The Orf Report

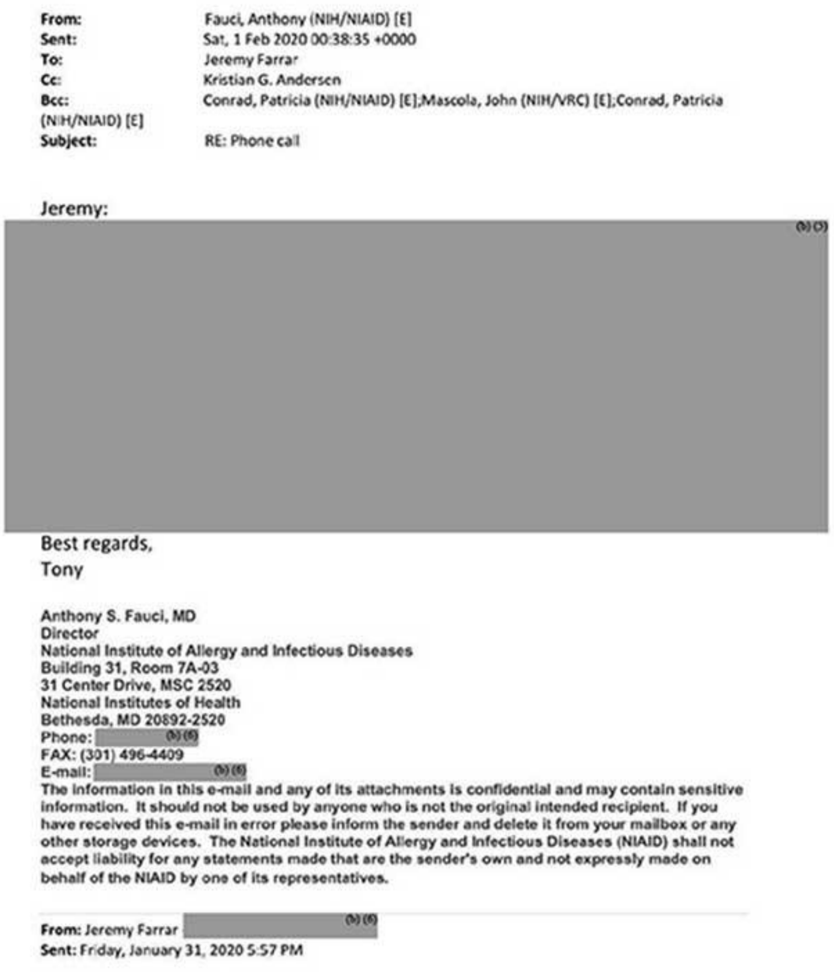
"COVID COVER UP"

Animation - Primary Sources

Matt Orfalea

Jul 24, 2023

Feb 1, 2020, email from Anthony Fauci to Jeremy Farrar. "I just got off the phone with Kristian Anderson and he related to me his concern about the Furine site mutation in the spike protein of the currently circulating 2019-nCoV..."



From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 00:38:35 +0000
To: Jeremy Farrar
Cc: Kristian G. Andersen
Bcc: Conrad, Patricia (NIH/NIAID) [E];Mascola, John (NIH/VRC) [E];Conrad, Patricia (NIH/NIAID) [E]
Subject: RE: Phone call

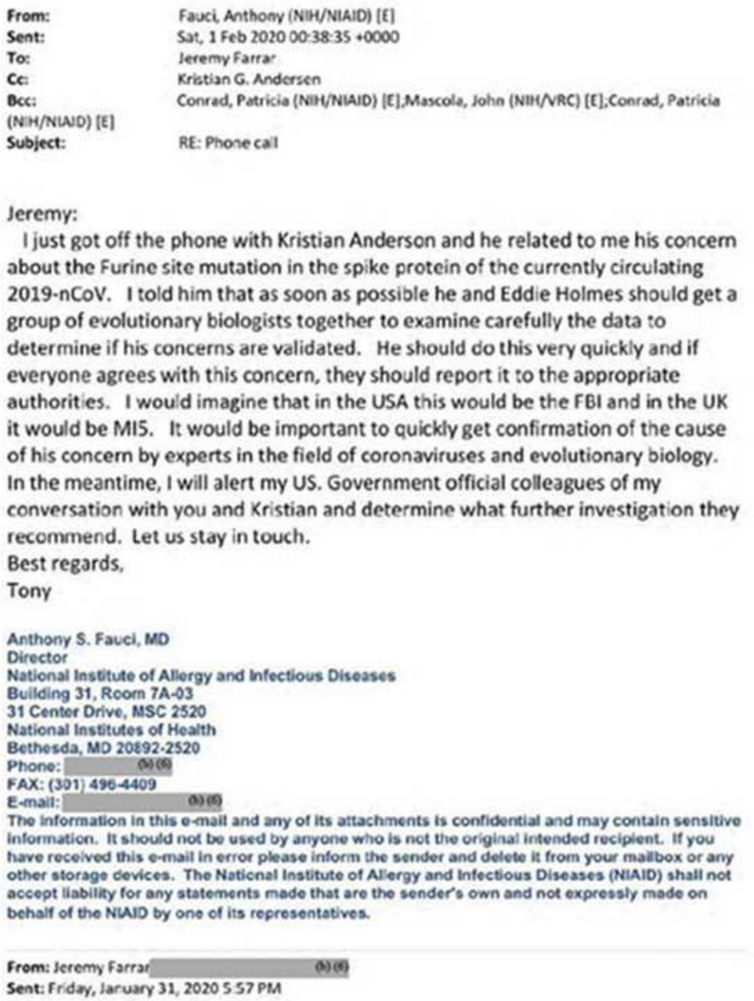
Jeremy:

(b)(5)

Best regards,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b)(6)
FAX: (301) 496-4409
E-mail: (b)(6)

From: Jeremy Farrar (b)(6)
Sent: Friday, January 31, 2020 5:57 PM



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Subject: RE: Phone call

Jeremy:

I just got off the phone with Kristian Anderson and he related to me his concern about the Furine site mutation in the spike protein of the currently circulating 2019-nCoV. I told him that as soon as possible he and Eddie Holmes should get a group of evolutionary biologists together to examine carefully the data to determine if his concerns are validated. He should do this very quickly and if everyone agrees with this concern, they should report it to the appropriate authorities. I would imagine that in the USA this would be the FBI and in the UK it would be MI5. It would be important to quickly get confirmation of the cause of his concern by experts in the field of coronaviruses and evolutionary biology. In the meantime, I will alert my US. Government official colleagues of my conversation with you and Kristian and determine what further investigation they recommend. Let us stay in touch.

Best regards,
Tony

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Director
National Institute of Allergy and Infectious Diseases
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31 Center Drive, MSC 2520
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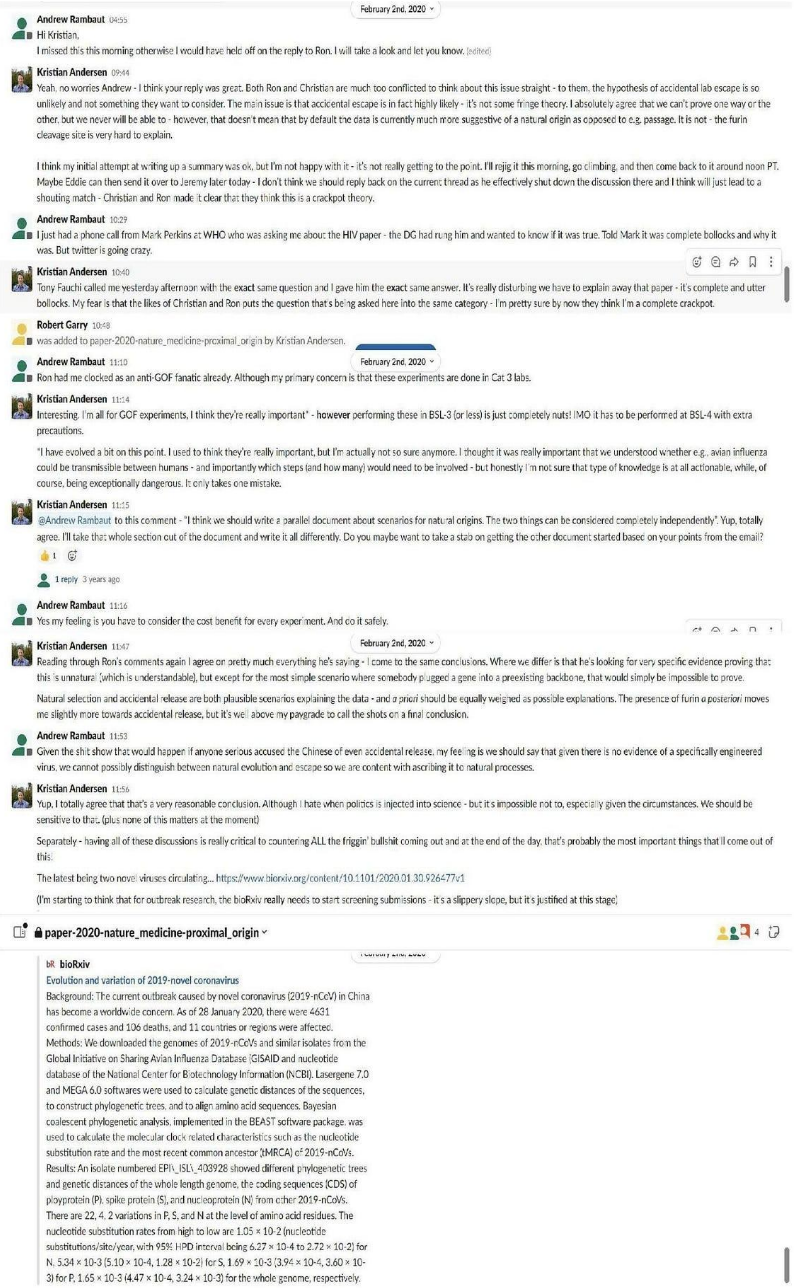
From: Jeremy Farrar (b)(6)
Sent: Friday, January 31, 2020 5:57 PM

Kristian Andersen on the laboratory-accident hypothesis for the origin of COVID-19, 02/02/2020 (i.e., *after* writing the first draft of "Proximal Origins"): "The main issue is that accidental escape is in fact highly likely–it's not some fringe theory."



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.

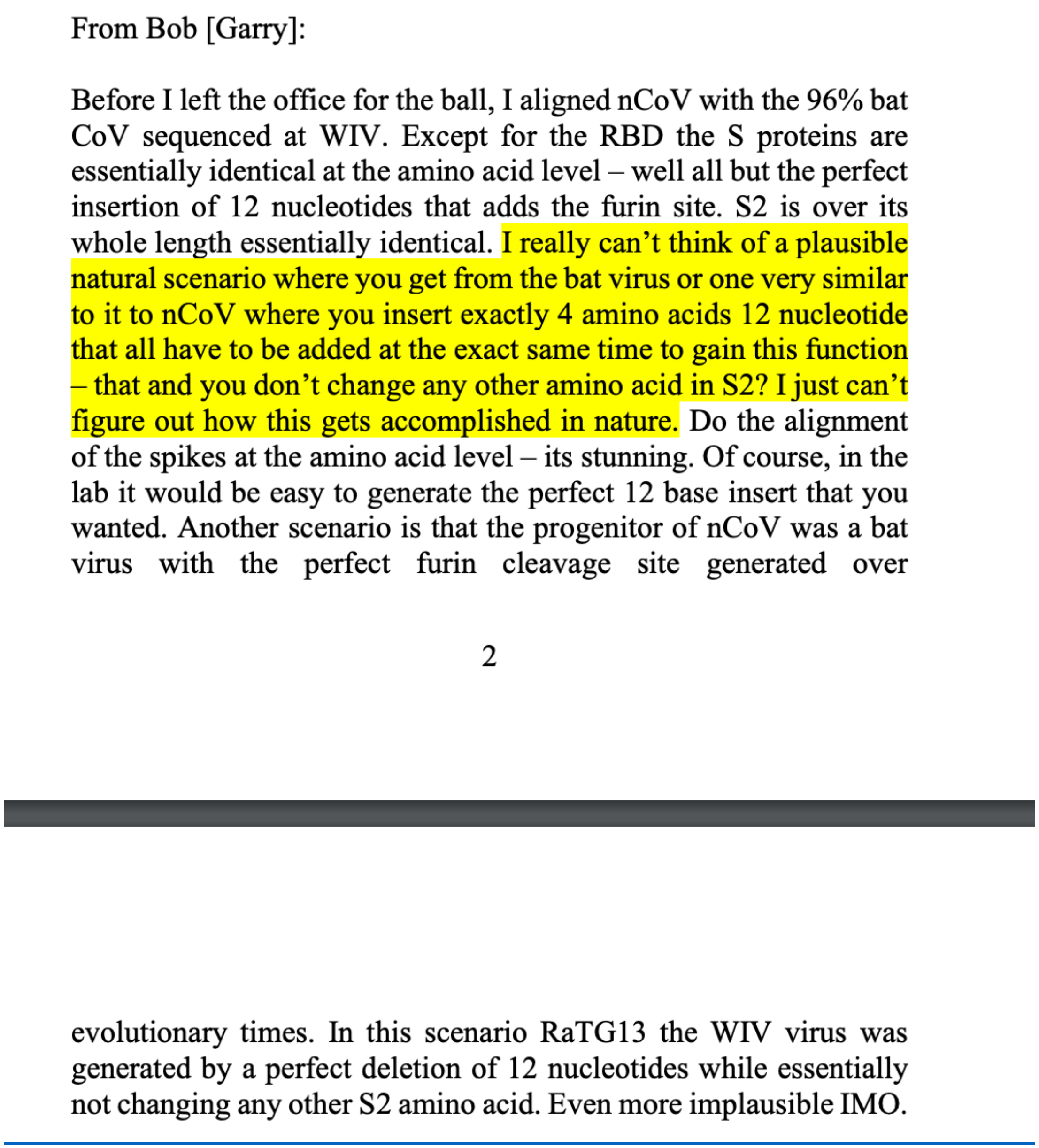
The latest being two novel viruses circulating... https://www.biorxiv.org/content/10.1101/2020.01.30.926477v1

(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.

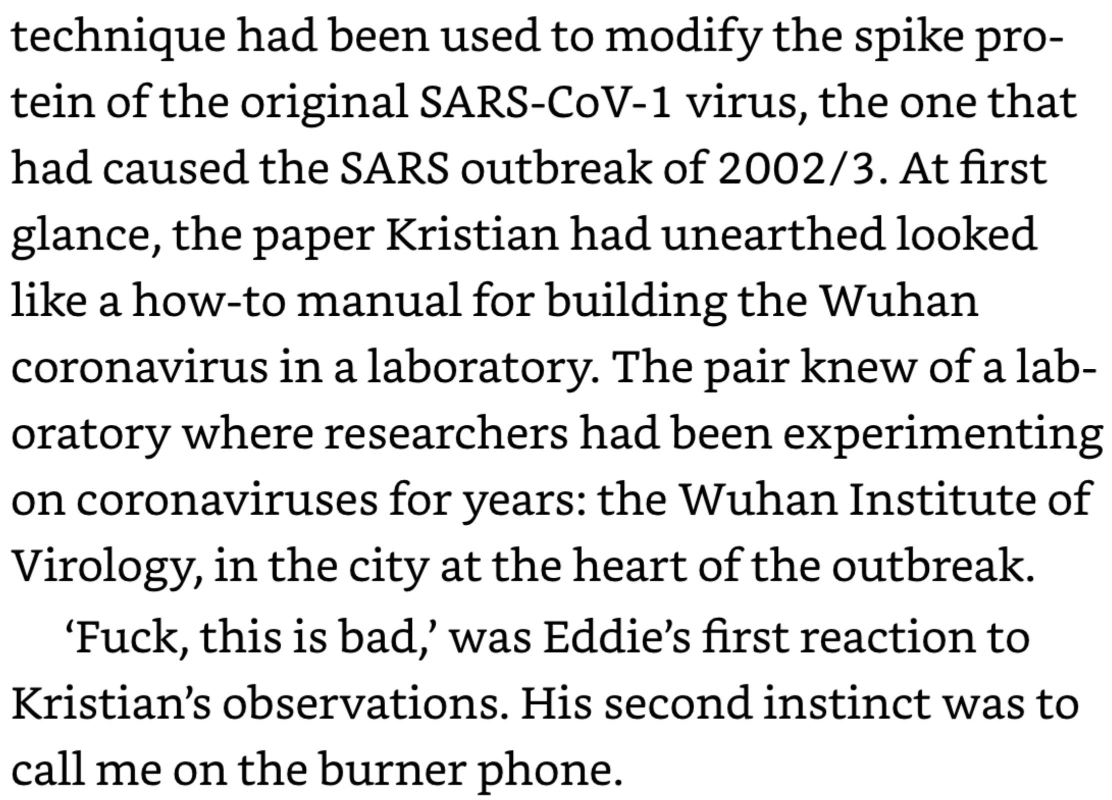
February 1, 2020, email transcribed and published by the House Oversight Committee:



From Bob [Garry]:

Before I left the office for the ball, I aligned nCoV with the 96% bat CoV sequenced at WIV. Except for the RBD the S proteins are essentially identical at the amino acid level – well all but the perfect insertion of 12 nucleotides that adds the furin site. S2 is over its whole length essentially identical. I really can't think of a plausible natural scenario where you get from the bat virus or one very similar to it to nCoV where you insert exactly 4 amino acids 12 nucleotide that all have to be added at the exact same time to gain this function – that and you don't change any other amino acid in S2? I just can't figure out how this gets accomplished in nature. Do the alignment of the spikes at the amino acid level – its stunning. Of course, in the lab it would be easy to generate the perfect 12 base insert that you wanted. Another scenario is that the progenitor of nCoV was a bat virus with the perfect furin cleavage site generated over evolutionary times. In this scenario RaTG13 the WIV virus was generated by a perfect deletion of 12 nucleotides while essentially not changing any other S2 amino acid. Even more implausible IMO.

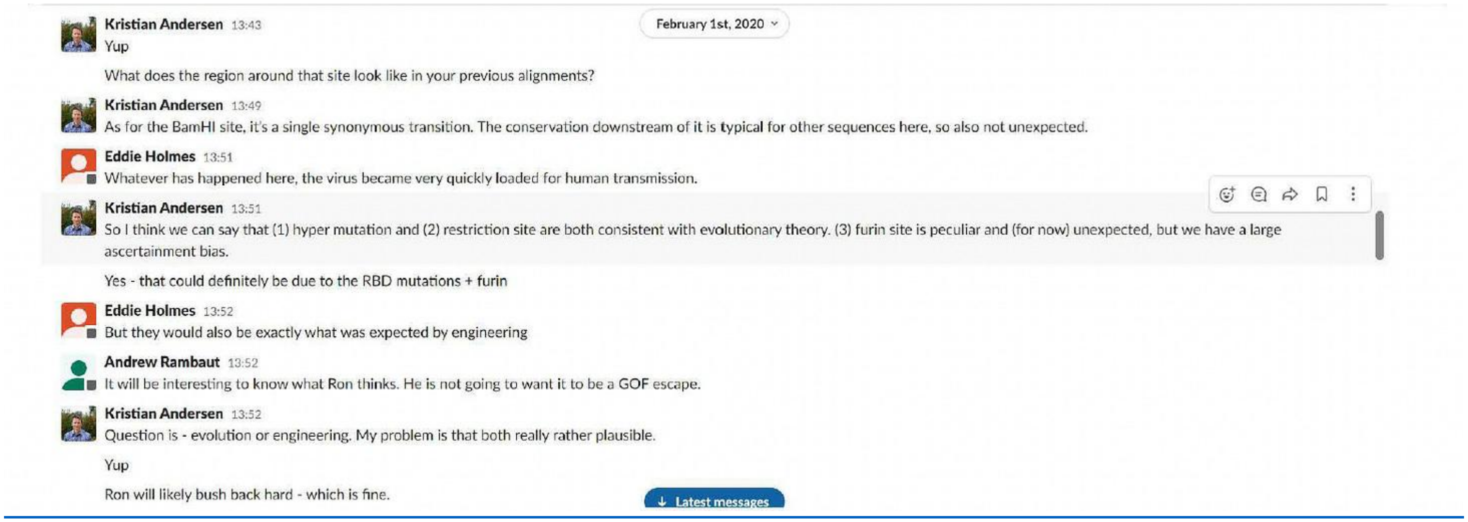
Jeremy Farrar, organizer and uncredited contributor to "Proximal Origin", wrote in his book that Andersen found a scientific paper that "looked like a how-to manual for building the Wuhan coronavirus in a laboratory…Fuck, this is bad,' was Eddie's first reaction to Kristian's observations. His second instinct was to call me on the burner phone."



technique had been used to modify the spike protein of the original SARS-CoV-1 virus, the one that had caused the SARS outbreak of 2002/3. At first glance, the paper Kristian had unearthed looked like a how-to manual for building the Wuhan coronavirus in a laboratory. The pair knew of a laboratory where researchers had been experimenting on coronaviruses for years: the Wuhan Institute of Virology, in the city at the heart of the outbreak.

'Fuck, this is bad,' was Eddie's first reaction to Kristian's observations. His second instinct was to call me on the burner phone.

February 1, 2020, Eddie Holmes and the rest discussed how elements of the virus look "exactly what was expected by engineering".



Kristian Andersen 13:43
Yup

What does the region around that site look like in your previous alignments?

Kristian Andersen 13:49
As for the BamHI site, it's a single synonymous transition. The conservation downstream of it is typical for other sequences here, so also not unexpected.

Eddie Holmes 13:51
Whatever has happened here, the virus became very quickly loaded for human transmission.

Kristian Andersen 13:51
So I think we can say that (1) hyper mutation and (2) restriction site are both consistent with evolutionary theory. (3) furin site is peculiar and (for now) unexpected, but we have a large ascertainment bias.

Yes - that could definitely be due to the RBD mutations + furin

Eddie Holmes 13:52
But they would also be exactly what was expected by engineering

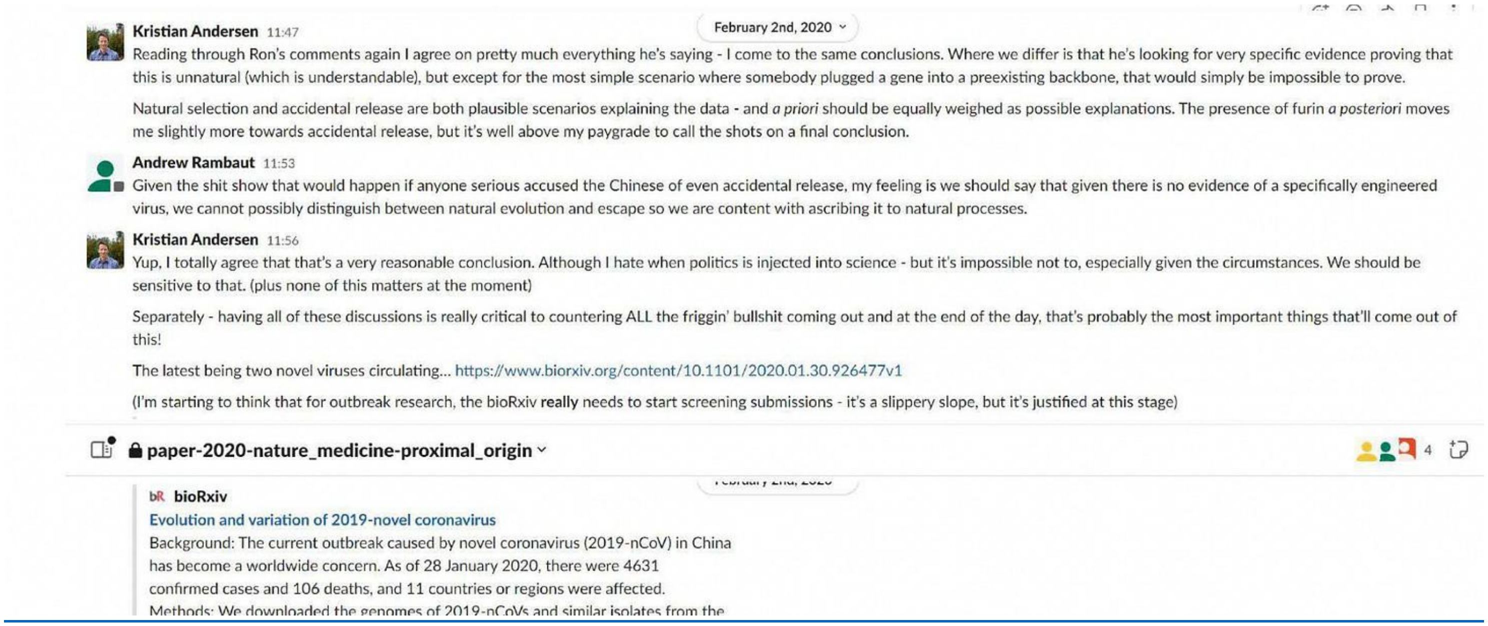
Andrew Rambaut 13:52
It will be interesting to know what Ron thinks. He is not going to want it to be a GOF escape.

Kristian Andersen 13:52
Question is - evolution or engineering. My problem is that both really rather plausible.

Yup

Ron will likely bush back hard - which is fine.

February 2, 2020, Rambaut discussed omitting the likely possibility of a lab leak to avoid a political "shit show". Andersen said, "I totally agree."



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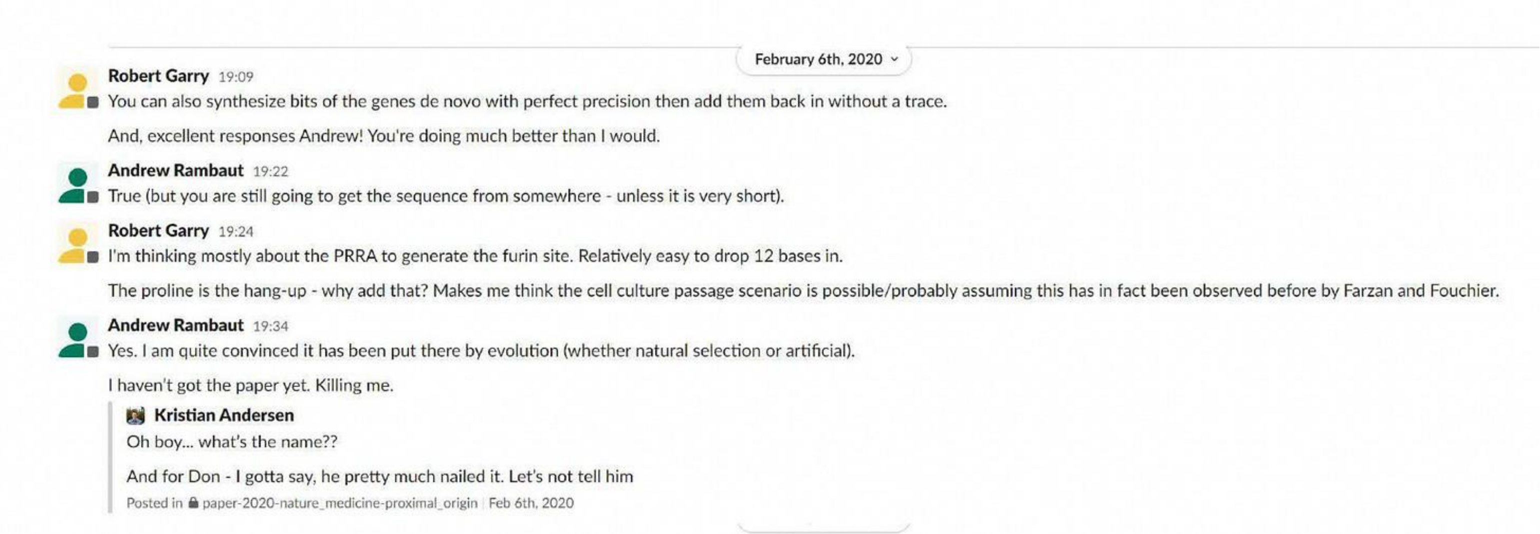
February 6, 2020, Rambaut: "I am quite convinced it has been put there by evolution (whether natural selection or artificial)."



February 6th, 2020

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.

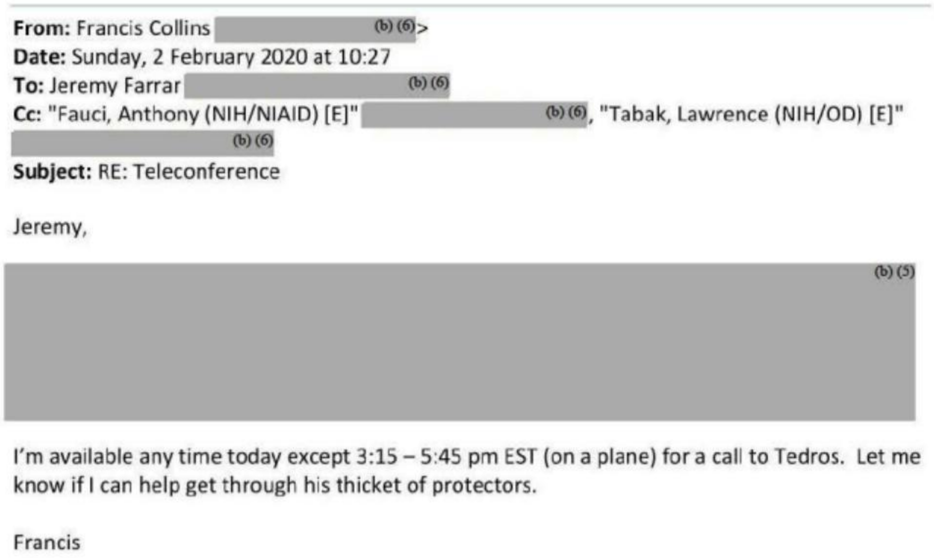
Andrew Rambaut 19:34
Yes. I am quite convinced it has been put there by evolution (whether natural selection or artificial).

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

Feb 2, 2020, NIH Director Collins emails Fauci and others, warning that a free and open debate about covid origins may do “great potential harm to science and the international harmony”. GOP Oversight Committee published the previously redacted text.

2. Email from Dr. Francis Collins to Drs. Jeremy Farrar, Anthony Fauci, and Lawrence Tabak



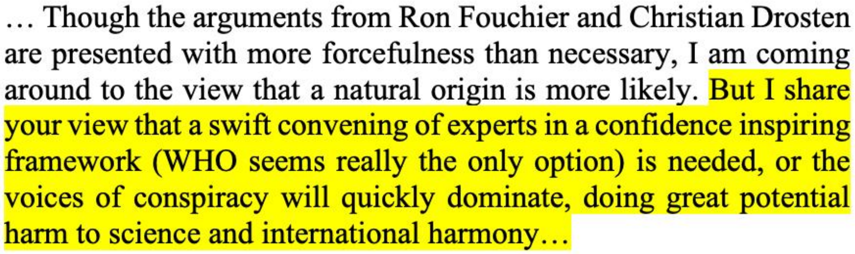
From: Francis Collins [redacted] (b) (6)>
Date: Sunday, 2 February 2020 at 10:27
To: Jeremy Farrar [redacted] (b) (6)
Cc: "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b) (6), "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)
Subject: RE: Teleconference

Jeremy,

[redacted] (b) (5)

I'm available any time today except 3:15 – 5:45 pm EST (on a plane) for a call to Tedros. Let me know if I can help get through his thicket of protectors.

Francis



… Though the arguments from Ron Fouchier and Christian Drosten are presented with more forcefulness than necessary, I am coming around to the view that a natural origin is more likely. But I share your view that a swift convening of experts in a confidence inspiring framework (WHO seems really the only option) is needed, or the voices of conspiracy will quickly dominate, doing great potential harm to science and international harmony…

Likewise, GOP Oversight Committee published redacted email text of NIH-funded gain of function researcher, Ron Fouchier saying the same: a debate about covid origins would "harm science".

3. Email from Dr. Andrew Rambaut to Drs. Jeremy Farrar, Anthony Fauci, Patrick Vallance, Christian Drosten, Marion Koopmans, Edward Holmes, Kristian Andersen, Paul Schreier, Mike Ferguson, Francis Collins, and Josie Golding

From: '[redacted] (b)(6)
Date: Sunday, 2 February 2020 at 09:38
To: Jeremy Farrar <[redacted] (b)(6)>
Cc: [redacted] (b)(6)>, "Fauci, Anthony (NIH/NIAID) [E]" [redacted] (b)(6), Patrick Vallance [redacted] (b)(6)>, "Drosten, Christian" [redacted] (b)(6), Marion Koopmans <[redacted] (b)(6), Edward Holmes [redacted] (b)(6) [redacted] (b)(6), "Kristian G. Andersen" [redacted] (b)(6), Paul Schreier [redacted] (b)(6) Michael FMedSci [redacted] (b)(6)>, Francis Collins [redacted] (b)(6) [redacted] (b)(6) Josie Golding [redacted] (b)(6)
Subject: Re: Teleconference

Dear Jeremey, Ron and all,

Thanks for inviting me on the call yesterday. [redacted] (b)(5) (b)(5)

[redacted] (b)(5)

Best,
Andrew

Thanks for inviting me on the call yesterday. I am also agnostic on this – I do not have any experience of laboratory virology and don't know what is likely or not in that context. From a (natural) evolutionary point of view the only thing here that strikes me as unusual is the furin cleavage site. It strongly suggests to me that we are missing something important in the origin of the virus. My inclination would be that it is a missing host species in which this feature arose because it was selected for in that host. We can see this insertion has resulted in an extremely fit virus in humans – we can also deduce that it is not optimal for transmission in bat species.

Eddie Holmes tells the story of how he exclaimed "Oh my god," thinking it wasn't just 60/40 likelihood of lab leak/natural but 80/20. *"I thought it might have been 80/20 at some point but that phase lasted like 3 days, and then very quickly I changed my mind, bc of the data."*

Holmes explains his questionable evolution: *"My colleagues at the University of Hong Kong emailed me and said I've got this sequence of a pangolin, it's kind of close...suddenly the pangolin, the same sequence, more or less is there...there it is in nature...that must be natural."*

Source: https://censorednews.substack.com/p/covid-covier-up-animation-primary