

[gtranslate]

Timeline: The proximal origin of SARS-CoV-2

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Posted on September 14, 2022 by Emily Kopp



Anthony Fauci shaped an editorial dismissing the idea COVID-19 emerged from the Wuhan Institute of Virology after being alerted to coronavirus work his institute funded there. (Photo credit: White House Archives)

Updated: September 29, 2022

Introduction

"The proximal origin of SARS-CoV-2" is one of the most influential scientific articles in history.

In February 2020 — about a month before a pandemic had been declared — five top virologists huddled to examine aspects of a rapidly emerging coronavirus that seemed primed to infect human cells. (The furin cleavage site kept one virologist up all night.) A few days later, they concluded the virus had not been engineered. In March, their conclusions were published in *Nature Medicine*.

“We do not believe that any type of laboratory-based scenario is plausible,” the article read.

The article assured much of the media, Washington and the broader infectious disease community that there was no need to scrutinize the labs at the pandemic’s epicenter in Wuhan, China. The Wuhan Institute of Virology is well known for research on SARS-like coronaviruses, including gain-of-function research. Though a “correspondence” and not a formal paper, the article has been cited in the press 2,127 times.

It took 15 months and a Freedom of Information Act lawsuit to reveal that each of the five authors had expressed private concerns about engineering or the Wuhan Institute of Virology’s store of novel coronaviruses.

Also troubling: A confidential teleconference organized by Wellcome Trust Director Jeremy Farrar had framed early drafts of the article. But several scientists on the call had undisclosed conflicts of interest.

Two authors were later found to have collaborated with the Wuhan lab or its American partner, EcoHealth Alliance. Another virologist who shaped the article’s central ideas without credit is synonymous with controversial viral engineering.

Also present on the call for “advice and leadership” but not publicly credited: director of the National Institutes of Health Francis Collins and director of the NIH’s National Institute of Allergy and Infectious Diseases Anthony Fauci. NIAID had funded the Wuhan Institute of Virology — a fact Fauci had been alerted to by late January.

The scientists’ familiarity with the Wuhan Institute of Virology’s work on novel coronaviruses calls into question a central premise of the paper — that SARS-CoV-2 could not have been engineered because it appeared to be novel.

Farrar said that “proximal origin” was motivated by the absence of an investigation by the WHO. However, emails show that Farrar simultaneously shepherded along the article and appealed to the WHO.

This timeline compiles several sources in an effort to flesh out the backstory of the enormously influential article. The timeline is likely to grow as more information emerges. All times have been approximated to Eastern Time.

The authors of the “proximal origin” article are Scripps Research virologist Kristian Andersen, University of Sydney virologist Edward Holmes, Tulane School of Medicine virologist Robert Garry, University of Edinburgh virologist Andrew Rambaut and Columbia University virologist Ian Lipkin.

“Just a few of us – Eddie, Kristian, Tony and I – were now privy to sensitive information that, if proved to be true, might set off a whole series of events that would be far bigger than any of us. It felt as if a storm was gathering,” Farrar wrote of the period leading up the publication of “proximal origin.”

Summary

January 27, 2020: Fauci learned he funds the Wuhan Institute of Virology.

January 29, 2020: Andersen discovered a paper describing gain-of-function techniques with coronaviruses involving the Wuhan Institute of Virology.

January 31, 2020: Fauci and Andersen spoke privately. Four virologists, including three authors of the article — Andersen, Holmes and Garry — found the virus to be “inconsistent with expectations from evolutionary theory.”

February 1, 2020: Farrar organized a secret teleconference between the virologists and NIH. Separately, Fauci sought to learn more about which projects NIAID funded at the lab.

February 2, 2020: The virologists exchanged thoughts. Several leaned toward a lab origin. Garry said he cannot understand how SARS-CoV-2 could have emerged naturally after comparing it to RaTG13.

February 4, 2020: A draft was circulated. Holmes, “60-40 lab,” said the draft “does not mention other anomalies as that will make us look like loons.” Andersen derided the idea of an engineered virus as “crackpot” and promoted the phrase “consistent with natural evolution” to scientists outside of the confab.

March 6, 2020: Andersen thanked Farrar, Collins and Fauci for their “advice and leadership.”

April 17, 2020: Fauci told reporters COVID-19 is “totally consistent with a jump of a species from an animal to a human,” citing the paper.

August 19, 2020: Collins and Fauci discussed the termination of an EcoHealth Alliance grant and the lab leak theory. Eight days later, a new grant is extended from NIAID to EcoHealth and Andersen’s lab.

June 20, 2021: Collins, Fauci, Andersen and Garry encouraged a researcher to rethink a preprint about early SARS-CoV-2 sequences that NIH improperly spiked from its database. Andersen proposed deleting it from a preprint server.

July 31, 2022: New entries to an NIH database indicated a relationship between Holmes and the Wuhan Institute of Virology, including work on RaTG13.

Timeline

‘Mid-January’: CDC director sounds the alarm

Robert Redfield, director of the Centers for Disease Control and Prevention and a virologist, voiced the concern that a lab accident occurred at the Wuhan Institute of Virology. He shared this concern with Fauci, Farrar, and World Health Organization Director-General Tedros Ghebreyesus, Vanity Fair reported.

Farrar noticed email chatter among credible scientists “suggesting the virus looked almost engineered to infect human cells” in the last week of January, according to his memoir Spike.

January 27, 2020: Fauci learns he funded the Wuhan Institute of Virology 6:59 a.m.

Farrar acquired a second phone for discussing the origin of SARS-CoV-2.

27 Jan 2020, at 11:59:

Special request!

Can I get a second phone today? Separate number, need to have one separate to my existing Wellcome one, I hope just for 3–6 months – can explain when we meet

Source: Spike (2021)

"We should use different phones; avoid putting things in emails; and ditch our normal email addresses and phone contacts," Farrar wrote in his memoir. "I didn't know the term then but I now had a burner phone, which I would use only for this purpose and then get rid of."

6:24 p.m.

By January 27, Fauci knows his institute funded work on coronaviruses at the Wuhan Institute of Virology through the EcoHealth Alliance, according to an email obtained by the House Oversight and Reform Committee.

From: [Folkers, Greg \(NIH/NIAID\) \[E\]](#)
To: [Routh, Jennifer \(NIH/NIAID\) \[E\]](#); [Fauci, Anthony \(NIH/NIAID\) \[E\]](#)
Cc: [Billet, Courtney \(NIH/NIAID\) \[E\]](#); [Stover, Kathy \(NIH/NIAID\) \[E\]](#); [Conrad, Patricia \(NIH/NIAID\) \[E\]](#); [Marston, Hilary \(NIH/NIAID\) \[E\]](#); [Lerner, Andrea \(NIH/NIAID\) \[E\]](#)
Subject: RE: For review (due to HHS for White House by 8:30 tonight): press conference talking points
Date: Monday, January 27, 2020 6:24:59 PM
Attachments: [Talking Points for NIAID Director Dr. Fauci.docx](#)

As a place folder looks good to me.

+ Andrea who is the lead on a CoV talk ASF is giving on Tuesday

Also --- when talking about CoV (not necessarily in this venue) we have on our team (Vincent and folks we fund, Peter Daszak, Ralph Baric, Ian Lipkin, etc.) probably the world's experts non-human coronaviruses.

From David M -- EcoHealth group (Peter Daszak et al), has for years been among the biggest players in coronavirus work, also in collaboration with Ralph Baric, Ian Lipkin and others.

NIAID has funded Peter's group for coronavirus work in China for the past 5 years through R01 1R01AI110964: "Understanding the Risk of Bat Coronavirus Emergence". That's now been renewed, with a specific focus to identify cohorts of people highly exposed to bats in China, and work out if they're getting sick from CoVs. Erik Stemmy is the Program Officer. Collaborators include Wuhan Institute of Virology (currently working on the nCoV), and Ralph Baric. The results of the work to date include:

(b) (5)

Source: House Oversight and Reform Committee

Details about EcoHealth's NIAID-funded research are shared with Fauci, but these details are redacted.

January 28, 2020: Discussions begin

Farrar called Holmes, concerned about chatter about the possibility of a lab accident and a recently published preprint on the server BioRxiv.

Farrar's memoir does not name the preprint.

But Holmes identified the preprint in a 2022 interview as "Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin," coauthored by Wuhan Institute of Virology Center for Emerging Infectious Diseases Director Zhengli Shi and published on January 23. The preprint described the sequence of SARS-CoV-2 and compared the virus to similar bat coronaviruses discovered by the Wuhan lab, including a coronavirus called RaTG13 with 96 percent similarity to SARS-CoV-2.

"I got an email from Jeremy Farrar saying, 'There is some chatter in the U.S. about whether this virus has come out of a lab, do you have time for a talk now?'" Holmes said. "I think this is started because Zhengli Shi posts her first paper that ends up in Nature that has her sequence and RaTG13."

"RaTG13 being the closest relative to SARS-CoV-2... so of course that leads to lots of chatter," Holmes continued.

(Patrick Vallance, chief scientific advisor to the United Kingdom, may have also been on the line, Holmes said.)

Holmes was "indifferent" to the similarity between SARS-CoV-2 and RaTG13, according to Farrar's memoir, finding the pattern of variation to be normal.

"I didn't think much of it, if I'm honest. I was busy traveling and trying to write a scientific paper," Holmes recounted to Farrar.

Holmes is a coauthor on partial sequences of RaTG13 alongside Shi. These partial sequences were submitted to NIH's database in 2018, but published in July 2022.

January 29, 2020: Andersen flags gain-of-function research

Andersen became alarmed that a bat coronavirus may have been engineered to infect humans, pointing to the receptor binding domain and furin cleavage site, according to Farrar's memoir.

He also flagged a gain-of-function study that "looked like a how-to manual for building the Wuhan coronavirus in a laboratory," the memoir states.

"Andersen found a scientific paper where exactly this 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," Farrar wrote. "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."

The title of this paper is unknown.

But it is clear that a 2015 paper involving gain-of-function work with a SARS-CoV backbone at the Wuhan Institute of Virology appears to have alarmed Fauci a few days later. The 2015 paper had been given an abbreviated title: "SARS Gain of function."

Andersen and Holmes arrange to meet a Zoom call.

"Kristian said, 'Eddie, can we talk? I need to be pulled off the ledge here,'" Holmes later recounted.

Andersen directs Holmes' attention to a concerning part of the genome.

"He said there's this furin cleavage site between the S1 and S2 junctions," Holmes recounted. "There are two restriction sites, BamHI, around it. And that section, between the restriction sites, looks like it has reduced variation."

In other words, the furin cleavage site — a feature of SARS-CoV-2 that makes it unusually infectious — had features characteristic of genetic engineering. Restriction sites are snippets of the genome recognized by restriction enzymes that cleave at or near that site. And the portion of the genome between these sites did not at first appear natural.

"Fuck, this is bad," Holmes said in response to Andersen's findings.

January 31, 2020: 'Inconsistent with expectations from evolutionary theory'

5:23 p.m.

Farrar asked to speak to Fauci.

From: Jeremy Farrar [REDACTED] (b) (6)
Sent: Friday, January 31, 2020 5:23 PM
To: Fauci, Anthony (NIH/NIAID) [E] [REDACTED] (b) (6)
Subject: Phone call

Tony
Really would like to speak with you this evening

It is 10pm now UK

Can you phone me on [REDACTED] (b) (6)

Jeremy

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Source: Jimmy Tobias, independent journalist

Farrar then told Fauci "the people involved" included three top virologists: Andersen, Garry and Holmes.

Fauci and Andersen also spoke privately.

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

To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: Re: Phone call

Thanks Tony

Can you phone Kristian Anderson

(b) (6)

He is expecting your call now.

The people involved are:

Kristian Anderson

<https://www.scripps.edu/faculty/andersen/>

Bob Garry

<https://medicine.tulane.edu/departments/microbiology-immunology-tulane-cancer-center/faculty/robert-f-garry-jr-phd>

Eddie Holmes

<https://sydney.edu.au/science/about/our-people/academic-staff/edward-holmes.html>

Source: Jimmy Tobias, independent reporter

8:43 p.m.

Science Magazine published the article "Mining coronavirus genomes for clues to the outbreak's origins" by staff writer Jon Cohen. The article quoted Holmes, Andersen and Rutgers Board of Governors Professor Richard Ebright, who told Cohen he had concerns about a new maximum biocontainment lab called the Wuhan Institute of Virology.

Fauci forwarded the article to Farrar and Andersen.

"It is of interest to the current discussion," he wrote.

10:32 p.m.

Andersen wrote back to Fauci.

While SARS-CoV-2 fits within the family tree of bat coronaviruses, that doesn't illustrate whether it has been engineered. Indeed, the virus looks unnatural to Andersen and three other virologists, he wrote.

"You have to look very closely at the genome to see features that are potentially engineered... I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome to be inconsistent with expectations from evolutionary theory," he wrote. "We have a good team lined up to look at this, so we should know more by the end of the weekend."

"Mike" referred to Michael Farzan, chair of the Scripps Research Department of Immunology and Microbiology, who has made key discoveries related to how SARS-CoV infects human cells.

Other members of the "team" looped into early conversations included Garry and Rambaut. Christian Drosten, director of the Institute of Virology at Charité Hospital, also participated in early discussions.

The "team" also sought the advice of a proponent of gain-of-function research, Erasmus MC virologist Ron Fouchier, and Erasmus MC Department of Viroscience Director Marion Koopmans.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 18:43:31 +0000
To: Kristian G. Andersen
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] (b) (6) >
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Jeremy Farrar [redacted] (b) (6) >
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

Source: Jimmy Tobias, independent journalist

At the time, Holmes was 80 percent sure the novel coronavirus had a lab origin, while Andersen favored a lab origin by about 60 to 70 percent, according to Farrar's memoir.

"Andrew and Bob were not far behind. I, too, was going to have to be persuaded that things were not as sinister as they seemed," Farrar wrote.

Andersen would later say he was intimidated by the idea of breaking the news to the world that the virus may be engineered.

"I was battling with the idea that, having raised the alarm, I might end up being the person who proved this new virus came from a lab," he told Farrar. "And I didn't necessarily want to be that person."

February 1, 2020: The teleconference

12:29 a.m.

"IMPORTANT," Fauci wrote in the subject line of an email to an aide a little after midnight — about two hours after Andersen told him the genome may not have evolved naturally.

"Hugh: It is essential that we speak this AM. Keep your cell phone on," he wrote.

He instructed Hugh Auchincloss, NIAID principal deputy director, to read the attached paper and added an urgent instruction: "You will have tasks today that must be done."

The attached paper was likely a 2015 Nature paper titled "A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence," a study NIH had funded through a grant to EcoHealth Alliance.

The file name included the phrase "SARS Gain of function."

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 12:29:01 +0000
To: Auchincloss, Hugh (NIH/NIAID) [C] (b) (6)
Cc: (b) (6)
Subject: IMPORTANT
Attachments: Baric, Shi et al - Nature medicine - SARS Gain of function.pdf

Hugh:

It is essential that we speak this AM. Keep your cell phone on. I have a conference call at 7:45 AM with Azar. It likely will be over at 8:45 AM. Read this paper as well as the e-mail that I will forward to you now. You will have tasks today that must be done.

Thanks,

Tony

Anthony S. Fauci, MD

Source: BuzzFeed News

The paper shows that a team co-led by Shi had spliced the spike protein of one coronavirus into a SARS-CoV backbone. The authors wrote that future experimentation on these viruses "may be too risky to pursue."

12:38 a.m.

Fauci emailed Farrar and Andersen, but the details are redacted.

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

Source: Jimmy Tobias, independent journalist

10:55 a.m.

Farrar invited Fauci to a teleconference later that day.

"My preference is to keep this [a] really tight group," Farrar wrote. "Obviously ask everyone to keep in total confidence."

From: Jeremy Farrar
Sent: Sat, 1 Feb 2020 10:55:15 +0000
To: Fauci, Anthony (NIH/NIAID) [E]
Subject: Re: Conf details
Attachments: IMG_1781[2].JPG

Could you join?

Trying to set up an initial call with

Kristian Anderson
Bob Garry
Christian Drosten
Tony Fauci
Ron Fouchier
Eddie Holmes
Marion Koopmans
Patrick Vallance - Chief Scientist UK

Time zones a challenge

Suggestion - Today 1st February (2nd Feb for Eddie) - I Will confirm later today. If you cannot make it, we will phone you afterwards to update.

6am Sydney
8pm CET
7pm GMT
2pm EST
9am West Coast

My preference is to keep this really tight group.

To listen to the work Eddie, Bob and Kristian have done.
Question it
And think through next steps.

Obviously ask everyone to treat in total confidence.

Source: Jimmy Tobias, independent journalist

An analysis that framed the February 1, 2020, teleconference was titled "Coronavirus sequence comparison[1].pdf." This document has not been released to the public.

Participants were asked to keep the call confidential until "next steps" are outlined.

11:47 a.m.

Auchincloss reported back to Fauci that the work was performed before a 2014 gain-of-function pause, but reviewed and approved by NIH after the pause was lifted in 2017.

This appears to be confusing, as Auchincloss reported back to Fauci that another NIH aide said that "no coronavirus work has gone through the P3 framework," a reference to the "pandemic potential pathogen" framework put in place to regulate gain-of-function research after the "pause."

In any case, this NIH aide will investigate "if we have any distant ties to this work abroad," Auchincloss says.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 17:51:31 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E]
Subject: RE: Continued

OK. Stay tuned.

-----Original Message-----

From: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6)>
Sent: Saturday, February 1, 2020 11:47 AM
To: Fauci, Anthony (NIH/NIAID) [E] <(b) (6)>
Subject: Continued

The paper you sent me says the experiments were performed before the gain of function pause but have since been reviewed and approved by NIH. Not sure what that means since Emily is sure that no Coronavirus work has gone through the P3 framework. She will try to determine if we have any distant ties to this work abroad.

Sent from my iPad

Source: BuzzFeed News

11:48 a.m.

Collins sent a recent preprint by Shi to Fauci. The preprint shared between NIH's leaders described several coronaviruses, including RaTG13.

"No evidence this work was supported by NIH," Collins wrote.

"I did see it, but did not check the similarities. Obviously we need more details," Fauci wrote back.

From: [Fauci, Anthony \(NIH/NIAID\) \[E\]](#)
To: [Collins, Francis \(NIH/OD\) \[E\]](#)
Subject: RE: BioRxiv report on 2019 nCoV from Shi et al.
Date: Saturday, February 1, 2020 11:48:58 AM

Thanks. I did see it, but did not check the similarities. Obviously we need more details.

-----Original Message-----

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Saturday, February 1, 2020 11:46 AM
To: Tabak, Lawrence (NIH/OD) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E]
(b) (6); Wolinetz, Carrie (NIH/OD) [E] (b) (6)
Subject: BioRxiv report on 2019 nCoV from Shi et al.

In case you haven't already seen this preprint from one week ago. (b) (5)

No evidence this work was supported by NIH.

Francis

Source: U.S. Right to Know

Any ties between the Wuhan Institute of Virology's work on coronaviruses and NIH were apparently top of mind for Fauci and Collins just two hours before they conferred with the authors of the "proximal origin" paper.

2 p.m.

Collins and Fauci joined the teleconference at 2 p.m. Washington time (7 p.m. GMT and 6 a.m. in Sydney) along with Farrar, Andersen and Holmes.

Garry and Rambaut were invited by Andersen and Holmes.

Others on the call included: Vallance; Fouchier; Koopmans; Drosten; Stefan Pohlmann, a virologist at the German Primate Centre in Gottingen; Mike Ferguson, Wellcome's deputy chair and a biochemist; Paul Schreier, also from Wellcome.

Despite his appeals both to Fauci and Farrar, Redfield is left out of the teleconference.

Andersen presented slides to the group, with Holmes providing some input. A discussion follows.

Virologists on the call insist the NIH grantmakers did not seek to spin the science.

"Tony Fauci says very little. Francis Collins says even less," Holmes recounted emphatically. "Their behavior was completely impeccable."

Gain-of-function research practitioners were clearly influential, however.

Fouchier — who ignited a debate about gain-of-function research when he altered the highly lethal H5N1 virus to be airborne between ferrets — was among the first to voice the argument that would become central to the paper, according to Holmes.

"People like Ron very correctly point out that if you were going to do this ... you would use a standard lab background, and this is not a standard lab background," Holmes said. "They gave a whole set of very cogent points about what you would do if you were going to do this."

Drosten and Koopmans, Fouchier's boss, both agreed, Farrar recollected.

"The conference call finished and the conclusion was that we should write something up, a sort of summary statement," Holmes said.

15.

From: [REDACTED]

Sent: 01 February 2020 19:37

To: Jeremy Farrar [REDACTED]

[REDACTED] Vallance, Patrick (GO-Science) [REDACTED]

Subject: Re: Teleconference

We need to talk about the backbone too, not just the insert?

Source: Ian Birrell, journalist

In an email sent after the call, one of the virologists referred to a viral "backbone" and "insert."

February 2, 2020: 'There are possible ways in nature, but highly unlikely'

After the call, Farrar collected some thoughts from the group and emailed Fauci and Collins.

"On a spectrum if 0 is nature and 100 is release – I am honestly at 50! My guess is that this will remain grey, unless there is access to the Wuhan lab – and I suspect that is unlikely!" Farrar said.

On a spectrum if 0 is nature and 100 is release – I am honestly at 50! My guess is that this will remain grey, unless there is access to the Wuhan lab – and I suspect that is unlikely!

Source: Spike (2021)

6:53 a.m.

Farrar relayed more thoughts from participants on the call to Fauci and Collins. These emails, first obtained through FOIA by BuzzFeed News, were viewed un-redacted by congressional staff *in camera* and reported by The Intercept.

From: Jeremy Farrar (b) (6)
Sent: Sunday, February 2, 2020 6:53 AM
To: Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Tabak, Lawrence (NIH/OD) [E]
(b) (6)
Subject: Re: Teleconference

Thank you

See thoughts overnight from others.

(b) (5)

Source: BuzzFeed News

"From Mike Farzan (discoverer of SARS receptor):

1. The RBD didn't look 'engineered' to him – as in, no human would have selected the individual mutations and cloned them into the RBD (I think we all agree)
2. Tissue culture passage can often lead to gain of basic sites – including furin cleavage sites (this is stuff they have seen with human coronaviruses)
3. He is bothered by the furin site and has a hard time explain that as an event outside the lab (though, there are possible ways in nature, but highly unlikely)
4. Instead of directed engineering, changes in the RBD and acquisition of the furin site would be highly compatible with the idea of continued passage of virus in tissue culture
5. Acquisition of the furin site would likely destabilize the virus but would make it disseminate to new tissues.

So, given above, a likely explanation could be something as simple as passage SARS-live CoVs in tissue culture on human cell lines (under BSL-2) for an extended period of time, accidentally creating a virus that would be primed for rapid transmission between humans via gain of furin site (from tissue culture) and adaption to human ACE2 receptor via repeated passage.

...So, I think it becomes a question of how do you put all this together, whether you believe in this series of coincidences, what you know of the lab in Wuhan, how much could be in nature – accidental release or natural event? I am 70:30 or 60:40."

From Mike Farzan (discoverer of SARS receptor):

1. The RBD didn't look 'engineered' to him – as in, no human would have selected the individual mutations and cloned them into the RBD (I think we all agree)
2. Tissue culture passage can often lead to gain of basic sites – including furin cleavage sites (this is stuff they have seen with human coronaviruses)
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...So, I think it becomes a question of how do you put all this together, whether you believe in this series of coincidences, what you know of the lab in Wuhan, how much could be in nature – accidental release or natural event? I am 70:30 or 60:40.

Source: House Oversight and Reform Committee

"You were doing gain of function research you would NOT use an existing close [clone] of SARS or MERSv. These viruses are already human pathogens. What you would do is close a bat virus th[at] had not yet emerged," Garry said.

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

2

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.

That is the big if.

You were doing gain of function research you would NOT use an existing close of SARS or MERSv. These viruses are already human pathogens. What you would do is close a bat virus th[at] had not yet emerged. Maybe then pass it in human cells for a while to lock in the RBS, then you reclone and put in the mutations you are interested – one of the first a polybasic cleavage site.

Source: House Oversight and Reform Committee

"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 3 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.

That is the big if.

You were doing gain of function research you would NOT use an existing close [clone] of SARS or MERSv. These viruses are already human pathogens. What you would do is close a bat virus th[at] had not yet emerged. Maybe then pass it in human cells for a while to lock in the RBS, then you reclone and put in the mutations you are interested – one of the first a polybasic cleavage site."

8:30 a.m.

Fouchier emailed Farrar, and apparently the other participants on the call, calling for further inquiry. However he also calls the question of the virus' origin a distraction for the moment, and possibly harmful to science and to China.

"Dear Jeremy and others,

"Thanks for a 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.

... 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 a 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."

... 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

7

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.

... 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 a 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.

Source: House Oversight and Reform Committee

9:38 a.m.

Under the subject line "Re: Teleconference," Rambaut emails Farrar, Fauci, and the other call's participants.

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.

... The biggest hinderance at the moment (for this and more generally) is the lack of data and information. There have been no genome sequences from Wuhan for cases more recent than the

beginning of January and reports, but no information, about virus from non-human animals in Wuhan. If the evolutionary origins of the epidemic were to be discussed, I think the only people with sufficient information or access to samples to address it would be the teams working in Wuhan.

"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.

... The biggest hinderance at the moment (for this and more generally) is the lack of data and information. There have been no genome sequences from Wuhan for cases more recent than the 6 beginning of January and reports, but no information, about virus from non-human animals in Wuhan. If the evolutionary origins of the epidemic were to be discussed, I think the only people with sufficient information or access to samples to address it would be the teams working in Wuhan."

10:27 a.m.

Collins emailed Farrar, Fauci, and NIH official Lawrence Tabak, raising concerns about the "potential harm to science and international harmony" a lab origin of COVID-19 could pose.

"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.

I'm available any time today except 3:15 p.m. – 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."

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

Jeremy,

(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...

Source: House Oversight and Reform Committee

11:28 a.m.

Farrar updated Collins and Fauci on his efforts to pressure the WHO, but the aim is unclear.

"Tedros and Bernard have apparently gone into conclave....they need to decide today in my view. If they do prevaricate, I would appreciate a call with you later tonight or tomorrow to think how we might take forward.

Meanwhile.....

<https://www.zerohedge.com/geopolitical/coronavirus-contains-hiv-insertions-stoking-fears-over-artificially-created-bioweapon>"

From: Jeremy Farrar (b) (6)
Sent: Sunday, February 2, 2020 11:28 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Tabak, Lawrence (NIH/OD) [E] (b) (6)>
Subject: Re: Teleconference

Tedros and Bernhard have apparently gone into conclave....they need to decide today in my view. If they do prevaricate, I would appreciate a call with you later tonight or tomorrow to think how we might take forward.

Meanwhile....

<https://www.zerohedge.com/geopolitical/coronavirus-contains-hiv-insertions-stoking-fears-over-artificially-created-bioweapon>

Source: BuzzFeed News

1:57 p.m. (approximate)

Twitter suspended Zero Hedge — the blog that Farrar had flagged to Fauci and Collins — apparently because of a separate post that shared the contact information of a Chinese scientist. The ban appeared to coincide with an effort by the WHO to work with social media companies to bar “misinformation.”

3:30 p.m.

Fauci weighed in on the virologists’ comments but the details are redacted.

From: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)>
Date: Sunday, 2 February 2020 at 15:30
To: Jeremy Farrar (b) (6)>, Francis Collins (b) (6)>
Cc: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Subject: RE: Teleconference

Jeremy:

Sorry that I took so long to weigh in on your e-mails with Francis and me. I was on conference calls.

(b) (5)
(b) (5)

Best regards,
Tony

Source: BuzzFeed News

4:49 p.m.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 16:49:35 +0000
To: Collins, Francis (NIH/OD) [E]
Cc: Tabak, Lawrence (NIH/OD) [E]
Subject: FW: Teleconference

Francis:
Do you have a minute for a quick call?
Tony

Source: BuzzFeed News

Fauci asked Collins for a private phone call.

At some point on February 2, Holmes received an email from University of Hong Kong Tommy Lam about a receptor binding domain found in pangolin coronaviruses that resembled the one in SARS-CoV-2, bolstering the natural origin theory, Holmes shared in a 2022 interview.

February 4, 2020: 'Did not mention other anomalies as this will make us look like loons'

2:01 a.m.

Farrar shared an early draft of "proximal origin" with Fauci and Collins, with the promise of a more polished version soon. Farrar said that he was "pushing WHO again today."

Holmes had emailed Farrar the summary, noting that it "did not mention other anomalies as this will make us look like loons."

From: Jeremy Farrar (b) (6)
Sent: Tuesday, February 4, 2020 2:01 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)
Subject: FW: Prevalence of infection and stage of the epidemic in Wuhan

Please treat in confidence – a very rough first draft from Eddie and team – they will send on the edited, cleaner version later.

Pushing WHO again today

From: Edward Holmes (b) (6)
Date: Tuesday, 4 February 2020 at 06:33
To: Jeremy Farrar (b) (6)
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

Here's our summary so far. Will be edited further.

It's fundamental science and completely neutral as written. Did not mention other anomalies as this will make us look like loons. As it stands it is excellent basic science I think, which is a service in itself.

Will finish as soon as we can.

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

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

Source: U.S. Right to Know

6:08 a.m.

Farrar reported to Fauci and Collins that Holmes is "60-40 lab," while Farrar is "50-50."

Email from Dr. Jeremy Farrar to Drs. Anthony Fauci and Francis Collins

From: Jeremy Farrar (b) (6)
Sent: Tuesday, February 4, 2020 6:08 AM
To: Collins, Francis (NIH/OD) [E] (b) (6) >
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6) >
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

(b) (4)

...[Eddie Holmes] 60-40 lab. I am 50-50...

Source: House Committee on Oversight and Reform

6:23 a.m.

From: [Fauci, Anthony \(NIH/NIAID\) \[E\]](#)
To: [Collins, Francis \(NIH/OD\) \[E\]](#); [Jeremy Farrar](#)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan
Date: Tuesday, February 4, 2020 6:23:47 AM

(b) (5) Very thoughtful summary and analysis. We really need to get WHO moving on getting the convening started.

Source: U.S. Right to Know

Fauci praised what appears to be an early draft of “proximal origin.”

“Very thoughtful summary and analysis. We really need to get the WHO moving on getting the convening started,” he wrote.

12:05 p.m.

As “proximal origin” progressed, Andersen also participated on a National Academies of Sciences, Engineering, and Medicine team responding to a request from the White House Office of Science and Technology Policy for next steps on determining the origin of the novel coronavirus.

Andersen was one of the eight experts tapped by NASEM, along with EcoHealth Alliance President Peter Daszak and University of North Carolina virologist Ralph Baric.

Andersen encouraged the NASEM to dispel the lab leak theory.

“Reading through the letter I think it’s great, but I do wonder if we need to be more firm on the question of engineering,” he wrote.

Andersen previewed the argument that would become a central premise of “proximal origin.”

“The main crackpot theories going around at the moment relate to this virus being engineered with intent and that is demonstrably not the case. Engineering can mean many things and could be done for either basic research or nefarious reasons, but the data conclusively show that neither was done (if in the nefarious scenario somebody would have used a SARS/MERS backbone and optimal ACE2 binding as previously described, and for the basic research scenario would have used one of the many already available reverse genetic systems),” he wrote.

As for communicating these ideas to the public, just a few days after emailing Fauci that he had found the genome to be “inconsistent with expectations from evolutionary theory,” Andersen encouraged the scientists to communicate the virus had arisen naturally using a similar phrase, only inverted: “consistent with natural evolution.”

“If one of the main purposes of this document is to counter those fringe theories, I think it’s very important that we do so strongly and in plain language (“consistent with [natural evolution] is a favorite of mine when talking to scientists, but not when talking to the public – especially conspiracy theorists),” he wrote.

To: Peter Daszak[daszak@ecohealthalliance.org]
Cc: Pope, Andrew[APope@nas.edu]; Chakravarti, Aravinda[Aravinda.Chakravarti@nyulangone.org]; Baric, Ralph S[rbaric@email.unc.edu]; Trevor Bedford (trevor@bedford.io)[trevor@bedford.io]; Gigi Gronvall[ggronvall@jhu.edu]; Tom Inglesby (tinglesby@jhu.edu)[tinglesby@jhu.edu]; Stanley Perlman (stanley-perlman@uiowa.edu)[stanley-perlman@uiowa.edu]; Shore, Carolyn[CShore@nas.edu]; Chao, Samantha[SChao@nas.edu]
From: Kristian G. Andersen[kga1]
Sent: Tue 2/4/2020 12:05:54 PM (UTC-05:00)
Subject: Re: URGENT: Please review by NOON if at all possible...

I too agree with all that has been said, but would caution against adding language suggesting that the virus might evolve (i.e., “mutate” to most people) towards better infectivity or transmission - a lot has been said about that for Ebola and other viruses, and it’s been driving fear because most people don’t fully understand what it means. I’m not arguing that it’s not something that might well happen - the SARS data beautifully show it - but I would be worried about the message it could send.

Reading through the letter I think it’s great, but I do wonder if we need to be more firm on the question of engineering. The main crackpot theories going around at the moment relate to this virus being somehow engineered with intent and that is demonstrably not the case. Engineering can mean many things and could be done for either basic research or nefarious reasons, but the data conclusively show that neither was done (in the nefarious scenario somebody would have used a SARS/MERS backbone and optimal ACE2 binding as previously described, and for the basic research scenario would have used one of the many already available reverse genetic systems). If one of the main purposes of this document is to counter those fringe theories, I think it’s very important that we do so strongly and in plain language (“consistent with” [natural evolution] is a favorite of mine when talking to scientists, but not when talking to the public - especially conspiracy theorists).

Best,
Kristian

Source: U.S. Right to Know

1:18 p.m.

Fauci sees an early version of the “proximal origin” paper and gives feedback — appearing to express confusion about “serial passage in ACE2-transgenic mice,” which may have been a phrase included in earlier versions.

Fauci: “?? Serial passage in ACE2-transgenic mice”

From: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)
Date: Tuesday, 4 February 2020 at 13:18
To: Francis Collins <(b) (6)>, Jeremy Farrar (b) (6)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

?? (b) (6)

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)

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...Serial passage in ACE2-transgenic mice

Source: House Oversight and Investigations Committee

The phrase refers to a way to adapt viruses in the laboratory to become more infectious.

February 5, 2020: 'I spoke with the WHO again this morning'

Farrar tells Fauci that their groups should "pressure" the WHO. He asked Fauci to recommend the names of individuals who could serve on an origins investigation, but none of the names Fauci recommends ultimately end up on any probe.

From: Jeremy Farrar (b) (6)
Sent: Wednesday, February 5, 2020 6:21 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Josie Golding (b) (6)
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

Francis and Tony

Couple of things:

- I spoke again with WHO this morning. I believe they have listened and acted. Let me know if you agree
 - At the WHO meeting next week they will set up the Group who will “look at the origins and evolution of 2019n-CoV”
 - They have asked for names to sit on that Group – please do send any names
 - We can have a call this week with a core group of that to frame the work of the Group including – if you could join?
 - I think this puts it under the umbrella of WHO, with action this week and into next
 - With names to be put forward into the Group from us and pressure on this group from your and our teams next week.
- The team will update the draft today and I will forward immediately – they will add further comments on the glycans

Does that sound reasonable to you?

Jeremy

Source: Jimmy Tobias, independent journalist

“Francis and Tony,

Couple of things:

- I spoke again with the WHO this morning. I believe they have listened and acted. Let me know if you agree
 - At the WHO meeting next week they will set up the Group who will “look at the origins and evolution of 2019n-CoV”
 - They have asked for names to sit on that Group – please do send any names
 - We can have a call this week with a core group of that to frame the work of the Group including – if you could join?
 - I think this puts it under the umbrella of WHO, with action this week and into next
 - With names to be put forward into the Group from us and pressure on this group from your and our teams next week

The team will update the draft today and I will forward it immediately – they will add further comments on the glycans”

February 7, 2020: ‘There’s always that concern’

Farrar emailed Victor Dzau, head of the National Academy of Medicine, to offer help investigating the origins of COVID-19.

The email followed the February 6 publication of a NAESM letter in response to the White House Office of Science and Technology Policy on the virus' origins. Despite Andersen's pressure, the letter did not explicitly rule out a lab origin.

"Tony (Francis) Patrick, myself and a close knit group have been looking at this for the last 10 days and might have some information to share which might help," Farrar writes, copying Fauci and Collins.

From: Jeremy Farrar
Sent: Fri, 7 Feb 2020 15:05:56 +0000
To: Victor Dzau;Fauci, Anthony (NIH/NIAID) [E];Vallance, Patrick (GO-Science)
Subject: Phone call

Victor

Let me know if a call on this would help, with either Tony, Patrick or I

<https://abcnews.go.com/Politics/white-house-asks-scientists-investigate-origins-coronavirus/story?id=68807304>

Tony (Francis), Patrick, myself and a close knit group have been looking at this for the last 10 days and might have some information to share which might help.

Best wishes Jeremy

Source: Jimmy Tobias, independent journalist

Farrar linked to an ABC News article reporting that the White House Office of Science and Technology Policy had called on the academies to lay out next steps in investigating the origins of COVID-19.

Fauci is quoted in the ABC article, and alludes to the drafting of "proximal origin."

"There's always that concern," Fauci said on the question of engineering. "And one of the things that people are doing right now is very carefully looking at sequences to see if there's even any possibility much less likelihood that that's going on. And you could ultimately determine that. So people are looking at it, but right now, the focus is on what are we going to do about what we have."

February 8, 2020: 'Summary.Feb7.pdf'

4:08 a.m.

Farrar shared a summary of discussions between the scientists with Dzau as well as the head of the National Academy of Sciences and the head of the White House Office of Science and Technology Policy.

The document — "Summary.Feb7.pdf" — is redacted in full.

"Eddie Holmes and a small group have been looking extensively at the origins and evolution of n-CoV including all theories," Farrar wrote in an email to Dzau, referring to an early abbreviation for the novel coronavirus.

"This is the latest summary, written as part of a series of [teleconference] discussions we set up and included [National Institute of Allergy and Infectious Diseases Director Anthony Fauci] and [National Institutes of Health Director Francis Collins] as well as a small group from USA, UK, Europe and Australia," Farrar wrote.

All seven pages are redacted.

From: Jeremy Farrar <(b) (6)>
Date: February 8, 2020 at 4:08:06 AM EST
To: "Dzau, Victor J." (b) (6), Edward Holmes (b) (6)
Subject: FW: 2019 N-CoV

Victor

Eddie Holmes and a small group have been looking extensively at the origins and evolution of n-CoV including all theories.

This is the latest summary, written as part of a series of TC discussions we set up and included Tony and Francis as well as a small group from USA UK, Europe and Australia.

Source: U.S. Right to Know

Responding to U.S. Right to Know reporting, Andersen said in a tweet that the idea this document arose out of a joint teleconference was a "conspiracy theory," but did not elaborate.

This same document, "SummaryFeb7.pdf," would later emerge when Fauci, Holmes and Andersen conferred on how to respond to an anonymous tip shared with Cohen, the reporter for Science Magazine.

February 11, 2020: 'A nightmare of circumstantial evidence'

9:01 a.m.

Lipkin emailed his coauthors about a "nightmare of circumstantial evidence" pointing to the Wuhan Institute of Virology, according to Vanity Fair.

On 11 Feb 2020, at 9:01 am, Ian Lipkin <> wrote:

It's well reasoned and provides a plausible argument against genetic engineering. It does not eliminate the possibility of inadvertent release following adaptation through selection in culture at the institute in Wuhan. Given the scale of the bat CoV research pursued there and the site of emergence of the first human cases we have a nightmare of circumstantial evidence to assess.

Ian

Source: Vanity Fair

"It's well reasoned and provides a plausible argument against genetic engineering. It does not eliminate the possibility of inadvertent release following adaptation through selection in culture at the institute in Wuhan," Lipkin wrote. "Given the scale of bat CoV research pursued there and the site of emergence of the first human cases we have a nightmare of circumstantial evidence to assess."

February 13, 2020: 'Not my area of expertise'

CDC National Center for Immunization and Respiratory Diseases Director Nancy Messonnier — who reports to Redfield — asked Fauci for more clarity on the National Academies' report on SARS-CoV-2's origin.

Fauci described the teleconferences and emails being convened by Farrar, and said that he has joined two of these calls.

"There is an ad hoc group informally led by Jeremy Farrar of Wellcome Trust," Fauci wrote. "This group has about 15 people, all of whom are highly respected scientists, mostly evolutionary biologists who are convening by email and conference calls (I have been on 2 of these calls since Jeremy invited me) to look at all of the bat, pangolin and human coronavirus sequence to try and determine the evolutionary origin."

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Thu, 13 Feb 2020 22:36:17 +0000
To: Messonnier, Nancy (CDC/DDID/NCIRD/OD)
Subject: RE: NAS

Nancy:

The official USG group will be convened by NAS. Bob Kadlec is the person with direct knowledge of that. In addition, there is an ad hoc group informally led by Jeremy Farrar of Wellcome Trust. This group has about 15 people, all of whom are highly respected scientists, mostly evolutionary biologists who are convening by e-mail and conference calls (I have been on 2 of these calls since Jeremy invited me) to look at all of the bat, pangolin and human coronavirus sequences to try and determine the evolutionary origin. This is not my area of expertise and so I have backed off and am leaving it all to Jeremy.

Best,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases

Source: BuzzFeed News

"This is not my area of expertise so I have backed off and am leaving it all to Jeremy," Fauci added.

February 17, 2020: Preprint publishes

February 19, 2020: 'Strongly condemn conspiracy theories'

To: Peter Daszak[daszak@ecohealthalliance.org]; Baric, Toni C[antoINETte_baric@med.unc.edu]
Cc: Alison Andre[andre@ecohealthalliance.org]; Aleksei Chmura[chmura@ecohealthalliance.org]
From: Baric, Ralph S[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=BB0D9CC80C184735A4E862C3BDD8A15D-RALPH S BAR]
Sent: Thur 2/6/2020 4:01:22 PM (UTC-05:00)
Subject: RE: No need for you to sign the "Statement" Ralph!!

I also think this is a good decision. Otherwise it looks self-serving and we lose impact. ralph

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Thursday, February 6, 2020 3:16 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Baric, Toni C <antoINETte_baric@med.unc.edu>
Cc: Alison Andre <andre@ecohealthalliance.org>; Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: No need for you to sign the "Statement" Ralph!!
Importance: High

I spoke with Linfa last night about the statement we sent round. He thinks, and I agree with him, that you, me and him should not sign this statement, so it has some distance from us and therefore doesn't work in a counterproductive way.

Jim Hughes, Linda Saif, Hume Field, and I believe Rita Colwell will sign it, then I'll send it round some other key people tonight. We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice.

Cheers,

Peter

Peter Daszak
President

Source: U.S. Right to Know

A letter in The Lancet to "strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin" includes Farrar as a signatory.

EcoHealth Alliance President Peter Daszak organized the letter but purposefully omitted EcoHealth's partnership with the Wuhan Institute of Virology and the name of University of North Carolina virologist Ralph Baric, a coronavirus engineering expert who works with EcoHealth and the lab, in order to feign impartiality.

The letter publicly called upon the WHO to play a role in curbing the lab leak theory.

The Lancet cited the National Academies letter, even though that letter had not asserted that the virus had a natural origin, despite Andersen's pressure.

It's not precisely clear when Farrar opted to sign The Lancet letter, but emails show that a first draft was sent to potential signatories on February 6.

March 6, 2020: 'Thanks for your advice and leadership'

The paper has been accepted by *Nature Medicine*. Andersen thanks Fauci, Farrar and Collins for "advice and leadership" with the paper, shares a press release, and asks if they have any further suggestions. Andersen loops in Garry, Rambaut and Lipkin.

Dear Jeremy, Tony, and Francis,

Thank you again for your advice and leadership as we have been working through the SARS-CoV-2 'origins' paper. We're happy to say that the paper was just accepted by Nature Medicine and should be published shortly (not quite sure when).

To keep you in the loop, I just wanted to share the accepted version with you, as well as a draft press release. We're still waiting for proofs, so please let me know if you have any comments, suggestions, or questions about the paper or the press release.

Tony, thank you for your straight talk on CNN last night - it's being noticed.

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](#)

Source: Jimmy Tobias, independent journalist

"Dear Jeremy, Tony, and Francis,

Thank you again for your advice and leadership as we have been working through the SARS-CoV-2 'origins' paper. We're happy to say that the paper was just accepted by Nature Medicine and should be published shortly (not quite sure when).

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Tony, thank you for the straight talk on CNN last night – it's being noticed."

March 8, 2020: 'Nice job on the paper'

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 8 Mar 2020 13:23:32 +0000
To: Kristian G. Andersen
Cc: Jeremy Farrar;Collins, Francis (NIH/OD) [E];Robert Garry;Edward Holmes;Andrew Rambaut;Ian Lipkin;Chris Emery
Subject: Re: SARS-CoV-2 article to be published in Nature Medicine

Kristian:
Thanks for your note. Nice job on the paper.
Tony

Source: Jimmy Tobias, independent journalist

Fauci replies: "Thanks for your note. Nice job on the paper."

March 17, 2020: 'Sorry, conspiracy theorists'

The paper is published in *Nature Medicine* and rejects the lab leak theory in even stronger terms than the preprint. The paper receives a lot of media attention.

Fox News: "The coronavirus did not escape from a lab: Here's how we know"

Vice News: "Once and for All, the New Coronavirus Was Not Made in a Lab"

ABC News: "Sorry, conspiracy theorists. Study concludes COVID-19 is not a laboratory construct"

Despite the strong statements by the scientists and definitive headlines, Holmes would say two and a half years later that the scientists never intended the paper to be the final word.

"It's just a paper. It's not a papal decree. It's not a government order. If you disagree with it, you can disagree with it," he said in late 2022. "It's science, right?"

March 26th, 2020: 'Some folks are even making outrageous claims'

Collins publishes a blog post amplifying the study, but does not mention his own involvement in its conception.

"Some folks are even making outrageous claims that the new coronavirus causing the pandemic was engineered in a lab and deliberately released to make people sick," he wrote. "A new study debunks such claims by providing scientific evidence that this novel coronavirus arose naturally."

April 16, 2020: 'Wondering if there is something NIH can do to help put down this very destructive conspiracy'

Under the subject line "conspiracy gains momentum" Collins asks Fauci — copying NIH subordinates Lawrence Tabak, Cliff Lane, John Burklow — for more ideas on how to "put down" the lab leak theory.

Wondering if there is something NIH can do to help put down this very destructive conspiracy, with what seems to be growing momentum:

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Thursday, April 16, 2020 5:02 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Tabak, Lawrence (NIH/OD) [E] (b) (6); Lane, Cliff (NIH/NIAID) [E] (b) (6); Burklow, John (NIH/OD) [E] (b) (6)
Subject: conspiracy gains momentum

(b) (3)

<https://www.mediaite.com/tv/foxs-bret-baier-sources-increasingly-confident-coronavirus-outbreak-started-in-wuhan-lab/>

(b) (3)

Francis

Wondering if there is something NIH can do to help put down this very destructive conspiracy, with what seems to be growing momentum:

<https://www.mediaite.com/tv/foxs-bret-baier-sources-increasingly-confident-coronavirus-outbreak-started-in-wuhan-lab/>

I hoped the Nature Medicine article on the genomic sequence of SARS-CoV-2 would settle this. But probably didn't get much visibility.

Anything more we can do? Ask the National Academy to weigh in?

Francis

Source: House Oversight and Reform Committee

I hoped the Nature Medicine article on the genomic sequence of SARS-CoV-2 would settle this. But probably didn't get much visibility. Anything more we can do? Ask the National Academy to weigh in?"

April 17, 2020: 'It is a shiny object that will go away in times'

2:45 p.m.

Fauci tells the concerned Collins: "I would not do anything about this right now. It is a shiny object that will go away in times."

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Fri, 17 Apr 2020 02:45:01 +0000
To: Collins, Francis (NIH/OD) [E]
Subject: RE: conspiracy gains momentum

Francis:

[REDACTED] (b) (5)

Best,
Tony

I would not do anything about this right now. It is a shiny object that will go away in times.

Source: House Oversight and Reform Committee

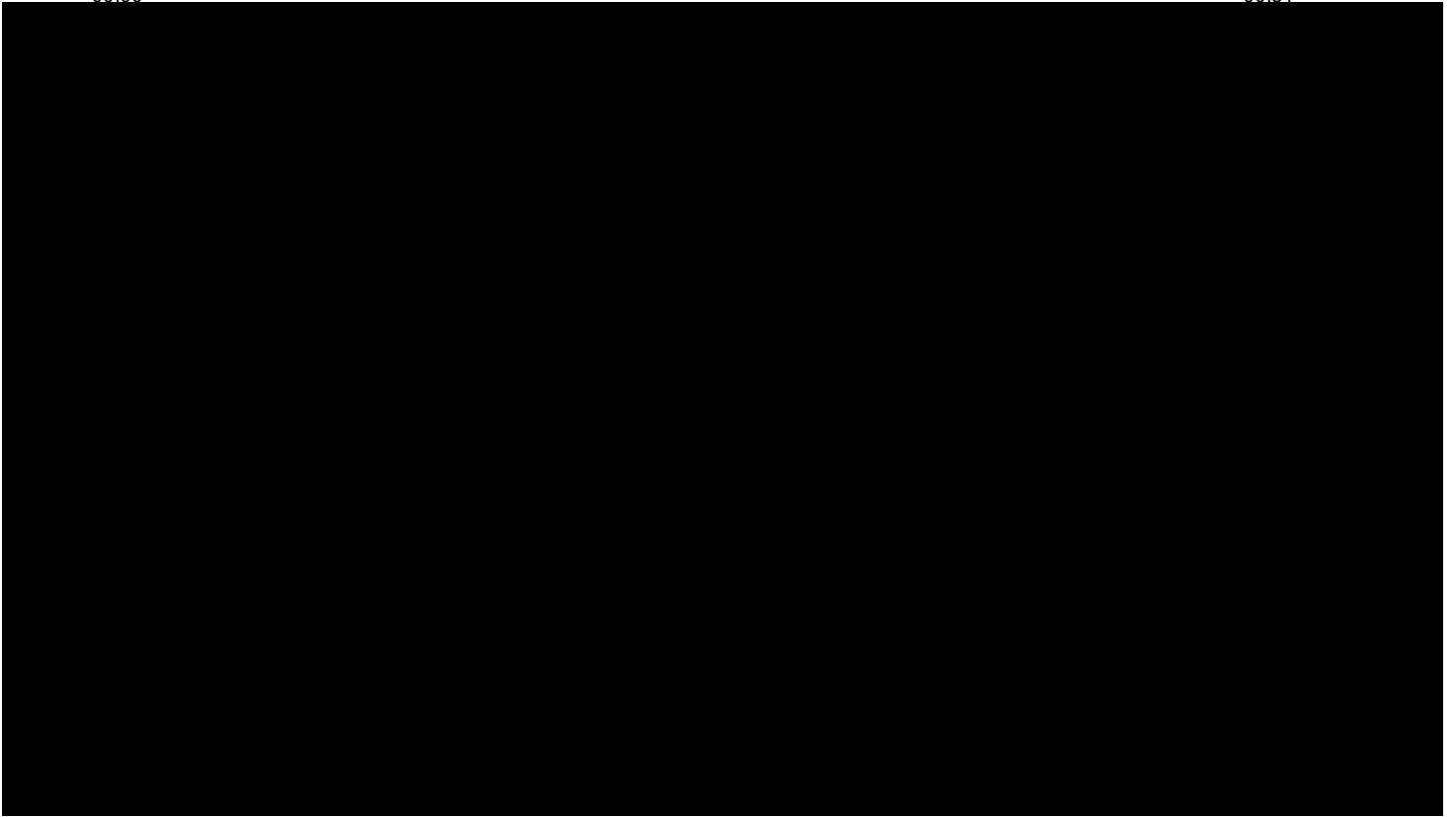
6:22 p.m.

At a White House press conference, Fauci cited "proximal origin" and told reporters that the virus certainly arose naturally. Fauci adopted the phrase that Andersen had recommended to the National Academies.

He described the genome as "totally consistent with a jump of a species from an animal to a human."

00:00

00:51



Bill:

Here are the links to the scientific papers and a commentary about the scientific basis of the origins of SARS-Cov-2.

The proximal origin of SARS-CoV-2. Andersen KG, Rambaut A, Lipkin WI, **Holmes** EC, Garry RF. Nat Med. 2020 Apr;26(4):450-452. doi: 10.1038/s41591-020-0820-9. No abstract available.

A Genomic Perspective on the Origin and Emergence of SARS-CoV-2.Zhang YZ, **Holmes** EC. Cell. 2020 Apr 16;181(2):223-227. doi: 10.1016/j.cell.2020.03.035. Epub 2020 Mar 26.

Also this statement from Eddie Holmes

<https://bit.ly/2ym1UGe>

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)

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On Apr 19, 2020, at 2:21 PM, Bill Gertz <bgertz@washingtontimes.com> wrote:

Katie,

Dr. Fauci on Friday said he would share a scientific paper with the press on the origin of the coronavirus. Can you please help me get a copy of that paper? Thanks in advance.

Bill Gertz

Source: Washington Examiner

Fauci personally replied, sharing the "proximal origin" paper. Fauci also shared a paper coauthored by Holmes titled "A genomic perspective on the origin and emergence of SARS-CoV-2" and Holmes' accompanying statement. Holmes argues in the statement that RaTG13 was sampled from Yunnan Province, while COVID-19 first appeared in Wuhan, and that the 20 to 50 years of evolution would be required to transform RaTG13 into SARS-CoV-2.

May 5, 2020: 'We deeply appreciate your efforts in steering and messaging'

Lipkin, a coauthor of the paper, forwarded Fauci an email exchange with Chen Zhu, China's former Minister of Health, about COVID-19's origins.

"We deeply appreciate your efforts in steering and messaging," he wrote.

----- Original -----

From: "Lipkin, Ian W." (b) (6);
Date: Tue, May 5, 2020 06:06 AM
To: "ZhuChen" (b) (6) >;
Subject: SARS-CoV-2

Dear Zhu,

The COVID-19 pandemic poses an unprecedented threat not only to global public health but also to economic and political stability. Uncertainty about the origin of COVID-19 pandemic is causing friction worldwide, particularly between China and the United States. There is agreement that the causative agent, SARS-CoV-2 originated in a bat. There is also a high level of confidence that the virus was not deliberately modified in any laboratory. What we do not know is the answers to two questions: (1) whether a precursor virus circulated in the human population before it evolved to become a pandemic virus and (2) whether a precursor virus adapted to humans by first passing through another animal. (b) (4)

Source: BuzzFeed News

The details of his exchange with Chen are mostly redacted.

"Uncertainty about the origin of COVID-19 pandemic is causing friction worldwide, particularly between China and the United States. There is agreement that the causative agent, SARS-CoV-2 originated in a bat. There is also a high level of confidence that the virus was not deliberately modified in any laboratory," Lipkin's note reads in part.

July 25-27, 2020: 'Here is what one person ... is saying behind your backs' 7:22 a.m.

An anonymous whistleblower emailed Cohen, the journalist with Science Magazine, about the unknown "bizarre backstory" behind the paper.

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

Several paragraphs of details shared by the tipster are redacted.

On Jul 25, 2020, at 7:22 AM, ofu8ledu8z [REDACTED] (b) (6) 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>).

[REDACTED] (b) (4)

Source: Jimmy Tobias, independent journalist

July 27, 3:02 p.m.

Cohen forwarded the message to two sources: Holmes and Andersen.

"Here is what one person who claims to have direct knowledge is saying behind your backs..." he wrote.

July 27, 6:05 p.m.

Andersen and Holmes conferred with Fauci and Farrar on how to respond.

"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)," Andersen wrote.

From: Kristian G. Andersen
Sent: Mon, 27 Jul 2020 18:05:59 -0700
To: Fauci, Anthony (NIH/NIAID) [E]
Cc: Jeremy Farrar; Edward Holmes
Subject: Fwd: [REDACTED] (b) (4), (b) (5)
[REDACTED]
Attachments: Summary.Feb7.pdf

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)** (b) (4), (b) (5)
[REDACTED] (b) (4), (b) (5)

(b) (4), (b) (5) 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

Source: Jimmy Tobias, independent journalist

"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 then Eddie and I will reply back to Jon. ... please let me know if you have any comments, questions or concerns in this regard," Andersen wrote.

Andersen also attached the "Summary.Feb7.pdf" document.

Cohen has thus far declined to release the email he received from an anonymous tipster or Holmes' response. But Cohen told U.S. Right to Know that he decided against writing about the tip because it involved a petty grievance over credit.

Why was Fauci looped in?

"They were being assailed for not sharing credit — which is a serious accusation in the world of science — with someone on the now famous 'Fauci call.' I imagine they wanted him in the loop on this attack on their credibility. Ironies never end," Cohen wrote. "I've said it before and I'll say it again: This is barking up a tree that has no animal in it."

August 19, 2020: 'A woeful attack on the traditional way'

Collins and Fauci confer with former NIH Director Harold Varmus about three news articles.

One article described a letter from Michael Lauer, NIH deputy director for extramural research, seeking lab books and an inspection of the Wuhan Institute of Virology through EcoHealth Alliance as a condition of reinstating a grant.

"This whole episode is just a woeful attack on the traditional way NIH has maintained its integrity," Varmus said in the article.

From: "Collins, Francis (NIH/OD) [E]" (b) (6)
Date: Wednesday, August 19, 2020 at 9:49 PM
To: "Harold E. Varmus" (b) (6)
Cc: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)
Subject: [EXTERNAL] Reaching out for a chance to talk

Harold,

(b) (6)

Tony and I would like the chance to speak with you about this – but for various personal reasons we can't do so until next week. How about a call then?

Meanwhile, (b) (6), I wonder if you have seen this article:
<https://www.independentsciencenews.org/commentaries/a-proposed-origin-for-sars-cov-2-and-the-covid-19-pandemic/>

Francis

Source: U.S. Right to Know

A second article postulated a lab origin of SARS-CoV-2.

A third article reported that NIAID had awarded a new grant to EcoHealth Alliance, despite not meeting the conditions set by Lauer.

August 27, 2020: NIAID awards funding to EcoHealth, Andersen

NIAID awarded \$82 million over 5 years to a network of new Centers for Research in Emerging Infectious Diseases, including Andersen's lab and the EcoHealth Alliance.

"The impact of the COVID-19 pandemic serves as a potent reminder of the devastation that can be wrought when a new virus infects humans for the first time," Fauci said in a statement. "The knowledge gained through this research will increase our preparedness for future outbreaks."

March 30, 2021: 'Extremely unlikely'

The World Health Organization's report on COVID's origins is released dismissing a lab origin as "extremely unlikely," but Director-General Tedros Adhanom Ghebreyesus immediately suggests the investigation is incomplete.

Daszak and Koopmans, two scientists who had dismissed the lab leak theory in February 2020 — Daszak through *The Lancet* and Koopmans through an undisclosed role in writing “proximal origin” — comprised two members of the team.

The annex of the WHO report showed that when investigators visited the Wuhan Institute of Virology, lab leadership cited “proximal origin.”

“A paper by leading virologists in Nature rebutted the idea of a bioengineered source,” Shi told the WHO team.

June 1, 2021: ‘A clear example of the scientific process’

Redacted emails released by BuzzFeed News following a FOIA lawsuit revealed that the virologists behind “proximal origin” had initially found the genome “inconsistent with expectations from evolutionary theory.”

Andersen denied the idea that NIH shaped the article. Andersen deleted tweets before temporarily disabling his Twitter account amid the backlash.

“What the email shows is a clear example of the scientific process,” he told the New York Times in an email.

June 20, 2021: ‘I want to be clear that I never suggested you delete ... the preprint’

Fred Hutchinson Cancer Research Center evolutionary biologist Jesse Bloom reached out to Collins and Fauci about a forthcoming preprint reporting that NIH deleted early SARS-CoV-2 genomic data sampled in Wuhan from its public database, and to ask about recovering other data that may have been deleted that could shed light on the virus’ evolution.

Collins scheduled a Zoom call for June 20, a Sunday, according to a Vanity Fair report.

The NIH leaders invited two of the coauthors of the “proximal origin” paper: Andersen and Garry.

Andersen urged Bloom to allow him to spike the preprint, according to Bloom’s notes. Fauci distanced himself from those comments by Andersen, but did ask Bloom not to use the word “surreptitiously.”

Bloom declined to delete his paper.

Kristian Andersen then said that he was a screener at *bioRxiv*, and so he could delete the preprint or revise it in a way that would leave no record that this had been done. I replied that although I appreciated the critiques, I was not going to delete the pre-print, and instead would go ahead with posting it. I also said that although I could imagine revising the pre-print, given the contentious nature of the meeting, I doubted it was appropriate to revise the pre-print in this context. At that point, both Anthony Fauci and Francis Collins clarified their views by each saying something to the effect: “Just for the record, I want to be clear that I never suggested you delete or revise the pre-print.” Kristian continued to press the point that he could use his capacity as a screener at *bioRxiv* to upload a revised version of the pre-print. At that point, one of the NIH attendees (I think it was Francis Collins but I am not certain) said something to the effect: “Kristian, if he’s already submitted the pre-print, it’s better if you don’t pressure him to revise it.”

Source: Jesse Bloom and Vanity Fair

January 12, 2022: ‘That will just add fuel to the conspiracists’

Congressional staff and NIH negotiated an agreement to view unredacted copies of the emails obtained by BuzzFeed in June *in camera*. In other words, congressional staff could view the emails at NIH, transcribe them, and describe their contents, but not reproduce copies.

The fully unredacted notes starkly showed concerns among the authors about unusual features of the genome.

Garry insisted that the participation of the NIH did not influence their analysis in emails to The Intercept.

"Neither Drs. Fauci or Collins edited our Proximal Origins paper in any way. The major feedback we got from the Feb 1 teleconference was: 1. Don't try to write a paper at all — it's unnecessary or 2. If you do write it don't mention a lab origin as that will just add fuel to the conspiracists," Garry said in an email to the outlet.

After the story published, Garry emailed a follow-up comment: "One thing that could be misconstrued is that neither Dr Fauci or Dr Collins suggested in any way that we not write the Proximal Origin paper. Likewise, neither one suggested that we not mention the possibility of a Lab origin. These were comments from others in emails after the call."

July 1, 2022: Lipkin revealed to be former EcoHealth partner

Lipkin, a coauthor of "proximal origin," was found to have once been featured as a "partner" on the EcoHealth Alliance website. This relationship, confirmed by EcoHealth Alliance, is not reported in the paper's conflict of interest section.

July 31, 2022: Tie between Holmes and Wuhan Institute of Virology

One hundred and sixty-three partial sequences describing SARS-like coronaviruses appeared on an NIH database, but quickly disappeared from the database's search results. (These partial sequences remain searchable to people who know their accession numbers.)

Two of the authors are Shi, senior scientist at the Wuhan Institute of Virology, and Holmes, a coauthor of the "proximal origin" paper.

The uploads included partial sequences of RaTG13, a cousin virus to SARS-CoV-2.

"The really shocking thing about these submissions was that my name was on them ... I couldn't compute. I thought, 'why am I on this?'" Holmes said in a September 2022 interview. "Then I looked back, and it turns out there was this paper that was never published."

Holmes had contributed analysis and helped write an unpublished paper about bat coronaviruses in January 2018 at the request of a Shanghai scientist named Jie Cui, he said.

"It's just some [phylogenetic] trees and some recombination analysis," Holmes said. "They're interested particularly in what they call the 'southern lineage,' and where there was SARS1, and where SARS1 bat viruses are found in Guangdong and Yunnan Province. ... Is there a lineage that goes along that southern part of China?"

A handful of journals reject the paper because it does not include full genomes. Cui struggles to obtain the full genomes. The paper was withdrawn in October 2018.

"This is why I completely forgot about it, because it was never published," Holmes said.

Holmes has provided the partial sequences to the World Health Organization's Scientific Advisory Group on the Origins of Novel Pathogens, which is investigating the origins of COVID-19.

Meanwhile, this apparent conflict of interest has also gone undisclosed in *Nature Medicine*.