

On 16 Feb 2020, at 7:24 pm, Garry, Robert F [REDACTED] wrote:

No problem either count

Jeremy has been amazing leader-should be author

Sent from my iPhone

On Feb 16, 2020, at 2:18 AM, Edward Holmes [REDACTED] wrote:

External Sender. Be aware of links, attachments and requests.

Ah. I so, I can submit on his behalf.

Jeremy wants to add something to the acknowledgments.

Just seen this: no GISAID acknowledgment as far as I can tell:

<https://www.tandfonline.com/doi/full/10.1080/20477724.2020.1725339>

PROFESSOR EDWARD C. HOLMES FAA FRS

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T
E [REDACTED]

On 16 Feb 2020, at 7:14 pm, Garry, Robert F [REDACTED] wrote:

One thing - I'm not sure when Kristian is returning to the connected world. Monday is a federal holiday.

Sent from my iPhone

On Feb 16, 2020, at 12:44 AM, Edward Holmes [REDACTED] wrote:

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Thanks Bob!

Sorry about the typo. I'll let Kristian fix that one.

Cheers,

Eddie

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T [REDACTED]
E [REDACTED]

On 16 Feb 2020, at 5:05 pm, Garry, Robert F [REDACTED] wrote:

Looking fine! Congrats all.

Minor: last sentence first paragraph covid-9 to covid-19

Sent from my iPhone

On Feb 15, 2020, at 10:46 PM, Edward Holmes [REDACTED] wrote:

[REDACTED] External Sender. Be aware of links, attachments and requests.

All, attached is what I propose is the final version of this paper. I've just given it a final wash-and-brush-up.
Looks great I reckon.

Can you please check your names, affiliations and acknowledgements.

I'll pass to Jeremy to see if he has any final comments and wants to be acknowledged.

This needs to go to Nature on Monday in somebody's time zone. Kristian I'll let you deal with this. You may need to provide more contact details. Figure also attached separately.

Cheers,

Eddie

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On 16 Feb 2020, at 12:09 pm, Garry, Robert F [REDACTED] wrote:

I formally agree.

Any guy that helps discover Jingmen tick viruses and Wuhan cricket virus must be trusted. Very important.

Going to dinner with my wife so will put down the phone.

Did I mention the Jingmen tick viruses have pretty spectacular mucin like domains? Would not have looks at CoVs otherwise.

Sent from my iPhone

On Feb 15, 2020, at 6:26 PM, Edward Holmes : [REDACTED] wrote:

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I will send through a final version that everyone can formally agree to later today. I'll also pass to Jeremy. Kristian can then do the formal submission, although I'll probably ping a copy to Magda and Clare anyway.

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On 16 Feb 2020, at 11:22 am, Ian Lipkin : [REDACTED] wrote:

Congratulations. It's a timely and well reasoned review.

Ian

On Feb 15, 2020, at 7:15 PM, Edward Holmes : [REDACTED] wrote:

Fab.

Just need to sort out author order. Kristian 1st and probably should correspond as he's chatted with Clare? Bob, I was thinking you might go last? I'd be nervous about putting my name there as I am amateur on the specific virological stuff we discuss. I feel I have only contributed to the writing. I don't mind Andrew going last either.

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I am done. Added in all the references (I think).

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Right, I need to get this finalised. Can I suggest that people stop editing the Google Docs version within the next hour (noon Sydney time) and I'll finish everything in normal Word. Need to draw a line under this very soon.

Thanks!

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contact – [REDACTED] | <http://tree.bio.ed.ac.uk> | tel : [REDACTED]

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<Andersen.Nature Perspective.docx>

<Andersen.Figure 1.pdf>

Message

From: Edward Holmes [REDACTED]
Sent: 2/16/2020 3:06:49 PM
To: Garry, Robert F [REDACTED]
CC: Ian Lipkin [REDACTED]; Kristian G. Andersen [REDACTED]; Andrew Rambaut [REDACTED]
Subject: Re: Paper

Just got this from Francis Collins.

"This is really well done, and I would argue ought to be made public ASAP (Jeremy sent it this morning).

Francis"

I'll submit and send to Magda/Clare this morning. If they ok we can then put on bioRxiv and perhaps [Virological.org](#) as well?

Cheers,

Eddie

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On 17 Feb 2020, at 9:52 am, Garry, Robert F [REDACTED] wrote:

Important to get this out.

<https://www.washingtonpost.com/politics/2020/02/16/tom-cotton-coronavirus-conspiracy/>

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I'll quickly check with Magda first.

Professor Edward C. Holmes FAA FRS
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On 17 Feb 2020, at 9:06 am, Garry, Robert F <[REDACTED]> wrote:

Sounds correct to me.

From: Edward Holmes <[REDACTED]>
Date: Sunday, February 16, 2020 at 4:04 PM
To: Robert Garry <[REDACTED]>
Cc: Ian Lipkin <[REDACTED]>, Kristian Andersen <[REDACTED]>, Andrew Rambaut <[REDACTED]>
Subject: Re: Paper

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Thanks Eddie!

Yes the NAID pics are nice.

The fusing SARS-CoV-2 pic is maybe not the prettiest one, but for me a clear indication that the polybasic site is functional.

You can observe this with flu v if you concentrate and treat with trypsin or some proper peptides. The virions fuse with each other.

Looks to me like SARS-CoV-2 gets at least partly activated coming out of the cells.

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Date: Sunday, February 16, 2020 at 2:50 PM
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Cc: Ian Lipkin <[REDACTED]>, Kristian Andersen <[REDACTED]>, Andrew Rambaut <[REDACTED]>
Subject: Re: Paper

[REDACTED] External Sender. Be aware of links, attachments and requests.

Great pics. Let's see what Nature say. I will get the paper out the door today.

Cheers,

Eddie

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Or maybe not.

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Date: Sunday, February 16, 2020 at 8:21 AM
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Subject: Re: Paper

They might need a cover. ☺

Seriously though NIH Took some pics that Tony would love to see on the Nature cover:

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<image001.png>

This one is actually VERY pertinent to our story BTW – notice that there are several fusing virions.

We've actually seen the same thing with fusion peptides that activate FluV.

SARS-CoV-2 is "activated!"

From: Ian Lipkin [REDACTED]
Date: Sunday, February 16, 2020 at 5:46 AM
To: Kristian Andersen [REDACTED], Robert Garry [REDACTED], Andrew Rambaut [REDACTED], Eddie Holmes [REDACTED]
Subject: Re: Paper

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Our audience includes the general public and policy makers as well as the scientific community. Once the paper is accepted we should ask Nature how it and we can promote broad visibility. At minimum we will need a short, powerful press release that hits the high points: who reviewed the data, what we considered, what we concluded, what needs to be done.

Ian

On Feb 16, 2020, at 5:58 AM, Andrew Rambaut · [REDACTED] wrote:

Just catching up on all this. Bob - you definitely should go last author. Without your expertise and knowledge (and your rummaging around the literature), we wouldn't have been able to write this. Happy to go second and Eddie can go second senior.

Andrew

On 16 Feb 2020, at 00:20, Garry, Robert F · [REDACTED] wrote:

Andrew should go last – he did the bulk of the heavy lifting.

¹ Tulane University, School of Medicine, Department of Microbiology and Immunology, New Orleans, LA, USA

² Zalgen Labs, LCC, Germantown, MD, USA

I have to list the latter because of the US Col rules.

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Cc: Robert Garry <[REDACTED]>, Kristian Andersen [REDACTED], Ian Lipkin [REDACTED]

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<Suggested cover v2 red1.pdf>

Message

From: Edward Holmes [REDACTED]
Sent: 2/16/2020 6:59:20 PM
To: Kristian G. Andersen [REDACTED]
CC: Andrew Rambaut [REDACTED]; Garry, Robert F [REDACTED]; Ian Lipkin [REDACTED]
Subject: Re: Paper

All came together very quickly in the end. Jeremy Farrar and Francis Collins are very happy. Works for me.

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T [REDACTED]
E [REDACTED]

On 17 Feb 2020, at 1:53 pm, Kristian G. Andersen [REDACTED] wrote:

Pure coincidence. The no-shower-since-Thursday will serve as evidence in case you need proof....

Great job lads!!

K

On Sun, Feb 16, 2020 at 6:48 PM Edward Holmes [REDACTED] wrote:

Well, that's suspicious...he comes back 15 minutes after I submit? A natural phenomenon? I'm not sure we can exclude the hypothesis of deliberately engineered responsibility shirking.

Anyway, it's done. Sorry the last bit had to be done without you...pressure from on high.

Fair point about bioRxiv. I've asked Nature what they want. Virological will work.

More rattlesnakes to come mate....

Cheers,

Eddie

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T [REDACTED]
E [REDACTED]

On 17 Feb 2020, at 1:41 pm, Kristian G. Andersen [REDACTED] wrote:

Gentlemen, it seems I should go to the desert more often... Only had three rattlesnake encounters, one near-death experience, and one running out of gas on the highway (with 1/4 left in the tank... it's a Jeep thing...), so all in all, pretty mellow. Fun though.

I'm still on my way back so not caught up yet - lemme know what's needed from me?

Eddie, bioRxiv is only for primary research and not this type of paper, so no need to submit.

Bob, pangolins... not me. But good idea.

Onwards.

K

On Sun, Feb 16, 2020 at 4:35 PM Edward Holmes [REDACTED] wrote:

Added (attached).

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T [REDACTED]

E [REDACTED]

On 17 Feb 2020, at 11:16 am, Andrew Rambaut [REDACTED] wrote:

The pangolin metagenomic data seems to have come ultimately from this paper:

<https://www.ncbi.nlm.nih.gov/pubmed/31652964>

We should cite it.

A.

On 16 Feb 2020, at 23:12, Garry, Robert F [REDACTED] wrote:

Sounds good...

From: Edward Holmes [REDACTED]

Date: Sunday, February 16, 2020 at 5:06 PM

To: Robert Garry [REDACTED]

Cc: Ian Lipkin [REDACTED], Kristian Andersen [REDACTED], Andrew Rambaut [REDACTED]

[REDACTED]
Subject: Re: Paper

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"This is really well done, and I would argue ought to be made public ASAP (Jeremy sent it this morning).

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Ian Lipkin

Subject: Re: Paper

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<Suggested cover v2 red1.pdf>

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[REDACTED] | <http://tree.bio.ed.ac.uk> | tel + [REDACTED]

From: Jeremy Farrar
Sent: Monday, February 17, 2020 10:42 AM EST
To: Ian Lipkin
Subject: Re: Connections COVID-19

Yes I know and in US - why so keen to get out ASAP.
I will push Nature

On 17 Feb 2020, at 16:41, Ian Lipkin [REDACTED] wrote:

Jeremy,

Thanks for shepherding this paper. Rumors of bioweaponeering are now circulating in China.

Ian

On Feb 17, 2020, at 10:28 AM, Jeremy Farrar [REDACTED] wrote:

When you have been able to update with the extra sentence and data can you forward on to me - keep that WHO see ASAP.

On 17 Feb 2020, at 12:09, Garry, Robert F [REDACTED] wrote:

This also means less concern about the Baric scenario where another mutation could kick SARS-CoV-2 into another gear. Binding already optimal.

Sent from my iPhone

On Feb 17, 2020, at 4:51 AM, Andrew Rambaut [REDACTED] wrote:

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Fixed.

On 17 Feb 2020, at 10:47, Edward Holmes [REDACTED] wrote:

Hang on...should be " recent binding studies indicate" not indict. One of the new edits.

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OK. Here is the version with all the changes and the updated references. As I manually changed the numbers (adding reference 7 and incrementing all numbers above 6) I would appreciate a check.

I also simplified Bob's text below.

I am going to start formatting this in virological so let me know if you spot any issues.

A.

On 17 Feb 2020, at 10:25, Garry, Robert F [REDACTED] wrote:

Another better version:

While these analyses suggest that SARS-CoV-2 may be capable of binding the human ACE2 receptor with high affinity, the interaction is not predicted to be optimal¹. Additionally, several of the key residues in the RBD of SARS-CoV-2 are different to those previously described as optimal for human ACE2 receptor binding⁶. In contrast to these computational assessments recent binding studies indicate that SARS-CoV-2 binds with high affinity to human ACE2 (insert ref). SARS-CoV-2 spike does not appear to have an artificial sequence designed in the laboratory. An artificial sequence would have used interactions predicted to be optimal for interaction with its receptor. Instead the

SARS-CoV-2 spike appears to be the result of selection on human or human-like ACE2 permitting another optimal binding solution to arise. This is strong evidence that SARS-CoV-2 is *not* the product of genetic engineering.

[redacted]
From: Andrew Rambaut [redacted]
Sent: Monday, February 17, 2020 10:23 AM
To: Garry, Robert F [redacted]
Cc: Eddie Holmes [redacted]; Kristian G. Andersen [redacted]; Ian Lipkin [redacted]; Jeremy Farrar [redacted]
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OK. I will add that. I am editing the document now.
Andrew

On 17 Feb 2020, at 10:20, Garry, Robert F [redacted] wrote:

While these analyses suggest that SARS-CoV-2 may be capable of binding the human ACE2 receptor with high affinity, the interaction is not predicted to be optimal¹. Additionally, several of the key residues in the RBD of SARS-CoV-2 are different to those previously described as optimal for human ACE2 receptor binding⁶. In contrast to these computational assessments recent binding studies indicate that SARS-CoV-2 binds with high affinity to human ACE2 (insert ref). SARS-CoV-2 spike does not appear to have an artificial sequence designed in the laboratory would have been designed for optimal binding and used interactions predicted to be optimal. Instead it appears to be the result of selection on human or human-like ACE2 permit another optimal binding solutions to arise. This is strong evidence that SARS-CoV-2 is *not* the product of genetic engineering.

[redacted]
From: Garry, Robert F [redacted]
Sent: Monday, February 17, 2020 10:02 AM
To: Edward Holmes [redacted]
Cc: Kristian G. Andersen [redacted]; Andrew Rambaut [redacted]; Ian Lipkin [redacted]; Jeremy Farrar [redacted]
Subject: Re: Connections COVID-19

put the "While these" back

[redacted]
From: Edward Holmes [redacted]
Sent: Monday, February 17, 2020 9:49 AM
To: Garry, Robert F [redacted]
Cc: Kristian G. Andersen [redacted]; Andrew Rambaut [redacted]

[REDACTED]; Ian Lipkin [REDACTED]; Jeremy Farrar

Subject: Re: Connections COVID-19

External Sender. Be aware of links, attachments and requests.

Ok. Pass a draft to me and I'll give it a quick read through.
No way I can stay up to your levels...

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 [REDACTED]
E [REDACTED]

On 17 Feb 2020, at 8:47 pm, Garry, Robert F [REDACTED] wrote:

agreed - i'm up - who needs to sleep
will take very quick swing at it now - yes a sentence or two will
likely do
15 minutes i'll be back

[REDACTED]
From: Edward Holmes [REDACTED]
Sent: Monday, February 17, 2020 9:45 AM
To: Garry, Robert F [REDACTED]
Cc: Kristian G. Andersen [REDACTED]; Andrew Rambaut [REDACTED]; Ian Lipkin [REDACTED]; Jeremy Farrar [REDACTED]
Subject: Re: Connections COVID-19

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Bob, if you or someone else wants to add a sentence now that's ok (refs.
will need to change as well), but we must get it out today. Things are
moving/changing so rapidly that we are always going to be out of date. We
need to draw a line somewhere.

PROFESSOR EDWARD C. HOLMES FAA FRS
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The University of Sydney | Sydney | NSW | 2006 | Australia

T [REDACTED]

E [REDACTED]

On 17 Feb 2020, at 8:39 pm, Garry, Robert F [REDACTED] wrote:

New preprint not affect any of the other three scenarios for selection on a human or human like ACE2, but a stronger still argument against bioengineering imo.

Sent from my iPhone

On Feb 17, 2020, at 2:50 AM, Edward Holmes [REDACTED]

wrote:

External Sender. Be aware of links, attachments and requests.

All,

We have the green light to preprint.

Kristian - even though bioRxiv deals with primary research papers I still feel we should send it there.

Andrew - I think you can put this in Virological and do some precision tweeting.

Very interesting to see the new ACE2 paper.

Best wishes,

Eddie

PROFESSOR EDWARD C. HOLMES FAA FRS
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School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia

T [REDACTED]

E [REDACTED]

Begin forwarded message:

From: Clare Thomas [REDACTED]
Subject: RE: Connections COVID-19
Date: 17 February 2020 at 7:07:01 pm AEDT
To: Edward Holmes [REDACTED], Magdalena Skipper [REDACTED]

Hi Eddie,

Thanks for this. I agree that you should deposit the preprint asap. I can see it in our system so I'll send it for expedited review today.

If the refs are positive it will likely need revising as it already seems out of date. See the preprint below, for example, which appeared on Saturday and which says that SARS-CoV-2 binds with higher affinity to ACE2 than SARS-CoV. And of course if the second pangolin paper surfaces that would also affect the conclusions, if their press release is to be believed.

<https://www.biorxiv.org/content/10.1101/2020.02.11.944462v1>

Anyway, thanks again for sending this and I'll try to return a decision soon.

All the best,

Clare

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<Andersen.Nature Perspective.Final_v2.docx>

<Andersen.Nature Perspective.Final_v2.docx>

From: Garry, Robert F
Sent: Monday, February 17, 2020 12:37 PM EST
To: Jeremy Farrar; Kristian G. Andersen
CC: Andrew Rambaut; Eddie Holmes; Ian Lipkin
Subject: Re: Connections COVID-19

Ian suggested a press release – it's very appropriate under the circumstances. Who will draft?

From: Jeremy Farrar [REDACTED]
Date: Monday, February 17, 2020 at 11:35 AM
To: Kristian Andersen [REDACTED]
Cc: Andrew Rambaut [REDACTED], Robert Garry [REDACTED], Eddie Holmes [REDACTED], Ian Lipkin [REDACTED]
Subject: Re: Connections COVID-19

External Sender. Be aware of links, attachments and requests.

Reason I ask about when to post is to coordinate press briefings etc etcto make sure the key messages are reasonably reported...

From: Jeremy Farrar [REDACTED]
Date: Monday, 17 February 2020 at 18:32
To: "Kristian G. Andersen" [REDACTED]
Cc: "a.rambaut@ed.ac.uk" [REDACTED], "Garry, Robert F" [REDACTED], Edward Holmes [REDACTED], Ian Lipkin [REDACTED]
Subject: Re: Connections COVID-19

No preference – whatever you all think best.

When do you plan to post?

From: "Kristian G. Andersen" [REDACTED]
Date: Monday, 17 February 2020 at 18:30
To: Jeremy Farrar [REDACTED]
Cc: "a.rambaut@ed.ac.uk" [REDACTED], "Garry, Robert F" [REDACTED], Edward Holmes [REDACTED], Ian Lipkin [REDACTED]
Subject: Re: Connections COVID-19

The bioRxiv unfortunately does not accept perspectives/reviews/comments - only original research papers so this, per standard policies, can't go on there. For that reason, my preference is to keep this on Virological and use that as the channel for dissemination, but if there's a need to try and bypass normal bioRxiv policies I can definitely reach out to Richard and John to ask them. I'm leading their efforts for

better screening of outbreak-related preprints and have another email out to them so can definitely bring it up. Jeremy, what's your preference?

K

On Mon, Feb 17, 2020 at 9:22 AM Jeremy Farrar [REDACTED] wrote:

Thank you

Any idea when likely to be released on pre-print server?

Is tomorrow OK?

Thinking about the publicity of it....

From: "Kristian G. Andersen" [REDACTED]

Date: Monday, 17 February 2020 at 18:11

To: Jeremy Farrar [REDACTED]

Cc: [REDACTED], "Garry, Robert F" [REDACTED], Edward Holmes [REDACTED], Ian Lipkin [REDACTED]

Subject: Re: Connections COVID-19

Sure, attached.

K

On Mon, Feb 17, 2020 at 9:02 AM Jeremy Farrar [REDACTED] wrote:

Sorry to micro-manage/microedit!

But would you be willing to change one sentence?

From

It is **unlikely** that SARS-CoV-2 emerged through laboratory manipulation of an existing SARS-related coronavirus.

To

It is **improbable** that SARS-CoV-2 emerged through laboratory manipulation of an existing SARS-related coronavirus.

From: [REDACTED]

Date: Monday, 17 February 2020 at 17:56

To: "Kristian G. Andersen"

Cc: Jeremy Farrar [REDACTED], "Garry, Robert F" [REDACTED], Edward Holmes [REDACTED], Ian Lipkin [REDACTED]

Subject: Re: Connections COVID-19

Sorry. This is the final version (v2.2).

Sent from my phone. Apologies for brevity or illiteracy.

On 17 Feb 2020, at 16:52, Kristian G. Andersen [REDACTED] wrote:

Just corrected a few more typos - but yes, I believe this is the final version for now. I'm sure Nature will have plenty of edits.

K

On Mon, Feb 17, 2020 at 8:47 AM Jeremy Farrar [REDACTED] wrote:

Andrew – is this the 'final' draft, pending any changes at Nature – with the additional information?

From: [REDACTED]
Date: Monday, 17 February 2020 at 17:08
To: Jeremy Farrar [REDACTED], "Garry, Robert F" [REDACTED],
Edward Holmes [REDACTED], "Kristian G. Andersen"
[REDACTED], Ian Lipkin [REDACTED]
Subject: Re: Connections COVID-19

Dear all,

I think this is now the same version as on Virological. First author's name corrected, 'SARs' corrected. Figure updated (and legend corrected).

Andrew

On 17 Feb 2020, at 15:28, Jeremy Farrar [REDACTED] wrote:

When you have been able to update with the extra sentence and data can you forward on to me - keep that WHO see ASAP.

On 17 Feb 2020, at 12:09, Garry, Robert F [REDACTED] wrote:

This also means less concern about the Baric scenario where another mutation could kick SARS-CoV-2 into another gear. Binding already optimal.

Sent from my iPhone

External Sender. Be aware of links, attachments and requests.

On Feb 17, 2020, at 4:51 AM, Andrew Rambaut [REDACTED] wrote:

Fixed.

On 17 Feb 2020, at 10:47, Edward Holmes [REDACTED] wrote:

Hang on...should be " recent binding studies indicate" not indict. One of the new edits.

PROFESSOR EDWARD C. HOLMES FAA FRS
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T [REDACTED]

E [REDACTED]

On 17 Feb 2020, at 9:44 pm, Garry, Robert F [REDACTED] wrote:

Looks great!

Sent from my iPhone

External Sender. Be aware of links, attachments and requests.

On Feb 17, 2020, at 4:41 AM, Andrew Rambaut [REDACTED] wrote:

OK. Here is the version with all the changes and the updated references. As I manually changed the numbers (adding reference 7 and incrementing all numbers above 6) I would appreciate a check.

I also simplified Bob's text below.

I am going to start formatting this in virological so let me know if you spot any issues.

A.

On 17 Feb 2020, at 10:25, Garry, Robert F [REDACTED] wrote:

Another better version:

While these analyses suggest that SARS-CoV-2 may be capable of binding the human ACE2 receptor with high affinity, the interaction is not predicted to be optimal¹. Additionally, several of the key residues in the RBD of SARS-CoV-2 are different to those previously described as optimal for human ACE2 receptor binding⁶. In contrast to these computational assessments recent binding studies indicate that SARS-CoV-2 binds with high affinity to human ACE2 (insert ref). SARS-CoV-2 spike does not appear to have an artificial sequence designed in the laboratory. An artificial sequence would have used interactions predicted to be optimal for interaction with its receptor. Instead the SARS-CoV-2 spike appears to be the result of selection on human or human-like ACE2 permitting another optimal binding solution to arise. This is strong evidence that SARS-CoV-2 is *not* the product of genetic engineering.

From: Andrew Rambaut [REDACTED]
Sent: Monday, February 17, 2020 10:23 AM
To: Garry, Robert F [REDACTED]
Cc: Eddie Holmes [REDACTED]; Kristian G. Andersen [REDACTED]; Ian Lipkin [REDACTED]; Jeremy Farrar [REDACTED]
Subject: Re: Connections COVID-19

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OK. I will add that. I am editing the document now.

Andrew

On 17 Feb 2020, at 10:20, Garry, Robert F [REDACTED] wrote:

While these analyses suggest that SARS-CoV-2 may be capable of binding the human ACE2 receptor with high affinity, the interaction is not predicted to be optimal¹. Additionally, several of the key residues in the RBD of SARS-CoV-2 are different to those previously described as optimal for human ACE2 receptor

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Sent: Monday, February 17, 2020 10:02 AM
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Cc: Kristian G. Andersen [REDACTED]; Andrew Rambaut [REDACTED]; Ian Lipkin [REDACTED]; Jeremy Farrar [REDACTED]
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put the "While these" back

From: Edward Holmes [REDACTED]
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Cc: Kristian G. Andersen [REDACTED]; Andrew Rambaut [REDACTED]; Ian Lipkin [REDACTED]; Jeremy Farrar [REDACTED]
Subject: Re: Connections COVID-19

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T [REDACTED]

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agreed - i'm up - who needs to sleep

will take very quick swing at it now - yes a sentence or two will likely do
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From: Edward Holmes [REDACTED]
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Cc: Kristian G. Andersen [REDACTED]; Andrew Rambaut [REDACTED]; Ian Lipkin [REDACTED]; Jeremy Farrar [REDACTED]
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[REDACTED] wrote:

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Very interesting to see the new ACE2 paper.

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Eddie

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T [REDACTED]
E [REDACTED]

Begin forwarded message:

From: Clare Thomas [REDACTED]
Subject: RE: Connections COVID-19
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To: Edward Holmes [REDACTED], Magdalena Skipper [REDACTED]

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If the refs are positive it will likely need revising as it already seems out of date. See the preprint below, for example, which appeared on Saturday and which says that SARS-CoV-2 binds with higher affinity to ACE2 than SARS-CoV. And of course if the second pangolin paper surfaces that would also affect the conclusions, if their press release is to be believed.

<https://www.biorxiv.org/content/10.1101/2020.02.11.944462v1>

Anyway, thanks again for sending this and I'll try to return a decision soon.

All the best,

Clare

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

<Andersen.Nature Perspective.Final_v2.docx>

<Andersen.Nature Perspective.Final_v2.docx>

<Andersen.Nature Perspective.Final_v2.2.docx>

Message

From: Clare Thomas [REDACTED]
Sent: 3/4/2020 11:44:43 PM
To: Kristian G. Andersen [REDACTED]
CC: Edward Holmes [REDACTED]
Subject: RE: Decision on Nature submission 2020-02-02583

Dear Kristian,

It looks like it's set up with you as the CA with your gmail address as the contact info kga1978@gmail.com.

I can see whether my assistant can merge the account with your other one: andersen@scripps.edu. I'll ask her to get in touch with you once she's done it. Alternatively you can just submit directly to Nature Medicine and if Joao needs to see the reports again I can send them to him by email.

I am indeed drowning in COVID-19 papers. Never been so busy. I cancelled my participation in the conference that Eddie is at, in part because I just don't have time to move from my desk... (sorry to miss you, Eddie).

I am sure you're frantically busy as well.

All the best,

Clare

From: Kristian G. Andersen [REDACTED]
Sent: 05 March 2020 02:06
To: Clare Thomas
Cc: Edward Holmes
Subject: Re: Decision on Nature submission 2020-02-02583

Dear Clare,

We're just about to send our manuscript over to Nature Medicine, which has been much improved due to some recent data. I just wanted to share the new material with you so you're in the loop.

Since the original manuscript was submitted under Eddie's account, would it be possible for you to please transfer everything over to my account so I can start the process of getting this to Nature Medicine? Eddie is in transit at the moment, so I think it'll be difficult for him to get this transferred in time. If you're not able to transfer to my account, don't worry - we'll figure it out.

Thanks again for giving us the opportunity - we thought this would have been a very good piece for Nature given the massive interest, but Nature Medicine (if accepted) will be a good audience too.

I hope you're not drowning in COVID-19 papers!

Best,
Kristian

On Thu, Feb 20, 2020 at 9:56 AM Kristian G. Andersen [REDACTED] wrote:

Yeah, no worries Clare - it's a tricky topic and I understand. And thanks for reaching out to your colleagues - much appreciated.

Best,
Kristian

On Thu, Feb 20, 2020 at 9:54 AM Clare Thomas [REDACTED] wrote:

Dear Kristian,

Ok, thanks for clarifying. I am sorry we could not return a more positive decision at Nature but I wish you all the best with publishing it elsewhere and I'm glad we could get you some other options at Nature Research, if that interests you.

All the best,

Clare

From: Kristian G. Andersen [REDACTED]
Sent: 20 February 2020 17:48
To: Clare Thomas
Subject: Re: Decision on Nature submission 2020-02-02583

Thanks Clare for letting me know so quickly. I'll discuss with the other authors to see what the best path would be - just one thing to make clear though, reviewer 2 is unfortunately wrong about "Once the authors publish their new pangolin sequences, a lab origin will be extremely unlikely". Had that been the case, we would of course have included that - but the more sequences we see from pangolins (and we have been analyzing/discussing these *very* carefully) the more unlikely it seems that they're intermediate hosts. They definitely harbor SARS-CoV-like viruses, no doubt, but it's unlikely they have a direct connection to the COVID-19 epidemic. Unfortunately none of this helps refute a lab origin and the possibility must be considered as a serious scientific theory (which is what we do) and not dismissed out of hand as another 'conspiracy' theory. We all really, really wish that we could do that (that's how this got started), but unfortunately it's just not possible given the data.

Thanks again for considering our manuscript and while we had of course hoped for a better outcome, we understand the decision.

Best,
Kristian

On Thu, Feb 20, 2020 at 8:52 AM [REDACTED] wrote:

20th February 2020

Dear Kristian,

Thank you for submitting your manuscript entitled "The Proximal Origin of SARS-CoV-2" to be considered for publication in Nature. We've now obtained two ref reports on the paper (appended below) and I've had the opportunity to discuss them with our chief editor Magdalena Skipper. In the light of the advice received I am afraid we have decided that we cannot offer to publish the Perspective in Nature.

While the Perspective is interesting and timely one of our referees raised concerns (also emphasised to the editors) about whether such a piece would feed or quash the conspiracy theories. But more importantly this reviewer feels, and we agree, that the Perspective would quickly become outdated when more scientific data are published (for example on potential reservoir hosts).

I did, however, take the liberty of consulting with my colleagues at Nature Medicine, Nature Ecology and Evolution and Nature Microbiology and I am happy to say that all three journals were interested in publishing a revised piece in some form.

Nature Medicine are interested in publishing it either as a Comment or a Correspondence. If you would like to pursue this option, please transfer the submission to Nature Medicine using the link provided below. Feel free to reach out to Joao Monteiro, chief editor, at joao..monteiro@us.nature.com if you want to discuss the transfer process or have questions.

Nature Ecology & Evolution would be interested in considering the manuscript as a Comment article. They would like to work with you to address the reviewers' concerns and restructure the manuscript to focus more on the plausible evolutionary scenarios. If this option is of interest, you can also use the link below to transfer, and please feel free to get in touch with Patrick Goymer (p.goymer@nature.com) to discuss it further.

Finally, Nature Microbiology would similarly be interested in considering a revised manuscript that addresses the main concerns from the referees as a Comment article. Should you be interested in this option, please use the link below to transfer and please feel free to contact Nonia Pariente (nonia.pariente@nature.com; who is currently out of the office but will be back on Feb 24th) and Paula Jauregui (paula.jauregui@nature.com) to discuss further.

I am sorry that we cannot be more positive on this occasion. We hope that our decision does not discourage you from submitting your work to us in future as we remain interested in publishing key developments in this area of research. We hope that you will find our referees' comments helpful.

With best wishes,

Clare

Clare Thomas
Senior Editor
Nature

Referees' comments:

Referee #1 (Remarks to the Author):

Anderson presented a timely manuscript to share their points of view about the origin of SARS-CoV-2. There are several rumors about the origin of this virus. However, these "hypotheses" are entirely based on very limited, if any, scientific evidences.

This reviewer sees most of the arguments raised by the authors are valid and convincing. However, the authors might want to consider these minor suggestions:

1. The sections for the RBD and cleavage site of Spike protein basically have summarized the existing findings from other recent publications. The authors might want to spell out that these two sections are

review summaries. In addition, the author can present these two sections in a more condense format and save some space for something else (also see points 6 and 7 below)

2. Fig. 1. This figure has 6 aligned sequences, but with only 5 sequence titles. The order of these titles are also not correct.

3. Lines 170 -174. It is correct that no adaptive mutation has been found in the spike of MERS-CoV. Deletions in other ORF regions, however, were detected in some human MERS-CoV viruses (PMID: 26981770). In addition, the 29nt deletion of human SARS-CoV (PMID: 12958366) was suggested to have effects on host adaptation. The authors should also consider these findings. It is premature to say that this would not happen in SARS-CoV-2.

4. Line 194. The accident at Singapore occurred in a BSL3, not BSL2, containment.

5. Line 194. Laboratory escapes of SARS occurred in Singapore, China and Taiwan (PMID: 16830004).

6. There are two recent reports about coronaviruses in pangolins (<https://www.biorxiv.org/content/10.1101/2020.02.13.945485v1.full.pdf>; <https://www.biorxiv.org/content/10.1101/2020.02.08.939660v2.full.pdf>). The authors might want to comments on these.

7. Optional: Can the authors share their views on the possibility of having a lab escape of a natural coronavirus? This is also one of the hypotheses that have been extensively discussed. The reviewer understand that this is entirely a different topic, but any insights are welcomed.

Referee #2 (Remarks to the Author):

This is a perspective discussing evidence against a hypothetical lab origin of SARS-CoV-2. The paper addresses suboptimal composition of ACE2-binding sites in the RBD, 3 predicted O-linked glycosylation sites and a furin cleavage site in the glycoprotein that was speculated upon before.

The paper is itself interesting, but unnecessarily speculative. It's not clear why the authors do not refute a hypothetical lab origin in their coming publication on the ancestors of SARS-CoV-2 in bats and pangolins. The tree showing diverse pangolin viruses has kindly been made available by some of the authors in GISAID. Once the authors publish their new pangolin sequences, a lab origin will be extremely unlikely. It is not clear why the authors rush with a speculative perspective if their central hypothesis can be supported by their own data. Please explain.

Another critical aspect of this text is the complete lack of referencing to a potential debate on a hypothetical lab origin. Who said this, why is this considered a problem? There are indeed a few apparently uninformed statements claiming the virus may be a Chinese bioweapon, but is this really problematic on a larger scale? The central reason for issuing this text must be exhaustively referenced and discussed.

The authors state that a predicted polybasic cleavage sites is unique to SARS-CoV-2 in SARS viruses. Who knows how many out of thousands undiscovered bat ancestors also acquired such a motif, the sampling bias in descriptions of remote bat viruses is dramatic. This should be discussed. Also state clearly that this site is only predicted so far and that experimental evidence for its biological function and its potential impact on pathogenesis are required.

The predicted O-linked glycosylation sites are mysterious. What do the authors imply with those sites? In

silico prediction of O-linked glycosylation sites is not robust and whether these sites indeed exist requires experimental validation. Even if those sites exist, why are they relevant? This is not addressed at all. If the authors assume these sites constitute part of a glycan shield, they should say so and weigh their assumption carefully.

Finally, the main argument against a hypothetical lab origin seems the required reconstruction of a backbone of a bat virus of unknown pathogenesis. It does not seem feasible that any scientist would disembark on such an uncertain endeavor. This difficulties of coronavirus reverse genetics should be stated clearly.

--

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Message

From: medicine@us.nature.com [medicine@us.nature.com]
Sent: 3/5/2020 1:03:48 PM
To: [REDACTED]
CC: medicine@us.nature.com; [REDACTED]@springernature.com
Subject: Decision on Nature Medicine submission NMED-LE102233-T

5th Mar 2020

Dear Kristian,

Thanks for working with us to improve your Letter for publication. I'm delighted to tell you that your manuscript NMED-LE102233-T has been accepted for publication in our Correspondence section, and that it has been scheduled for publication in our April print issue. Please note that we are fast-tracking the online publication of this piece, so please make sure to return the copyrights form to our editorial assistant asap, and to respond to any queries from our production promptly to avoid delays. As soon as we have the online publication date set, our production will let you know. This piece will be in front of the paywall for time being.

All the best,
Joao

Joao Monteiro
Chief Editor

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Message

From: Edward Holmes [REDACTED]
Sent: 3/5/2020 5:24:59 PM
To: Kristian G. Andersen [REDACTED]
CC: Clare Thomas [REDACTED]
Subject: Re: Decision on Nature submission 2020-02-02583

Thanks Both!

Sorry if I confused things.

Sorry to miss you Clare! It was a really good meeting and largely free of coronavirus stuff. I had some nice conversations with the Nature staff that attended...who have already sent me papers to review!

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 [REDACTED]
E [REDACTED]

On 6 Mar 2020, at 2:08 am, Kristian G. Andersen [REDACTED] wrote:

Hi Clare,

Yes, sorry - I was confused. Eddie started the process and that emailed a link to me so we should be good. Thanks again.

COVID-19 will be a marathon, not a sprint, so hopefully we'll all get some time to breathe soon ;).

Best,
Kristian

On Wed, Mar 4, 2020 at 11:45 PM Clare Thomas [REDACTED] wrote:

Oh, I was looking at my emails backwards... I see you've already done it ☺

From: Clare Thomas
Sent: 05 March 2020 07:45
To: 'Kristian G. Andersen'

Cc: Edward Holmes
Subject: RE: Decision on Nature submission 2020-02-02583

Dear Kristian,

It looks like it's set up with you as the CA with your gmail address as the contact info
[REDACTED]

I can see whether my assistant can merge the account with your other one: [REDACTED]. I'll ask her to get in touch with you once she's done it. Alternatively you can just submit directly to Nature Medicine and if Joao needs to see the reports again I can send them to him by email.

I am indeed drowning in COVID-19 papers. Never been so busy. I cancelled my participation in the conference that Eddie is at, in part because I just don't have time to move from my desk... (sorry to miss you, Eddie).

I am sure you're frantically busy as well.

All the best,

Clare

From: Kristian G. Andersen [REDACTED]
Sent: 05 March 2020 02:06
To: Clare Thomas
Cc: Edward Holmes
Subject: Re: Decision on Nature submission 2020-02-02583

Dear Clare,

We're just about to send our manuscript over to Nature Medicine, which has been much improved due to some recent data. I just wanted to share the new material with you so you're in the loop.

Since the original manuscript was submitted under Eddie's account, would it be possible for you to please transfer everything over to my account so I can start the process of getting this to Nature Medicine? Eddie is in transit at the moment, so I think it'll be difficult for him to get this transferred in time. If you're not able to transfer to my account, don't worry - we'll figure it out.

Thanks again for giving us the opportunity - we thought this would have been a very good piece for Nature given the massive interest, but Nature Medicine (if accepted) will be a good audience too.

I hope you're not drowning in COVID-19 papers!

Best,

Kristian

On Thu, Feb 20, 2020 at 9:56 AM Kristian G. Andersen <[REDACTED]> wrote:

Yeah, no worries Clare - it's a tricky topic and I understand. And thanks for reaching out to your colleagues - much appreciated.

Best,

Kristian

On Thu, Feb 20, 2020 at 9:54 AM Clare Thomas <[REDACTED]> wrote:

Dear Kristian,

Ok, thanks for clarifying. I am sorry we could not return a more positive decision at Nature but I wish you all the best with publishing it elsewhere and I'm glad we could get you some other options at Nature Research, if that interests you.

All the best,

Clare

From: Kristian G. Andersen
Sent: 20 February 2020 17:48
To: Clare Thomas
Subject: Re: Decision on Nature submission 2020-02-02583

Thanks Clare for letting me know so quickly. I'll discuss with the other authors to see what the best path would be - just one thing to make clear though, reviewer 2 is unfortunately wrong about "Once the authors publish their new pangolin sequences, a lab origin will be extremely unlikely". Had that been the case, we would of course have included that - but the more sequences we see from pangolins (and we have been analyzing/discussing these very carefully) the more unlikely it seems that they're intermediate hosts. They definitely harbor SARS-CoV-like viruses, no doubt, but it's unlikely they have a direct connection to the COVID-19 epidemic. Unfortunately none of this helps refute a lab origin and the possibility must be considered as a serious scientific theory (which is what we do) and not dismissed out of hand as another 'conspiracy' theory. We all really, really wish that we could do that (that's how this got started), but unfortunately it's just not possible given the data.

Thanks again for considering our manuscript and while we had of course hoped for a better outcome, we understand the decision.

Best,

Kristian

On Thu, Feb 20, 2020 at 8:52 AM [REDACTED] wrote:

20th February 2020

Dear Kristian,

Thank you for submitting your manuscript entitled "The Proximal Origin of SARS-CoV-2" to be considered for publication in Nature. We've now obtained two ref reports on the paper (appended below) and I've had the opportunity to discuss them with our chief editor Magdalena Skipper. In the light of the advice received I am afraid we have decided that we

cannot offer to publish the Perspective in Nature.

While the Perspective is interesting and timely one of our referees raised concerns (also emphasised to the editors) about whether such a piece would feed or quash the conspiracy theories. But more importantly this reviewer feels, and we agree, that the Perspective would quickly become outdated when more scientific data are published (for example on potential reservoir hosts).

I did, however, take the liberty of consulting with my colleagues at Nature Medicine, Nature Ecology and Evolution and Nature Microbiology and I am happy to say that all three journals were interested in publishing a revised piece in some form.

Nature Medicine are interested in publishing it either as a Comment or a Correspondence. If you would like to pursue this option, please transfer the submission to Nature Medicine using the link provided below. Feel free to reach out to Joao Monteiro, chief editor, at [REDACTED] if you want to discuss the transfer process or have questions.

Nature Ecology & Evolution would be interested in considering the manuscript as a Comment article. They would like to work with you to address the reviewers' concerns and restructure the manuscript to focus more on the plausible evolutionary scenarios. If this option is of interest, you can also use the link below to transfer, and please feel free to get in touch with Patrick Goymer [REDACTED] to discuss it further.

Finally, Nature Microbiology would similarly be interested in considering a revised manuscript that addresses the main concerns from the referees as a Comment article. Should you be interested in this option, please use the link below to transfer and please feel free to contact Nonia Pariente ([REDACTED] who is currently out of the office but will be back on Feb 24th) and Paula Jauregui [REDACTED] to discuss further.

I am sorry that we cannot be more positive on this occasion. We hope that our decision does not discourage you from submitting your work to us in future as we remain interested in publishing key developments in this area of research. We hope that you will find our referees' comments helpful.

With best wishes,

Clare

Clare Thomas
Senior Editor
Nature

Referees' comments:

Referee #1 (Remarks to the Author):

Anderson presented a timely manuscript to share their points of view about the origin of SARS-CoV-2. There are several rumors about the origin of this virus. However, these "hypotheses" are entirely based on very limited, if any, scientific evidences. This reviewer sees most of the arguments raised by the authors are valid and convincing.

However, the authors might want to consider these minor suggestions:

- 1.The sections for the RBD and cleavage site of Spike protein basically have summarized the existing findings from other recent publications. The authors might want to spell out that these two sections are review summaries. In addition, the author can present these two sections in a more condense format and save some space for something else (also see points 6 and 7 below)
2. Fig. 1. This figure has 6 aligned sequences, but with only 5 sequence titles. The order of these titles are also not correct.
3. Lines 170 -174. It is correct that no adaptive mutation has been found in the spike of MERS-CoV. Deletions in other ORF regions, however, were detected in some human MERS-CoV viruses (PMID: 26981770). In addition, the 29nt deletion of human SARS-CoV (PMID: 12958366) was suggested to have effects on host adaptation. The authors should also consider these findings. It is premature to say that this would not happen in SARS-CoV-2.
4. Line 194. The accident at Singapore occurred in a BSL3, not BSL2, containment.
5. Line 194. Laboratory escapes of SARS occurred in Singapore, China and Taiwan (PMID: 16830004).
6. There are two recent reports about coronaviruses in pangolins (<https://www.biorxiv.org/content/10.1101/2020.02.13.945485v1.full.pdf>; <https://www.biorxiv.org/content/10.1101/2020.02.08.939660v2.full.pdf>). The authors might want to comments on these.
7. Optional: Can the authors share their views on the possibility of having a lab escape of a natural coronavirus? This is also one of the hypotheses that have been extensively discussed. The reviewer understand that this is entirely a different topic, but any insights are welcomed.

Referee #2 (Remarks to the Author):

This is a perspective discussing evidence against a hypothetical lab origin of SARS-CoV-2. The paper addresses suboptimal composition of ACE2-binding sites in the RBD, 3 predicted O-linked glycosylation sites and a furin cleavage site in the glycoprotein that was speculated upon before.

The paper is itself interesting, but unnecessarily speculative. It's not clear why the authors do not refute a hypothetical lab origin in their coming publication on the ancestors of SARS-CoV-2 in bats and pangolins. The tree showing diverse pangolin viruses has kindly been made available by some of the authors in GISAID. Once the authors publish their new pangolin sequences, a lab origin will be extremely unlikely. It is not clear why the authors rush with a speculative perspective if their central hypothesis can be supported by their own data. Please explain.

Another critical aspect of this text is the complete lack of referencing to a potential debate on a hypothetical lab origin. Who said this, why is this considered a problem? There are indeed a few apparently uninformed statements claiming the virus may be a Chinese bioweapon, but is this really problematic on a larger scale? The central reason for issuing this text must be

exhaustively referenced and discussed.

The authors state that a predicted polybasic cleavage sites is unique to SARS-CoV-2 in SARS viruses. Who knows how many out of thousands undiscovered bat ancestors also acquired such a motif, the sampling bias in descriptions of remote bat viruses is dramatic. This should be discussed. Also state clearly that this site is only predicted so far and that experimental evidence for its biological function and its potential impact on pathogenesis are required.

The predicted O-linked glycosylation sites are mysterious. What do the authors imply with those sites? In silico prediction of O-linked glycosylation sites is not robust and whether these sites indeed exist requires experimental validation. Even if those sites exist, why are they relevant? This is not addressed at all. If the authors assume these sites constitute part of a glycan shield, they should say so and weigh their assumption carefully.

Finally, the main argument against a hypothetical lab origin seems the required reconstruction of a backbone of a bat virus of unknown pathogenesis. It does not seem feasible that any scientist would disembark on such an uncertain endeavor. This difficulties of coronavirus reverse genetics should be stated clearly.

--

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Message

From: Joao Monteiro [REDACTED]
Sent: 3/5/2020 10:17:45 AM
To: Kristian G. Andersen [REDACTED]; Edward Holmes [REDACTED]
Subject: RE: Interest in "Proximal Origins of hCoV-19"?

Thanks, Kristian.

Our Editorial Assistant, Sarah will send you the copyright assignment form. Please return it to her today if possible. Otherwise we are good to go.

Joao

From: Kristian G. Andersen [REDACTED]
Sent: Thursday, March 05, 2020 12:29 PM
To: Edward Holmes
Cc: Joao Monteiro
Subject: Re: Interest in "Proximal Origins of hCoV-19"?

Hi Joao,

Just to let you know the manuscript has been transferred over - NMED-C102233-T.

Please let me know if you need anything else or have any questions.

Best,
Kristian

On Wed, Mar 4, 2020 at 7:04 PM Edward Holmes [REDACTED] wrote:

Excellent, many thanks.

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 [REDACTED]
E [REDACTED]

On 4 Mar 2020, at 7:02 pm, Kristian G. Andersen [REDACTED] wrote:

Yup, links work - all good, I'll get this done in the morning.

K

On Wed, Mar 4, 2020 at 7:01 PM Edward Holmes [REDACTED] wrote:

Ok! I started the transfer process but I've just aborted.

Kristian - can you just check that the link works.

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 [REDACTED]
E [REDACTED]

On 4 Mar 2020, at 6:59 pm, Kristian G. Andersen [REDACTED] wrote:

Ah, I have the email - I see the link. I'll update a few things and get this transferred over - should be completed tomorrow morning.

K

On Wed, Mar 4, 2020 at 6:57 PM Joao Monteiro [REDACTED] wrote:

Hi,

If you are listed as corresponding author, you can just go ahead and transfer the paper using the link in the decision letter from Nature that you received. You may also be able to make Kristien a corresponding author, if you have access to your account.

Sent from my iPhone, please excuse the brevity.

On Mar 4, 2020, at 9:54 PM, Edward Holmes [REDACTED] wrote:

Apologies! I'm in LAX now and will be for a few hours.

Please let me know what I need to do get this resolved.

Best wishes,

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 [REDACTED]
E [REDACTED]

On 4 Mar 2020, at 4:33 pm, Kristian G. Andersen [REDACTED] wrote:

Once I have clarity on HCoV-19/SARS-CoV-2 I have all the edits in.

As for the previous submission - that's actually under Eddie's account - are you able to transfer it over to mine (krisandersen)? Otherwise, I'll forward all the material to Eddie and then he can transfer - I believe he's *en route* to Sydney at the moment.

K

On Wed, Mar 4, 2020 at 3:32 PM Kristian G. Andersen [REDACTED] wrote:

Great, thanks Joao - I can incorporate.

A couple of specific comments:

- "Proximal" is included since we're talking about the most recent origin - not deeper origins (e.g., in bats). I have heard from a number of people that they really like that bit, so I was hoping to keep it?
- The naming of the virus is tricky and I'm hoping to push back a little here - but of course will do whatever you prefer. The name "SARS-CoV-2" was chosen by ICTV without consulting any Chinese authorities or any of the people involved in its discovery. The WHO - while they now acknowledge SARS-CoV-2 as the official name of the virus, they refuse to use it because of stigma and other issues. HCoV-19 was suggested by a number of leading Chinese scientists involved in the discovery of the virus to (a) avoid stigma, and (b) make it more consistent with the name of the disease. [https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(20\)30419-0/fulltext](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30419-0/fulltext). Again, we'll of course do whatever you think is best, but my personal opinion (shared by my co-authors) is that HCoV-19 is more appropriate than SARS-CoV-2.

<Screen Shot 2020-03-04 at 3.30.34 PM.png>

On Wed, Mar 4, 2020 at 3:22 PM Joao Monteiro [REDACTED] wrote:

Hi Kristian,

Thanks for the quick reply. I have added a couple notes to the file, for you to review plus some stylistic edits. Once you're done, can you transfer the submission from Nature to our system and upload the files to include the revised finalized version, the point-by-point response and the figure file separately, please? The main text should be an editable word doc.

LMK if you have any questions. I'll be on and off for the next hour or so. If you can turn this back to me before end of the week, would be fab.

ATB

Joao

From: Kristian G. Andersen [REDACTED]
Sent: Wednesday, March 04, 2020 5:56 PM
To: Joao Monteiro
Subject: Re: Interest in "Proximal Origins of hCoV-19"?

Hi Joao,

Please find attached a version cut to the suggested size. Please let me know if you have any questions or if you need anything else.

Best,

Kristian

On Tue, Mar 3, 2020 at 5:27 PM Kristian G. Andersen [REDACTED] wrote:

Hi Joao,

Thanks for getting back to me. Sounds good - we'll cut it to size and get back to you asap (hopefully tomorrow).

K

On Tue, Mar 3, 2020 at 11:02 AM Joao Monteiro [REDACTED] wrote:

Hi Kristian,

Thanks for sending the files and sorry about the delay to respond.

We're interested in the piece, though I must it has grown significantly since the version I saw in consultation with Nature. Our plan was going to pursue publication within our Correspondences section, given the tone and overall type of discussion in the piece. I could offer ~2200 words, and up to 30 references, so you'd need to trim this back down more or less the size of the Nature version, while retaining the major changes in response to the reviewers.

Does this sound a reasonable plan to you? I believe that using this route, we could move ahead with publication fairly quickly.

Please let me know.

All the best,

Joao

From: Kristian G. Andersen [REDACTED]
Sent: Saturday, February 29, 2020 7:22 PM
To: Joao Monteiro
Subject: Re: Interest in "Proximal Origins of hCoV-19"?

Hi Joao,

Sorry for the delay in getting this over to you. I have attached the manuscript (PDF + Word), figure, and the response to the questions raised after our first submission. Please let me know if you have any questions or if you want me to submit this via your formal submission system.

Best,

Kristian

On Thu, Feb 27, 2020 at 9:17 PM Kristian G. Andersen [REDACTED] wrote:

Hi Joao,

Sounds great. I need to get a few final edits in to make our conclusions a little less open ended (to make clearer that this *does* have a natural origin), but I'm hoping to get that done tomorrow in the AM. I'll send it over to you as soon as that's done.

K

On Thu, Feb 27, 2020 at 18:53 Joao Monteiro [REDACTED] wrote:

Hi Kristian,

Thanks for reaching out. Yes, we are very interested in the comment, and since it's been already peer reviewed, we were hoping to. I've ahead with fairly quickly. I'm at a conference right now, back to the office tomorrow. In the meanwhile, could you send me the revised version you're working on? I can work in that fri. The editorial side, so that when you transfer, we can move ahead with accepting it straight away.

All the best,

Joao

Sent from my iPhone, please excuse the brevity.

On Feb 27, 2020, at 7:34 PM, Kristian G. Andersen [REDACTED] wrote:

Dear Joao,

I believe Clare over at Nature might have mentioned our commentary on the proximal origins of the hCoV-19 virus last week. We have been incorporating some critical changes to the reviewer's comments so I just wanted to reach out to you to see if you're still interested in having a look at this manuscript? We're still incorporating a few changes but will have all of this wrapped up shortly as we're on a tight deadline - the media interest in this has been enormous and hasn't slowed down (we have refrained from commenting until formal publication). The public interest

has also been very high, with more than 65,000 reads of the blog post version over the last week.

Best,

Kristian

Kristian G. Andersen, PhD

Associate Professor, Scripps Research

Director of Infectious Disease Genomics, Scripps Research Translational Institute

Director, Center for Viral Systems Biology

The Scripps Research Institute

10550 North Torrey Pines Road, [REDACTED]

Department of Immunology and Microbial Science

La Jolla, CA 92037

p: [REDACTED]

c: [REDACTED]

t: @K_G_Andersen

e: [REDACTED]

w: www.andersen-lab.com

Assistant: [REDACTED]



Message

From: Chris Emery [REDACTED]
Sent: 3/17/2020 1:21:41 PM
To: Kristian Andersen Gmail Forward [REDACTED]
Subject: FW: COVID-19 preprint of interest - now published

You probably know this, but the paper is live. Press release is up here: <https://www.scripps.edu/news-and-events/press-room/2020/20200317-andersen-covid-19-coronavirus.html>

From: "Coleman, Amanda (NIH/NIAID) [C]" [REDACTED]
Date: Tuesday, March 17, 2020 at 1:15 PM
To: "Shabman, Reed (NIH/NIAID) [E]" [REDACTED]
Cc: "Brown, Liliana (NIH/NIAID) [E]" [REDACTED]; Chris Emery [REDACTED]
Subject: RE: COVID-19 preprint of interest - now published

Thanks so much, Reed. I'll let the Office of Communications know.

Thank you,

Amanda Coleman [C]
[REDACTED]

From: Shabman, Reed (NIH/NIAID) [E] [REDACTED]
Sent: Tuesday, March 17, 2020 3:01 PM
To: Coleman, Amanda (NIH/NIAID) [C] [REDACTED]
Cc: Brown, Liliana (NIH/NIAID) [E] [REDACTED]; Chris Emery [REDACTED]
Subject: RE: COVID-19 preprint of interest - now published

Hi Amanda,

Following-up on this email chain. The paper, **The proximal origin of SARS-CoV-2**, is now online at Nature Medicine. Disregard my note if you have already heard from Chris at Scripps, but just wanted to close the loop.

Reed

Link: <https://www.nature.com/articles/s41591-020-0820-9#Ack1>

From: Shabman, Reed (NIH/NIAID) [E]
Sent: Wednesday, February 19, 2020 3:30 PM
To: Coleman, Amanda (NIH/NIAID) [C] [REDACTED]
Cc: Brown, Liliana (NIH/NIAID) [E] [REDACTED]; Chris Emery [REDACTED]
Subject: RE: COVID-19 preprint of interest

Hi Amanda,

I reached out to Kristian and team and copied his response below in italics. As you can see from his note, the text is submitted to Nature. Kristian suggests that the Office of Communications can communicate directly with Chris Emery (copied here).

Thanks,

Reed

Yes, it's been submitted for peer review (in Nature) and we are holding off on giving further comments to the media until it's been through that and published. Chris Emery from our communications department (cc'd here) is taking the lead on creating a press release / summary in lay language, as well as a Q&A with questions the public and policy makers might have - Wellcome is involved as well to help out. If there's interest on NIAID's side, I'm sure Chris and the team would welcome coordination/collaboration, so if you can please reach out to him directly.

*Best,
Kristian*

From: Coleman, Amanda (NIH/NIAID) [C] [REDACTED]
Sent: Wednesday, February 19, 2020 1:21 PM
To: Shabman, Reed (NIH/NIAID) [E] [REDACTED]
Cc: Brown, Liliana (NIH/NIAID) [E] [REDACTED]
Subject: RE: COVID-19 preprint of interest

Hi Reed – The Office of Communications asked if we could alert them if this paper is accepted in a peer reviewed journal. Do you know if the authors have submitted it to a journal?

Thank you,

Amanda Coleman [C]
[REDACTED]

Message

From: Kristian G. Andersen [REDACTED]
Sent: 3/31/2020 8:59:49 PM
To: Michael Farzan [REDACTED]
Subject: Re: Furin...

Hey Mike,

Still chugging along here in SoCal... As per our previous conversations, I thought this was pretty interesting:

<http://virological.org/t/identification-of-a-common-deletion-in-the-spike-protein-of-sars-cov-2/451>

Not quite sure what to make of it - but definitely interesting!

K

On Mon, Feb 17, 2020 at 9:26 AM Kristian G. Andersen [REDACTED] wrote:
Hey Mike,

Thanks - I was actually in the desert when that got pushed out, so a little rushed IMO. But pressure from the higher ups to get it out.

Thanks for your comment on the structure/binding - this is actually *really* important. We have been discussing that bioRxiv paper this morning since it appears to show that -2 does indeed bind as well - or better - than -1. There is other data to suggest that too, but good to know that this isn't gospel!

Four pangolin sequences just dropped as well - unfortunately these are similar to the previous and not similar in the RBD. I'm starting to think that one pango that stands out might not actually be correct. Hopefully more to come!

Cheers,
K

On Mon, Feb 17, 2020 at 9:17 AM Michael Farzan <[REDACTED]> wrote:

Yep.

Hey just saw your review. Nice!

Fyi: Jason McClellan's otherwise gorgeous S-protein structure includes a probably wrong assertion that the SARS2 S protein binds with "20-fold" higher affinity than that of SARS1. This is almost certainly wrong, and based in thei paper on an apples to oranges comparison. I suspect that will be in the press soon but thought I would mention it in case you were asked, "the jury is still out on that conclusion".

From: Kristian G. Andersen [REDACTED]
Sent: Sunday, February 16, 2020 9:45 PM
To: Michael Farzan
Subject: Re: Furin...

Hey Mike,

Yup, one of the pangolin sequences have a very similar RBD (the others are more like bat and further from human still). It's not the elusive "99% pangolin" though as that sequence was never published nor was a study produced - I think they might have spoken a little too soon. The one that's online and close in the RBD is from merging a couple of metagenomic datasets and is very incomplete, so I'm not quite sure what to make of it. I really hope they'd come up with the 99% sequence - that'd be cool!

Cheers,
Kristian

On Sat, Feb 15, 2020 at 9:42 AM Michael Farzan [REDACTED] wrote:

Hi Kristian, you probably know this by now but the RBM of the 99% pangolin-derived virus is virtually identical to SARS2 but the furin-site 4-aa insertion is missing. Mike

From: Michael Farzan
Sent: Thursday, February 6, 2020 11:07 PM
To: Kristian G. Andersen [REDACTED]
Subject: RE: Furin...

Hey Kristian,

It's a bit complicated but here is the best I can find.

There are two MHV variants A59 and BHK. BHK is lab adapted and has extended host range, and no longer is cleaved in the producer cell by furin. It also appears to be independent of the murine (or human) CEACAM receptor, relying on heparan sulfate.

The furin site has not changed in BHK, rather two amino acids immediately downstream account for the phenotype.

https://jvi.asm.org/content/79/22/14451?ijkey=709aa5da9513e80f42db103ec19b539ed1cc350b&keytype2=tf_ipsecsha

Virus-Cell Interactions

Message

From: Jeremy Farrar [REDACTED]
Sent: 2/8/2020 1:27:14 PM
To: Kristian G. Andersen [REDACTED] Drosten, Christian [REDACTED]
CC: Edward Holmes [REDACTED] Andrew Rambaut [REDACTED]; rfgarry [REDACTED]; r.fouchier [REDACTED]; P.Vallance1 [REDACTED]; collinsf [REDACTED]; afauci [REDACTED]; Josie Golding [REDACTED]; m.koopmans [REDACTED]; Mike Ferguson [REDACTED]
Subject: Re: [ext] 2019 N-CoV

We now have (and we will get more) the pangolin data (Eddie has) we think we can tie this up even tighter with the next iteration and make a conclusive statement which will then be the go to scientific statement to refer to.

Eddie and I have just come off a call with the National Academy of Medicine in the US – who the White House has asked to produce a report on this....

From: "Kristian G. Andersen" [REDACTED]
Date: Saturday, 8 February 2020 at 21:16
To: "Drosten, Christian" [REDACTED]
Cc: Jeremy Farrar [REDACTED], Edward Holmes [REDACTED], "a.rambaut" [REDACTED], "rfgarry" [REDACTED], "r.fouchier" [REDACTED], "P.Vallance1" [REDACTED], Francis Collins [REDACTED], "afauci" [REDACTED], Josie Golding [REDACTED], Marion Koopmans [REDACTED], Mike Ferguson [REDACTED]
Subject: Re: [ext] 2019 N-CoV

A lot of good discussion here, so I just wanted to add a couple of things for context that I think are important - and why what we're considering is far from "another conspiracy theory", but rather is taking a valid scientific approach to a question that is increasingly being asked by the public, media, scientists, and politicians (e.g., I have been contacted by Science, NYT, and many other news outlets over the last couple of days about this exact question).

To Ron's question, passage of SARS-like CoVs have been ongoing for several years, and more specifically in Wuhan under BSL-2 conditions - see references 12-15 in the document for a few examples. The fact that Wuhan became the epicenter of the ongoing epidemic caused by nCoV is likely an unfortunate coincidence, but it raises questions that would be wrong to dismiss out of hand. Our main work over the last couple of weeks has been focused on trying to *disprove* any type of lab theory, but we are at a crossroad where the scientific evidence isn't conclusive enough to say that we have high confidence in any of the three main theories considered. Like Eddie - and I believe Bob, Andrew, and everybody on this email as well - I am very hopeful that the viruses from pangolins will help provide the missing pieces. For now, giving the lab theory serious consideration has been highly effective at countering many of the circulating conspiracy theories, including HIV recombinants, bioengineering, etc. - here's just one example: <https://www.factcheck.org/2020/02/baseless-conspiracy-theories-claim-new-coronavirus-was-bioengineered/>.

As to publishing this document in a journal, I am currently not in favor of doing so. I believe that publishing something that is open-ended could backfire at this stage. I think it's important that we try to gather additional evidence - including waiting on the pangolin virus sequences and further scrutinize the furin cleavage site and O-linked glycans - before

publishing. That way we can (hopefully) come out with some strong conclusive statements that are based on the best data we have access to. I don't think we are there yet.

Best,
Kristian

On Sat, Feb 8, 2020 at 12:38 PM Drosten, Christian [REDACTED] wrote:

OK, I see. We should then introduce references to these informal sources in the beginning of the text. Else it reads a bit funny.

Christian

--

Professor Christian Drosten

Director, Institute of Virology
Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin
Campus Charité Mitte

[REDACTED]
Germany

E-Mail: [REDACTED]

<https://virologie-ccm.charite.de/>

<https://globalhealth.charite.de/>

Von: Jeremy Farrar [REDACTED]
Datum: Samstag, 8. Februar 2020 um 21:21
An: Edward Holmes [REDACTED], Christian Drosten [REDACTED]
Cc: "kga1978" [REDACTED], Andrew Rambaut [REDACTED], "rgarry" [REDACTED], "r.fouchier" [REDACTED], "P.Vallance1" [REDACTED], "collinsf" [REDACTED], <collinsf" [REDACTED], "afauci" [REDACTED], Josie Golding [REDACTED], "m.koopmans" [REDACTED], Mike Ferguson [REDACTED]
Betreff: Re: [ext] 2019 N-CoV

The theory of the origin of the has gathered considerable momentum not in social media, but increasingly among some scientists, in main stream media, and among politicians.

The aim of this was to bring a neutral, respected, scientific group together to look at the data and in a neutral, considered way provide an opinion and we hoped to focus the discussion on the science, not on any conspiracy or

other theory and to lay down a respected statement to frame whatever debate goes on – before that debate gets out of hand with potentially hugely damaging ramifications.

With the additional information on the pangolin virus, information not available even 24 hours ago, I think the argument is even clearer.

My preference is that a carefully considered piece of science, early in the public domain, will help mitigate more polarised debate. If not, that debate will increasingly happen and science will be reacting to it. Not a good position to be in.

From: Edward Holmes [REDACTED]
Date: Saturday, 8 February 2020 at 20:11
To: Christian Drosten [REDACTED]
Cc: Jeremy Farrar [REDACTED], "kga1978" [REDACTED]
"a.rambaut" [REDACTED], "rfgarry" [REDACTED]
"r.fouchier" [REDACTED], "P.Vallance1" [REDACTED]
[REDACTED], Francis Collins [REDACTED], "afauci" [REDACTED]
[REDACTED], Josie Golding [REDACTED] Marion Koopmans
[REDACTED], Mike Ferguson [REDACTED]
Subject: Re: [ext] 2019 N-CoV

Hi Christian,

I don't know where this story came from, but it has nothing whatsoever to do with the HIV nonsense. Please don't associate this with that. This is a broader story.

Ever since this outbreak started there have been suggestions that the virus escaped from the Wuhan lab, if only because of the coincidence of where the outbreak occurred and the location of the lab. I do a lot of work in China and I can tell you that a lot of people there believe this and believe they are being lied to. Things were made worse when Wuhan lab published the bat virus sequence - a bat sampled in a different province for which they have a large collection of samples.

I believe the aim/question here is whether we, as scientists, should try to write something balanced on the science behind this? There are arguments for and against doing this.

Personally, with the pangolin virus possessing 6/6 key sites in the receptor binding domain, I am in favour of the natural evolution theory.

Best wishes,

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 [REDACTED]

E [REDACTED]

On 9 Feb 2020, at 6:52 am, Drosten, Christian [REDACTED] wrote:

Dear All,

I am overloaded with nCoV patient-related work and will need a few days before I can work on this text.

Can someone help me with one question: didn't we congregate to challenge a certain theory, and if we could, drop it? This whole text reads as if the hypothesis was obvious, or was brought up by some external source, forcing us to respond. Is this the case? It does not seem as if this was linked to the HIV nonsense.

Who came up with this story in the beginning? Are we working on debunking our own conspiracy theory?

Christian

—

Professor Christian Drosten

Director, Institute of Virology

Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin

Campus Charité Mitte

[REDACTED]
Germany

E-Mail: [REDACTED]

<https://virologie-ccm.charite.de/>

<https://globalhealth.charite.de/>

Von: Jeremy Farrar [REDACTED]

Datum: Samstag, 8. Februar 2020 um 10:45

An: Edward Holmes [REDACTED], "kga1978@charite.de" [REDACTED]

Andrew Rambaut "rfgarry@
Cc: "r.fouchier@
<P.Vallance1@
, "collinsf@
Josie Golding "m.koopmans@
, Christian Drosten Mike Ferguson
[REDACTED]

Betreff: [ext] FW: 2019 N-CoV

APOLOGIES WITH ALL CORRECT EMAILS

Kristen, Andrew, Bob, Eddie have reworked the summary and it is attached here.

We are pushing to get the sequence data from the reports on the pangolins, but do not have currently, clearly that is very important to incorporate.

Interested in your views

- Is this reasonably balanced given the data?
- Is there anything anyone disagrees with?
- Is there anything more in relation to what would seem to be the two possibilities
 - Nature, Intermediate host, evolution and passage
- Future data you may have
- Advice on whether KA, AR, RG and EH should publish this.

These and other thoughts welcome in confidence.

Message

From: Edward Holmes
[REDACTED]
Sent: 7/28/2020 4:23:46 AM
To: Kristian G. Andersen
[REDACTED]
CC: Garry, Robert F
[REDACTED]
Andrew Rambaut
[REDACTED]
Subject: Re: Teleconference

External Sender. Be aware of links, attachments and requests.

All, I've spoken to Jeremy and he wants a little more of the time-line incorporated, which helps make or case stronger. Also happens to be true. He's also agreed to be cc'd on the reply to Jon which is great because he will be able to confirm.

So, I've edited the draft email to Jon accordingly (Kristian, I've moved some sentences around).

Jeremy's comms person at Wellome also had some suggestions and I'll forward that in a sec.

Cheers,

Eddie

Hi Jon,

Here are the facts:

1. On Jan 27 Jeremy Farrar called one of us (Eddie) to say that some rumours were coming out of the US that the virus may be a lab escape and could he determine whether this had any scientific credibility. By coincidence, on Jan 31 Kristian independently contacted Eddie to note that there was some features in the SARS-CoV-2 genome that at the time appeared unusual, particularly the furin cleavage site and the receptor binding domain.
2. At this stage we thought it was wise to ask for additional opinion on this, so a conference call was rapidly arranged for Feb 1 (Feb 2 Eddie's time). There were indeed other coronavirus experts on the call, chosen by Jeremy and Eddie. It is worth pointing out at this point that the senior author on our paper - Bob Garry - has published a significant number of papers on coronaviruses, including on the SARS spike protein, and even commented on this on the virological.org website prior to the call taking place (<https://virological.org/t/analysis-of-wuhan-coronavirus-deja-vu/357>).
3. Clearly, some people on the call were very strongly of the opinion that the possibility of a lab escape was implausible and gave reasons why it should be dismissed (although there was also some initial confusion about whether we were referring to the crazy HIV origins theory that had just been touted - obviously we were not). Some of those comments we agreed with, others we did not.

4. A take-home message from the call was that we should investigate further and write a scientific paper to clearly set-out the background on the topic and our findings. Indeed, one of the emailed agenda items for discussion after the call was: "Advice on whether KA, AR, RG and EH should publish this".

Hence, we eventually wrote up our findings as a scientific (peer reviewed) paper. Critically, drafts of this paper were sent to all the people on the call, including those with the information that has been emailed to you. We have attached our first draft of what would eventually become our paper from Feb 7, which was circulated to everyone on the call. As you can see, it is essentially the basis of our final study and people on the call commented on it.

5. Very shortly after the call, the pangolin data came out. This was critical, and as Eddie wrote in an email to everyone on the call on Feb 9th:

"Personally, with the pangolin virus possessing 6/6 key sites in the receptor binding domain, I am in favour of the natural evolution theory."

With Andrew Rambaut replying:

"I am of the view that the natural selection hypothesis is the most likely (specifically the non-bat reservoir). And as Eddie mentioned this is becoming more likely from day to day with the pangolin story."

6. Hence, it is completely and utterly false to claim that we (i) all thought it was a lab escape, (ii) that we were corrected ("schooled") in our views by the coronavirus experts on the call, and (iii) then submitted a Nature paper without anyone else knowing about it. The truth is that we had a range of views among us, our paper included the pangolin data that was not available at the time of the call, and we circulated drafts of our document to everyone. Importantly, our study was an evolutionary study based on genomic information, which is the only way to investigate the origins of SARS-CoV-2 - we believe all the authors on our paper have a strong demonstrated record in answering exactly those types of questions for a multitude of viruses.

7. We also categorically deny that we were "spreading the rumor" that the virus was human engineered. As you can see from point 1 this did not come from us. Indeed, at the time, there were indeed rumours - which persists to this day - that SARS-CoV-2 was an engineered virus, but these certainly did not come from us. As you know, the White House OSTP asked for expert opinions on this question too (spurred by the HIV nonsense preprint), and Kristian was part of that panel (<https://www.the-scientist.com/news-opinion/lab-made-coronavirus-triggers-debate-34502>). Our study directly addressed these rumours in a scientific way by considering that a lab escape could have occurred. We did not dismiss this possibility out of hand, but we scientifically investigated it.

8. We strongly reject the idea that we should not have raised nor discussed the possibility of lab escape: as scientists we have to present all the data and discuss it openly. That's what we did. To not have considered or mentioned the possibility of a lab escape would have been negligent. Is the person who emailed you seriously suggesting that we should not have discussed these issues? Wouldn't that be a cover-up? Indeed, the great irony is that 99.9% of the feedback we have received on our paper - including death threats - are people accusing us of dismissing the lab escape theory too quickly. Can you imagine if we had not mentioned - or considered - it all as suggested by some "coronavirus experts"?

To us, this clearly appears to be a case of sour grapes based on half-truths that lack the full history, gossip, and likely stimulated by your recent (great) article with quotes from us on the questions you raised with Dr. Zhengli. It's telling that the person who emailed you is anonymous. We have absolutely no problem with people knowing that our views on this issue have evolved as more data have appeared - and continues to evolve to this day, should more data become available. That's

science. And it's the only way to do it well. Indeed, we have told our history of thinking on this to many people: the way we set this up was a study of alternative hypotheses equally weighted priors, which we tested - our posterior clearly favors the hypothesis that this is a natural virus. As far as we can tell we are only 'guilty' of following the proper scientific method - but maybe we offended an ivory tower "coronavirus expert" in the process. It likely won't be the last time.

Best,

Eddie and Kristian

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 [REDACTED]
E [REDACTED]

On 28 Jul 2020, at 6:21 pm, Andrew Rambaut [REDACTED] wrote:

I agree - most likely Ron doing the leaking. Whoever it was that talked to the emailer was indignant that 'non-coronavirus-experts' were involved. I can't see any of the others having this sort of pompous, arrogant view of the world. Marion approached me well after this to help analyse the Dutch data. Christian I have worked with before on MERS. I doubt even that Ron was that bothered - probably just told the story to whoever it was and misremembered or 'enhanced' it for effect.

A

On 28 Jul 2020, at 03:58, Edward Holmes [REDACTED] wrote:

Pohlmann as on it and very good. Christian was also v. interested in the furin cleavage site (I've other emails).

Despite this, I'm 100% sure it is Ron who leaked it - he was the most angry - and I still think it was like Baric who emailed Jon Cohen.

I just thought "I would conclude that a follow-up discussion on the possible origin of 2019-nCoV would be of much interest" was very interesting.

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 [REDACTED]
E [REDACTED]

On 28 Jul 2020, at 12:54 pm, Kristian G. Andersen [REDACTED] wrote:

Interesting - I don't actually remember this from Ron. Was Stefan Pohlmann on the call too? Surely he knows Ralph very well.

On Mon, Jul 27, 2020 at 7:47 PM Edward Holmes [REDACTED] wrote:
Ron thought it was useful at the time.

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 [REDACTED]
E [REDACTED]

Begin forwarded message:

From: "R.A.M. Fouchier" [REDACTED]
Subject: Re: Teleconference
Date: 2 February 2020 at 7:30:12 pm AEDT
To: Jeremy Farrar [REDACTED], "Fauci, Anthony (NIH/NIAID) [E]"
[REDACTED] >, Patrick Vallance [REDACTED]
Cc: "Drosten, Christian" : [REDACTED], "M.P.G. Koopmans"
<[REDACTED]>, Edward Holmes <[REDACTED]>
"spoehlmann" [REDACTED], Andrew Rambaut <[REDACTED]>, "Kristian
G. Andersen" [REDACTED], Paul Schreier [REDACTED]
"rfgarry" [REDACTED], "Ferguson, Mike"
Francis Collins <collinst@[REDACTED]>, "lawrence.tabak" [REDACTED] Josie
Golding [REDACTED]

Dear Jeremy and others,

This was a very useful teleconference. Given the evidence presented and the discussions around it, I would conclude that a follow-up discussion on the possible origin of 2019-nCoV would be of much interest. However, I doubt if it needs to be done on very short term, given the importance of other activities of the scientific community, WHO and other stakeholders at present. It is my opinion that a non-natural origin of 2019-nCoV is highly unlikely at present. Any conspiracy theory can be approached with factual information. I have written down some of the counter-arguments. It is a bit long (below) but wanted to share it with you anyway.

Thanks for organizing this on such short notice,

Kind regards

Ron

Ron's notes:

An accusation that nCoV-2019 might have been engineered and released into the environment by humans (accidental or intentional) would need to be supported by strong data, beyond reasonable doubt. It is good that this possibility was discussed in detail with a team of experts. However, further debate about such accusations would unnecessarily distract top researchers from their active duties and do unnecessary harm to science in general and science in China in particular. At present, the arguments that nCoV-2019 could have emerged from an animal source is much stronger than other possibilities.

Observations about the genome that were inferred to be suggestive for a non-animal origin:

1. HIV-like sequences in the spike protein.
 2. Level of mutations in the spike protein region.
 3. Presence of a furin cleavage site in the middle of spike
 4. BamH1 restriction site at the end of the spike sequence
 5. An F-to-Y substitution in the receptor-binding domain of spike
 6. Potential O-linked glycan sites protecting the cleavage site of spike
1. The biorxiv publication by Prashant Pradhan and colleagues from Delhi ("Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag") has already been heavily debated on biorxiv and virological.org. The similarity between the inserts in 2019-nCoV spike and sequences of HIV-1 is accidental. These are very short insert sequences that are highly similar to many Genbank entries. Such similarities are explained by pure chance alone.
 2. Andrew Rambaut analyzed the level of mutations in the spike region of SARS-CoV with that of its closest bat virus relative and of 2019-nCoV and its closest bat virus relative. The level of mutations between the two pairs of viruses was in the same range. Thus, this level of mutations can arise under circumstances of natural emergence.
 3. Bat coronaviruses generally do not have a furin cleavage site in the spike protein. Some human coronaviruses do have a furin cleavage site in spike, which must have evolved naturally. As animal reservoir and spill-over hosts are highly under-sampled, the presence of a furin cleavage site in spike in such species is unknown. When coronaviruses jump host barriers, this frequently involved adaptation of cleavage sites that may be targeted by various proteases. Given the presence of furin-like sites in human coronavirus and the mutation of protease cleavage sites upon coronavirus host-jumps in general, a natural origin of the furin site is certainly not impossible.
 4. The BamHI restriction endonuclease site evolved due to a single (silent) nucleotide substitution as compared to the closest relative bat virus genome sequence. Restriction sites of 6 nucleotides can be found in every sequence, all over the genome, when 1 of the 6 positions is allowed to vary. We now find BamHI, next time it might be one of the plethora of other 6-nucleotide sequence motifs. This can be explained by pure chance.
 5. The F-Y substitution in the spike receptor binding domain was observed in mouse-adapted SARS-CoV and in 2019-nCoV. It is generally absent in bat coronaviruses. This substitution is associated with host adaptation in mice. It may point to (natural) host adaption of 2019-nCoV (in mice, humans or unknown hosts) as well. It is possible that scientists would like to test the effect of F-Y because it was found in a mouse adaptation experiment. However, the logical way to test it would be in the original (SARS-CoV) virus backbone. There is no other reason to insert the F-Y substitution in an engineered virus.
 6. It is unclear if the potential O-linked glycosylation sites 1) are used during glycosylation; 2) have a functional role for the spike protein; 3) were present in the ancestral virus from the original host. This is not an argument in the discussion on the origin of 2019-nCoV.

Additional arguments:

- A. All focus is on spike. Spike is a highly variable protein in general, crucial for host adaptation and under strong natural selection.

B. The virus backbone (beyond spike) is not an indicator of a human source of 2019-nCoV emergence. The virus itself has not been described or characterized previously and no reverse genetics system has been described for this virus. Any scientist wanting to investigate spike function (e.g. to study protease cleavage or the receptor-binding domain) would have used a well-characterized reverse genetics system that is already available (making accidental lab-escape unlikely). Anyone with malicious intent would have used a well-characterized virulent strain (SARS-CoV, MERS-CoV) described and characterized (by others) in the literature.

C. The patterns of mutations we observe in the receptor-binding domain and the protease cleavage sites of spike are typical for host-switched naturally evolving viruses. We can infer it for the naturally evolved human coronaviruses, we have seen it for the natural zoonoses of SARS-CoV and MERS-CoV. Convergent (parallel) evolutionary events are common in virology. Also for influenza, we see the same mutations emerge during the pandemics of 1918 (H1N1), 1957 (H2N2) and 1968 (H3N2), in the 2013 zoonotic H7N9 virus and e.g. an epizootic in seals in 2014 (H10N7). Regardless of the divergent subtype, we see identical substitutions in the receptor-binding domains, identical substitutions in polymerase, and non-identical substitutions with identical phenotypic consequences (e.g. stability) in the genome. The fact that we (think we) see recognizable traits in spike does not mean it must be man-made.

D. We do not know the source of 2019-nCoV. There is “~30 years of evolutionary gap” between 2019-nCoV and the closest bat virus relative. These 30 years may have been in any host. We have no idea what might have happened (in evolutionary sense) between BatCov/RaTG13 and 2019-nCoV. We should rest our case until we have a close relative of 2019-nCoV.

Van: Jeremy Farrar [REDACTED]

Datum: zaterdag 1 februari 2020 om 21:59

Aan: "Fauci, Anthony (NIH/NIAID) [E]" [REDACTED], Patrick Vallance [REDACTED]
[REDACTED]

CC: Christian Drosten [REDACTED], "M. Koopmans" [REDACTED]

"R.A.M. Fouchier" [REDACTED]

Edward Holmes [REDACTED]

"spoehlmann" [REDACTED], Andrew Rambaut [REDACTED], "Kristian G." [REDACTED]

Andersen" [REDACTED]

Paul Schreier [REDACTED]

, "rfgarry" [REDACTED]

"Ferguson, Mike" [REDACTED]

, Francis Collins [REDACTED]

<collinsf@[REDACTED]

"lawrence.tabak" [REDACTED]

Josie Golding [REDACTED]

Onderwerp: Re: Teleconference

Thank you to everyone for joining.

There is clearly much to understand understand in this. This call was very helpful to hear some of our current understanding and the many gaps in our knowledge. I do not believe this is a question of a binary outcome, it is more a question of “What are the evolutionary origins of 2019-nCoV, important for future risk assessment and understanding of animal/human coronaviruses”.

I do know there are papers being prepared, there will media interest and there is already chat on Twitter/WeChat.

We on this call are not the only ones with scientific expertise in this area and this was an ad hoc group that came together to air some thoughts. It is clearly not the sole group to take this forward, that will need a broader range of input and a respected international body to ask an expert group to explore this, with a completely open mind. In order to stay ahead of the conspiracy theories and social media I do think there is an urgency for a body to convene such a group and commission some work to – (draft) “To understand the evolutionary origins of 2019-nCoV, important for this epidemic and for future risk assessment and understanding of animal/human coronaviruses”.

In other words a completely open minded and neutral question bringing in the best minds, and under the umbrella of a respected international agency

I hope that is a reasonable approach, please send any thoughts or suggestions.

Once again, thank you for making time over a weekend and for such an informed discussion on a complex issue.

Thank you and best wishes Jeremy

From: Jeremy Farrar [REDACTED]

Date: Saturday, 1 February 2020 at 15:34

To: "Fauci, Anthony (NIH/NIAID) [E]" [REDACTED], Patrick Vallance [REDACTED]

Cc: "Drosten, Christian" [REDACTED], Marion Koopmans [REDACTED]

"r.fouchier" [REDACTED], Edward Holmes [REDACTED]

"spoehlmann" [REDACTED] "a.rambaut" [REDACTED] "Kristian G." [REDACTED]

Andersen" [REDACTED] Paul Schreier [REDACTED] "rfgarry" [REDACTED]

<rfgarry> [REDACTED] Michael FMedSci [REDACTED]

Subject: Teleconference

1st February (2nd Feb for Eddie)

Information and discussion is shared in total confidence and not to be shared until agreement on next steps.

Dial in details attached.

Please mute phones.

I will be on email throughout – email Paul or I Paul if any problems

If you cannot make it, I will phone you afterwards to update.

One Hour

6am Sydney

8pm CET

7pm GMT

2pm EST

11am PST

(*Hope I have the times right!*)

Thank you for the series of calls and for agreeing to join this call.

Agenda

- Introduction, focus and desired outcomes - JF
- Summary – KA
- Comments – EH
- Q&A – All
- Summary and next steps - JF

Kristian Anderson
Bob Garry - I have not been able to contact Bob. Please forward if you can.
Christian Drosten
Tony Fauci
Mike Ferguson
Ron Fouchier
Eddie Holmes
Marion Koopmans
Stefan Pohlmann
Andrew Rambaut
Paul Schreier
Patrick Vallance

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Message

From: Jeremy Farrar [REDACTED]
Sent: 7/28/2020 12:36:51 AM
To: Edward Holmes [REDACTED]
CC: Kristian G. Andersen [REDACTED]; Fauci, Anthony (NIH/NIAID) [E] [REDACTED]
Subject: Re: The authors who wrote the paper saying that SARS-CoV-2 is not human engineered first tried convincing Anthony Fauci of the opposite.

Thanks Eddie.

I will recheck emails and phones, I will try and do that today.

I think it really starts on the 8/9th January and the calls you and I had with China and the original sequence.

And others were also on those calls – Francis Collins, Mike Ferguson, Patrick Vallance.

I would suggest we get the sequence of events absolutely right before replying.

Best wishes Jeremy

From: Edward Holmes [REDACTED]
Date: Tuesday, 28 July 2020 at 08:30
To: Jeremy Farrar [REDACTED]
Cc: "Kristian G. Andersen" [REDACTED]; "Fauci, Anthony (NIH/NIAID) [E]" [REDACTED]
Subject: Re: The authors who wrote the paper saying that SARS-CoV-2 is not human engineered first tried convincing Anthony Fauci of the opposite.

Hi Jeremy,

Here is the exact time-line which I have now checked.

1. Jan 26. You call me (I was in Switzerland) to talk about some concerns coming out the US that the virus might be a lab escape. Patrick Vallance might have been on that call, I can't recall. You later forward me an email from Marc Lipsitch and others containing some comments from Richard Ebright. I take a quick look at the sequence and say that I saw no evidence for lab escape in SARS-CoV-2 because its pattern of variability was the same as in RaTG13.

2. Jan 31. Kristian contacts me to say that he has spotted some strange things in the issue - specifically the furin cleavage site and restriction sites - that we were concerned about. Given our conversation earlier that week, I called you and informed you of Kristian's findings. We then decided to have a broader discussion with key parties on this ASAP. I think Kristian told Tony at this point but he can confirm. You and I then decided that Ron Fouchier, Christian Drosten and Marion Koopmans would be good to include. Christian also wanted Stephan Pollmnan involved.

3. Feb 1 (6 am on Feb 2 for me). We have the conference call and then start an email chain about how we should deal with this. Writing it up for a paper was on the agenda and discussed. I have all the emails on this.

For Tony's benefit a revised draft of the email to Jon is pasted below.

I can't for the life of me see what we have done wrong here. I strongly believe we have just tried to get on top of a very vexing question as quickly and openly as possible.

Cheers,

Eddie

Hi Jon,

Here are the facts:

1. In early Feb we had spotted some features in the SARS-CoV-2 genome that at the time appeared unusual - particularly the furin cleavage site and the receptor binding domain.
2. At this stage we thought it was wise to ask for other expert's opinions on this, so a conference call was arranged. There were indeed other coronavirus experts on the call. It is worth pointing out that the senior author on our paper - Bob Garry - has published a significant number of papers on coronaviruses, including on the SARS spike protein, and even commented on this on the [virological.org website](https://virological.org/t/analysis-of-wuhan-coronavirus-deja-vu/357) prior to the call taking place (<https://virological.org/t/analysis-of-wuhan-coronavirus-deja-vu/357>). Importantly, our study was an evolutionary study based on genomic information, which is the only way to investigate the origins of SARS-CoV-2 - we believe all the authors on our paper have a strong demonstrated record in answering exactly those types of questions for a multitude of viruses.
3. Clearly, some people on the call were very strongly of the opinion that the possibility of a lab escape was ridiculous and listed reasons why it should be dismissed out of hand (although there was also some initial confusion about whether we were referring to the crazy HIV origins theory that had just been touted - obviously we were not). Some of those comments we agreed with, others we did not. A take-home message from the call was that we should investigate further and write a scientific paper to clearly set-out the background on the topic and our findings. Indeed, one of the emailed agenda items for discussion after the call was "Advice on whether KA, AR, RG and EH should publish this".
4. We eventually wrote up our findings as a scientific (peer reviewed) paper. Critically, drafts of this paper were sent to all the people on the call, including those with the information that has been emailed to you. We have attached our first draft of what would eventually become our paper from Feb 7, which was circulated to everyone on the call. As you can see, it is essentially the basis of our final study and people on the call commented on it.
5. Very shortly after the call, the pangolin data came out. This was critical and as Eddie wrote in an email to everyone on the call on Feb 9th:

"Personally, with the pangolin virus possessing 6/6 key sites in the receptor binding domain, I am in favour of the natural evolution theory."

and Rndrew Rambaut replied to this stating:

"I am of the view that the natural selection hypothesis is the most likely (specifically the non-bat reservoir). And as Eddie mentioned this is becoming more likely from day to day with the pangolin story."

6. Hence, it is completely and utterly false to claim that we (1) all thought it was a lab escape, (2) that we were corrected ("schooled") in our views by the coronavirus experts on the call, and (3) then submitted a Nature paper without anyone else knowing about it. The truth is that we had a range of views among us, our paper included the pangolin data that was not available at the time of the call, and we circulated drafts of our document to everyone.

7. We categorically deny that we were "spreading the rumor" that the virus was human engineered. At the time, there were indeed rumours - which persists to this day - that SARS-CoV-2 was an engineered virus, but these certainly did not come from us. As you know, the White House OSTP asked for expert opinions on this question too (spurred by the HIV

nonsense preprint), and Kristian was part of that panel (<https://www.the-scientist.com/news-opinion/lab-made-coronavirus-triggers-debate-34502>). Our study directly addressed these rumours in a scientific way by considering that a lab escape could have occurred. We did not dismiss this possibility out of hand, but we scientifically investigated it.

We strongly reject the idea that we should not have raised nor discussed the possibility of lab escape: as scientists we have to present all the data and discuss it openly. That's what we did. To not have considered or mentioned the possibility of a lab escape would have been negligent. Is the person who emailed you seriously suggesting that we should not have discussed these issues? Wouldn't that be a cover-up? Indeed, the great irony is that 99.9% of the feedback we have received on our paper - including death threats - are people accusing us of dismissing the lab escape theory too quickly. Can you imagine if we had not mentioned - or considered - it all as suggested by some "coronavirus experts"?

This clearly appears to be a case of sour grapes based on half-truths and likely stimulated by your recent (great) article with quotes from us on the questions you raised with Dr. Zhengli. It's telling that the person who emailed you is anonymous. We have absolutely no problem with people knowing that our views on this issue have evolved as more data have appeared - and continues to evolve to this day, should more data become available. That's science. And it's the only way to do it well. Indeed, we have told this to many people: the way we set this up was a study of alternative hypotheses equally weighted priors, which we tested - our posterior clearly favors the hypothesis that this is a natural virus. As far as we can tell we are only 'guilty' of following the proper scientific method - but maybe we offended an ivory tower "coronavirus expert" in the process. It likely won't be the last time.

Best,

Eddie and Kristian

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 [REDACTED]
E [REDACTED]

On 28 Jul 2020, at 4:54 pm, Jeremy Farrar [REDACTED] wrote:

Thanks for forwarding this and the other emails.

I would like to get the sequence of events absolutely right from the start. Eddie the start goes back to the calls you and I had on the 8/9th January.

Can we get that sequence of events right and agreed before a substantive reply goes back to Jon?

Jeremy

On 28 Jul 2020, at 02:07, Kristian G. Andersen [REDACTED] wrote:

Dear Tony,

I am sorry to be contacting you, as I know you have critically important priorities, including developing a vaccine for COVID-19. **We just received the email below from Jon Cohen** (from Science) about our conversations back in February investigating the **origins of SARS-CoV-2**. As you know, we considered the theory that SARS-CoV-2 could have been a lab escape and therefore did what any good scientist should do - investigate likely hypotheses and let the data decide. As you know, the data strongly suggests that this is a natural virus and clearly this person gets a lot of things wrong about how this all played out.

We need to reply back to Jon, which would have to include confirming that this meeting did indeed take place with you and Jeremy present. Please let me know if you have any comments or concerns in this regard.

At the very end of this email, I have added a draft email that Eddie put together. I have a few clarifying points that I will add and then Eddie and I will reply back to Jon.

Again, sorry to take up your time - please let me know if you have any comments, questions, or concerns. **We are planning to email Jon tomorrow afternoon.**

Best,
Kristian

Kristian G. Andersen, PhD

Professor | Scripps Research
Director of Infectious Disease Genomics | Scripps Research Translational Institute
Vice President | Viral Hemorrhagic Fever Consortium
Principal Investigator | Center for Viral Systems Biology
Principal Investigator | West African Emerging Infectious Disease Research Center

The Scripps Research Institute

10550 North Torrey Pines Road, [REDACTED]
Department of Immunology and Microbial Science
La Jolla, CA 92037

p: [REDACTED]
t: [@K_G_Andersen](#)
e: [REDACTED]
w: www.andersen-lab.com

Assistant: [REDACTED]

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

From: **Jon Cohen** [REDACTED]

Date: Mon, Jul 27, 2020 at 3:02 PM

Subject: Re: The authors who wrote the paper saying that SARS-CoV-2 is not human engineered first tried convincing Anthony Fauci of the opposite.

To: Kristian G. Andersen [REDACTED], Edward Holmes [REDACTED]

Here's what one person who claims to have inside knowledge is saying behind your backs...

Jon

On Jul 25, 2020, at 7:22 AM, ofu8ledu8z <ofu8ledu8z@REDACTED> wrote:

[EXTERNAL EMAIL]

Hello Jon

Given your recent mentions of the origin of SARS-CoV-2 I thought you might be interested to hear the bizarre back-story of the paper "The proximal origin of SARS-CoV-2" (<https://www.nature.com/articles/s41591-020-0820-9>).

In summary, four of the authors managed to organize a conference call with Anthony Fauci and others, after quietly raising the alarm (or "spreading the rumor", as Jeremy Farrar apparently put it) that the virus **WAS** in fact human engineered. On the call were two world-class virologists who actually work on coronaviruses, who set them straight in great detail. That seemed to be the end of the affair.

But, incredibly, Andersen et al. turned around and submitted the Proximal paper to *Nature* with the exact opposite claim, i.e., that the virus was **NOT** human engineered. They used (without acknowledgment, of course) all the arguments provided by the coronavirologists on the initial call in which they had tried to raise the human-engineered alarm.

I don't think it would be too hard to verify all this, if you feel like digging a little. If you're wondering if this could all possibly be true: ask yourself how this group of authors, none of whom work on coronaviruses, could have such detailed arguments about why SARS-CoV-2 was not human-engineered. The answer is that they couldn't (and didn't) - they were schooled by the coronavirus experts on the call.

For the phone conference, Anthony Fauci called in Jeremy Farrar (Director of the Wellcome Trust). Farrar asked the coronavirus experts to join the call to listen to the claims. The call took place on a Saturday in early February (either the 1st or 8th, I'm not sure but I could probably find out). On the call making the claim were: Kristian G. Andersen, Andrew Rambaut, Edward C. Holmes, Robert F. Garry, but not Ian Lipkin.

The coronavirus experts listened for a while and both quickly concluded that the reasoning was completely flawed, that the non-coronavirus virologists had no idea what they were talking about, and that the human-engineered claim was totally wrong. One of the coronavirus experts was entertaining guests that day and told the people on the conference call that they wanted to give their opinion and then go back to the guests. So they told them it was nonsense, gave them a list of reasons why, and got off the call. The other coronavirus expert stayed on the call, gave a similar opinion and the morning afterwards sent a detailed list of the reasons why the claim was certainly wrong.

After the paper with the exact opposite claim was received at *Nature*, senior editor, Clare Thomas sent it out for review to some of the best people in the world... Not surprisingly, this happened to include a very close colleague of one of the experts who had been on the conference call. You can perhaps imagine the shock. Thomas was quickly apprised of the situation and *Nature* rejected the paper. It was then sent to *Nature Medicine*, where it was soon published.

One author on the paper was not on the conference call: Ian Lipkin. It's not clear how much of the back-story he is aware of. It might be worth giving him a call to ask, in case you feel like investigating. If his co-authors left him in the dark as to what actually happened and he's worried about the possible fallout he may want to help.

I apologize for mailing you without revealing my name (at least for now). I work in the field and have heard this story from two people who were on the initial call with Fauci. I'm not keen to be personally involved, but I find the situation so outrageous, hypocritical, and shameless that I also find I can't keep silent. It doesn't change anything with respect to knowledgeable thinking about the origin of the virus, of course, but it's a pretty ugly situation that I (obviously) think should be exposed.

----- EMAIL REPLY DRAFT -----

Hi Jon,

Here are the facts:

1. In early Feb we had spotted some features in the SARS-CoV-2 genome that at the time appeared unusual - particularly the furin cleavage site and the receptor binding domain.
2. At this stage we thought it was wise to ask for some other expert opinion on this, so a conference call was arranged. There were indeed some coronavirus experts on the call who we chose.
3. Clearly, some people on the call were very strongly of the opinion the possibility of a lab escape was ridiculous and listed reasons why it was unlikely (although there was also some initial confusion about whether we were referring to the crazy HIV origins theory that had just been touted - obviously we were not). Some of those comments we agreed with, others we didn't. There was a long email discussion about what the data said. A take-home message from the call was that we should go away and write something to clearly set-out the background science on the issue.
4. So, we eventually wrote up a paper. Critically, however, drafts of this paper were sent to all the people on the call, including those that have leaked out the information. I've attached here the draft of the document from Feb 7 that was circulated to everyone. As you can see, it is essentially the basis of the document and people on the call commented on it.

5. Very shortly after the call the pangolin data came out. This was critical. As I wrote in an email to everyone on the call on Feb 9th:

"Personally, with the pangolin virus possessing 6/6 key sites in the receptor binding domain, I am in favour of the natural evolution theory."

6. Hence, it is completely and utterly false to claim that we all thought it was a lab escape, we were corrected in our views by the coronavirus experts on the call, and then submitted a Nature paper without anyone else knowing about it. The truth is that we had a range of views among us, our paper included the pangolin data that was not available at the time of the call, and we circulated drafts of our document to everyone.

I also strongly reject the idea that we should not have raised nor discussed the possibility of lab escape: as scientists we have to present all the data and discuss it openly. That's all we did. To have not mentioned the possibility of lab escape would have been negligent. Is the person who emailed you seriously suggesting that we should have not discussed these issues? Wouldn't that be a cover-up? Indeed, the great irony is that 99.9% of the feedback I've had on the paper - including death threats - are people accusing me of dismissing the lab escape theory too quickly!! Can you imagine if we had not mentioned it all?

This is clearly just case of sour grapes based on some half-truths. It's telling that the person who emailed you is anonymous. I've absolutely no problem with people knowing that my views on this issue have evolved as more data have appeared. That's science. Indeed, I've told this to many people: the way see it is that we set-up an hypothesis and then tested it. As far I can tell we are only 'guilty' of following the proper scientific method.

Hope this helps.

Eddie

<Summary.Feb7.pdf>