Images found in the original version of the report:

Select Subcommittee on the Coronavirus Pandemic
Chairman Bard Wenstrup

The Proximal Origin of a Cover-Up:
Did the “Bethesda Boys” Downplay a Lab Leak:

Interim Majority Staff Report
July 11, 2023

by the technique described below. Page numbers are those in red at the bottom right of each page, add 2 for the PDF page.

The original version of the report was available at:

https://oversight.house.gov/wp-content/uploads/2023/07/2023.07.11-SSCP-Interim-Staff-Report-Re.-Proximal-Origin_FINAL.pdf

This file and the original report PDF is available via:

https://vitamindstopscovid.info/07-origins/

This document was prepared in Microsoft Word, saved as a PDF and then OCRed with PDF-XChange Editor Plus with the intention of making the text embodied in the images appear on the text layer of the final PDF. I have not checked the accuracy of this OCRing.

I have not read the report yet, nor the text in these images.

The question of the origins of SARS-CoV-2 is obviously of immense importance. It is equally important to investigate, understand and fully expose any effort, made by anyone, anywhere, to impede the full discovery and public disclosure of these origins.

Everyone knows that the Chinese government has covered up the origins of SARS-VoV-2.

Everyone should now know that multiple virologists and other academics and public health officials in the USA, most or all of whose work is paid for directly or indirectly by United States taxpayers, also went out of their way to obscure the origins of the virus, in 2020, since then and up to the present day with the recent Congressional hearings.

The progress made by this and related Congressional committees was made by Republican members and, as far as I know, was not helped at all and so was arguably impeded by its Democrat members. So these Democrats, and arguably the entire Democratic party, has been and is still actively covering up the origins of SARS-CoV-2.

All this is of the highest order importance, concerning justice, accountability and the prevention of further such pandemics – such as by banning gain of function research, since lab escapes, including by infecting lab workers, cannot be entirely prevented.

However, it is even more important to recognise that without proper vitamin D3 supplementation, such as 0.125 mg (5000 IU) a day for 70 kg 154 lb body weight without obesity, most people do not attain the 50 ng/mL 125 nmol/L circulating 25-hydroxyvitamin D their immune system needs to function properly.

Without proper supplementation, at rates 8 or more times higher than governments currently recommend, most people have only 1/10 to 1/2 of this, unless they have recently had a lot of UV-B skin exposure.

If everyone had at least 50 ng/mL circulating 25-hydroxyvitamin D (made in the liver from vitamin D3), there would have been no pandemic, since those infected, in general, would have had much milder symptoms than they did – with consequently far fewer viruses shed, which would reduce R0 to well below the 1.0 value which causes pandemic transmission. Nor would there be much influenza at any time of year. The incidence of sepsis, which kills about 11 million people a year would be vastly reduced. “5000 IU” a day sounds like a lot, but it is a gram every 22 years, and pharma-grade vitamin D3 costs about USD$2.50 a gram, ex-factory. All of humanity needs about a tonne a day. At current costs this would be about USD$1B a year.

Please read the research articles cited and discussed at:

https://vitamindstopscovid.info/00-evi/

and

https://brownstone.org/articles/vitamin-d-everything-you-need-to-know/

Robin Whittle

Independent researcher, Daylesford, Victoria, Australia

rw@firstpr.com.au

https://twitter.com/RobinWhittle3/

Regarding the images of text of emails or other messages which are actually contained in the PDF of the first version of the report, but which are cropped and so only part of them are visible, here are some articles which mention some of what can be seen by changing the cropping:

https://www.zerohedge.com/covid-19/not-some-fringe-theory-flip-flopping-virologist-thought-lab-leak-highly-likely-toeing

https://www.dailymail.co.uk/health/article-12289007/Scientist-denounced-Covid-lab-leak-theory-said-privately-highly-likely.html

Following a link in a Zerohedge article, I think the one above, I downloaded what I guess is the original version of the report, 35,782,714 bytes, from:

https://oversight.house.gov/wp-content/uploads/2023/07/2023.07.11-SSCP-Interim-Staff-Report-Re.-Proximal-Origin_FINAL.pdf

That file is no longer available. The Zerohedge article now points to this second 10,392,267 byte file:

https://oversight.house.gov/wp-content/uploads/2023/07/Final-Report-7.pdf

which appears much the same, but was made (open in PDF XChange Editor Plus and use File > Document Properties) with "Adobe Acrobat Pro (32-bit) 23.3.20215" rather than with "Acrobat PDFMaker 23 for Word" which was used for the original version.

I suspect that the second one was made by taking the page images of the first one - exactly what we see on the screen of a PDF reader - and creating a new PDF from that, with OCR to create the text layer, which is what you get when selecting text and copying it to the clipboard. The second report therefore has text layer representation of the emails or messages which are visible the image boxes, while the first report does not. (Use Beyond Compare to see the differences.)

I was not able to get the same results from the second version of the report as those described below, since the innards of this second PDF are structured entirely differently, and do not reflect what the Word PDF creation process generated, only what the results looked like.

Using Inkscape 1.2.2 on Windows 10 I imported the first report. This takes it 5 to perhaps 10 minutes to display all the pages. It may be necessary to scroll up and down to get the horizonal scroll bar to scale to the full width of all 55 pages side by side in the Inkscape work area.

I scrolled to the right to find the page labelled 13 at the bottom right, which is PDF page 15. Below the top para "The Select Committee . . ." is a frame with an image of part of an email, "From Mike Ferguson, Sent 2/9/2020 12:00:46 PM . . . "

It seems that this object, which is a group of other objects, contains a larger image than is visible at first, and which is cropped by the visible frame. Just clicking on this image selects the whole group. However, by holding down the Ctrl key and clicking in the image area, Inkscape selects the larger image, which is part of the group, so I saw a dotted line outline of the larger object I just selected. Then, I could drag the image by clicking in the visible image area, holding the left mouse/trackball button down, and moving the mouse/trackball around. I could drag the underlying image around and see different parts of it through the frame.

Better still, with this underlying image selected, I could use Ctrl C to copy the underlying image to the clipboard. Then I could create a new file in Inkscape and use Ctrl V to paste the image there and see the whole thing at once.

It was easier to make a new Word file and paste the images into that.

I went through the whole report, trying every frame. Some contained only am image exactly the same as what was visible. For all those with a larger image, I copied this to the clipboard and pasted it into this Word file. However, I later found it was best to copy the image into a new Inkscape document, export it to a very high resolution image PNG, edit that with Photoshop to be an 1800 pixel wide image, insert that into Word and then export to PDF with: File > Export > PDF and then: More Options (>Options > PDF Options > Optimize for image quality) and > Tools > Compress Pictures > High fidelity: preserve quality of the original picture.

Message

From: Jeremy Farrar [J.Farrar@wellcome.ac.uk]
Sent: 7/28/2020 12:36:51 AM
To: Edward Holmes [edward.holmes@sydney.edu.au]
CC: Kristian G. Andersen [andersen@scripps.edu]; Fauci, Anthony (NIH/NIAID) [E] [afauci@niaid.nih.gov]
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 <edward.holmes@sydney.edu.au>
Date: Tuesday, 28 July 2020 at 08:30
To: Jeremy Farrar <J.Farrar@wellcome.ac.uk>
Cc: "Kristian G. Andersen" <andersen@scripps.edu>, "Fauci, Anthony (NIH/NIAID) [E]" <afauci@niaid.nih.gov>
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.

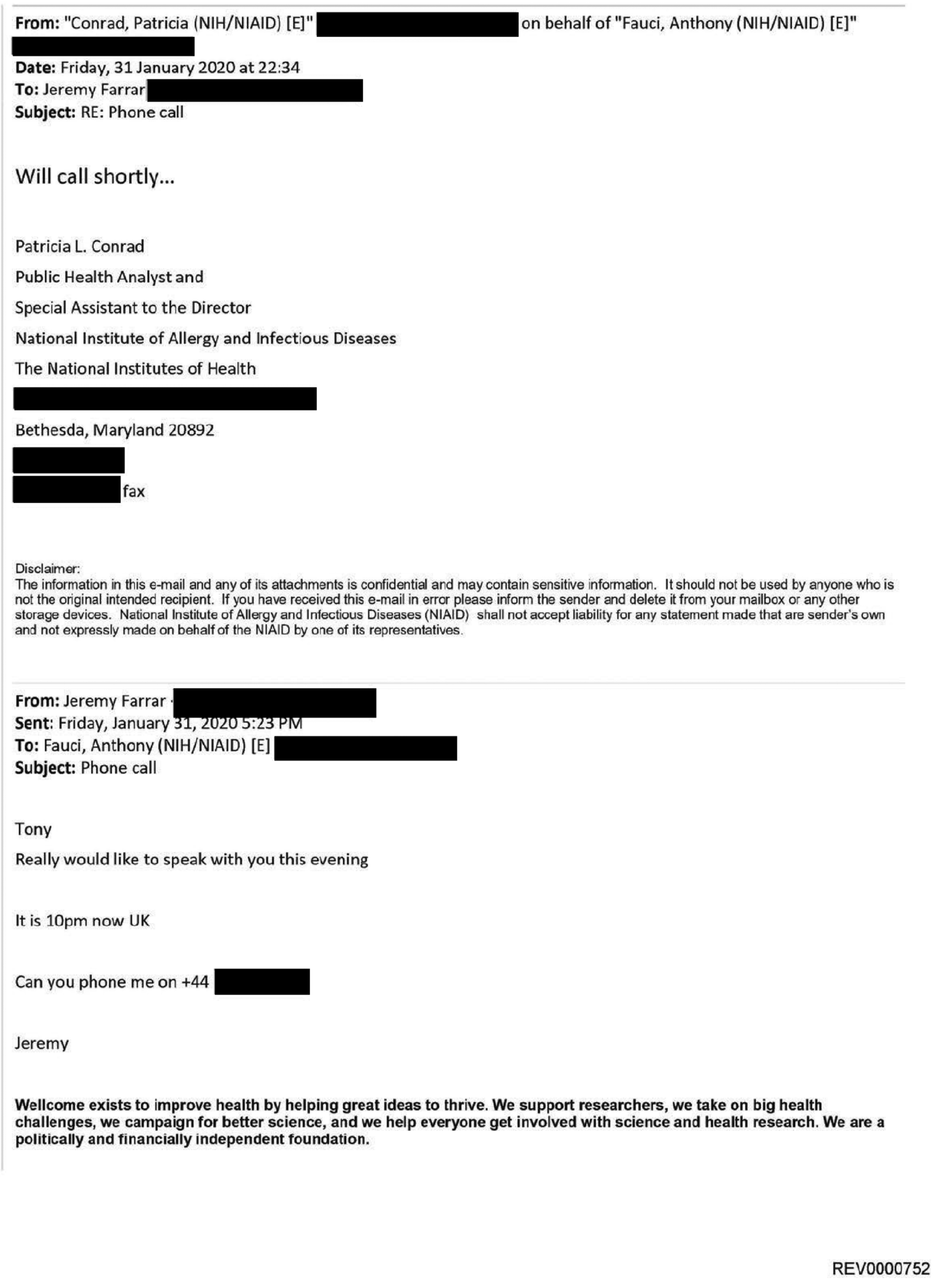
1. Jan 26. You call me (I was in Switzerland) to talk about some concerns coming out the US that the virus might be a lab escape. Patrick Vallance might have been on that call, I can't recall. You later forward me an email from Marc Lipsitch and others containing some comments from Richard Ebright. I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

Page 6:



From: "Conrad, Patricia (NIH/NIAID) [E]" [redacted] on behalf of "Fauci, Anthony (NIH/NIAID) [E]" [redacted]
Date: Friday, 31 January 2020 at 22:34
To: Jeremy Farrar [redacted]
Subject: RE: Phone call

Will call shortly...

Patricia L. Conrad
Public Health Analyst and
Special Assistant to the Director
National Institute of Allergy and Infectious Diseases
The National Institutes of Health
[redacted]
Bethesda, Maryland 20892
[redacted]
[redacted] fax

From: Jeremy Farrar [redacted]
Sent: Friday, January 31, 2020 5:23 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted]
Subject: Phone call

Tony

Really would like to speak with you this evening

It is 10pm now UK

Can you phone me on +44 [redacted]

Jeremy

Page 7 top and bottom frames show two parts of one image. The only parts not visible in the report are low-key disclaimers.

Message

From: Fauci, Anthony (NIH/NIAID) [E] [redacted]
Sent: 2/1/2020 10:43:31 AM
To: Kristian G. Andersen [redacted]
Subject: RE: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Thanks, Kristian. Talk soon on the call.

From: Kristian G. Andersen [redacted]
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted]
Cc: Jeremy Farrar [redacted]
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

On Fri, Jan 31, 2020 at 18:47 Fauci, Anthony (NIH/NIAID) [E] [redacted] wrote:

> Jeremy/Kristian:
>
> This just came out today. You may have seen it. If not, it is of interest to the current discussion.
>
> Best,
>
> Tony
>
> ---
>
> **From:** Folkers, Greg (NIH/NIAID) [E] [redacted]
> **Sent:** Friday, January 31, 2020 8:43 PM
> **Subject:** Science: Mining coronavirus genomes for clues to the outbreak's origins

Page 13:

Message

From: Mike Ferguson [redacted]
Sent: 2/9/2020 12:00:46 PM
To: Jeremy Farrar [redacted] Edward Holmes [redacted] kga1978[redacted];
Andrew Rambaut [redacted]; rfgarry([redacted]
CC: r.fouchier@ P.Vallance1[redacted] collinsf[redacted]; afauci([redacted]; Josie Golding
[redacted] m.koopmans[redacted]; christian.drosten([redacted]
Subject: Re: 2019 N-CoV
Attachments: Summary.Feb7_MF.pdf

Dear Jeremy et al

I have made some comments and suggestions on the pdf attached.

I am not an expert on protein O-glycosylation - however, Dr Tabak, who was on the call last weekend, is and if I were to consult anyone else on this it would be Henrik Clausen
https://icmm.ku.dk/english/research-groups/clausen-group/

However, from what I do know of general glycobiology, I am not sure one can conclude that an immune system would be required to select for O-glycosylation sites. Once an alpha-helix is disturbed by the introduction of a proline, adjacent Ser and Thr residues will be (over-)predicted to have O-glycosylation potential - hard to know the functional consequences/significance without knowing whether the potential O-sites are actually occupied.

Regards

Mike

From: Jeremy Farrar [redacted]
Sent: 08 February 2020 09:45
To: Edward Holmes [redacted]; kga1978[redacted] Andrew Rambaut
[redacted]; rfgarry[redacted] [redacted]
Cc: r.fouchier[redacted]; P.Vallance1([redacted]
[redacted]; collinsf[redacted] afauci[redacted]; Josie Golding
[redacted] m.koopmans@[redacted]
christian.drosten[redacted]; Mike Ferguson [redacted]
Subject: 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

Message

From: Clare Thomas [redacted]
Sent: 2/13/2020 2:34:29 AM
To: Kristian G. Andersen [redacted]
Subject: RE: Interest in commentary/hypothesis on SARS-CoV-2 origins?

Dear Kristian,
Yes please! It sounds possibly like a Perspective. I would love to take a look and consider whether it might be suitable for Nature.
All the best,
Clare

From: Kristian G. Andersen [redacted]
Sent: 12 February 2020 23:09
To: Clare Thomas
Subject: Interest in commentary/hypothesis on SARS-CoV-2 origins?

Dear Clare,

I can only imagine you must be crazy busy at the moment! I wanted to reach out to you to see if there would be interest in receiving a commentary/hypothesis piece on the evolutionary origins of SARS-CoV-2? There has been a lot of speculation, fear mongering, and conspiracies put forward in this space and we thought that bringing some clarity to this discussion might be of interest to Nature.

Prompted by Jeremy Farrah, Tony Fauci, and Francis Collins, Eddie Holmes, Andrew Rambaut, Bob Garry, Ian Lipkin, and myself have been working through much of the (primarily) genetic data to provide agnostic and scientifically informed hypotheses around the origins of the virus. We are not quite finished with the writeup and we still have some loose ends, but I wanted to reach out to you to see if this might potentially be of interest? We see this more as a commentary/hypothesis, as opposed to a more long-form Letter or Article.

Best,
Kristian

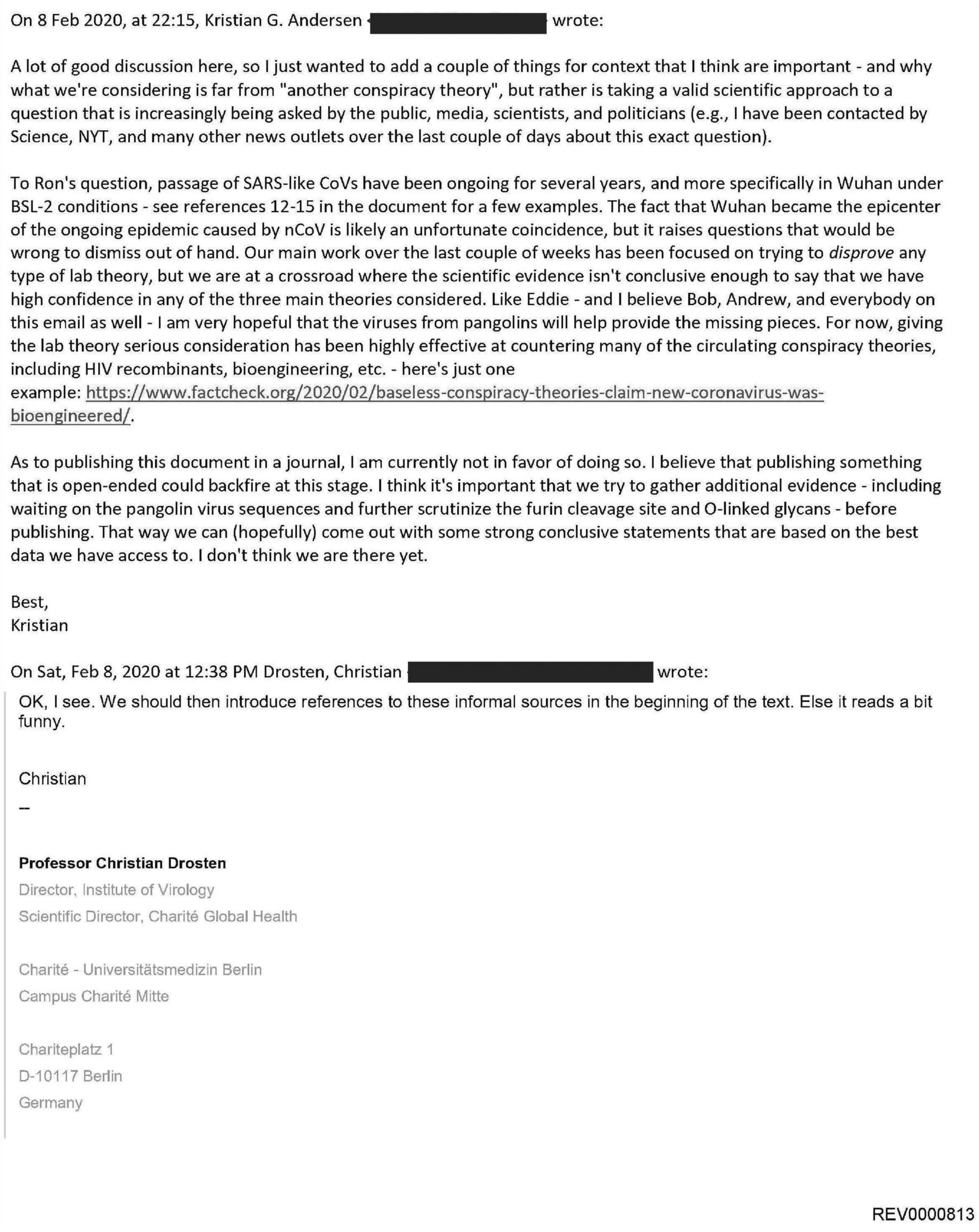
Kristian G. Andersen, PhD
Associate Professor, Scripps Research
Director of Infectious Disease Genomics, Scripps Research Translational Institute
Director, Center for Viral Systems Biology

The Scripps Research Institute
10550 North Torrey Pines Road, SGM-300A
Department of Immunology and Microbial Science
La Jolla, CA 92037

p: [redacted]
c:
t:
e:
w:

Assistant: [redacted]

Page 19 top frame:



On 8 Feb 2020, at 22:15, Kristian G. Andersen [redacted] wrote:

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/.

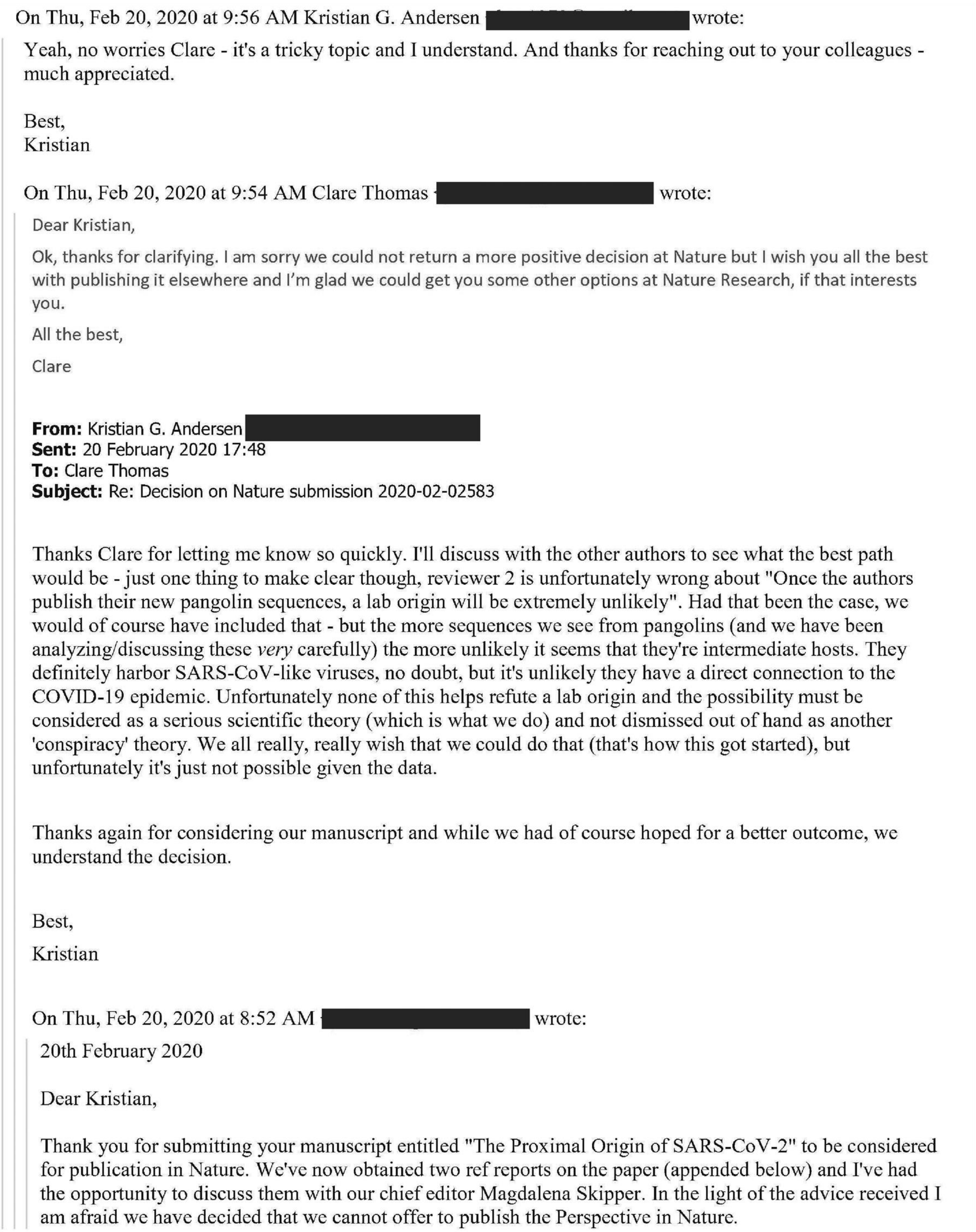
As to publishing this document in a journal, I am currently not in favor of doing so. I believe that publishing something that is open-ended could backfire at this stage. I think it's important that we try to gather additional evidence - including waiting on the pangolin virus sequences and further scrutinize 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
>
> Chariteplatz 1
> D-10117 Berlin
> Germany

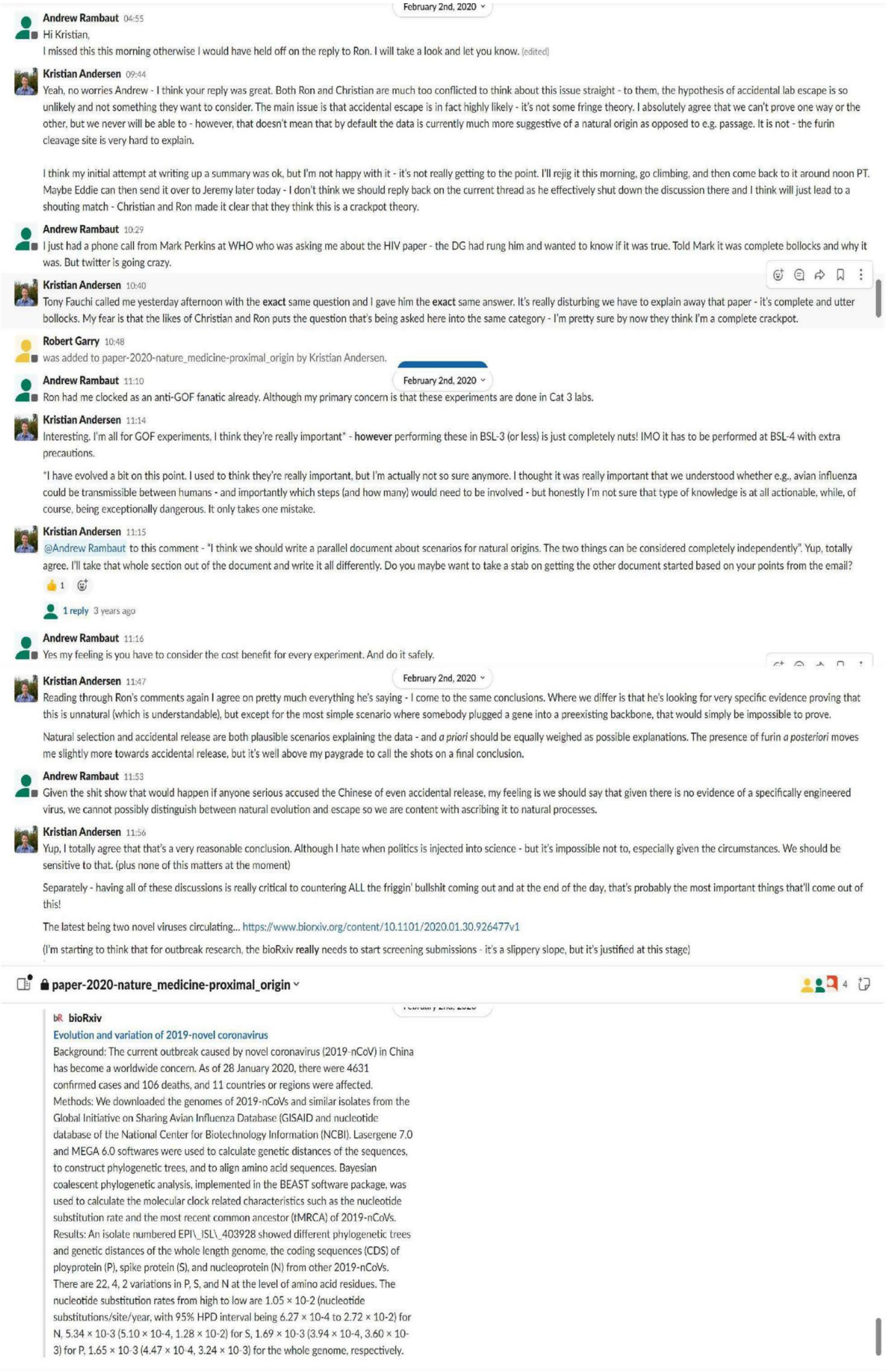
Page 19 bottom frame:



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.

Page 20, both frames contain the same image.



February 2nd, 2020

Andrew Rambaut 04:55
Hi Kristian,
I missed this this morning otherwise I would have held off on the reply to Ron. I will take a look and let you know. (edited)

Kristian Andersen 09:44
Yeah, no worries Andrew - I think your reply was great. Both Ron and Christian are much too conflicted to think about this issue straight - to them, the hypothesis of accidental lab escape is so unlikely and not something they want to consider. The main issue is that accidental escape is in fact highly likely - it's not some fringe theory. I absolutely agree that we can't prove one way or the other, but we never will be able to - however, that doesn't mean that by default the data is currently much more suggestive of a natural origin as opposed to e.g. passage. It is not - the furin cleavage site is very hard to explain.

I think my initial attempt at writing up a summary was ok, but I'm not happy with it - it's not really getting to the point. I'll rejig it this morning, go climbing, and then come back to it around noon PT. Maybe Eddie can then send it over to Jeremy later today - I don't think we should reply back on the current thread as he effectively shut down the discussion there and I think will just lead to a shouting match - Christian and Ron made it clear that they think this is a crackpot theory.

Andrew Rambaut 10:29
I just had a phone call from Mark Perkins at WHO who was asking me about the HIV paper - the DG had rung him and wanted to know if it was true. Told Mark it was complete bollocks and why it was. But twitter is going crazy.

Kristian Andersen 10:40
Tony Fauchi called me yesterday afternoon with the **exact** same question and I gave him the **exact** same answer. It's really disturbing we have to explain away that paper - it's complete and utter bollocks. My fear is that the likes of Christian and Ron puts the question that's being asked here into the same category - I'm pretty sure by now they think I'm a complete crackpot.

Robert Garry 10:48
was added to paper-2020-nature_medicine-proximal_origin by Kristian Andersen.

February 2nd, 2020

Andrew Rambaut 11:10
Ron had me clocked as an anti-GOF fanatic already. Although my primary concern is that these experiments are done in Cat 3 labs.

Kristian Andersen 11:14
Interesting. I'm all for GOF experiments, I think they're really important* - **however** performing these in BSL-3 (or less) is just completely nuts! IMO it has to be performed at BSL-4 with extra precautions.

*I have evolved a bit on this point. I used to think they're really important, but I'm actually not so sure anymore. I thought it was really important that we understood whether e.g., avian influenza could be transmissible between humans - and importantly which steps (and how many) would need to be involved - but honestly I'm not sure that type of knowledge is at all actionable, while, of course, being exceptionally dangerous. It only takes one mistake.

Kristian Andersen 11:15
@Andrew Rambaut to this comment - "I think we should write a parallel document about scenarios for natural origins. The two things can be considered completely independently". Yup, totally agree. I'll take that whole section out of the document and write it all differently. Do you maybe want to take a stab on getting the other document started based on your points from the email?
👍 1

1 reply 3 years ago

Andrew Rambaut 11:16
Yes my feeling is you have to consider the cost benefit for every experiment. And do it safely.

February 2nd, 2020

Kristian Andersen 11:47
Reading through Ron's comments again I agree on pretty much everything he's saying - I come to the same conclusions. Where we differ is that he's looking for very specific evidence proving that this is unnatural (which is understandable), but except for the most simple scenario where somebody plugged a gene into a preexisting backbone, that would simply be impossible to prove.

Natural selection and accidental release are both plausible scenarios explaining the data - and *a priori* should be equally weighed as possible explanations. The presence of furin *a posteriori* moves me slightly more towards accidental release, but it's well above my paygrade to call the shots on a final conclusion.

Andrew Rambaut 11:53
Given the shit show that would happen if anyone serious accused the Chinese of even accidental release, my feeling is we should say that given there is no evidence of a specifically engineered virus, we cannot possibly distinguish between natural evolution and escape so we are content with ascribing it to natural processes.

Kristian Andersen 11:56
Yup, I totally agree that that's a very reasonable conclusion. Although I hate when politics is injected into science - but it's impossible not to, especially given the circumstances. We should be sensitive to that. (plus none of this matters at the moment)

Separately - having all of these discussions is really critical to countering ALL the friggin' bullshit coming out and at the end of the day, that's probably the most important things that'll come out of this!

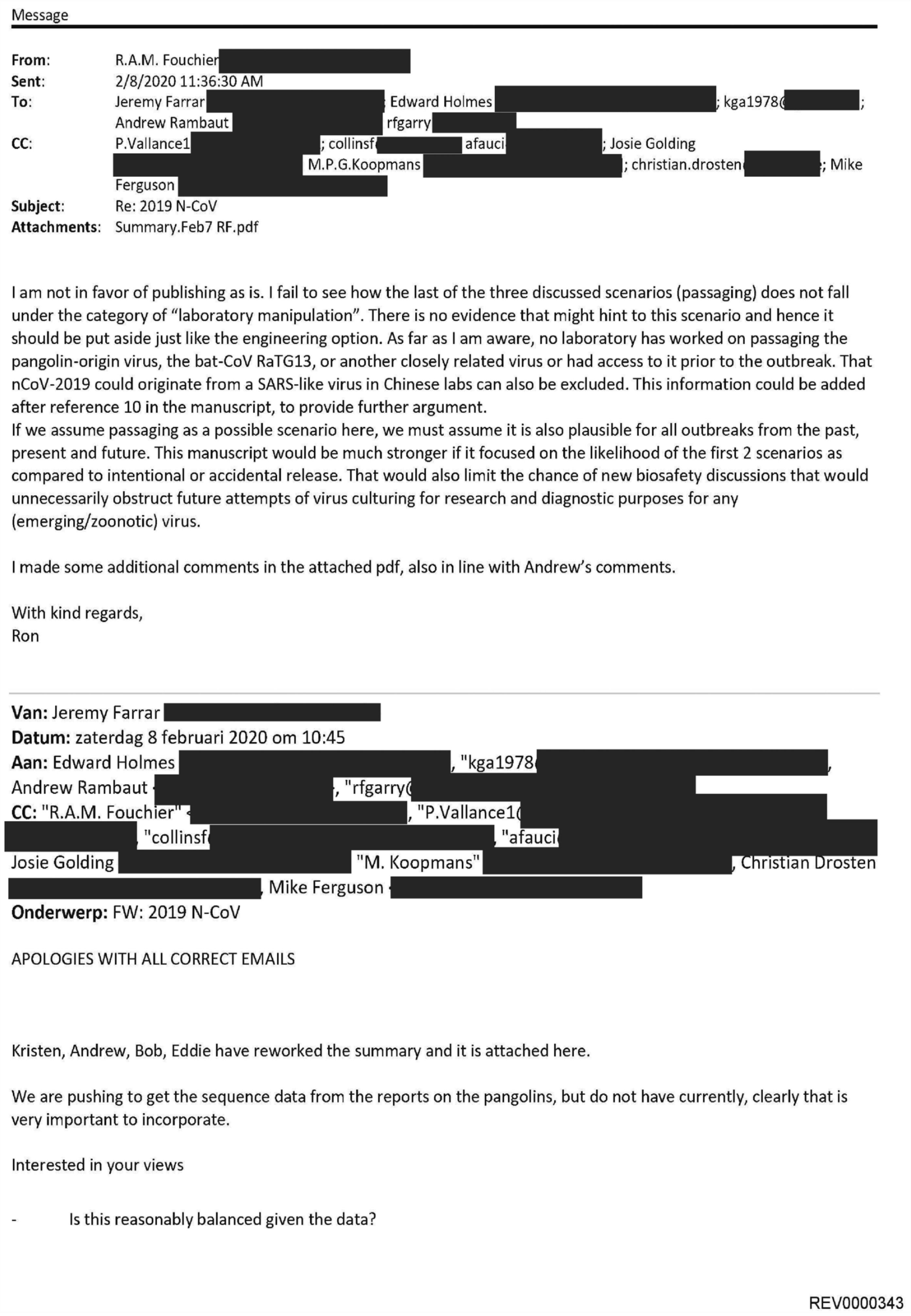
The latest being two novel viruses circulating... https://www.biorxiv.org/content/10.1101/2020.01.30.926477v1

(I'm starting to think that for outbreak research, the bioRxiv **really** needs to start screening submissions - it's a slippery slope, but it's justified at this stage)

paper-2020-nature_medicine-proximal_origin

bR **bioRxiv**
Evolution and variation of 2019-novel coronavirus
Background: The current outbreak caused by novel coronavirus (2019-nCoV) in China has become a worldwide concern. As of 28 January 2020, there were 4631 confirmed cases and 106 deaths, and 11 countries or regions were affected. Methods: We downloaded the genomes of 2019-nCoVs and similar isolates from the Global Initiative on Sharing Avian Influenza Database (GISAID and nucleotide database of the National Center for Biotechnology Information (NCBI). Lasergene 7.0 and MEGA 6.0 softwares were used to calculate genetic distances of the sequences, to construct phylogenetic trees, and to align amino acid sequences. Bayesian coalescent phylogenetic analysis, implemented in the BEAST software package, was used to calculate the molecular clock related characteristics such as the nucleotide substitution rate and the most recent common ancestor (tMRCA) of 2019-nCoVs. Results: An isolate numbered EPI_ISL_403928 showed different phylogenetic trees and genetic distances of the whole length genome, the coding sequences (CDS) of ployprotein (P), spike protein (S), and nucleoprotein (N) from other 2019-nCoVs. There are 22, 4, 2 variations in P, S, and N at the level of amino acid residues. The nucleotide substitution rates from high to low are 1.05 × 10-2 (nucleotide substitutions/site/year, with 95% HPD interval being 6.27 × 10-4 to 2.72 × 10-2) for N, 5.34 × 10-3 (5.10 × 10-4, 1.28 × 10-2) for S, 1.69 × 10-3 (3.94 × 10-4, 3.60 × 10-3) for P, 1.65 × 10-3 (4.47 × 10-4, 3.24 × 10-3) for the whole genome, respectively.

Page 23:



Message

From: R.A.M. Fouchier [redacted]
Sent: 2/8/2020 11:36:30 AM
To: Jeremy Farrar [redacted] Edward Holmes [redacted]; kga1978[redacted];
Andrew Rambaut [redacted] rfgarry[redacted]
CC: P.Vallance1[redacted]; collinsf[redacted] afauci[redacted]; Josie Golding
[redacted] M.P.G.Koopmans [redacted]; christian.drosten[redacted]; Mike
Ferguson [redacted]
Subject: Re: 2019 N-CoV
Attachments: Summary.Feb7 RF.pdf

I am not in favor of publishing as is. I fail to see how the last of the three discussed scenarios (passaging) does not fall under the category of "laboratory manipulation". There is no evidence that might hint to this scenario and hence it should be put aside just like the engineering option. As far as I am aware, no laboratory has worked on passaging the pangolin-origin virus, the bat-CoV RaTG13, or another closely related virus or had access to it prior to the outbreak. That nCoV-2019 could originate from a SARS-like virus in Chinese labs can also be excluded. This information could be added after reference 10 in the manuscript, to provide further argument.
If we assume passaging as a possible scenario here, we must assume it is also plausible for all outbreaks from the past, present and future. This manuscript would be much stronger if it focused on the likelihood of the first 2 scenarios as compared to intentional or accidental release. That would also limit the chance of new biosafety discussions that would unnecessarily obstruct future attempts of virus culturing for research and diagnostic purposes for any (emerging/zoonotic) virus.

I made some additional comments in the attached pdf, also in line with Andrew's comments.

With kind regards,
Ron

Van: Jeremy Farrar [redacted]
Datum: zaterdag 8 februari 2020 om 10:45
Aan: Edward Holmes [redacted], "kga1978[redacted],
Andrew Rambaut [redacted], "rfgarry[redacted]
CC: "R.A.M. Fouchier" [redacted], "P.Vallance1[redacted]
[redacted], "collinsf[redacted], "afauci[redacted]
Josie Golding [redacted] "M. Koopmans" [redacted], Christian Drosten
[redacted], Mike Ferguson [redacted]
Onderwerp: 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?

Page 24 top frame:

Jeremy is passing to Tony and Francis first.

Professor Edward C. Holmes FAA FRS
The University of Sydney

On 5 Feb 2020, at 8:12 am, Garry, Robert F [redacted] wrote:

On the broad topic of O-linked glycans on viruses from China I've attached a model of Alongshan virus, which I know Eddie has a particular interest.

It's instructive to see the mucin-like domains with a high concentration of serines, threonines and prolines.

This sequence in HKU1 CoV is also a mucin like domain:
481 fassckshkp psascpigtn yrscesttvl dhtdwcrcsc lpdpitaydp rscsqkkslv

Again several predicted O-linked glycans (also several at the furin site).

In the crystal structure 5i08 it is disordered because of the o-linked glycans..

From: Kristian Andersen [redacted]
Date: Tuesday, February 4, 2020 at 2:39 PM
To: Edward Holmes [redacted]
Cc: Robert Garry <[redacted], "rambaut@[redacted]
Subject: Re: Summary - Invitation to edit

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

Sounds good Eddie!

I was on a conference call hosted by the National Academy of Sciences yesterday and a statement about this not being "engineering" should be coming out from them - I believe Tony called that meeting. Let's see what comes out of that as well.

The idea of engineering and bioweapon is definitely not going away and I'm still getting pinged by journalists. I have noticed some of them starting to ask more broadly about "lab escape" and for now I have just ignored them - there might be a time where we need to tackle that more directly head on, but I'll let the likes of Jeremy and Tony figure out how to do that.

K

On Tue, Feb 4, 2020 at 12:36 PM Edward Holmes <[redacted]> wrote:

I've just passed to Jeremy.

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
E [redacted]

Outside my expertise, but I don't necessarily think that passage in animals would add the glycans. It's more that the glycans could suggest some sort of immune system as the glycans often work to 'shield' epitopes. So if the acquisition of glycans is adaptive, that would be suggestive of an immune system.

We didn't write this in the report, but the residues on which the glycans (S, T, and S) are all conserved in the bat virus - it's the addition of the P that makes it a specific glycan site though (not conserved in the bat, hence not predicted to be O-glycans). It's entirely possible that the 'P' works as a flexible residue for the furin cleavage site and by proxy creates the (predicted) O-linked glycans.

I'll let Bob weigh in as well - definitely not my area of expertise.

K

On Tue, Feb 4, 2020 at 2:59 PM Edward Holmes [redacted] wrote:

Agreed. Timing is perfect.

Bob - a question from Jeremy:

"Quick question though - why could passage in animals in lab work add the glycans?"

Any thoughts?

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

On 5 Feb 2020, at 9:53 am, Garry, Robert F [redacted] wrote:

Ironically the prevailing theory now in the underbelly if the internet is that the us or other enemy engineered this bio weapon and released it on China

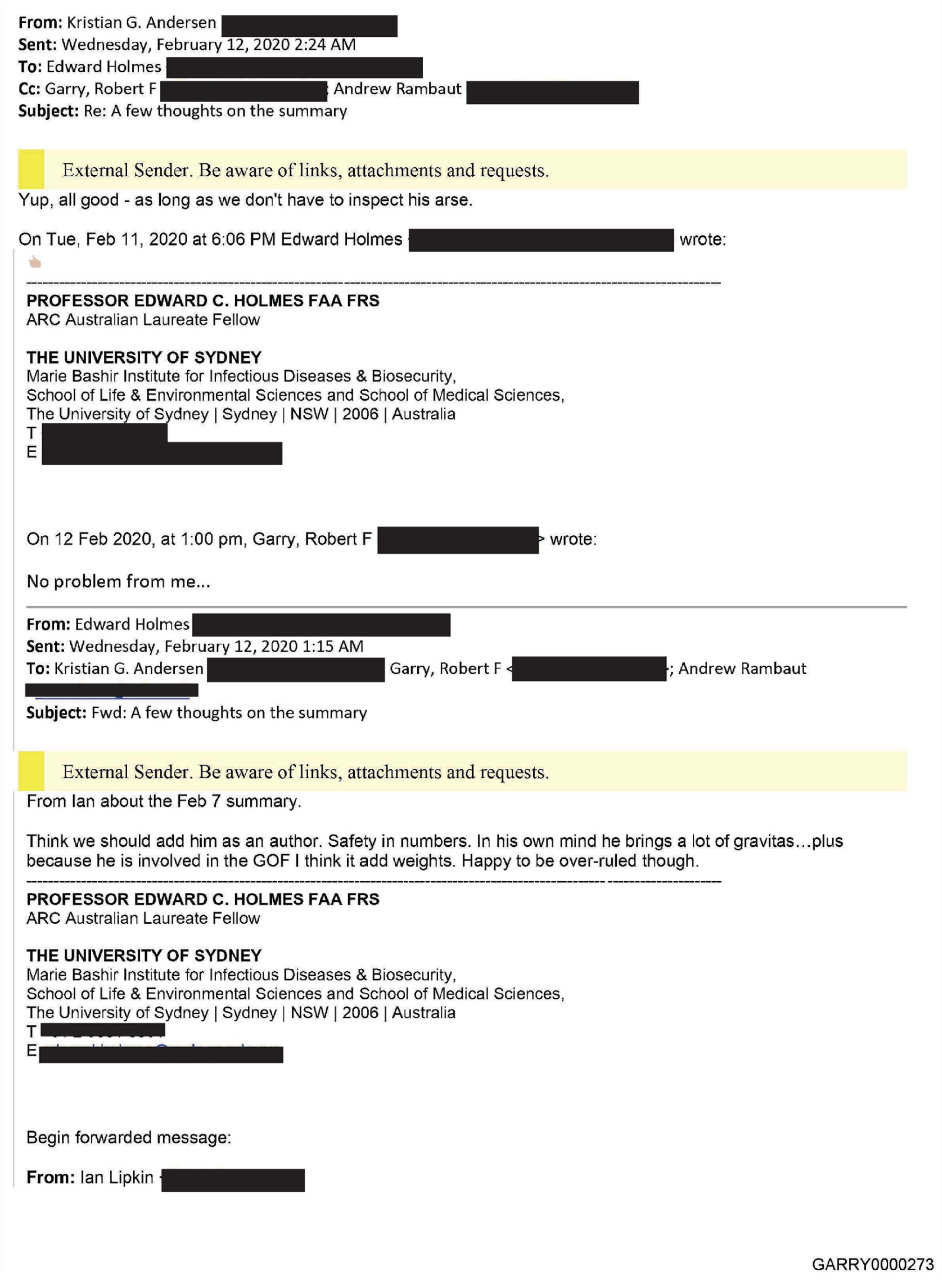
If the public health aspects of this were not bad enough the political fallout would be.

Good to have cogent science against the bio weapon scenario which is why I favor getting who involved in the "controversy"

Accidental release is a scenario many will not be comfortable with but it would be irresponsible to dismiss the possibility out of hand.

Sent from my iPhone

On Feb 4, 2020, at 3:28 PM, Edward Holmes [redacted] wrote:



From: Kristian G. Andersen [redacted]
Sent: Wednesday, February 12, 2020 2:24 AM
To: Edward Holmes [redacted]
Cc: Garry, Robert F [redacted]; Andrew Rambaut [redacted]
Subject: Re: A few thoughts on the summary

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

Yup, all good - as long as we don't have to inspect his arse.

On Tue, Feb 11, 2020 at 6:06 PM Edward Holmes [redacted] wrote:

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 12 Feb 2020, at 1:00 pm, Garry, Robert F [redacted]> wrote:

No problem from me...

From: Edward Holmes [redacted]
Sent: Wednesday, February 12, 2020 1:15 AM
To: Kristian G. Andersen [redacted] Garry, Robert F <[redacted]; Andrew Rambaut
[redacted]
Subject: Fwd: A few thoughts on the summary

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

From Ian about the Feb 7 summary.

Think we should add him as an author. Safety in numbers. In his own mind he brings a lot of gravitas…plus because he is involved in the GOF I think it add weights. Happy to be over-ruled though.

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: Ian Lipkin [redacted]

Page 32:

There are no framed images here. However, the main body of text of the document has three black boxes over some lines. With Inkscape I deleted these boxes so the original text was visible. The third redaction box had no text behind it.

The same pattern continued on pages 33, 34, 37 and 38. In all these cases, the obscured text is of the form: “CDR Jean-Paul Chretien.”, “CDR Chretien” and “Jean-Paul Chretien, Ph.D., M.D.”.

Anyone can do this by selecting the text in the original PDF, when viewing it in PDF-XChange Editor, or probably any other PDF reader.

Variation on the theme in HKU1, a virus that probably does have intense transmission infecting millions of people each year. Here the insert is three Serine residues, which pushes this site to a mucin-like patch (there are already a couple of prolines and the SSS is a turn as well)

Funny thing – not on the attachments, but those strains of MHV and HKU-1 that have o-linked glycans and the furin site ALSO have a larger patch - sometimes very large patch - of predicted o-linked glycans at the top of the prefusion form. When you see the pattern repeat itself in different viruses you start to believe it.

From: Robert Garry [redacted]
Date: Tuesday, February 4, 2020 at 5:56 PM
To: Kristian Andersen [redacted], Edward Holmes [redacted]
Cc: "rambaut[redacted]
Subject: Re: Summary - Invitation to edit

Kristian that's correct about everything he said for the P residue. It's what's shifted me to thinking that the insert of the furin site is the result of cell culture passage [or less likely intense transmission in a nonbat host]. Really need to see the data from Ron about generating the furim cleavage site on in vitro passage. Really!

CoV come with or without a furin site. CoV without a furin site are said to be non-cleaved and rely on endosomal proteases like cathepsin for entry. However if you infect a virus like SARS in culture in the presense of exogenous protease like trypsin its 100X more effective at entering because the spike gets cleaved and it can enter at the cell surface.

You have to infect flu viruses (the ones without the multibasic cleavage site) in the presence of trypsin, and include trypsin in the overlay if you want to get virus spread aka plaques.

This also contributes to the pathogenicity of - well - highly pathogenic flu virus – different tissues have different proteases and are able to "activate" flu to different extents - if the flu v has a furin cleavage site it has a lot more choices and canmore easil go systemic.

This is an excellent review on CoV fusion – deals with all the complexities:
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3397359/

Bottom line – I think that if you put selection pressure on a Cov without a furin cleavage site in cell culture you could well generate a furin cleavage site after a number of passages (but let's see the data Ron!). It will infect a lot better if it can effectively fuse at the cell surface and doesn't have to rely on endosomal cleavage and receptor mediated endocytosis..

From: Kristian Andersen [redacted]
Date: Tuesday, February 4, 2020 at 5:08 PM
To: Edward Holmes [redacted]
Cc: Robert Garry [redacted], "rambaut[redacted]
Subject: Re: Summary - Invitation to edit

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

Outside my expertise, but I don't necessarily think that passage in animals would add the glycans. It's more that the glycans could suggest some sort of immune system as the glycans often work to 'shield' epitopes. So if the acquisition of glycans is adaptive, that would be suggestive of an immune system.

Page 36 top frame:

Robert Garry 19:09
You can also synthesize bits of the genes de novo with perfect precision then add them back in without a trace.

And, excellent responses Andrew! You're doing much better than I would.

Andrew Rambaut 19:22
True (but you are still going to get the sequence from somewhere - unless it is very short).

Robert Garry 19:24
I'm thinking mostly about the PRRA to generate the furin site. Relatively easy to drop 12 bases in.

The proline is the hang-up - why add that? Makes me think the cell culture passage scenario is possible/probably assuming this has in fact been observed before by Farzan and Fouchier.

Andrew Rambaut 19:34
Yes. I am quite convinced it has been put there by evolution (whether natural selection or artificial).

I haven't got the paper yet. Killing me.

> **Kristian Andersen**
> Oh boy... what's the name??
>
> And for Don - I gotta say, he pretty much nailed it. Let's not tell him
>
> Posted in 🔒 paper-2020-nature_medicine-proximal_origin | Feb 6th, 2020

Apparently the manuscript is still being finalised. It will be preprinted and sent to the WHO at the same time.

> **Eddie Holmes**
> Can't believe that the ICTV did not preprint their paper.
>
> Posted in 🔒 paper-2020-nature_medicine-proximal_origin | Feb 6th, 2020

Robert Garry 19:44
I've known Don for 30 years. First time my work made the front page of NYTimes. I saw him at Trop Med meeting a few months ago. Very smart man - don't quite know wher he is going to go with this - curious as to the high in the USG is.

his source. It would be prudent to continue to pre-think responses.

I do like Wuhan snake flu virus for the name BTW.

Too bad they didn't test turtle codon usage.

Then it could be Wuhan Turtle Flu virus - WTFV

🤣 1

Eddie Holmes 19:49
Nailed it.

Andrew - thanks! Important typo.

Kristian Andersen 20:28
My drafted reply to Don. I'll chew on it a bit more, but lemme know if you have any suggestions.

```
Dear Don,

It's good to hear from you, and yes I of course remember our great conversations about Zika and Ebola. It's an interesting question you're asking, but I'm afraid I might not be the best person to answer, as we are mostly looking at what's going on during the epidemic (not before). Mostly, unless the virus was a really obvious recombinant virus, I'm not quite sure what a virus from culture vs an intermediate host would look like - I think they'd probably be indistinguishable.

A couple of things I can say based on the data so far though:

1. A lot of the conspiracy theories are talking about this being either a lab strain that had previously been produced (Nature Medicine paper) or some new recombinant. These rumours are demostratively false - we would have been able to easily pick that up if that were the case, however it is not.

2. The virus is highly related to bat SARS-like coronaviruses so we can with strong evidence say that the reservoir host is also a bat. Likely there was an amplifying host involved before the virus got into humans, but we don't yet know what it might be. I'm sure there's a lot of investigations going on addressing that exact question.

3. As you mention, we can clearly see from the sequence data produced so far that the introduction into the human population was a single event. This could either be from a single infected host to a single human, or a small cluster of hosts into a small cluster of people. The virus has then been spreading human to human ever since.

4. While the RaTG13 bat sequence is interesting, it still too divergent from nCoV to have anything to do with the current epidemic - the genetic distance is simply too great.

5. From a genomics perspective, the theories Richard Ebright lay out I expect would look the same - there would be no way to distingush between them.

I hope some of these answers were helpful.

Best,
Kristian
```

Robert Garry 20:31
PItch pergect responses.As I'm sure you'll know Ebright is the guy who thinks Yoshi and the of GOF researc should be locked up with the key thrown away. A little knowledge being the most danger ous thing. I suspect Ebright [i'm working with a bit of historical experience] is going to flat-out say this is for sure a lab escape - not unlike the underbelly article. Reporters aside I do not think any of this is going away.

Kristian Andersen 20:37
Agreed - this'll amplify over the next couple of weeks. I just wish there was a way to conclusively say one or the other, but without that intermediate host or very earlier cases, there's just no telling IMO. Which all means it's back to opinions - and honestly, for this type of question I don't think opinions are helpful - unless they have some damn strong science behind them.

Robert Garry 20:40
"So, he argued, it could have entered humans from the cave in Yunnan or another cave, or a wet market. Or, alternatively, it could have escaped into a human from the lab"

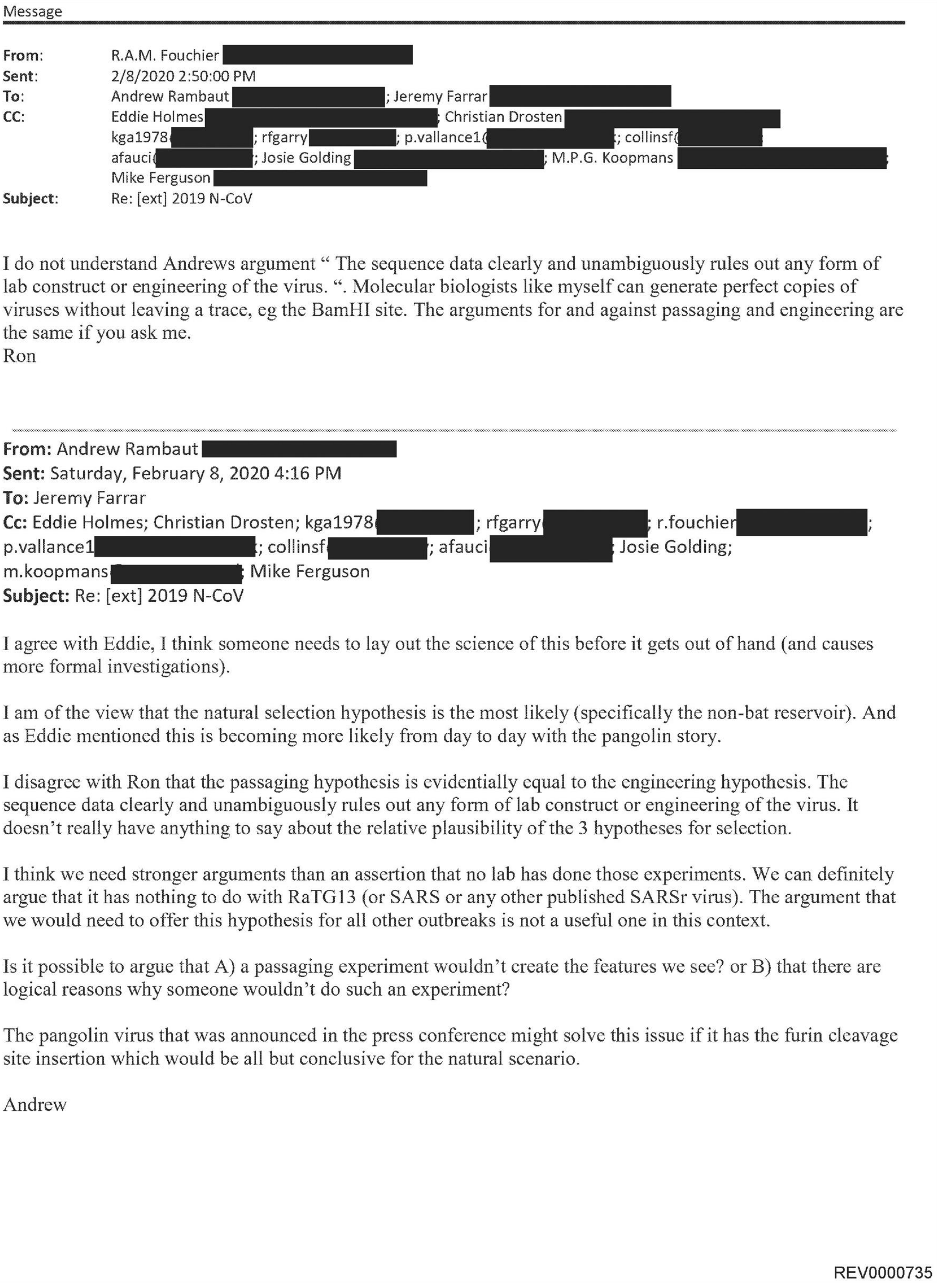
Three hypotheses here.

1. not likely a bat virus right into a human - could have happen long ago but not so likely.

2. Wet market -ok maybe an intermediate host. I think pangolin viruses sequences still too far afield but could be part of an animal circulation that generated the virus.

3. lab passage I'm open to and can't discount - that just because I don't know the data and few others do. Either furin sites have been generated or they haven't. If they have I'm suspicious of lab escape, but not conclusive evidence. If furin sites have not been generated on cell culture passive, then were looking at either a long circulation or a very intense circulation in either humans or animals.

Page 36 bottom frame:



Message

From: R.A.M. Fouchier [redacted]
Sent: 2/8/2020 2:50:00 PM
To: Andrew Rambaut [redacted]; Jeremy Farrar [redacted]
CC: Eddie Holmes [redacted]; Christian Drosten [redacted]
kga1978 [redacted]; rfgarry [redacted]; p.vallance1([redacted]; collinsf([redacted];
afauci([redacted]; Josie Golding [redacted]; M.P.G. Koopmans [redacted];
Mike Ferguson [redacted]
Subject: Re: [ext] 2019 N-CoV

I do not understand Andrews argument " The sequence data clearly and unambiguously rules out any form of lab construct or engineering of the virus. ". Molecular biologists like myself can generate perfect copies of viruses without leaving a trace, eg the BamHI site. The arguments for and against passaging and engineering are the same if you ask me.
Ron

From: Andrew Rambaut [redacted]
Sent: Saturday, February 8, 2020 4:16 PM
To: Jeremy Farrar
Cc: Eddie Holmes; Christian Drosten; kga1978 [redacted]; rfgarry [redacted]; r.fouchier [redacted];
p.vallance1 [redacted]; collinsf [redacted]; afauci [redacted]; Josie Golding;
m.koopmans [redacted]; Mike Ferguson
Subject: Re: [ext] 2019 N-CoV

I agree with Eddie, I think someone needs to lay out the science of this before it gets out of hand (and causes more formal investigations).

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.

I disagree with Ron that the passaging hypothesis is evidentially equal to the engineering hypothesis. The sequence data clearly and unambiguously rules out any form of lab construct or engineering of the virus. It doesn't really have anything to say about the relative plausibility of the 3 hypotheses for selection.

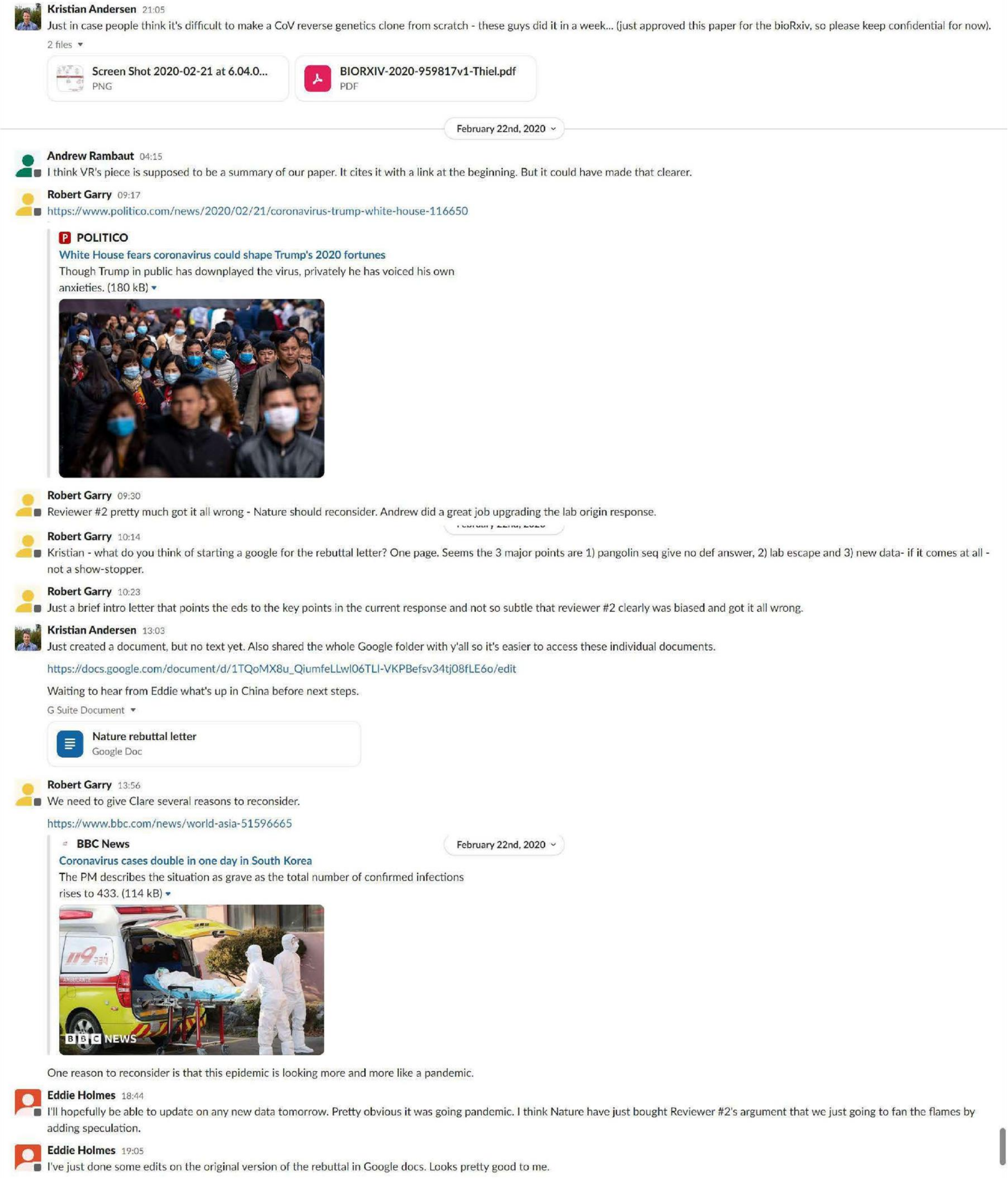
I think we need stronger arguments than an assertion that no lab has done those experiments. We can definitely argue that it has nothing to do with RaTG13 (or SARS or any other published SARSr virus). The argument that we would need to offer this hypothesis for all other outbreaks is not a useful one in this context.

Is it possible to argue that A) a passaging experiment wouldn't create the features we see? or B) that there are logical reasons why someone wouldn't do such an experiment?

The pangolin virus that was announced in the press conference might solve this issue if it has the furin cleavage site insertion which would be all but conclusive for the natural scenario.

Andrew

Page 38 top frame (REV0002958):



Kristian Andersen 21:05
Just in case people think it's difficult to make a CoV reverse genetics clone from scratch - these guys did it in a week... (just approved this paper for the bioRxiv, so please keep confidential for now).

2 files ▾

Screen Shot 2020-02-21 at 6.04.0...
PNG

BIORXIV-2020-959817v1-Thiel.pdf
PDF

February 22nd, 2020 ⌄

Andrew Rambaut 04:15
I think VR's piece is supposed to be a summary of our paper. It cites it with a link at the beginning. But it could have made that clearer.

Robert Garry 09:17
https://www.politico.com/news/2020/02/21/coronavirus-trump-white-house-116650

POLITICO
White House fears coronavirus could shape Trump's 2020 fortunes
Though Trump in public has downplayed the virus, privately he has voiced his own anxieties. (180 kB) ▾

Robert Garry 09:30
Reviewer #2 pretty much got it all wrong - Nature should reconsider. Andrew did a great job upgrading the lab origin response.

Robert Garry 10:14
Kristian - what do you think of starting a google for the rebuttal letter? One page. Seems the 3 major points are 1) pangolin seq give no def answer, 2) lab escape and 3) new data- if it comes at all - not a show-stopper.

Robert Garry 10:23
Just a brief intro letter that points the eds to the key points in the current response and not so subtle that reviewer #2 clearly was biased and got it all wrong.

Kristian Andersen 13:03
Just created a document, but no text yet. Also shared the whole Google folder with y'all so it's easier to access these individual documents.

https://docs.google.com/document/d/1TQoMX8u_QiumfeLLwl06TLI-VKPBefsv34tj08fLE6o/edit

Waiting to hear from Eddie what's up in China before next steps.

G Suite Document ▾

Nature rebuttal letter
Google Doc

Robert Garry 13:56
We need to give Clare several reasons to reconsider.

https://www.bbc.com/news/world-asia-51596665

February 22nd, 2020 ⌄

BBC News
Coronavirus cases double in one day in South Korea
The PM describes the situation as grave as the total number of confirmed infections rises to 433. (114 kB) ▾

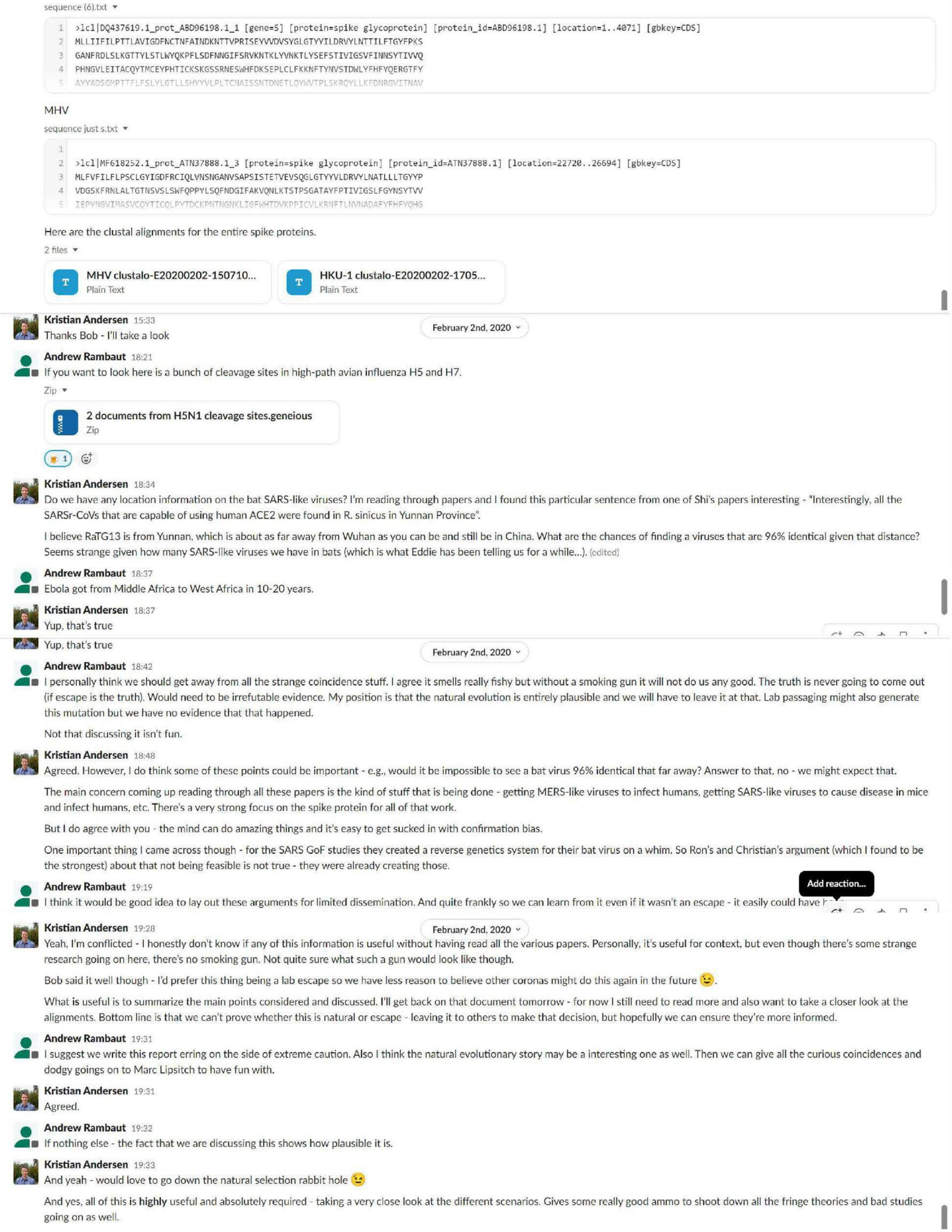
One reason to reconsider is that this epidemic is looking more and more like a pandemic.

Eddie Holmes 18:44
I'll hopefully be able to update on any new data tomorrow. Pretty obvious it was going pandemic. I think Nature have just bought Reviewer #2's argument that we just going to fan the flames by adding speculation.

Eddie Holmes 19:05
I've just done some edits on the original version of the rebuttal in Google docs. Looks pretty good to me.

I had to delete this before I could select:

Page 38 bottom frame (REV0002906):



sequence (6).txt

```
>lcl|DQ437619.1_prot_ABD96198.1_1 [gene=S] [protein=spike glycoprotein] [protein_id=ABD96198.1] [location=1..4071] [gbkey=CDS]
MLLIIFILPTTLAVIGDFNCTNFAINDKNTTVPRISEYVVDVSYGLGTYYILDRVYLNTTILFTGYFPKS
GANFRDLSLKGTTYLSTLWYQKPFLSDFNNGIFSRVKNTKLYVNKTLYSEFSTIVIGSVFINNSYTIVVQ
PHNGVLEITACQYTMCEYPHTICKSKGSSRNESWHFDKSEPLCLFKKNFTYNVSTDWLYFHFYQERGTFY
AYYADSGMPTTFLFSLYLGTLLSHYYVLPLTCNAISSNTDNETLQYWVTPLSKRQYLLKFDNRGVITNAV
```

MHV

sequence just s.txt

```

>lcl|MF618252.1_prot_ATN37888.1_3 [protein=spike glycoprotein] [protein_id=ATN37888.1] [location=22720..26694] [gbkey=CDS]
MLFVFILFLPSCLGYIGDFRCIQLVNSNGANVSAPSISTETVEVSQGLGTYYVLDRVYLNATLLLTGYYP
VDGSKFRNLALTGTNSVSLSWFQPPYLSQFNDGIFAKVQNLKTSTPSGATAYFPTIVIGSLFGYNSYTVV
IEPYNGVIMASVCQYTICQLPYTDCKPNTNGNKLIGFWHTDVKPPICVLKRNFTLNVNADAFYFHFYQHG
```

Here are the clustal alignments for the entire spike proteins.

2 files

Kristian Andersen 15:33

Thanks Bob - I'll take a look

Andrew Rambaut 18:21

If you want to look here is a bunch of cleavage sites in high-path avian influenza H5 and H7.

Zip

Kristian Andersen 18:34

Do we have any location information on the bat SARS-like viruses? I'm reading through papers and I found this particular sentence from one of Shi's papers interesting - "Interestingly, all the SARSr-CoVs that are capable of using human ACE2 were found in R. sinicus in Yunnan Province".

I believe RaTG13 is from Yunnan, which is about as far away from Wuhan as you can be and still be in China. What are the chances of finding a viruses that are 96% identical given that distance? Seems strange given how many SARS-like viruses we have in bats (which is what Eddie has been telling us for a while...). (edited)

Andrew Rambaut 18:37

Ebola got from Middle Africa to West Africa in 10-20 years.

Kristian Andersen 18:37

Yup, that's true

Yup, that's true

Andrew Rambaut 18:42

I personally think we should get away from all the strange coincidence stuff. I agree it smells really fishy but without a smoking gun it will not do us any good. The truth is never going to come out (if escape is the truth). Would need to be irrefutable evidence. My position is that the natural evolution is entirely plausible and we will have to leave it at that. Lab passaging might also generate this mutation but we have no evidence that that happened.

Not that discussing it isn't fun.

Kristian Andersen 18:48

Agreed. However, I do think some of these points could be important - e.g., would it be impossible to see a bat virus 96% identical that far away? Answer to that, no - we might expect that.

The main concern coming up reading through all these papers is the kind of stuff that is being done - getting MERS-like viruses to infect humans, getting SARS-like viruses to cause disease in mice and infect humans, etc. There's a very strong focus on the spike protein for all of that work.

But I do agree with you - the mind can do amazing things and it's easy to get sucked in with confirmation bias.

One important thing I came across though - for the SARS GoF studies they created a reverse genetics system for their bat virus on a whim. So Ron's and Christian's argument (which I found to be the strongest) about that not being feasible is not true - they were already creating those.

Andrew Rambaut 19:19

I think it would be good idea to lay out these arguments for limited dissemination. And quite frankly so we can learn from it even if it wasn't an escape - it easily could have

Kristian Andersen 19:28

Yeah, I'm conflicted - I honestly don't know if any of this information is useful without having read all the various papers. Personally, it's useful for context, but even though there's some strange research going on here, there's no smoking gun. Not quite sure what such a gun would look like though.

Bob said it well though - I'd prefer this thing being a lab escape so we have less reason to believe other coronas might do this again in the future 😉.

What is useful is to summarize the main points considered and discussed. I'll get back on that document tomorrow - for now I still need to read more and also want to take a closer look at the alignments. Bottom line is that we can't prove whether this is natural or escape - leaving it to others to make that decision, but hopefully we can ensure they're more informed.

Andrew Rambaut 19:31

I suggest we write this report erring on the side of extreme caution. Also I think the natural evolutionary story may be a interesting one as well. Then we can give all the curious coincidences and dodgy goings on to Marc Lipsitch to have fun with.

Kristian Andersen 19:31

Agreed.

Andrew Rambaut 19:32

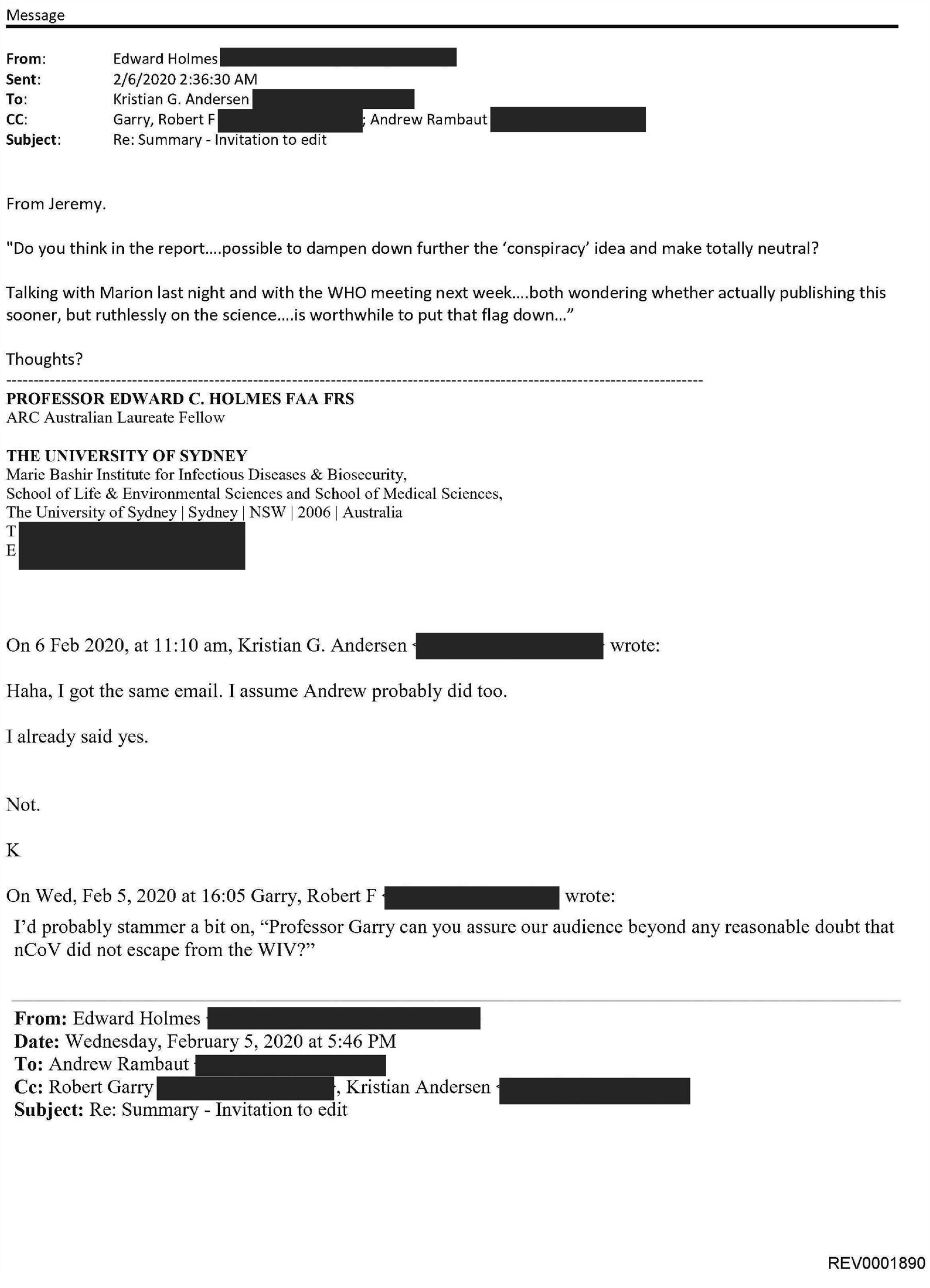
If nothing else - the fact that we are discussing this shows how plausible it is.

Kristian Andersen 19:33

And yeah - would love to go down the natural selection rabbit hole 😉

And yes, all of this is highly useful and absolutely required - taking a very close look at the different scenarios. Gives some really good ammo to shoot down all the fringe theories and bad studies going on as well.

Page 39 top frame:



Message

From: Edward Holmes [redacted]
Sent: 2/6/2020 2:36:30 AM
To: Kristian G. Andersen [redacted]
CC: Garry, Robert F [redacted]; Andrew Rambaut [redacted]
Subject: Re: Summary - Invitation to edit

From Jeremy.

"Do you think in the report....possible to dampen down further the 'conspiracy' idea and make totally neutral?

Talking with Marion last night and with the WHO meeting next week....both wondering whether actually publishing this sooner, but ruthlessly on the science....is worthwhile to put that flag down..."

Thoughts?

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

On 6 Feb 2020, at 11:10 am, Kristian G. Andersen [redacted] wrote:

Haha, I got the same email. I assume Andrew probably did too.

I already said yes.

Not.

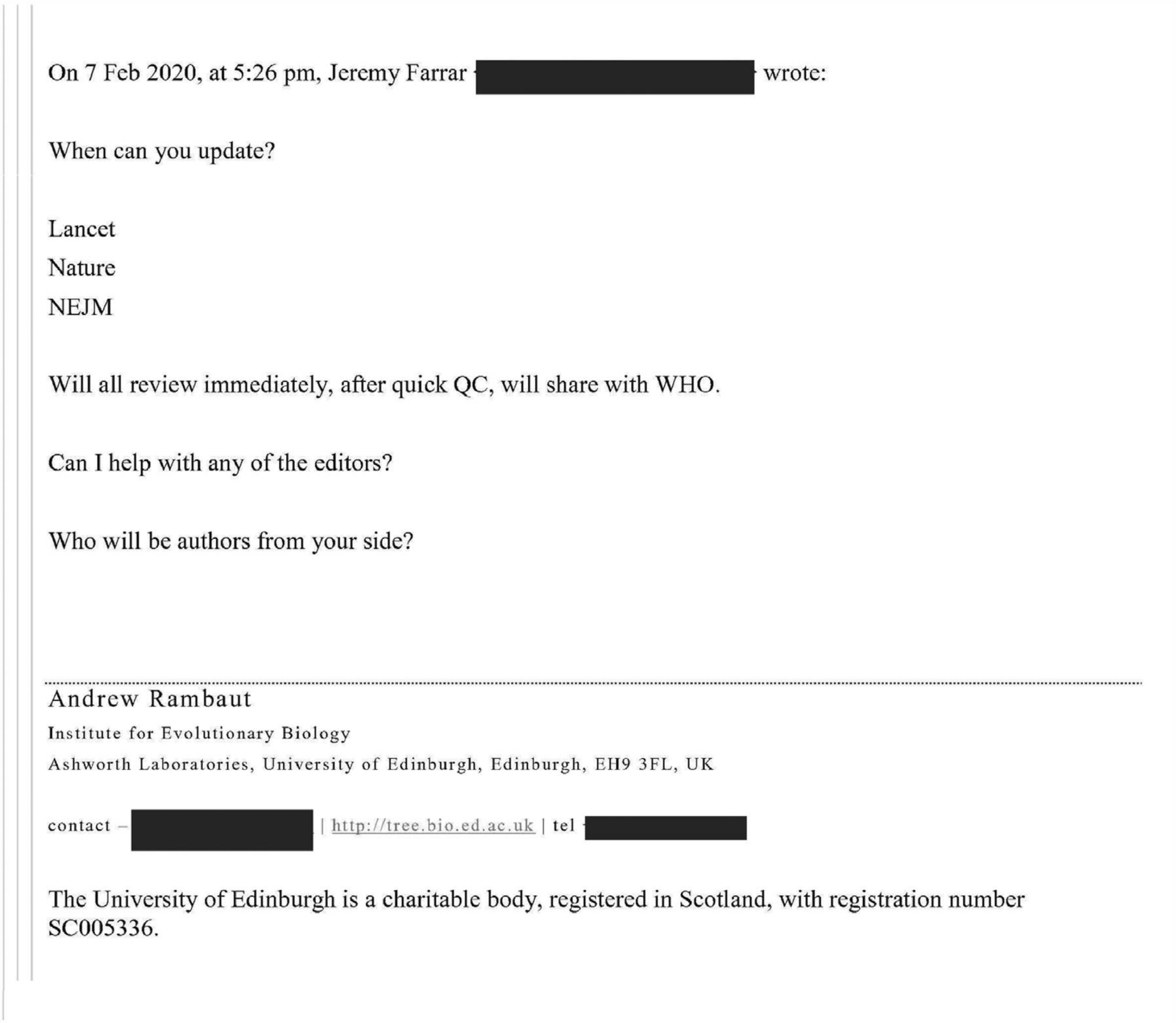
K

On Wed, Feb 5, 2020 at 16:05 Garry, Robert F [redacted] wrote:

> I'd probably stammer a bit on, "Professor Garry can you assure our audience beyond any reasonable doubt that nCoV did not escape from the WIV?"

From: Edward Holmes [redacted]
Date: Wednesday, February 5, 2020 at 5:46 PM
To: Andrew Rambaut [redacted]
Cc: Robert Garry [redacted], Kristian Andersen [redacted]
Subject: Re: Summary - Invitation to edit

Page 39 bottom frame:



On 7 Feb 2020, at 5:26 pm, Jeremy Farrar [redacted] wrote:

When can you update?

Lancet
Nature
NEJM

Will all review immediately, after quick QC, will share with WHO.

Can I help with any of the editors?

Who will be authors from your side?

Andrew Rambaut
Institute for Evolutionary Biology
Ashworth Laboratories, University of Edinburgh, Edinburgh, EH9 3FL, UK

contact – [redacted] | http://tree.bio.ed.ac.uk | tel [redacted]

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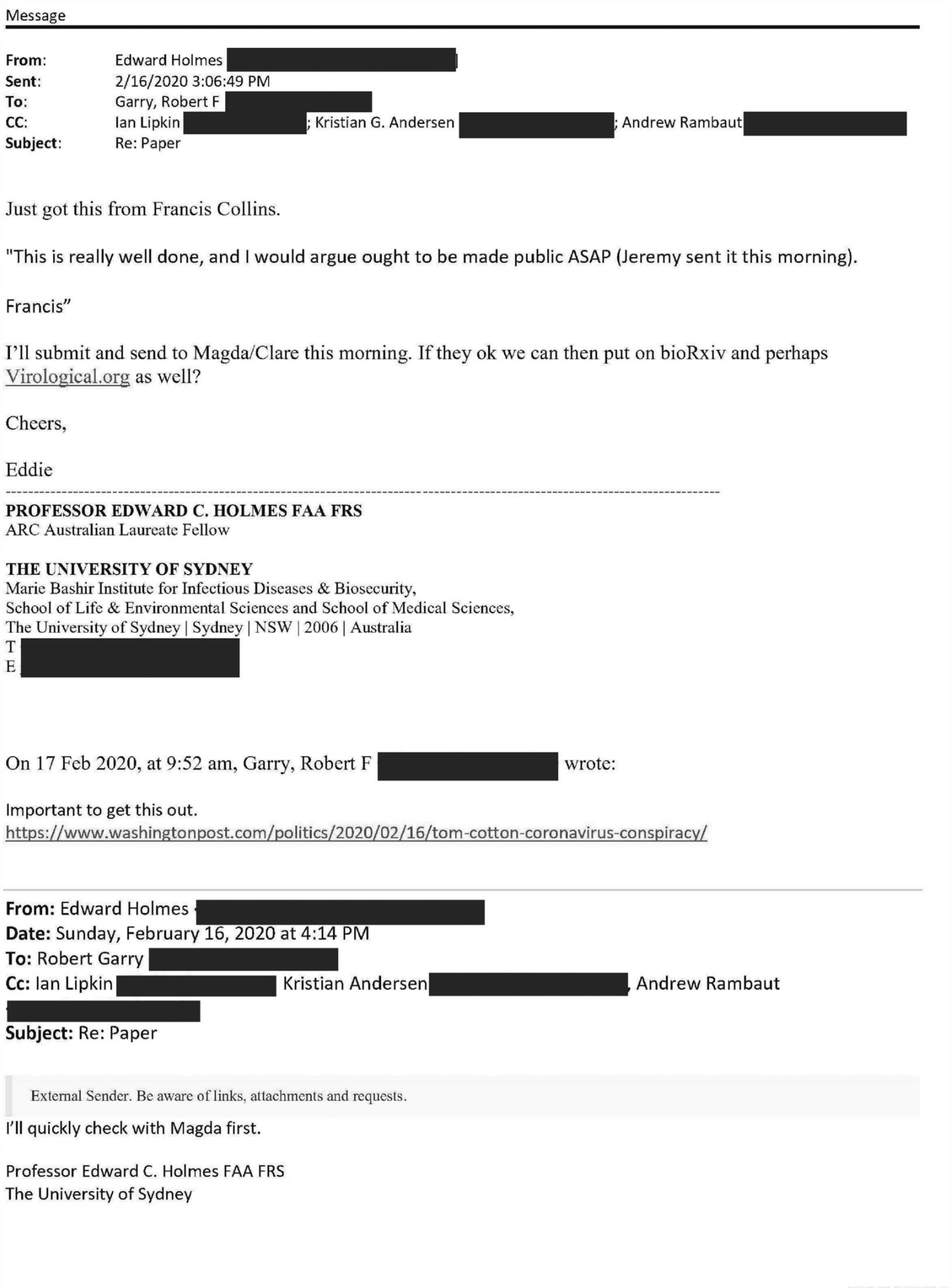

Message

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/

From: Edward Holmes [redacted]
Date: Sunday, February 16, 2020 at 4:14 PM
To: Robert Garry [redacted]
Cc: Ian Lipkin [redacted] Kristian Andersen [redacted], Andrew Rambaut
[redacted]
Subject: Re: Paper

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

I'll quickly check with Magda first.

Professor Edward C. Holmes FAA FRS
The University of Sydney

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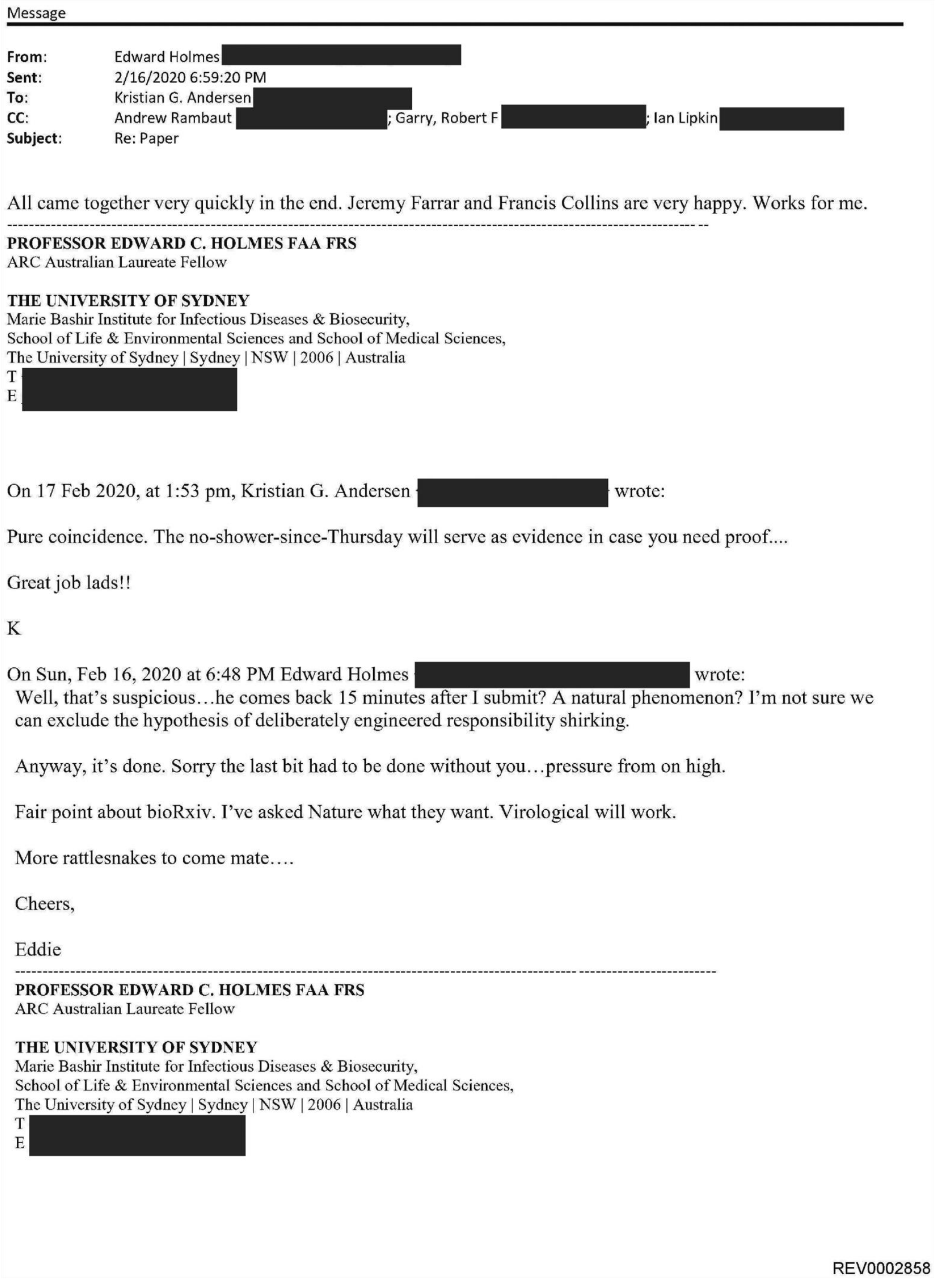

Message

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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THE UNIVERSITY OF SYDNEY
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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
>
> --
>
> **PROFESSOR EDWARD C. HOLMES FAA FRS**
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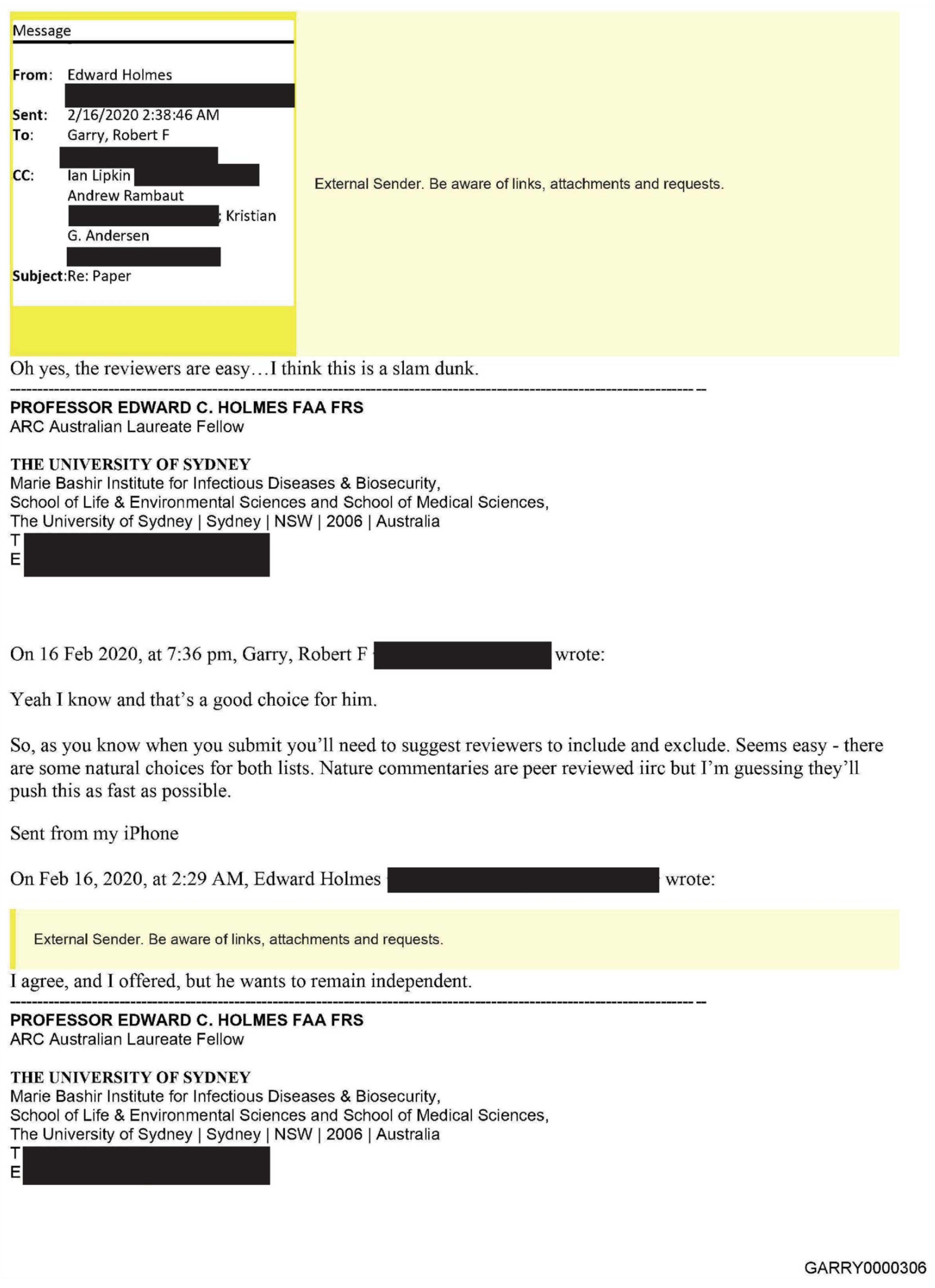
Page 42 and page 43:



Message

From: Edward Holmes [redacted]
Sent: 2/16/2020 2:38:46 AM
To: Garry, Robert F [redacted]
CC: Ian Lipkin [redacted] Andrew Rambaut [redacted]; Kristian G. Andersen [redacted]
Subject: Re: Paper

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

Oh yes, the reviewers are easy…I think this is a slam dunk.

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On 16 Feb 2020, at 7:36 pm, Garry, Robert F [redacted] wrote:

Yeah I know and that's a good choice for him.

So, as you know when you submit you'll need to suggest reviewers to include and exclude. Seems easy - there are some natural choices for both lists. Nature commentaries are peer reviewed iirc but I'm guessing they'll push this as fast as possible.

Sent from my iPhone

On Feb 16, 2020, at 2:29 AM, Edward Holmes [redacted] wrote:

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I agree, and I offered, but he wants to remain independent.

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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

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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.

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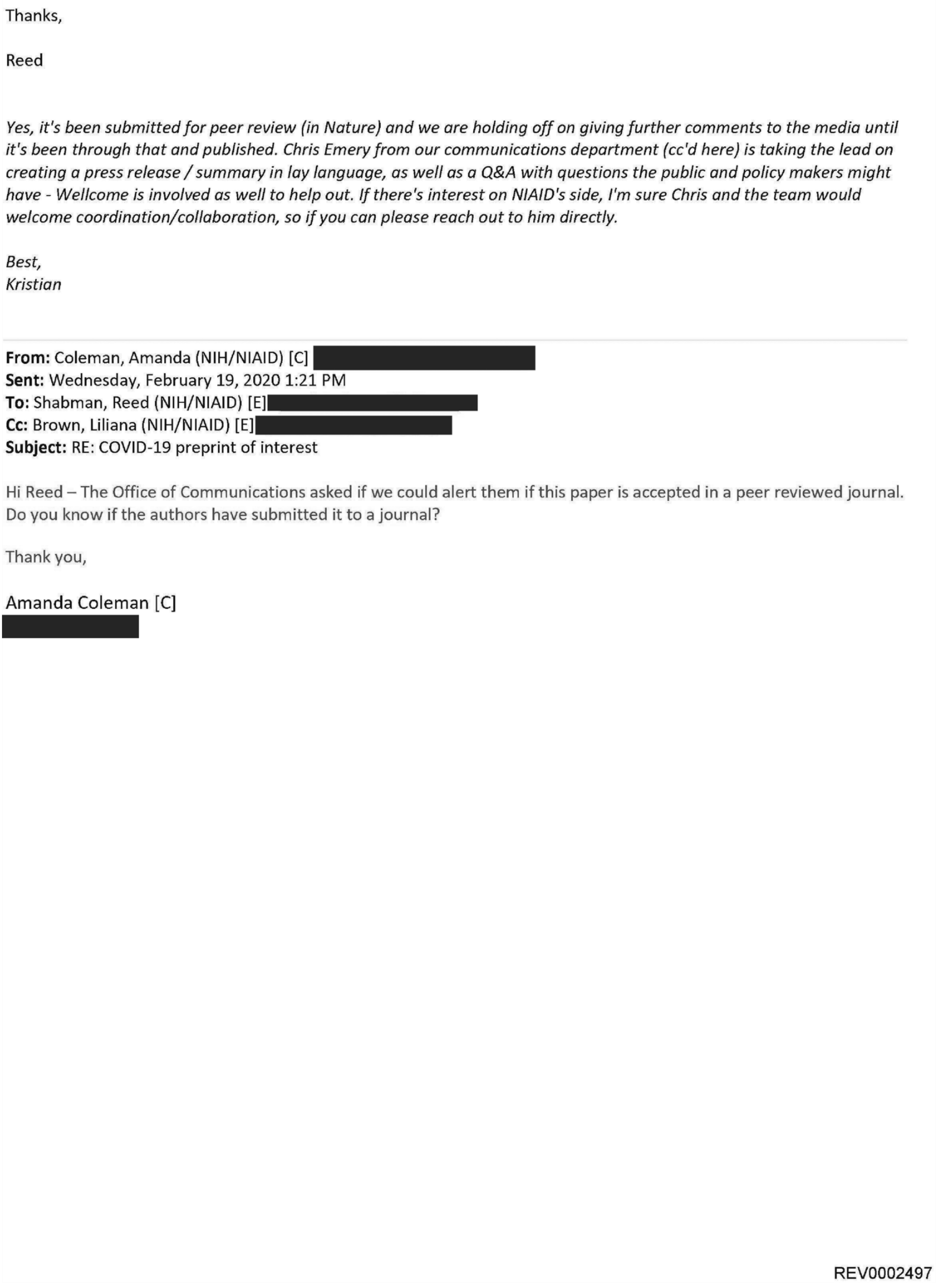

Thanks,

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]

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