Linfa; Munster, Vincent (NIH/NIAID) [E]; Perera,Rushika; Geiss,Brian
Cc: Maria Kaczmarek; epstein
Subject: Grant status
Attachments: R24 Grant_MEK_ts010721.docx

All, attached is the very rough skeleton of the R24 proposal. I've noted areas for each of you to work on, but of course please feel free to edit any other places you want. It's certainly going to change a bit before the final submission, but Jon and I want to get it to you sooner rather than later. Keep in mind that R24s are not supposed to be hypothesis-driven; they are really about resource development. The NIAID program officers gave us permission to do experimental challenges (Aim 3) so that's the place where we can do some science. We need to keep the Research Strategy to 12 pages (like an R01), so that means that means your sections should be a page to a page and a half. For your references, please just insert the PMID number and I'll get it the references inserted and formatted. It would be great if you could get your edits to us by Friday, but no later than Monday morning so that Jon and I can tidy up the proposal in preparation for submission on January 22.

For R24s, the Resource Sharing plan is critically important since the mechanism is directed to distribution of materials to the greater research community. We haven't started on that but I expect that once the proposal starts to shape up, this section will be mostly self-populating (but of course everone will get to see it before it is submitted).

Susan Rogers here at CSU is assembling the budgets and I think it will start routing through CSU's internal review process. If there are any problems, I'll be sure to let you know ASAP.

Jon and I have lined up several people who will provide letters of support for the proposal and I will be working on draft letters for each of them today.

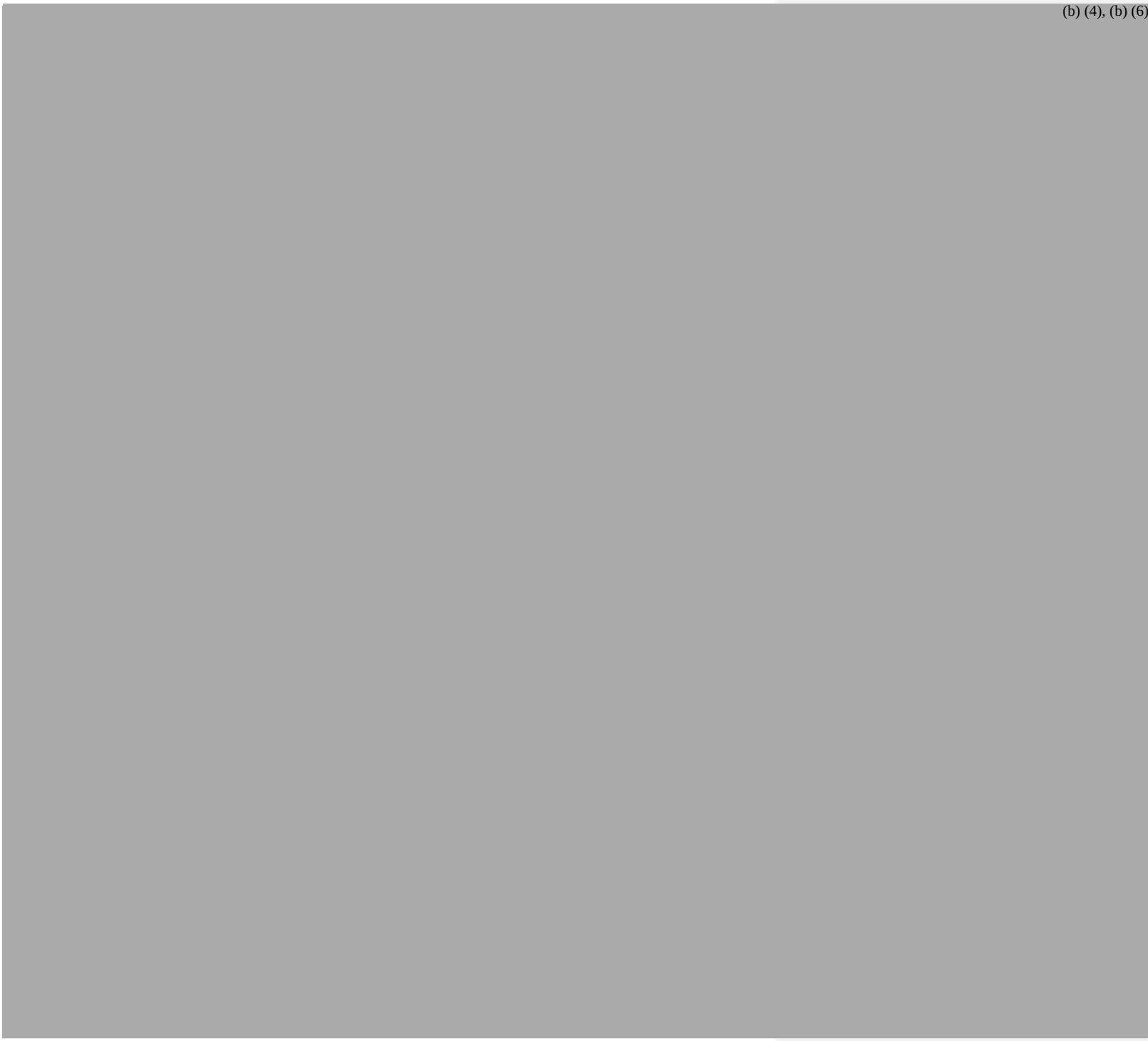
Let me know if you have questions.

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)




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


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


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


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


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


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


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


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


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


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

From: Plowright, Raina
Sent: Tue, 12 Jan 2021 02:00:21 +0000
To: LaTrielle, Sara; (b) (6) (b) (6) Barbara Han; Cara Brook; Colin Ross Parrish; Emily Gurley; Hamish McCallum; Hector Aguilar-Carreno; (b) (6) (b) (6) Nita Bharti; Olivier Restif; Peggy Eby; Hudson, Peter John; Schountz, Tony; Munster, Vincent (NIH/NIAID) [E]; Hoegh, Andrew; Cara Brook
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)
Attachments: MSU_PREEMPT_Phase_I_Review_Feb_2021.pptx

Hi Everyone,

Thanks for the productive call today.

Here is an updated version of the Phase I review outline. I incorporated the changes we discussed on the call and played with the timing to get us to 75 minutes. Use the proposed timing as a rough ball-park as we may adjust the scope of each section when we see the full slide deck.

Please send your slides to Sara by 27th January (2.5 weeks from now) and of course we will accept late-breaking data to be added to slides on the week of Feb 4th!

Raina

From: Plowright, Raina <(b) (6)
Date: Monday, January 11, 2021 at 12:37 PM
To: LaTrielle, Sara <(b) (6) (b) (6)
<(b) (6) (b) (6) <(b) (6) Barbara Han
<(b) (6) Cara Brook <(b) (6) Colin Ross Parrish
<(b) (6) Emily Gurley <(b) (6) Hamish McCallum
<(b) (6) Hector Aguilar-Carreno <(b) (6)
(b) (6) <(b) (6) (b) (6)
<(b) (6) Nita Bharti <(b) (6) Olivier Restif <(b) (6)
Peggy Eby <(b) (6) Hudson, Peter John <(b) (6) Schountz,Tony
<(b) (6) (b) (6) <(b) (6)
Hoegh, Andrew <(b) (6) Cara Brook <(b) (6)
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Hi Everyone,

Here is an outline for our Phase I Review presentation. Instructions are on the first pages. I've suggested a format and potential presenters and I'd like to make final decisions on the call today. Some of the headings are wonky bc DARPA have gone back to the original BAA and aligned our SOW with the original goals/language.

Also, prioritize analysis of phase I data that could be finalized by the deadline (at least a couple of days before Feb 4th) so we can include it in the final presentation. I'm thinking of the nutritional stress experiments in Artibeus bats, calibration of bioelectric impedance, initial cortisol analyses, or whatever is feasible in less than a month. Think about what is most strategic and please work with your teams to prioritize these data.

Talk to you in 1.5 hours.

Raina

From: LaTrielle, Sara <(b) (6)
Date: Monday, January 11, 2021 at 10:48 AM
To: (b) (6) < (b) (6) (b) (6) < (b) (6) Barbara Han < (b) (6) Cara Brook < (b) (6) Colin Ross Parrish < (b) (6) Emily Gurley < (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno < (b) (6) (b) (6) < (b) (6) (b) (6) < (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6) Peggy Eby < (b) (6) Hudson, Peter John < (b) (6) Plowright, Raina < (b) (6) Schountz,Tony < (b) (6) (b) (6) < (b) (6) Hoegh, Andrew < (b) (6) Cara Brook < (b) (6)
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

Reminder for today's PI meeting 2-3pm MST. Thanks to the few who already informed me that they will not be able to attend.

Join Zoom Meeting
https://zoom.us/j/ (b) (6)
*full call-in (dial) details below

agenda

From: LaTrielle, Sara
Sent: Monday, December 30, 2019 10:13 AM
To: (b) (6), < (b) (6) (b) (6) < (b) (6) Barbara Han < (b) (6) Cara Brook < (b) (6) Colin Ross Parrish < (b) (6) Emily Gurley < (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno < (b) (6) (b) (6) < (b) (6) (b) (6) < (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6) Peggy Eby < (b) (6) Hudson, Peter John < (b) (6) Plowright, Raina < (b) (6) Schountz,Tony < (b) (6)

(b) (6) < (b) (6) Hoegh, Andrew
(b) (6)
Cc: (b) (6) < (b) (6)
Subject: PREEMPT PI Monthly meeting (updated 2020)
When: Monday, January 11, 2021 2:00 PM-3:00 PM.
Where: https://zoom.us/j/ (b) (6)

Due to a date conflict our PI meeting is shifting to a week later.

All,

Please use this calendar invite with zoom and agenda links for our regular monthly meetings.

agenda

Zoom here:
PREEMPT is inviting you to a scheduled Zoom meeting.

Topic: PREEMPT PI Monthly Mtg

Join Zoom Meeting
https://zoom.us/j/ (b) (6)

Meeting ID: (b) (6)

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

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

PREEMPT Phase I Review

MSU

February 4th or 5th 2021

instructions

OPEN SESSION: February 4-5

The time allocated to your team's presentation during the Open Session is 75 minutes (Sub teams and other members included). Co-PIs, Postdocs, and students are welcome to present, however, you should manage to keep the presentation within the allotted time.

Presentations should focus on Phase I activities only, with a particular focus on findings/results, technical challenges addressed and remaining to be addressed, and transition plans. For any performers continuing into Phase II, those discussions will not take place during this meeting.

Performer presentations must include:

1. Your project goals and approach.

2. Key results since project inception. Note that most of the time should be focused on these updates.

3. Technical challenges and issues encountered by the team (including COVID19-related).

4. Any other information relevant to the PREEMPT community.

5. A concrete plan for transition including expected deliverables at the end of the program for both TA1 and TA2. Please include any transition partners (potential or realized) with whom you have engaged.

If potential transition partners have been identified by your team, or are likely transition partners, please send their contact information to [redacted] (b) (6) to issue them an invitation to the meeting on behalf of DARPA.

A short 15-minute discussion will follow each presentation. Please note that this time is in addition to the time allotted to you for the presentation (therefore, total time for presentation + discussion is 90 minutes).

The Open Session will be attended by all meeting participants including performers, DARPA employees and contractors, and potential transition partners from the government and private sectors. Each Open Session presentation should provide sufficient detail to enable general understanding of the effort without revealing proprietary details.

Team instructions

- Each designated presenter to address:

1. Your project goals and approach.
2. Key results since project inception. Note that most of the time should be focused on these updates.
3. Technical challenges and issues encountered by the team (including COVID19-related).
4. Any other information relevant to the PREEMPT community.
5. A concrete plan for transition including expected deliverables at the end of the program for both TA1 and TA2. Please include any transition partners (potential or realized) with whom you have engaged.

- Note that the last one is not relevant for all goals (e.g., field data)

Draft presentation (75 min)

- TA1
  1. Field data collection 20 min
     - Spatiotemporal virology data 15 min
     - Metadata 5 min
     - Tony's bat experiments (CeV experiment, VLP experiment) 5 min
  2. Bat virus shedding modeling 10 min
     - Olivier's models
  3. Bat virus sequence data 5 min
     - Field phylogeography
     - G & F sequences
     - New variants

     Transition between sequences and phenotyping with HNV G-P work 5 min
     - Experiments
     - Modeling
  1. Novel virus transmission phenotype system 10 min
     - Lab work
     - Models
- TA2
  1. HeV predictive models and eco-countermeasures 15 min
     - Multi-layer approach (use to summarize our studies) 5 min
     - Rough-cut early version with Bayesian network model spillover prediction 10 min
  2. HNV vaccination 5 min
     - Hector's work
- Conclusion 5 min

TA 1

TA1 Milestone 1: Collect field surveillance data

Goal/Metric	Identified up to 4 pulses of henipavirus shedding and collected environmental data and host immune data from these events.
Status	Complete: Identification of 8 pulses of henipavirus shedding in Australia and 4 pulses of shedding in Bangladesh and collection of environmental data and host immune data from these events.

Blue boxes are from DARPA

Develop a pipeline of in situ sampling, data analysis, and modeling **to detect viral shedding events in real time**. Knowing where and when bats are shedding zoonotic pathogens will allow resources to be focused on the highest risk places and times.

Yellow i
narrativ

Report from the 4 field teams on the data collection and analysis. What insights are derived so far?
-Australia
-Bangladesh
-Ghana
-Madagascar

To report: Ali or Emily to report

Milestone 1 continued….

- Metadata on bats and shedding events
  - Environmental data (Nita)
  - Immunology data (Dan/Caylee/Aga/Tony)
  - Diet data and microbiome data (mention this is in progress, in technical challenges)
  - Cortisol data (Liam)
  - Body condition data (Liam)
- make a strategy for what can be presented in early February.

--Raina to present?
--Sara to contact team members for single slide, or graph, and bullet points (note that unless the results are substantial, it will be a single bullet point)

Milestone 1 continued

- Data from Artibeus experiments
  - VLP nutritional stress
  - Cedar virus

Tony to present

TA1 Milestone 3: Initial mathematical models that assess risk of virus jump

Goal/Metric	**Developed statistical models that predict risk of spillover based on environmental, viral, and host population characteristics based on data collected in year 2. Predictive accuracy of models is 2X that obtained at 12 months.**
Status	In progress: Developing a statistical model coupled to a mechanistic model for virus circulation in and shedding from bat populations, and establishing seasonal drivers from Australian data. Work to fit the model to the last 2 years of data in process.

Focus on models that allow understanding of drivers of shedding
Olivier's team
-Emma's model
-Aaron's model
-in progress model

Olivier to present
(leave ML prediction to TA2 section)

TA1 Milestone 2: Multi-species lab test data

Goal/Metric	Identified a set of genetic signatures that differ among viral strains with different growth kinetics, attack rates or transmission rates.
Status	Big win: Describe 35 novel G and 37 novel F sequences of Hendra viruses and 1 full-sequence of a previously unknown henipavirus (from Madagascar). Identify (but not yet described) novel sequences from Ghana and Bangladesh.

Sequence data from the study
-Kwe phylogenetic work
-Hector sequences

Hector to report; lead into G-P work

This section will be a short transition between sequences and phenotyping

TA1 Milestone 4: Establish testbeds for validation of model predictions

Goal/Metric	Conducted infection experiments in hamster model to measure infection, shedding, & QS in model hosts.
Status	Complete: First full panel live virus in vitro HNV experiments. In progress: On-going studies in hamsters including transmission studies. SARS-CoV-2 vaccine hamster and mouse studies underway.

HNV G-P work
-Hector's team to summarize
-Jamie's team to summarize

-Jamie and Hector to report

Hectors HNV vaccine work in Hamsters – present this in TA2

New work on transmission phenotyping

Establish an integrated virology-to-modeling pipeline to quantify drivers of human-to-human spread in real time. This will enable rapid prioritization of countermeasures to contain early outbreaks (cf. masks over hand washing for SARS-CoV-2), while laying the foundation for *a priori* assessment of pandemic emergence risk for viruses in nature.

- Explain the transition from G-P work to virus transmission phenotype work (they don't want us to discuss phase II work, only phase I)
  - Jamie's modeling
  - Vincent's experiments

--Jamie to describe the concept of phenotyping and how experiments feed into phenotyping pipeline & new strain
--Vincent to describe some key experiments
Both to explain that G-P work transitioned to COVID bc of necessity

TA 2

TA2 Milestone: Proof of concept demonstration of preemptive approach that reduces either the probability of virus jump or the frequency of virus QS variants at high risk for species

Goal/Metric	**Demonstrated that >75% of individual subtropical Pteropus bats will abandon urban habitat in preference for native flowering and that bats do not differ in their use of regenerated and remnant native habitat, therefore providing POC for an ecological intervention for spillover. Demonstrated statistically significant protection against viral infection in hamsters.**
Status	Big win: Demonstrate that 60-78% of individual subtropical Pteropus abandoned urban habitat in preference for native flowering. In progress: Viral infection protection studies in hamsters underway.

See next slides

Proof of concept eco-countermeasure

Use artificial intelligence to integrate field data and mechanistic models to predict bat-borne viral spillover risk in space and time. If successful, this will allow **development of an early warning system for spillover of zoonotic pathogens from bats** and targeted deployment of countermeasures.

- Barbara's work
  - Progress and technical challenges on ML for prediction of spillover
  - Tie all the layers together in discussion of ML multi-scale (summary of all the different levels of data and models that feed into multi-scale work)
  - Distinguish these models that allow prediction from Olivier's models that allow understanding
- Rough-cut for Australia system is successful
  - Present all the predictive work in the Australian system including
  - ML factors that predict food shortage
  - Andy Hoegh's Bayesian network model on flowering and food shortages

To report: Barbara, Peggy, Andy, Pete, and Raina to brainstorm

HNV vaccine

- We characterized the sequence diversity, and then we understood the drivers of shedding, and we predicted the shedding events, so then we developed a multi-valent vaccination that can be applied to preempt spillover during these events
- Hector to report

Conclusion

- Pete and Raina

From: Plowright, Raina
Sent: Mon, 11 Jan 2021 19:37:16 +0000
To: LaTrielle, Sara; (b) (6) (b) (6) Barbara Han; Cara Brook; Colin Ross Parrish; Emily Gurley; Hamish McCallum; Hector Aguilar-Carreno; (b) (6) (b) (6) Nita Bharti; Olivier Restif; Peggy Eby; Hudson, Peter John; Schountz, Tony; Munster, Vincent (NIH/NIAID) [E]; Hoegh, Andrew; Cara Brook
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)
Attachments: MSU_PREEMPT_Phase_I_Review_Feb_2021.pptx

Hi Everyone,

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Also, prioritize analysis of phase I data that could be finalized by the deadline (at least a couple of days before Feb 4th) so we can include it in the final presentation. I'm thinking of the nutritional stress experiments in Artibeus bats, calibration of bioelectric impedance, initial cortisol analyses, or whatever is feasible in less than a month. Think about what is most strategic and please work with your teams to prioritize these data.

Talk to you in 1.5 hours.

Raina

From: LaTrielle, Sara <(b) (6)
Date: Monday, January 11, 2021 at 10:48 AM
To: (b) (6) < (b) (6) (b) (6) < (b) (6) Barbara Han < (b) (6) Cara Brook < (b) (6) Colin Ross Parrish < (b) (6) Emily Gurley < (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno < (b) (6) (b) (6) < (b) (6) (b) (6) < (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6) Peggy Eby < (b) (6) Hudson, Peter John < (b) (6) Plowright, Raina < (b) (6) Schountz,Tony < (b) (6) (b) (6) < (b) (6) Hoegh, Andrew < (b) (6) Cara Brook < (b) (6)
Subject: Re: PREEMPT PI Monthly meeting (updated 2020)

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https://zoom.us/j/ (b) (6)
*full call-in (dial) details below

agenda

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Sent: Monday, December 30, 2019 10:13 AM
To: (b) (6) < (b) (6) (b) (6) < (b) (6) Barbara Han < (b) (6) Cara Brook < (b) (6) Colin Ross Parrish < (b) (6) Emily Gurley < (b) (6) Hamish McCallum < (b) (6) Hector Aguilar-Carreno < (b) (6) (b) (6) < (b) (6) (b) (6) < (b) (6) Nita Bharti < (b) (6) Olivier Restif < (b) (6) Peggy Eby < (b) (6) Hudson, Peter John < (b) (6) Plowright, Raina < (b) (6) Schountz,Tony < (b) (6) (b) (6) < (b) (6) Hoegh, Andrew < (b) (6)
Cc: (b) (6) < (b) (6)
Subject: PREEMPT PI Monthly meeting (updated 2020)
When: Monday, January 11, 2021 2:00 PM-3:00 PM.
Where: https://zoom.us/j/ (b) (6)

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All,

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agenda

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PREEMPT is inviting you to a scheduled Zoom meeting.

Topic: PREEMPT PI Monthly Mtg

Join Zoom Meeting
https://zoom.us/j/ (b) (6)

Meeting ID: (b) (6)

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

Dial by your location
+1 669 900 9128 US (San Jose)
+1 646 558 8656 US (New York)

Meeting ID: (b) (6)
Find your local number: https://zoom.us/u/adzPR7PsUq

PREEMPT Phase I Review

MSU

February 2021

instructions

OPEN SESSION: February 4-5

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- Note that the last one is not relevant for all goals (e.g., field data)

Draft presentation

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  1. Field data collection
     - Virology data
     - Metadata
     - Tony's bat experiment
  2. Bat virus shedding modeling
     - Olivier's models
  3. Bat virus sequence data
     - Field phylogeography
     - G & F sequences
     - New variants
  4. HNV G-P work
     - Experiments
     - Models
- TA2
  1. HeV predictive models and eco-countermeasures
     - ML food shortages, and Bayesian flowering models
  2. HNV vaccination
     - Hector's work
  3. Novel virus transmission phenotype system
     - Modeling
     - Lab work

TA 1

TA1 Milestone 1: Collect field surveillance data

Goal/Metric	Identified up to 4 pulses of henipavirus shedding and collected environmental data and host immune data from these events.
Status	Complete: Identification of 8 pulses of henipavirus shedding in Australia and 4 pulses of shedding in Bangladesh and collection of environmental data and host immune data from these events.

Blue boxes are from DARPA

Develop a pipeline of in situ sampling, data analysis, and modeling **to detect viral shedding events in real time**. Knowing where and when bats are shedding zoonotic pathogens will allow resources to be focused on the highest risk places and times.

Yellow i
narrativ

Report from the 4 field teams on the data collection and analysis. What insights are derived so far?
-Australia
-Bangladesh
-Ghana
-Madagascar

To report: Ali or Emily to report

Milestone 1 continued….

- Metadata on bats and shedding events
  - Environmental data (Nita)
  - Immunology data (Dan/Caylee/Aga/Tony)
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  - Cortisol data (Liam)
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- **Let's make a strategy for what can be presented in early February.

--Raina to present?
--Sara to contact team members for single slide, or graph, and bullet points (note that unless the results are substantial, it will be a single bullet point)

Milestone 1 continued

- ? Data from Artibeus nutritional stress experiments

Tony?

TA1 Milestone 3: Initial mathematical models that assess risk of virus jump

Goal/Metric	**Developed statistical models that predict risk of spillover based on environmental, viral, and host population characteristics based on data collected in year 2. Predictive accuracy of models is 2X that obtained at 12 months.**
Status	In progress: Developing a statistical model coupled to a mechanistic model for virus circulation in and shedding from bat populations, and establishing seasonal drivers from Australian data. Work to fit the model to the last 2 years of data in process.

Olivier's team
-Emma's model
-Aaron's model
-in progress model

Olivier to report
(should we do ML Australia prediction here or in TA2—I think leave to TA2)

TA1 Milestone 2: Multi-species lab test data

Goal/Metric	Identified a set of genetic signatures that differ among viral strains with different growth kinetics, attack rates or transmission rates.
Status	Big win: Describe 35 novel G and 37 novel F sequences of Hendra viruses and 1 full-sequence of a previously unknown henipavirus (from Madagascar). Identify (but not yet described) novel sequences from Ghana and Bangladesh.

Sequence data from the study
-Kwe phylogenetic work
-Hector sequences

Hector to report; lead into G-P work (present after Olivier)

TA1 Milestone 4: Establish testbeds for validation of model predictions

Goal/Metric	Conducted infection experiments in hamster model to measure infection, shedding, & QS in model hosts.
Status	Complete: First full panel live virus in vitro HNV experiments. In progress: On-going studies in hamsters including transmission studies. SARS-CoV-2 vaccine hamster and mouse studies underway.

HNV G-P work
-Hector's team to summarize
-Jamie's team to summarize

-Jamie and Hector to report

Hectors HNV vaccine work in Hamsters – present this in TA2

TA 2

TA2 Milestone: Proof of concept demonstration of preemptive approach that reduces either the probability of virus jump or the frequency of virus QS variants at high risk for species

Goal/Metric	**Demonstrated that >75% of individual subtropical Pteropus bats will abandon urban habitat in preference for native flowering and that bats do not differ in their use of regenerated and remnant native habitat, therefore providing POC for an ecological intervention for spillover. Demonstrated statistically significant protection against viral infection in hamsters.**
Status	Big win: Demonstrate that 60-78% of individual subtropical Pteropus abandoned urban habitat in preference for native flowering. In progress: Viral infection protection studies in hamsters underway.

See next slides

Proof of concept eco-countermeasure

Use artificial intelligence to integrate field data and mechanistic models to predict bat-borne viral spillover risk in space and time. If successful, this will allow **development of an early warning system for spillover of zoonotic pathogens from bats** and targeted deployment of countermeasures.

- Present all the predictive work in the Australian system including
  - ML factors that predict food shortage
  - Andy Hoegh's Bayesian network model on flowering and food shortages
- Barbara's work
  - Progress and technical challenges on ML for prediction of spillover

To report: Barbara, Peggy, Andy, and Raina to brainstorm

HNV vaccine

- Hector to report

New work on Phenotyping

Establish an integrated virology-to-modeling pipeline to quantify drivers of human-to-human spread in real time. This will enable rapid prioritization of countermeasures to contain early outbreaks (cf. masks over hand washing for SARS-CoV-2), while laying the foundation for *a priori* assessment of pandemic emergence risk for viruses in nature.

- Explain the transition from G-P work to virus transmission phenotype work (they don't want us to discuss phase II work, only phase I)
  - Jamie's modeling
  - Vincent's experiments

--Jamie to describe the concept of phenotyping and how experiments feed into phenotyping pipeline
--Vincent to describe some key experiments
Both to explain that G-P work transitioned to COVID bc of necessity

From: Plowright, Raina
Sent: Sun, 10 Jan 2021 17:13:08 +0000
To: Munster, Vincent (NIH/NIAID) [E]
Cc: Jamie Lloyd-Smith
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Ok I'll check in with Trent. He works one on one with Manuel to stagger samples.

Sent from my iPhone

On Jan 10, 2021, at 10:03 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6)> wrote:

Stress on my end is actually fine, its more the demands on Kwe and Trent I need to manage carefully as I don't want them to burn out.

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

From: Plowright, Raina <(b) (6)>
Sent: Sunday, January 10, 2021 9:52 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)>
Cc: Jamie Lloyd-Smith <(b) (6)>
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi Vincent,
Sounds very stressful. Let me know how we can alleviate the load.
Raina

Sent from my iPhone

On Jan 10, 2021, at 9:37 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6)> wrote:

Hi guys,

Just a couple of points of continuous concern.

The demands on my group from both the PREEMPT team have been increasing, this is not attainable.

As an example:

- Having Trent and another Myndi do PCR extractions for Raina's students
- Having Kwe, Trent and Myndi spend over 10 hours over Christmas trying to inventory a shipment from Bangladesh because the Bangladesh team made a complete mess of things
- Having Amandine/UCLA use Steph, Bob, Kwe, Trent for her research
- Having Ali approach everything as an emergency for her students thesis

I have a feeling that your lack of experience in how much time all these combined things my lab actually costs results in a over demand of the available human resources in my lab. We are really struggling here. E.g. having UCLA adding time-point to Trent's experiments is not useful. On one end from a logistic in lab high containment perspective, on the other hand as it will completely overdo what we are setting out to ask ourselves. Even after multiple times I have tried to get this across this has not seem to have sank in completely.

After last time with the temperature – stability delays, I'm already having a hard time to keep my staff motivated to work with modelers as there is prevailing sense that the data which was gathered extremely fast was then put into an UCLA black hole and didn't emerge until way later. Especially Kwe and Trent feel completely side-lined there. I'm not arguing that that was what's needed, but there is the prevailing sense that there is not true collaboration there.

Obviously, I'm extremely dedicated to our work together, but need your help. Please consider the what the request means for my team members first, before you put it in . We are not in an ideal world, we are in the middle of a pandemic and I'm juggling at least 15 competing projects.

Cheers,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sun, 10 Jan 2021 16:13:45 +0000
To: Bushmaker, Trenton (NIH/NIAID) [E]; Plowright, Raina
Subject: RE: aerosol experiment prep

Great!

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Friday, January 8, 2021 2:35 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina
<(b) (6)
Subject: RE: aerosol experiment prep

Last update…
The chamber was ran at 10C @ 85%RH. It ran really well. I think we are good to go unless I heard back from you two.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Thursday, January 7, 2021 4:23 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina
(b) (6)
Subject: RE: aerosol experiment prep

The environmental chamber is running nicely. I did 30C at 65%RH last night it ran well.

I'm doing 10C at 40%RH tonight and will check tomorrow.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, December 3, 2020 9:57 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Plowright, Raina
(b) (6)
Subject: RE: aerosol experiment prep

Sounds good,

- CC me in with the conversations with biosafety

- Run a couple of trial runs to ensure the chamber works and holds temp / humidity the way it's supposed to

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, December 3, 2020 9:53 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina (b) (6)
Subject: RE: aerosol experiment prep

Vincent/Raina,
The environmental chamber looks to be completed. It doesn't look the most professional for the exhaust port with the red handle in the "Side view" picture. They tried to make the unit air tight and the black putty mixture came out a little bit.

The next step will be to start the conversation with biosafety regarding the use of the Goldberg drum inside the environmental unit. This will probably take the most of this month and will require an update to the SOP for the environmental chamber. I will update you both along the way.

When we feel the approval will be granted I will talked with BSL4 scheduling crew to see when we can get the unit into BSL4. Probably start this conversation in the next 2 weeks.

Let me know if you have questions.

-Trent

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Sent: Saturday, November 21, 2020 9:53 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Subject: RE: aerosol experiment prep

perfect

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Friday, November 20, 2020 3:38 PM

To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: RE: aerosol experiment prep

All the parts came in for the environmental chamber. Darren said he will start on it next week on schedule to be completed by the end of the month.

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, November 19, 2020 2:08 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: aerosol experiment prep

Vincent,
Quick update:

1. Most of the parts are in for the conversion of the environmental equipment for BSL4. I will talk with Darren tomorrow(Friday). This is on schedule for what I told you at the start of the month.
2. Plan to start the conversation with Biosafety after next week Wednesday regarding the use of the equipment in BSL4.
3. During the retrofit of the environmental chamber/ talked with Biosafety, the plan for December is to work on the stability of the RH% issues we talked about with Jamie/Dylan/Amandine with the Goldberg drum unit in the BSC(not the environmental chamber).
4. I will work on an outline of the experiments after next Wednesday.

Most of this will start after next Wednesday. I'm trying to concentrate on my finals for the next 6 days, working on confirming my committee for graduate school, and picking classes for next semester while I provide my support position.

I will be adding Raina on to emails like this so she knows what is going on. Also I would like to discuss adding her to the conversation with Jamie's crew.

I will be in tomorrow the whole day(Friday).

-Trent

From: Vincent Munster <(b) (6)
Date: Wednesday, November 18, 2020 at 9:29 AM
To: Trenton Bushmaker <(b) (6)
Subject: FW: aerosol experiment prep

Hi Trent,

What is te status on this?

It would be good if you start preparing:

- A complete overview of the planned experiments with a precise delineation of what assays you use, how your analyzing it etc.

- Do a retrospective analyses of the aerosol and PCR data and try to understand why. I want you to analyze the data, and not hand them over to a third party. If there are still samples available, I would do multiple extraction or plan for multiple extractions to see the variation in your procedures
- Make a complete time-line in gant chart form to get a sense when you will be doing which experiment exactly and provide an overview where we are exactly at currently

Cheers,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Monday, October 19, 2020 9:43 AM
To: Bushmaker, Trenton (NIH/NIAID) [E] (b) (6)
Cc: van Doremalen, Neeltje (NIH/NIAID) [E] < (b) (6) Holbrook, Myndi (NIH/NIAID) [C] < (b) (6)
Subject: aerosol experiment prep

Hi Trent,

- For the prepping of the upcoming experiments, it would be good if you start growing a large stock for your work of the Marcus Daly D614G isolate to be able to compare between WA1 and this one.
- Secondly, the titers are higher if titrated on the TMPRSII cells, so you need to titrate your stability experiment stock of WA1 on these cells as well (this will allow you to go in higher with the drum experiment), or if you do not have WA1 grow a big stock on the TMPRSII cells as well.
- Make sure all the titrations are done on the TMPRSII cells as well (more sensitive so better resolution).

Cheers,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sun, 10 Jan 2021 16:13:07 +0000
To: Plowright, Raina; Alison Peel; Bushmaker, Trenton (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]
Subject: RE: Update on shipment

Hi Raina,

For our analyses it shouldn't matter too much.

No virus isolation was attempted yet, and will likely not be done until later this spring given the pandemic.

Kwe/Trent can you comment as I thought that some of the boxes were still frozen upon arrival?

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

From: Plowright, Raina < (b) (6)
Sent: Saturday, January 9, 2021 9:08 PM
To: Alison Peel < (b) (6) Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] < (b) (6) Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Subject: Re: Update on shipment

Hi Everyone,
This shows that all samples from all boxes would have defrosted and they didn't even top the samples up with ice after the defrosting was discovered.
Hard to fathom this given the 10K price tag (and the hundreds of thousands spent to collect the samples).
RML folks, do you have a sense of which samples for which analyses will be most affected?
Did you attempt viral isolation on any samples?
Raina

From: Alison Peel < (b) (6)
Date: Thursday, January 7, 2021 at 2:47 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] < (b) (6) Munster, Vincent (NIH/NIAID) [E] (b) (6), Plowright, Raina < (b) (6)
Subject: Re: Update on shipment

Hi all,

Vincent - the quote is semi-fixed, but there can sometimes be extra charges associated with changed routes, delays requiring extra dry ice topup etc. I spoke with Mandy, and in fact the invoices are closer to expectations than I realised (USD $9400 for the RML shipment).

Thanks very much Kwe.

Vincent/Kwe/Trent - how concerned are you about the temperature records? I see that the temperature logs for all boxes show that they were >4 degrees C for 48-72 hours (including all boxes being at 7-9 degrees for 24 hours). It's shattering to think of the many thousands of hours that went into collecting and preparing these samples, and the uncertainty around the effect of this.

	-20 alarm triggered	Peak	Duration at peak	11-Dec	12-Dec	13-Dec	14-Dec	15-Dec	16-Dec	17-Dec	18-Dec	19-Dec	(dates are midday AEST)
Box 1	15 Dec 10:51 PM AEST	7 degrees	24 hours	-70	-70	-70	-70	-55	0	1	7	7	
Box 2	15 Dec 9:39 PM AEST	9 degrees	24 hours	-70	-70	-70	-70	-50	3	4	8	9	
Box 3	15 Dec 7:27 PM AEST	10 degrees	short, but 24 hours at 8 degrees	-70	-70	-70	-70	-55	5	6	8	9	
Box 4	16 Dec 5:23 AM AEST	9 degrees	24 hours	-70	-70	-70	-70	-70	-3	0	9	9	
Box 5	16 Dec 1:59 PM AEST	9 degrees	24 hours	-70	-70	-70	-70	-70	-14	5	7	9	
									* notified				

Looking at the tracking log, it seems like the dry ice may not have been topped up after it was transferred to Air NZ, or certainly not when it arrived in NZ.
After the boxes were detected as thawed, it seems like attempts to keep them at 4 degrees failed completely.
I think at some point they changed hands from WC to Fedex? When did that happen?
Have you had any experience with thawed shipments with WC in the past? It seems unfair to pay full price for this, but perhaps they will just shift the blame to AirNZ.

Tracking Event Log

House Waybill: 610318701

Job: 5275

Event	Log Date	Log Time
Shipment Ready at NATHAN QLD 4111 Australia	Dec 11 20	14:00
Picked Up at NATHAN QLD 4111 Australia	Dec 11 20	13:30
Tendered to AIR NEW ZEALAND at BRISBANE BRISBANE Australia	Dec 12 20	08:00
Air Transfer Confirmed to AIR NEW ZEALAND at AUCKLAND AUCKLAND New Zealand	Dec 14 20	
Shipment Recovered to AIR NEW ZEALAND at LOS ANGELES INTERNATIONAL LOS ANGELES United States	Dec 16 20	22:21
Shipment Recovered to FX CARGO at MISSOULA COUNTY MISSOULA UNITED STATES	Dec 18 20	15:00
Delivered at HAMILTON MT MT59840 United States	Dec 18 20	15:45

SHIPMENT STATUS	HWB
Delivered at HAMILTON MT MT59840 United States	610318701

SHIPPER	CONSIGNEE	PICK-UP	POD	PIECES	WEIGHT
NATHAN QLD 4111 AUS	HAMILTON MT MT59840 USA	Dec 11/2020 13:30	Dec 18/2020 15:45	5	220.46 LBs 100.0 KGs

TEMP:	REFRIG TYPE:
frozen	dry ice

REFRIGERANT ADDED: LOS ANGELES USA Date: Thu December 17, 2020 Time: 1725 / SENT TO: REFRIG: Gel Packs - refrig. Wgt: 0 LB

Thanks - appreciate any thoughts you have.
Ali

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: 08 January 2021 05:19
To: Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Alison Peel <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Update on shipment

Thank you Kwe, I did see that. Good work like you always do.

From: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6)
Date: Thursday, January 7, 2021 at 11:58:33 AM
To: "Bushmaker, Trenton (NIH/NIAID) [E]" <(b) (6) "Alison Peel" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Update on shipment

Trent,

I send the data to Ali already. Maybe you missed that email.

Thanks

Kwe

From: "Bushmaker, Trenton (NIH/NIAID) [E]" <(b) (6)
Date: Thursday, January 7, 2021 at 9:51 AM
To: Alison Peel <(b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Update on shipment

Ali- I will check-in with Kwe this afternoon and see if he needs some help. I would expect it by this weekend.

Kwe- How about we talk this afternoon when I am in, after 1pm.

-Trent

From: Alison Peel <(b) (6)
Date: Wednesday, January 6, 2021 at 7:50 PM

To: Trenton Bushmaker <(b) (6) Yinda Kwe <(b) (6)
Vincent Munster <(b) (6) "Plowright, Raina"
<(b) (6)
Subject: Re: Update on shipment

Thanks Trent,
What would be a reasonable timeframe to download the data? I need to respond to World Courier, and I think the temperature data is an important piece of information in my discussions with them.
Thanks
Ali

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: 06 January 2021 02:24
To: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F]
<(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Update on shipment

Ali,
I think Kwe has them on his desk but little busy doing inventory.

-Trent

From: Alison Peel <(b) (6)
Date: Monday, January 4, 2021 at 2:22 PM
To: Yinda Kwe <(b) (6) Trenton Bushmaker <(b) (6)
Vincent Munster <(b) (6) "Plowright, Raina"
<(b) (6)
Subject: Update on shipment

Hi all,
How did everything end up looking with the shipment temperature loggers? I'm interested to know obviously for the samples sake, but World Courier has send through an exorbitant bill without any further explanation and it would be helpful to have whatever detail from you on the loggers and your communications with world courier that would hep with arguing them down.
Thanks!
Ali

From: Plowright, Raina
Sent: Sun, 10 Jan 2021 03:57:23 +0000
To: Munster, Vincent (NIH/NIAID) [E]; Schountz, Tony; Olivier Restif
Cc: Schountz, Tony; Adney, Danielle (NIH/NIAID) [F]; (b) (6)
Subject: Re: deer-mice

Yes Angie would be the perfect person. Good thinking Olivier! Hope she is able to do this.
Raina

From: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Date: Friday, January 8, 2021 at 8:50 AM
To: Schountz, Tony <(b) (6) Olivier Restif <(b) (6)
Cc: Plowright, Raina <(b) (6) Schountz, Tony
<(b) (6) Adney, Danielle (NIH/NIAID) [F] <(b) (6)
(b) (6) <(b) (6)
Subject: RE: deer-mice

I'll reach out to her and CC you it,

She gave a presentation here a couple of years ago. Great suggestion btw Olivier!

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

From: Schountz,Tony <(b) (6)
Sent: Friday, January 8, 2021 8:49 AM
To: Olivier Restif <(b) (6)
Cc: Raina Plowright <(b) (6) Schountz, Tony <(b) (6)
Adney, Danielle (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E]
<(b) (6) (b) (6)
Subject: Re: deer-mice

Vincent, I can contact Angie if you'd like. I know her from the hantavirus days.

T.
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street

1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 8, 2021, at 1:13 AM, Olivier Restif <(b) (6) wrote:

Thanks Raina and Vincent. Happy to discuss this project indeed, but my first reaction is that the ideal person to talk to is your neighbour Angie Luis in Misoula.
https://www.cfc.umt.edu/research/disease-ecology/research/default.php

Best wishes,

Olivier

On 7 Jan 2021, at 21:54, Plowright, Raina <(b) (6) wrote:

It's a great idea. I don't have anyone in the lab who could do it right now but I have a former postdoc who is great with SIRS models and could potentially help. Olivier should be engaged as well as he is a 'real' modeler! I've cc'd him.

From: Schountz,Tony <(b) (6)
Date: Thursday, January 7, 2021 at 2:37 PM
To: Adney, Danielle (NIH/NIAID) [F] <(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6) (b) (6) <(b) (6) Schountz,Tony <(b) (6)
Subject: Re: deer-mice

I'm available Thursday from 9-1 and Friday all day.

Tony
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street

1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 7, 2021, at 1:41 PM, Adney, Danielle (NIH/NIAID) [F] <(b) (6) wrote:

Hi all,

Would people have time next week to touch base about possible studies? What is your availability next Thursday or Friday afternoon?

Best,
Danielle

--
Danielle Adney, DVM, PhD
Virus Ecology Section
Laboratory of Virology
NIH/NIAID

If you are receiving this email outside of your typical working hours, I hope you feel no pressure to read or respond until your schedule and workload permit.

From: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6)
Date: Thursday, January 7, 2021 at 10:03 AM
To: "Plowright, Raina" <(b) (6) "(b) (6)
<(b) (6) "Schountz, Tony" <(b) (6)
Cc: "Adney, Danielle (NIH/NIAID) [F]" <(b) (6)
Subject: deer-mice

Hi Raina and Jamie,

I'm sure you heard of Tony' s great work with the deer mice and SARS-CoV-2. Danielle from my lab is part of an interagency one-health workgroup with CDC, largely focusing on mink. The situation surrounding infected mink farms would have a high-risk of spill-over from mink into the deer-mouse population.

I thought one cool question for the epi modelers to look at is doing some classic SEIR modelling on the deer-mice. Get some population data and make some assessment what the risk (probably low, but who knows) of the establishment of deer mice as a reservoir based upon virological, transmission, sero-conversion and re-challenge data.

Let me know what your thoughts are,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Fri, 8 Jan 2021 18:55:36 +0000
To: Bushmaker, Trenton (NIH/NIAID) [E]; Amandine Gamble; Jamie Lloyd-Smith; Dylan H. Morris
Cc: Plowright, Raina
Subject: RE: Goldberg drum - WA1, UK, and SA variants

Hey guys,

Please do understand the technical limitation of the set-up in a high containment laboratory. I favor shorter experiments, which will allow us to more rapidly determine whether there are differences between the isolates.
Given that the transmission window is likely under 3 hours, I'm not particularly in favor making these experiments longer in duration than absolutely necessary. Anything over a 3 hour window will have massive implication on the way we conduct experiments.

My main priority is not running a model, but a providing good comparison between the different strains, which should be done in under 3 hours. A limited analyses as was done in the NEJM should be sufficient (I'm not against running a model, but human resources are extremely limited and I think it would be best to have an experimental design which would get us the best result with the least effort). Also this data is urgent, and I don't want to have any delays with getting this data out.

Of note, you don't "lose" 2 logs during the spray, that's just the experimental system (from collision to collection), this is fixed for every experiment so no difference is expected there between variants (or viruses)

As discussed this week, at the moment no isolates are in yet (again, try to understand that this is a massive undertaking and is a process of several weeks), but titers are expected in the WA1 range

Cheers,

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

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: Thursday, January 7, 2021 8:14 PM
To: Amandine Gamble <(b) (6) Jamie Lloyd-Smith <(b) (6) Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Dylan H. Morris <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Thank you for the quick reply, I like the points you made. I have some time tomorrow in BSL4 from 9-2pm to think and reply, thanks crew.

-Trent

From: "Amandine Gamble" <(b) (6)
Date: Thursday, January 7, 2021 at 7:01:22 PM
To: "Jamie Lloyd-Smith" <(b) (6) "Bushmaker, Trenton (NIH/NIAID) [E]" (b) (6) "Dylan H. Morris" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Goldberg drum - WA1, UK, and SA variants

Hi everyone,

Thanks Trent for all the info and your work on those new strains (among other things!). I only have two minor thoughts following up on Jamie's e-mail:

- As Jamie noted, the longer we wait before taking the second time point, the more precise our estimate of decay rate / half-life will be (as long as we are still above the LOD), so I would also be tempted to target 4 or 5h rather than 3h based on the data we had for the NEJM paper and the fact that you are now using a more sensitive titration protocol (if we understood well), however that obviously depends on the starting dose (the intercept on the graph Jamie put) so, my question is: **do you have any idea of the stock concentrations for the new variants**, and whether we have any reason to expect more loss during spraying? It looks from the NEJM paper that we lose around 2 log10 during spraying with WA1 (and SARS-CoV-1). I guess you all already thought about this, but just writing down in case (there are lots of things to think about!). Also, if you already have an idea on the stock concentration, Dylan can run some analyses on mock data (as mentioned by Jamie) accounting for this, the loss at spraying and potential decay rates, as pointed by Jamie.

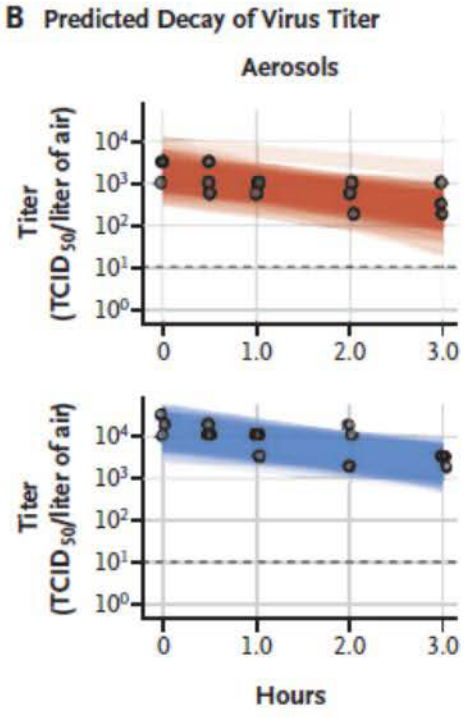
- The second point can be discussed after you got the data as it is only about formatting. I see from the raw data attached to one of the e-mails (the scan of the hand-written data) that some wells are blank, although in the Excel file we received, all the wells were classified as + or -. I assume that you did not collect data from those blank wells because you could assume they were all positive (based on higher dilutions being positive) or negative (based on lower dilutions being negative), right? Dylan can correct me, but I think his model would run perfectly on the raw data, even if they are "incomplete". In other words, I think we can let the model do what you were already doing when you complete the blank wells so there is no need for you to do this. So in the future, **we are happy to work on the raw data (i.e., with +, - and blanks [that you can note "NA" so we know it is not just a forgotten well]), rather the completed version (with only + and -)**. You can even just send us a scan of your data and we can generate the Excel file if you prefere.

With all this, I also with you all the best for 2021 =)

Amandine

Le jeu. 7 janv. 2021 à 16:53, Jamie Lloyd-Smith < (b) (6) a écrit :
Hi Trent, hi everyone (also copying in Amandine since she's the one on our side with most experience with the raw data),

Great to hear this -- a few quick responses.
- 22/65 makes sense to me
- great to add the SA strain!
- I hope we are planning to collect new data on the WA1 strain, not reuse the NEJM data. There were enough differences in design with the original experiments that I think it would be MUCH stronger science to study all three strains using the same design (updated to avoid some of the challenges of the first round). (Actually from your comment about 'another 9 days' to add a timepoint, i.e. 3 viruses times 3 replicates, I think we're on the same page here.)
- I think the 5% decline in RH due to settling should be OK, if it's basically consistent across the viruses. We can think about whether to account for it in the modelling... my instinct is that we can leave it out of the model unless it differs significantly across replicates and viruses.
- Great to hear about T=0. That's especially crucial if we're just doing the one later time-point.
- Regarding the timing of the later timepoint, I was surprised by your statement, since my memory from the NEJM paper was that the above-LOD detections would have continued well beyond 3 hours. i.e. look at the plots:



The SARS-CoV-2 data (red) started at a lower titer, but given the slopes it looks like there'd still be useful super-LOD data out to 5 and probably 6 hours. The SARS-CoV-1 data (blue) show the same slope with a

higher intercept, and look like they'd stay above LOD out to 6 hours and beyond. Looking at the raw well data, the difference in + counts across time points isn't so striking, i.e. it's not like we're losing a dilution per hour - which makes sense, given the estimated half-life of ~3 hrs. Also if I'm not mistaken, Neetlje or Vincent mentioned that you guys have changed protocols (spin inoculation and different cell line) to get higher sensitivity in culture.
Bottom line: again, it will depend on the titers achievable at T=0, but unless I'm misreading things badly I think there would be value in extending that later timepoint. I know there are complexities about how long you can spend in BSL4, etc, but I'm just talking about the raw information content.

Dylan, Amandine, any further/other thoughts? Dylan, do you want to do a quick analysis with mock data (and reasonable noise) to think about the power we'd have to distinguish differences among variants using this design (i.e. 3 replicates of a single uninterrupted decay window)? And how that might change if we stretch the window to longer time periods? Or if we need more information to get better estimates, do we do as well by adding a 4th replicate at the long time point, rather than adding intermediate time points? (nothing magic about intermediate time points, except for prettier decay graphs. one replicate at 5h might be equivalent to 2 at 2h, in terms of information gained)

cheers,
Jamie

On Thu, Jan 7, 2021 at 3:51 PM Bushmaker, Trenton (NIH/NIAID) [E] <[redacted] (b) (6)
wrote:
Jamie/Dylan,
First, I have added the pervious email so we can all stay on the same page(UK variant shams).

Next, I have talked with Vincent today but would like your input. For a quick paper, I think we should do condition at 22C @ 65%RH - hospital setting. Is everyone ok with this? This was the same setting as we had in the NEJM paper.

Third, we will do the UK variant (VOC), South African (SA) variants, and the original NEJM paper Washington (WA1) for the comparison.

Four, will a 5% percent decrease over 3 hours of the relative humidity cause issues with anything? This happens when nothing is pulled out of the drum, it just happens because of the time frame of 3 hours with the deposition. It should be ok for this decay model(linear regression) correct? I just want to confirm.

Lastly and most important, we will "for sure" have a timepoint at 0 minutes to check for the start values. However, we need to discuss the last timepoint. The LOD for our titrations with our cell culture seems to happen between 180-240 mins, so I would stick with the 180 minute timepoint (titrations attached- "2019-nCoV titrations goldberg drum.jpeg"). Do you agree with this? It would give you two points at timepoint 0 and 180 minutes.

I will collect (4) qRT-PCR per timepoint 0 and (4) more during the later timepoint.

How does this sound? Think about the later timepoint. Each run is a day of work in BSL4 and 10ml of virus. If in addition you want to collect at a middle timepoint this will adding another 9 days of BSL4 work, that will have to be spread out over 3 weeks. We can also think about a later timepoint. The titrations will be useless but qRT-PCR might be interesting. I think this will be usefully for a later experiment because we want to get this out quickly.

-Trent

--
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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 7 Jan 2021 22:18:31 +0000
To: Plowright, Raina; Schountz, Tony; Adney, Danielle (NIH/NIAID) [F]
Cc: (b) (6) Schountz, Tony; Olivier Restif
Subject: RE: deer-mice

awesome

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

From: Plowright, Raina <(b) (6)
Sent: Thursday, January 7, 2021 2:55 PM
To: Schountz, Tony <(b) (6) Adney, Danielle (NIH/NIAID) [F]
<(b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) (b) (6) Schountz,
Tony <(b) (6) Olivier Restif <(b) (6)
Subject: Re: deer-mice

It's a great idea. I don't have anyone in the lab who could do it right now but I have a former postdoc who is great with SIRS models and could potentially help. Olivier should be engaged as well as he is a 'real' modeler! I've cc'd him.

From: Schountz,Tony <(b) (6)
Date: Thursday, January 7, 2021 at 2:37 PM
To: Adney, Danielle (NIH/NIAID) [F] (b) (6)
Cc: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina
<(b) (6) (b) (6) <(b) (6)
Schountz,Tony <(b) (6)
Subject: Re: deer-mice

I'm available Thursday from 9-1 and Friday all day.

Tony
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street

1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 7, 2021, at 1:41 PM, Adney, Danielle (NIH/NIAID) [F] <(b) (6) wrote:

Hi all,

Would people have time next week to touch base about possible studies? What is your availability next Thursday or Friday afternoon?

Best,
Danielle

--
Danielle Adney, DVM, PhD
Virus Ecology Section
Laboratory of Virology
NIH/NIAID

If you are receiving this email outside of your typical working hours, I hope you feel no pressure to read or respond until your schedule and workload permit.

From: "Munster, Vincent (NIH/NIAID) [E]" (b) (6)
Date: Thursday, January 7, 2021 at 10:03 AM
To: "Plowright, Raina" (b) (6), "(b) (6)
<(b) (6) "Schountz, Tony" <(b) (6)
Cc: "Adney, Danielle (NIH/NIAID) [F]" <(b) (6)
Subject: deer-mice

Hi Raina and Jamie,

I'm sure you heard of Tony' s great work with the deer mice and SARS-CoV-2. Danielle from my lab is part of an interagency one-health workgroup with CDC, largely focusing on mink. The situation surrounding infected mink farms would have a high-risk of spill-over from mink into the deer-mouse population.

I thought one cool question for the epi modelers to look at is doing some classic SEIR modelling on the deer-mice. Get some population data and make some assessment what the risk (probably low, but who knows) of the establishment of deer mice as a reservoir based upon virological, transmission, sero-conversion and re-challenge data.

Let me know what your thoughts are,

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 7 Jan 2021 17:22:06 +0000
To: Schountz,Tony
Cc: Schountz, Tony
Subject: RE: modelling

Sounds good, just let mee know. Whatever is fastest, looks cool though.

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, January 7, 2021 10:13 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Schountz, Tony <(b) (6)
Subject: Re: modelling

Let me check my budget. All I would need to do is submit an amendment, which would only take a couple of weeks.

T.
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 7, 2021, at 10:07 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Yes I think so, we could put in a rapid ASP and do some re-challenge studies?

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, January 7, 2021 9:57 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Schountz, Tony <(b) (6)
Subject: Re: modelling

Don't you still have the deer mice from the hantavirus work Heinz had going?

If you want to coordinate a Zoom call with the modelers I'll join in. I teach Tu/Th from 2-5, and have weekly meetings on Mon 1-3, Wed 9-10 and Wed 3-5.

T.
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 7, 2021, at 9:54 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

If needed we could easily do some studies here to alleviate some of the $$$

We could get the ball rolling with MSU/modellers, I think largely they would need some shedding, transmission and re-infection data.

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, January 7, 2021 9:51 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Schountz, Tony <(b) (6)
Subject: Re: modelling

Yes, we can chat with the MSU crew about it. I'd rather not get too involved until after the R24 grant is submitted on January 25. We're still pulling together a lot of the supplemental documents that have to be submitted with it.

We definitely want to do rechallenge experiments. The biggest issue is the cost because we will have to keep them in the BSL3 for a few months at about $27 per day. I don't have any deer mouse money right now (submitted an R21 in October) so I'm "borrowing" money from other grants to subsidize the work.

T.

—

Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 7, 2021, at 9:37 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Some re-challenge data would be good to have

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

From: Schountz,Tony <(b) (6)
Sent: Thursday, January 7, 2021 8:23 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: modelling

Yes, for sure. Juergen just called and I'm on the phone with him….

—

Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine

Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 7, 2021, at 8:20 AM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

We should discuss with the DARPA / MSU crew so they can do some modelling?

Think that would make a nice paper with some little effort. Do you know whether the RML deer mice are the same?

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 7 Jan 2021 08:18:49 -0700
To: Kwe Claude, Yinda (NIH/NIAID) [F]; Alison Peel; Bushmaker, Trenton (NIH/NIAID) [E]; Plowright, Raina
Subject: Re: Update on shipment

When did they arrive at RML again?

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

From: "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6)
Date: Thursday, January 7, 2021 at 8:05 AM
To: Alison Peel <(b) (6) Trenton Bushmaker <(b) (6) "(b) (6) <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Update on shipment

Hi Ali,

I have attached the files from the temp logs and they are in attachment.

Thanks

Kwe

From: Alison Peel <(b) (6)
Date: Wednesday, January 6, 2021 at 7:50 PM
To: "Bushmaker, Trenton (NIH/NIAID) [E]" <(b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Update on shipment

Thanks Trent,
What would be a reasonable timeframe to download the data? I need to respond to World Courier, and I think the temperature data is an important piece of information in my discussions with them.
Thanks
Ali

From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: 06 January 2021 02:24
To: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Update on shipment

Ali,
I think Kwe has them on his desk but little busy doing inventory.

-Trent

From: Alison Peel <(b) (6)
Date: Monday, January 4, 2021 at 2:22 PM
To: Yinda Kwe <(b) (6) Trenton Bushmaker <(b) (6) Vincent Munster <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Update on shipment

Hi all,
How did everything end up looking with the shipment temperature loggers? I'm interested to know obviously for the samples sake, but World Courier has send through an exorbitant bill without any further explanation and it would be helpful to have whatever detail from you on the loggers and your communications with world courier that would hep with arguing them down.
Thanks!
Ali

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Thu, 7 Jan 2021 07:31:20 -0700
To: Alison Peel; Bushmaker, Trenton (NIH/NIAID) [E]; Kwe Claude, Yinda (NIH/NIAID) [F]; Plowright, Raina
Subject: Re: Update on shipment

Isn't the price of a shipment fixed?

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

From: Alison Peel <(b) (6)
Date: Wednesday, January 6, 2021 at 7:50 PM
To: Trenton Bushmaker <(b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) "(b) (6) <(b) (6) "Plowright, Raina" <(b) (6)
Subject: Re: Update on shipment

Thanks Trent,
What would be a reasonable timeframe to download the data? I need to respond to World Courier, and I think the temperature data is an important piece of information in my discussions with them.
Thanks
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From: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6)
Sent: 06 January 2021 02:24
To: Alison Peel <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Plowright, Raina <(b) (6)
Subject: Re: Update on shipment

Ali,
I think Kwe has them on his desk but little busy doing inventory.

-Trent

From: Alison Peel <(b) (6)
Date: Monday, January 4, 2021 at 2:22 PM
To: Yinda Kwe <(b) (6) Trenton Bushmaker <(b) (6) Vincent Munster <(b) (6) "Plowright, Raina"

<[redacted] (b) (6)
Subject: Update on shipment

Hi all,
How did everything end up looking with the shipment temperature loggers? I'm interested to know obviously for the samples sake, but World Courier has send through an exorbitant bill without any further explanation and it would be helpful to have whatever detail from you on the loggers and your communications with world courier that would hep with arguing them down.
Thanks!
Ali

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Wed, 6 Jan 2021 22:39:57 +0000
To: Dylan H. Morris
Cc: Bushmaker, Trenton (NIH/NIAID) [E]; Jamie Lloyd-Smith; Plowright, Raina
Subject: RE: SARS-CoV-2 Goldberg drum study

Got family working with the Biden administration but they shouldn't be in the capitol area

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

-----Original Message-----
From: Dylan H. Morris < (b) (6)
Sent: Wednesday, January 6, 2021 3:39 PM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6)
Cc: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) Jamie Lloyd-Smith
< (b) (6) Plowright, Raina < (b) (6)
Subject: Re: SARS-CoV-2 Goldberg drum study

Wife and I checked in with a friend of ours who works there. He's home safely, fortunately.

> On Jan 6, 2021, at 5:37 PM, Munster, Vincent (NIH/NIAID) [E] < (b) (6) wrote:
>
> Good thing we are not the east coast NIH, what a mess
>
> Vincent Munster, PhD
> Chief Virus Ecology Section
> Rocky Mountain Laboratories
> NIAID/NIH
>
> -----Original Message-----
> From: Dylan H. Morris < (b) (6)
> Sent: Wednesday, January 6, 2021 3:36 PM
> To: Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6)
> Cc: Jamie Lloyd-Smith (b) (6); Munster, Vincent (NIH/NIAID) [E]
> < (b) (6) Plowright, Raina < (b) (6)
> Subject: Re: SARS-CoV-2 Goldberg drum study
>
> Thanks for this! Will take a look tonight, assuming I can concentrate on work, else tomorrow.
>
>> On Jan 6, 2021, at 5:35 PM, Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) wrote:
>>
>> <TEMP & RH.txt>
>

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 4 Jan 2021 23:18:16 +0000
To: Schountz,Tony
Subject: RE: carollia

That makes it easy

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

From: Schountz,Tony <(b) (6)
Sent: Monday, January 4, 2021 4:09 PM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Subject: Re: carollia

Vinnie, unfortunately, we don't have any Carollia's left. The ones we had didn't breed so the remaining 6 or 7 were euthanized a couple of years ago.

Tony
—
Tony Schountz, PhD
Associate Professor
Center for Vector-borne Infectious Diseases
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
200 West Lake Street
1685 Campus Delivery
Fort Collins, CO 80523-1692
(b) (6)
(b) (6)

On Jan 4, 2021, at 3:54 PM, Munster, Vincent (NIH/NIAID) [E] <(b) (6) wrote:

Hi Tony,

Would we be able to get some Carolia for infection studies?

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

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Mon, 4 Jan 2021 21:38:50 +0000
To: LaTrielle, Sara
Cc: Plowright, Raina
Subject: RE: DARPA mtg: present (rescheduled) next Friday 15th?

Happy new year!

This unfortunately won't work for me as my workload has increased over the last 3 weeks with the novel variants emerging. Never a dull moment I guess,

Sorry for that,

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

From: LaTrielle, Sara <(b) (6)
Sent: Monday, January 4, 2021 8:53 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: DARPA mtg: present (rescheduled) next Friday 15th?

Vincent,

Happy New Year to you! Great article in the Missoulian last week with you and Emmie and..... on both being awarded the Golden Goose Award.

Looking to reschedule your presentation to DARPA- hoping next **Friday, Jan 15th (1pm MST)** will work for you? If possible, to also give a debrief of the ppt to the PI's next Monday, Jan 11th, 2pm MST? You can of course use the same slides- or update if you like.

Best,
Sara

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Sun, 3 Jan 2021 16:06:28 +0000
To: Port, Julia (NIH/NIAID) [F]; Bushmaker, Trenton (NIH/NIAID) [E]; Fischer, Robert (NIH/NIAID) [F]; Kwe Claude, Yinda (NIH/NIAID) [F]
Cc: Plowright, Raina
Subject: RE: New Environmental chamber 12/31/2020.

I think we should stay focused, the priority should be on the initial drum comparison at ambient temperatures:

Compare WA1 and UK, as we discussed.

Trent: get this started asap, you'll need to start growing and titration of WA1 to do the experiment the way we discussed

This should be 2-3 weeks work and then a short communication to EID

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

From: Port, Julia (NIH/NIAID) [F] (b) (6)
Sent: Saturday, January 2, 2021 7:57 PM
To: Munster, Vincent (NIH/NIAID) [E] < (b) (6) Bushmaker, Trenton (NIH/NIAID) [E] < (b) (6) Fischer, Robert (NIH/NIAID) [F] < (b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] < (b) (6)
Cc: Plowright, Raina < (b) (6)
Subject: Re: New Environmental chamber 12/31/2020.

Happy to be a pair of hands if useful, even if only titrations or cutting discs! Would love to learn how the chamber works etc.

From: "Munster, Vincent (NIH/NIAID) [E]"
Date: Sat, Jan 2, 2021, 10:52 AM
To: "Port, Julia (NIH/NIAID) [F]" , "Bushmaker, Trenton (NIH/NIAID) [E]" , "Fischer, Robert (NIH/NIAID) [F]" , "Kwe Claude, Yinda (NIH/NIAID) [F]"
CC: "Plowright, Raina"
Subject: RE: New Environmental chamber 12/31/2020.

Lets get that project rolling and start with the UK variant asap!

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

From: Port, Julia (NIH/NIAID) [F] <(b) (6)
Sent: Friday, January 1, 2021 2:49 PM
To: Bushmaker, Trenton (NIH/NIAID) [E] <(b) (6) Munster, Vincent (NIH/NIAID) [E] <(b) (6) Fischer, Robert (NIH/NIAID) [F] <(b) (6) Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: Re: New Environmental chamber 12/31/2020.

Thanks for the update Trent!

From: "Bushmaker, Trenton (NIH/NIAID) [E]" <(b) (6)
Date: Thursday, December 31, 2020 at 1:53 PM
To: "Munster, Vincent (NIH/NIAID) [E]" <(b) (6) "Fischer, Robert (NIH/NIAID) [F]" (b) (6) "Kwe Claude, Yinda (NIH/NIAID) [F]" <(b) (6) "Port, Julia (NIH/NIAID) [F]" <(b) (6)
Cc: "Plowright, Raina" (b) (6)
Subject: RE: New Environmental chamber 12/31/2020.

The Environmental chamber was good at 10C all day today. Next week I will run at high humidity with high temperature(might do a low temperature in addition).

-Trent

From: Bushmaker, Trenton (NIH/NIAID) [E]
Sent: Thursday, December 31, 2020 8:44 AM
To: Munster, Vincent (NIH/NIAID) [E] <(b) (6) Fischer, Robert (NIH/NIAID) [F] (b) (6); Kwe Claude, Yinda (NIH/NIAID) [F] <(b) (6) Julia (NIH/NIAID) Port [F] (b) (6)
Cc: Plowright, Raina <(b) (6)
Subject: New Environmental chamber 12/31/2020.

The Environmental chamber is in a cold room in BSL4. I ran the unit at 30C last night and it looked good this morning. I am currently running it at 10C today to see how it reacts. Next week I will run the unit at a 30C with high humidity (85%RH).

In addition I have talked with Darren about getting parts to connect the unit to the HVAC system. He will get a parts list to me and we will order it next week.

I will be working on the SOP to add the Goldberg drum operations. I will need to get this to Biosafety by the January 11th.

-Trent