

The Origins of the Coronavirus Pandemic, Including but Not Limited to the Federal Government’s Funding of Gain-of-Function Research

I. The Unknown Origins of COVID-19

FINDING: SARS-CoV-2, the Virus that Causes COVID-19, Likely Emerged Because of a Laboratory or Research Related Accident.

Four years after the onset of the worst pandemic in 100 years, the weight of the evidence increasingly supports the lab leak hypothesis. Since the Select Subcommittee commenced its work in February 2023, more and more senior intelligence officials, politicians, science editors, and scientists increasingly have endorsed the hypothesis that COVID-19¹ emerged as the result of a laboratory or research related accident.

In January 2021, the State Department published an unclassified Fact Sheet entitled, “Fact Sheet: activity at the Wuhan Institute of Virology,” [hereinafter “Fact Sheet”] that stated the following.

- 1) “The U.S. government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illness.”² The June 2023 ODNI Assessment entitled, “Potential Links Between the Wuhan Institute of Virology and the Origin of the COVID-19 Pandemic,” [hereinafter “June 2023 ODNI Assessment”] supported this conclusion.³
- 2) “The WIV has a published record of conducting “gain-of-function” research to engineer chimeric viruses.”⁴ The June 2023 ODNI Assessment supported this conclusion and went further, stating, “[s]cientists at the WIV have created chimeras, or combinations of SARS-like coronaviruses through genetic engineering, attempted to clone other unrelated viruses, and used reverse genetic cloning techniques on SARS-like coronaviruses.”⁵ The June 2023 ODNI Assessment continued, “[s]ome of the WIV’s genetic engineering projects on coronaviruses involved techniques that could make it difficult to detect intentional changes.”⁶
- 3) “Despite the WIV presenting itself as a civilian institution, the United States had determined that the WIV collaborated on publications and secret projects with China’s military...since at least 2017.”⁷ Again, the June 2023 ODNI Assessment supported this

¹ Throughout this Report, “COVID-19” is used to describe SARS-CoV-2.

² FACT SHEET: ACTIVITY AT THE WUHAN INSTITUTE OF VIROLOGY, U.S. DEP’T OF STATE (Jan. 15, 2021) [hereinafter “Fact Sheet”].

³ POTENTIAL LINKS BETWEEN THE WUHAN INSTITUTE OF VIROLOGY AND THE ORIGIN OF THE COVID-19 PANDEMIC, OFFICE OF THE DIR. OF NAT’L INTELLIGENCE (June 2023) [hereinafter “June 2023 ODNI Assessment”].

⁴ Fact Sheet, *supra* note 2.

⁵ June 2023 ODNI Assessment, *supra* note 3.

⁶ *Id.*

⁷ Fact Sheet, *supra* note 2.

conclusion, stating, "...WIV personnel have worked with scientists associated with the PLA on public health-related projects and collaborated on biosafety and biosecurity projects."⁸

Further, the June 2023 ODNI Assessment stated, "[s]ome WIV researchers probably did not use adequate biosafety precautions at least some of the time prior to the pandemic in handling SARS-like coronaviruses, increasing the risk of accidental exposure to viruses."⁹

In February and March of 2023, DOE and FBI publicly acknowledged their respective assessments that COVID-19 was the likely result of a lab incident—FBI with moderate confidence and DOE with low confidence.¹⁰ Other intelligence elements assess COVID-19's emergence was likely zoonotic, albeit all with low confidence.¹¹

On March 8, 2023, Dr. Redfield testified:

Dr. Robert Redfield (March 8, 2023)

From the earliest days of the pandemic, my view was that both theories about the origin of COVID-19 needed to be aggressively and thoroughly examined. Based on my initial analysis of the data, I came to believe—and still believe today—that it indicates COVID-19 infections more likely were the result of an accidental lab leak than the result of a natural spillover event. This conclusion is based primarily on the biology of the virus itself, including its rapid high infectivity for human-to-human transmission which would then predict rapid evolution of new variants, as well as a number of other important factors to include the unusual actions in and around Wuhan in the fall of 2019...¹²

One month later in April 2023, Mr. Ratcliffe testified:

The Honorable John Ratcliffe (April 18, 2023)

First, let me state the bottom-line up front. My informed assessment as a person with as much access as anyone to our government's intelligence during the initial year of the pandemic has been and continues to be that a lab leak is the only explanation credibly supported by our intelligence, by science, and by commonsense. From a view inside the IC, if our intelligence and evidence supporting a lab leak theory was placed side-by-

⁸ June 2023 ODNI Assessment, *supra* note 3.

⁹ *Id.*

¹⁰ Hannah Rabinowitz, *FBI Director Wray acknowledges bureau assessment that Covid-19 likely resulted from lab incident*, CNN (updated Mar. 1, 2023); Jeremy Herb & Natasha Bertrand, *US Energy Department assesses Covid-19 likely resulted from lab leak, furthering US intel divide over virus origin*, CNN (Feb. 27, 2023).

¹¹ June 2023 ODNI Assessment, *supra* note 3.

¹² Investigating the Origins of COVID: Hearing Before the Select Subcomm. on the Coronavirus Pandemic, 118th Cong, 1, (Mar. 8, 2023) [hereinafter "Investigating the Origins of COVID-19"].

side with our intelligence and evidence pointing to a natural origins or spillover theory, the lab leak side of the ledger would be long, convincing, even overwhelming, while the spillover side would be nearly empty and tenuous.¹³

In January 2024, Mr. Wade voiced his increasing support for a lab incident origin.¹⁴ Mr. Wade astutely noted that “SARS2 possesses a furin cleavage site, found in none of the other 871 known members of its viral family, so it cannot have gained such a site through the ordinary evolutionary swaps of genetic material within a family.”¹⁵ With the natural evolution of a furin cleavage site being nonexistent, Mr. Wade further noted that EcoHealth and the WIV’s DEFUSE proposal, which was rejected by DARPA, sought to do what nature had not been ever known to do—insert a furin cleavage site into a SARS2 virus.¹⁶ It is, therefore, more than just a coincidence that COVID-19 emerged from the city with a lab preparing to conduct this research under cost-effective yet risky BSL-2 protocols.¹⁷

In June 2024, Dr. Chan explained five key points that support the lab leak scenario as more plausible than a zoonotic spillover.¹⁸

First, COVID-19 emerged in Wuhan, the city that happens to be the location of the China’s foremost research lab for SARS-like viruses.¹⁹ Dr. Shi, has been researching SARS-like viruses for over a decade and even initially wondered if the outbreak came from the WIV.²⁰

Next, in 2018, a year before the outbreak, EcoHealth, in partnership with the WIV, in a grant application to DARPA proposed to create a virus with SARS-CoV-2’s defining features. In their application to DARPA, EcoHealth and its WIV partners stated their intent to create a SARS-like virus with a furin cleavage site, which is the exact same feature that made humans susceptible to COVID-19 infection.²¹

Third, the WIV has a track record of engaging in this type of airborne viral research under low biosafety conditions.²² At the WIV, it was known that Chinese researchers conducted this type of research under BSL-2 protocols, which do not require masking at all times and involves less protective equipment.²³ In the U.S., this type of research would be conducted under BSL-3 protocols, which require stricter personal respirator use at all times and more protective

¹³ Investigating the Origins of COVID Part 2: China and the Available Intelligence: Hearing Before the Select Subcomm. on the Coronavirus Pandemic, 118th Cong, 1, (Apr. 18, 2023) [hereinafter “Investigating the Origins of COVID Part 2: China and the Available Intelligence”].

¹⁴ Nicholas Wade, *The Story of the Decade*, CITY JOURNAL (Jan. 25, 2024).

¹⁵ *Id.*

¹⁶ *Id.*

¹⁷ *Id.*

¹⁸ Alina Chan, *Why the Pandemic Probably Started in a Lab, in 5 Key Points*, THE N.Y. TIMES (June 3, 2024) [hereinafter “Chan”].

¹⁹ *Id.*

²⁰ *Id.*

²¹ *Id.*

²² *Id.*

²³ *Id.*

equipment.²⁴ In fact, in a draft proposal for the grant to DARPA, Dr. Daszak acknowledged that some of the SARS-CoV-2 research would be conducted at BSL-2 at the WIV.²⁵

The modeling team will use these data to build models of 1) risk of viral evolution and spillover, and 2) strategies to maximize inoculation strategy. Data on the diversity of bat spike proteins, prevalence of recombinant CoVs, ability to bind and infect human cells, degree of clinical signs in mouse models, will be used to estimate evolutionary rates, rates of recombination, and capacity to generate novel strains capable of human infection. Using dynamic metapopulation models, we will estimate the flow of genes within each bat cave, based on the known host and viral assemblages. This will inform how rapidly new CoV strains with distinct phenotypic characteristics evolve. Because of our unique collaboration among world-class modelers, and coronavirologists, we will be able to test model predictions of viral capacity for spillover by conducting spike protein-based binding and cell culture experiments. The BSL-2 nature of work on SARSr-CoVs makes our system highly cost-effective relative to other bat-virus systems (e.g. Ebola, Marburg, Hendra, Nipah), which require BSL-4 level facilities for cell culture.

We will use modeling approaches, the data above, and other biological and ecological data to estimate how rapidly high-risk SARSr-CoVs will re-colonize a bat population following immune boosting or priming. We will obtain model estimates of the frequency of inoculation required for both approaches, what proportion of a population needs to be reached to have effective viral dampening, and whether specific seasons, or locations within a cave would be more effective to treat. We will then model

Commented [BRS17]: IN the US, these recombinant SARS CoV are studied under BSL3, not BSL2, especially important for those that are able to bind and replicate in primary human cells. In china, might be growin these virus under bsl2. US reseachers will likely freak out.

Fourth, the evidence supporting that COVID-19 came from an animal at the Huanan Seafood Market in Wuhan is tenuous.²⁶ Dr. Chan points of that “the existing genetic and early case data show that all known COVID-19 cases probably stem from a single introduction of SARS-CoV-2 into people, and the outbreak at the Wuhan market probably happened after the virus had already been circulating in humans.”²⁷ Furthermore, no infected animal has been verified at the Wuhan market or its supply chain.²⁸

Finally, key evidence that would be expected if the virus had emerged from the wildlife trade is still missing.²⁹ In previous outbreaks, such as SARS in 2002 and MERS in 2012, infected animals were found, the earliest cases occurred in people exposed to live animals, and ancestral variants of the virus found in animals were discovered, but none of this evidence has been discovered for COVID-19.³⁰

In September 2024, Mr. Boris Johnson, former British Prime Minister, stated his belief that the COVID-19 pandemic originated via a laboratory or research related accident in Wuhan.³¹

²⁴ *Id.*

²⁵ Emily Kopp, *American scientists misled Pentagon on research at the Wuhan Institute of Virology*, U.S. RIGHT TO KNOW (Dec. 18, 2023).

²⁶ Chan, *supra* note 18.

²⁷ *Id.*

²⁸ *Id.*

²⁹ *Id.*

³⁰ *Id.*

³¹ Jane Dalton, *Boris Johnson claims Covid originated in lab, in sudden U-turn in his views*, INDEPENDENT (Sept. 29, 2024).

Mr. Johnson noted that the pandemic “now looks overwhelmingly likely that the mutation was the result of some botched experiment in a Chinese lab.”³²

In November 2024, Biden-Harris Administration COVID-19 Response Coordinator, Dr. Ashish K. Jha, wrote that Chinese “senior military officers have been writing for years about the potential benefits of offensive biological warfare.”³³ He also acknowledged that the COVID-19 virus might have accidentally leaked from a lab.³⁴

On November 21, 2024, Dr. Tim Spector, Professor at King’s College London, who played a significant role in the pandemic response in the United Kingdom, recently doubled down on his belief that the lab leak is the most likely source of the pandemic.³⁵ Dr. Spector noted that “[i]t’s looking increasingly like that was a bit of a cover-up and the most likely source of this was a lab leak from Wuhan.”³⁶

Over the course of the pandemic, there have also been studies suggesting COVID-19’s emergence was zoonotic and transferred from an animal to a human.³⁷ Dr. Lipkin described two of these studies as “armchair epidemiology,”³⁸ Dr. Baric described one as having a “major problem,”³⁹ and Dr. Holden Thorp, the Editor-in-Chief of *Science* (the publisher of two of these studies) testified these studies “do not conclusively prove [] the theory of natural origin.”⁴⁰

As Mr. Ratcliffe testified, the ledger on the side of lab leak is full of convincing evidence while the spillover side is nearly empty. Since January 2020, the body of evidence has only grown stronger in support of a lab leak theory.

FINDING: “The Proximal Origin of SARS-CoV-2” Was “Prompted” by Dr. Anthony Fauci to “Disprove” the Lab Leak Theory.

On February 16, 2020, Dr. Rambaut, on behalf of himself and his co-authors, Dr. Andersen, Dr. Lipkin, Dr. Holmes, and Dr. Garry posted “The Proximal Origin of SARS-CoV-2”

³² *Id.*

³³ Ashish K. Jha, *et al.*, *The U.S. could soon face a threat ‘more powerful’ than nuclear weapons*, THE WASH. POST (Nov. 11, 2024).

³⁴ *Id.*

³⁵ Sarah Knapton, *Lab leak most likely source of Covid, says Prof Tim Spector*, THE TELEGRAPH (Nov. 21, 2024).

³⁶ *Id.*

³⁷ Alexander Crits-Christoph, *et al.*, *Genetic tracing of market wildlife and viruses at the epicenter of the COVID-19 pandemic*, CELL 187: 5468-5482; Edward Holmes, *et al.*, *The origins of SARS-CoV-2: A critical review*, CELL 184: 4848-4856; Jonathan Pekar, *et al.*, *The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2*, SCIENCE 377:960-966; Michael Worobey, *et al.*, *The Hunan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic*, SCIENCE 377: 951-959; Edward Holmes, *et al.*, *The emergence and evolution of SARS-CoV-2*, ANN. REV. VIROL. (Sept. 11, 2024).

³⁸ Transcribed Interview of Ian Lipkin, M.D., John Snow Professor of Epidemiology, Columbia Univ. (Apr. 6, 2023) [hereinafter “Lipkin TI”].

³⁹ Transcribed Interview of Ralph Baric, Ph.D., Professor, University of N. Carolina, at 102 (Jan. 22, 2024) [hereinafter “Baric TI”].

⁴⁰ Academic Malpractice: Examining the Relationship Between Scientific Journals, the Government, and Peer Review: Hearing Before the Select Subcomm. on the Coronavirus Pandemic, 118th Cong, (Apr. 11, 202) (Statement of Dr. Holden Thorp, Editor-in-Chief, Science Journals).

on the website *Virological*.⁴¹ One month later, on March 17, 2020, “The proximal origin of SARS-CoV-2” [hereinafter “Proximal Origin”] was published in *Nature Medicine*.⁴²

The authors of Proximal Origin stated two primary conclusions: (1) “...[COVID-19] is not a laboratory construct or a purposefully manipulated virus,” and (2) “we do not believe that any type of laboratory-based scenario is plausible.”⁴³

January 2020

According to Dr. Farrar, the initial discussions regarding the sequence of COVID-19 and any unusual aspects began on January 8 or 9.⁴⁴ At that point it is unclear what the concerns were or who exactly was involved, however e-mails suggest that Dr. Farrar called both Chinese officials and Dr. Collins.⁴⁵

Message

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

Thanks Eddie.

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

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

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

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

Best wishes Jeremy

According to Dr. Farrar he became aware of “chatter” suggesting the virus looked almost engineered to infect human cells in the last week of January.⁴⁶ In Dr. Farrar’s own words, “[t]hat got my mind racing. This was a brand-new virus that seemingly sprang from nowhere. Except

⁴¹ Kristian Andersen, Ph.D., *et. al.*, *The Proximal Origin of SARS-CoV-2*, *VIROLOGICAL* (Feb. 16, 2020), <https://virological.org/t/the-proximal-origin-of-sars-cov-2/398>.

⁴² Kristian Andersen, Ph.D., *et. al.*, *The proximal origin of SARS-CoV-2*, *NATURE MEDICINE* (Mar. 17, 2020) [hereinafter “Proximal Origin”].

⁴³ *Id.*

⁴⁴ E-Mail from Jeremy Farrar, Dir., Wellcome Trust, to Eddie Holmes, Ph.D., *et. al.*, Professor, University of Sydney (July 28, 2020, 12:36 AM).

⁴⁵ *Id.* (Dr. Collins did not recall being on any calls with Chinese officials or Dr. Farrar, separately or together, during this time period.)

⁴⁶ Jeremy Farrar, *Spike: The Virus vs. The People – The Inside Story* (Profile Books 2021) [hereinafter “Spike: The Virus vs. The People – The Inside Story”].

that this pathogen had surfaced in Wuhan, a city with a BSL-4 virology lab which is home to an almost unrivalled collection of bat viruses.”⁴⁷ Dr. Farrar’s first concern was, “[c]ould the novel-coronavirus be anything to do with ‘gain-of-function’ (GOF) studies?”⁴⁸ This is a type of research that Dr. Farrar, much like Dr. Fauci, believed to be “ultimately useful.”⁴⁹

Around this same time, Dr. Andersen shared his concerns regarding the possibility the COVID-19 pandemic was the result of a lab leak and that it had properties that may have been genetically modified or engineered—specifically the furin cleavage site—with Dr. Holmes.⁵⁰ According to Dr. Holmes, Dr. Andersen texted, “Eddie, can we talk? I need to be pulled off a ledge here.”⁵¹

Dr. Andersen went on to express concerns regarding two distinct aspects of the virus—the RBD and the furin cleavage site. Dr. Andersen also found a paper written by Dr. Baric and Dr. Shi [hereinafter “Baric/Shi Paper”] that purported to have inserted furin cleavage sites into SARS. As recounted by Dr. Farrar, this paper was a “how-to-manual for building the Wuhan coronavirus in a laboratory.”⁵² Dr. Holmes responded, “fuck, this is bad” and “oh my god what worse words than that.”⁵³

On January 30, 2020, Dr. Holmes relayed Dr. Andersen’s concerns to Dr. Farrar via his burner phone.⁵⁴ Dr. Andersen recalled Dr. Holmes saying that Dr. Farrar acted as Dr. Holmes’ “handler.”⁵⁵ Then, as Dr. Holmes characterized it, the conversations went from “zero to 100.”⁵⁶

January 31, 2020

In a transcribed interview, Dr. Andersen testified that after discussing his concerns with Dr. Farrar, they began to organize a conference call [hereinafter “February 1 Conference Call”].⁵⁷ The February 1 Conference Call was a forum for Dr. Andersen to “walk through my concerns and then...discuss it.”⁵⁸

Dr. Kristian Andersen (June 16, 2023)

And Jeremy [Farrar] gets all of this set up. He, I’m sure, has been in touch with Tony Fauci at the time, reaches out to Dr. Fauci, asks him to call me.⁵⁹

⁴⁷ *Id.*

⁴⁸ *Id.*

⁴⁹ *Id.*

⁵⁰ Vincent Racaniello, This Week in Virology 940 (Sept. 28, 2022) [hereinafter “Racaniello”].

⁵¹ *Id.*

⁵² Spike: The Virus vs. the People, *supra* note 46.

⁵³ *Id.*; Racaniello, *supra* note 50.

⁵⁴ *Id.*

⁵⁵ Transcribed Interview of Kristian Andersen, Ph.D., Professor, Scripps Research, at 16 (June 16, 2023) (hereinafter “Andersen TI”).

⁵⁶ Racaniello, *supra* note 50.

⁵⁷ Andersen TI, *supra* note 55, at 16.

⁵⁸ *Id.*

⁵⁹ *Id.*

It is unclear whether Dr. Farrar and Dr. Fauci had significant contact prior to the call, but it was at this point that Dr. Farrar alerted Dr. Fauci to potential concerns and they began orchestrating a conference call.⁶⁰ Dr. Fauci's assistant replied, "Will call shortly..."⁶¹

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

Tony
Really would like to speak with you this evening

It is 10pm now UK

Can you phone me on +44 [REDACTED]

Jeremy

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

Will call shortly...

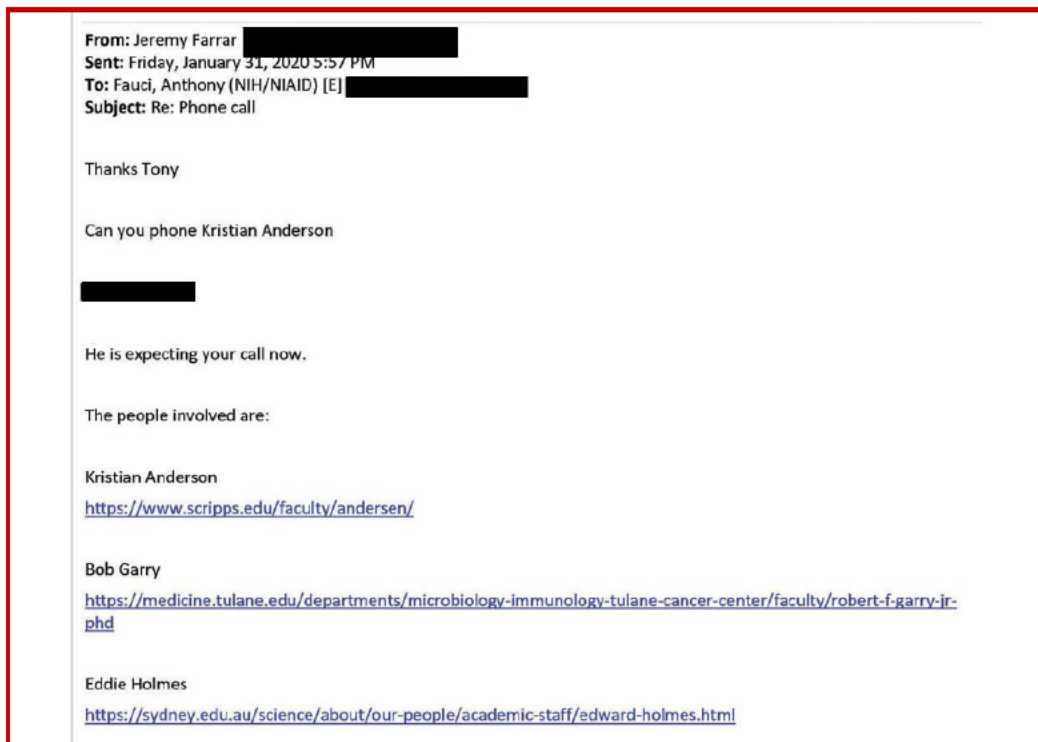
Patricia L. Conrad
Public Health Analyst and
Special Assistant to the Director
National Institute of Allergy and Infectious Diseases
The National Institutes of Health
[REDACTED]
Bethesda, Maryland 20892
[REDACTED]
[REDACTED] fax

Presumably, Dr. Fauci and Dr. Farrar discussed the concerns raised by Dr. Andersen and Dr. Holmes because after their call, Dr. Farrar responds to Dr. Fauci and asks him to call Dr. Andersen, stating, "[t]he people involved are: Kristian Andersen..., Bob Garry..., Eddie Holmes."⁶²

⁶⁰ E-Mail from Jeremy Farrar, Ph.D., Dir., Wellcome Trust, to Anthony Fauci, M.D., Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health (Jan. 31, 2020, 5:23 PM).

⁶¹ E-Mail from Patricia Conrad, Special Asst. to the Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, to Jeremy Farrar, Ph.D., Dir., Wellcome Trust (Jan. 31, 2020, 22:34).

⁶² E-Mail from Jeremy Farrar, Ph.D., Dir., Wellcome Trust, to Anthony Fauci, M.D., Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health (Jan. 31, 2020, 5:57 PM).



Dr. Fauci memorialized his January 31, 2020 conversation with Dr. Andersen.⁶³ In this e-mail, Dr. Fauci raised direct concerns regarding the furin cleavage site, directed Dr. Andersen to “get a group of evolutionary biologists together to examine carefully the data to determine if his concerns are validated,” and stated that if there is a possibility COVID-19 came from a lab leak, they would need to “report it to the appropriate authorities.”⁶⁴ This appears to be Dr. Fauci’s first mention of setting up a conference call and drafting a report. Dr. Fauci concluded by saying, “...I will alert my U.S. Government official colleagues of my conversation...and determine what further investigation they recommend.”⁶⁵

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⁶³ E-Mail from Anthony Fauci, M.D., Dir., Nat’l Inst. of Allergy & Infectious Diseases, Nat’l Insts. of Health, to Jeremy Farrar, Ph.D., Dir., Wellcome Trust, & Kristian Andersen, Ph.D., Professor, Scripps Research (Jan. 31, 2020, 4:38 PM).

⁶⁴ *Id.*

⁶⁵ *Id.*

On Fri, Jan 31, 2020 at 4:38 PM Fauci, Anthony (NIH/NIAID) [E] [REDACTED] wrote:

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

Anthony S. Fauci, MD
Director

REV0000750

National Institute of Allergy and Infectious Diseases

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Dr. Andersen testified that January 31 was the first time he spoke to Dr. Fauci personally, outside of potential interactions at conferences.⁶⁶ Accordingly, it was also on the January 31 phone call between Dr. Fauci and Dr. Andersen when the first discussion of a paper regarding a possible lab leak took place.⁶⁷

Dr. Kristian Andersen (June 16, 2023)

Q. Was this the first time that you had ever spoken to Dr. Fauci, like personally?

A. Probably. Yeah...

Q. Outside of conferences or - -?

A. Sure. Yes. Yes. Yes. Absolutely, yes.

⁶⁶ Andersen TI, *supra* note 55, at 16.

⁶⁷ *Id.*

Q. So, I think you testified, and you can correct me if this isn't a fair characterization, that Dr. Fauci suggested a peer-reviewed paper of some kind. When did that suggestion happen?

A. That happened - - again, the first phone call I had with him, which was immediately prior - - I think a day prior [January 31], right, to the conference call itself [February 1] where I relayed my initial concerns and findings. He specifically suggested considering writing a peer-reviewed publication on it, and specifically I remember hearing him saying that if you think this came from a lab, you should write this up as a peer-reviewed paper, so it can be judged by the peer community basically, yeah.⁶⁸

Then, Mr. Folkers forwarded Dr. Fauci an article entitled, "Mining coronavirus genomes for clues to the outbreak's origins."⁶⁹ This article directly mentions the Baric/Shi Paper that Dr. Andersen found alarming, and links directly EcoHealth to the WIV.⁷⁰ Dr. Fauci forwarded the article to Dr. Farrar and Dr. Andersen and said, "[t]his just came out today. You may have seen it. If not, it is of interest to the current discussion."⁷¹ Dr. Andersen responded:⁷²

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

Hi Tony,

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

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

Best,
Kristian

⁶⁸ *Id.*

⁶⁹ E-Mail from Greg Folkers, Chief of Staff, Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, to Anthony Fauci, M.D., Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health (Jan. 31, 2020); Jon Cohen, *Mining coronavirus genomes for clues to the outbreaks' origins*, SCIENCE (Jan. 31, 2020).

⁷⁰ Jon Cohen, *Mining coronavirus genomes for clues to the outbreaks' origins*, SCIENCE (Jan. 31, 2020).

⁷¹ E-Mail from Anthony Fauci, M.D., Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, to Jeremy Farrar, Ph.D., Dir., Wellcome Trust, & Kristian Andersen, Ph.D., Professor, Scripps Research (Jan. 31, 2020).

⁷² E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Anthony Fauci, M.D., Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, to Jeremy Farrar, Ph.D., Dir., Wellcome Trust (Jan. 31, 2020, 10:32 PM).

Dr. Andersen clarified what “unusual features” he was referencing.

Dr. Kristian Andersen (June 16, 2023)

Q. Which features, at that time, were you talking about?

A. Yeah, I’m talking about, like, the furin cleavage site, the receptor binding domain, and a few things associated with that, the BamHI restriction site that I mentioned, as well as some features associated with that - - basically, what I ended up presenting the next day at that conference call.⁷³

Dr. Andersen subsequently confirmed that when he said the “genome inconsistent with expectations from evolutionary theory” he meant he thought COVID-19 could have been engineered.

Dr. Kristian Andersen (June 16, 2023)

Q. ...[W]as it the furin cleavage site and the RBD that looked inconsistent from evolutionary theory?

A. And when I’m saying the genome is inconsistent with expectations from evolutionary theory, it’s a bit of *a fancy way of basically saying, like, look, guys, I think this could be engineered.*⁷⁴

The next day, February 1, 2020, a group of scientists, including Dr. Fauci, gathered via conference call for Dr. Andersen to present these findings and discuss a path forward.

February 1, 2020

On February 1, 2020, Dr. Farrar emailed a large group to set up the February 1 Conference Call to discuss Dr. Andersen’s concerns about the origins of COVID-19. The original attendee list included:

Kristian Andersen
Bob Garry
Christian Drosten
Tony Fauci
Mike Ferguson
Ron Fouchier
Eddie Holmes

⁷³ Andersen TI, *supra* note 55, at 16.

⁷⁴ *Id.*

Marion Koopmans
Stefan Pohlmann
Andrew Rambaut
Paul Schreier
Patrick Vallance.⁷⁵

Despite Dr. Farrar sending the invitation on February 1, Dr. Andersen testified he was aware of the potential of a call prior to February 1.

Dr. Kristian Andersen (June 16, 2023)

Q. When did you first learn of this call? Was it when the roster was sent out, February 1st?

A. No. I knew that the call was going to happen, because Eddie, myself had talked about it, and I talked to Jeremy Farrar... This is where I became aware of all the details surrounding the conference call.⁷⁶

In a transcribed interview, Dr. Garry testified he was also aware of the potential conference call prior to February 1.

Dr. Robert Garry (June 9, 2023)

Q. How were you invited to this call?

A. I believe I received an email from Jeremy Farrar.

Q. ...[T]o the best of your recollection, what day was that?

A. Probably the day before or - - at most 2 days before, but I think it was the day before.⁷⁷

In addition to Dr. Fauci, at least two other federal government officials were on the call despite not being on the official roster—Dr. Collins and Dr. Tabak.

E-mails suggest that Dr. Fauci personally invited Dr. Collins.⁷⁸

⁷⁵ E-Mail from Jeremy Farrar, Ph.D., Dir., Wellcome Trust, to Anthony Fauci, M.D., *et. al.*, Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health (Feb. 1, 2020).

⁷⁶ Andersen TI, *supra* note 55, at 16.

⁷⁷ Transcribed Interview of Robert Garry, Ph.D., Professor, Tulane University School of Medicine, at 16 (June 9, 2023) [hereinafter "Garry TI"].

⁷⁸ E-Mail from Anthony Fauci, M.D., Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, to Jeremy Farrar, Ph.D., Dir., Wellcome Trust, & Francis Collins, M.D., Ph.D., Dir., Nat'l Insts. of Health (Feb. 1, 2020, 15:48); E-Mail from Anthony Fauci, M.D., Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, to Robert Garry, Ph.D., Professor, Tulane School of Medicine, *et. al.* (Feb. 1, 2020, 15:50).

From: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6) >
Date: Saturday, 1 February 2020 at 15:48
To: Jeremy Farrar (b) (6)
Cc: Francis Collins (b) (6)
Subject: RE: Teleconference

Jeremy:
Francis will be on the call. He is trying to phone you.
Tony

From: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)
Date: Saturday, 1 February 2020 at 15:50
To: "Garry, Robert F" (b) (6), Jeremy Farrar (b) (6)
Cc: Patrick Vallance (b) (6), "Drosten, Christian" (b) (6), Marion Koopmans (b) (6), Edward Holmes (b) (6), "Kristian G. Andersen" (b) (6), Paul Schreier (b) (6), Michael FMedSci (b) (6), Francis Collins (b) (6), "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Subject: RE: Teleconference

Please include Francis Collins (copied here) on all subsequent correspondence regarding this call. Thanks.

On March 24, 2023, the Select Subcommittee requested Dr. Fauci clarify whether he personally invited Dr. Collins to the conference call.⁷⁹ On March 27, 2023, Dr. Fauci responded, via Counsel, “[a]s one would reasonably expect, Dr. Fauci advised his immediate supervisor, Dr. Francis Collins, that the call was taking place. Dr. Collins expressed an interest in joining the call.”⁸⁰ In a transcribed interview, Dr. Fauci further clarified this sequence of events.

Dr. Anthony Fauci (January 9, 2024)

Q. So I want to talk about the first forward of yours to Dr. Collins. Did Dr. Collins request to be on the call? Like, how did the process -- you obviously forwarded the call-in details to Dr. Collins. How did that process play out?

A. Well, Dr. Collins is my boss. So this seemed like a pretty important call for NIH, so I thought it would be a good idea to let my boss know.

⁷⁹ Letter from Hon. Brad Wenstrup, Chairman, Select Subcomm. on the Coronavirus Pandemic, to Anthony Fauci, M.D. Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health (Mar. 24, 2023).

⁸⁰ Letter from David Schertler & Danny Ornato, Counsel for Dr. Anthony S. Fauci, to Hon. Brad Wenstrup, Chairman, Select Subcomm. on the Coronavirus Pandemic (Mar. 27, 2023).

Q. So you got invited -- or you had the January 31st call, got invited to the conference call after Farrar set it all up, and then went and was like, "Dr. Collins, there's this call happening. Would you like to take part?" Is that fair?

A. I believe that's the way it went, because -- yeah, I believe that's the way it went.

Q. Okay. It's been in the news for a while and Dr. Redfield has talked about this a lot and testified in front of us in March that he was not included in the call. He was very clear to say he was not -- he's not testifying that he was intentionally excluded, just that he was not included. At any point, did --

A. Actually, he said that I kept him out of the call because he had a different viewpoint.

Q. He did say that --

A. He said that clearly.

Q. Do you recall having any conversations with --

A. Sorry.

Q. No. No problem. Do you recall having any conversations with Dr. Redfield about the call?

A. No. No.

Q. Why not?

A. Because why would I do that? This was a call that was organized by Jeremy Farrar, who was the organizer of the call, and it wasn't my call who was in and on. But it was perfectly appropriate for me to notify my boss.

Q. This is the beginning of a pandemic, discussing how to respond to the pandemic.

A. Yeah. Yeah.

Q. Dr. Redfield is the head of the CDC --

A. No, I'm sorry, I disagree with you.

Q. Okay.

A. I disagree with you completely. It is my responsibility to notify my boss. The next morning, I notified the chief of staff of the Department of Health and Human Services, who is the chief of staff to the Secretary, who is Bob Redfield's boss.

Q. Did you have any conversations with Dr. Redfield after the fact regarding the call?

A. I don't recall.⁸¹

Dr. Tabak was also on the February 1 Conference Call.⁸²

Message

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

Dear Jeremy et al

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

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

Dr. Lawrence Tabak (January 5, 2024)

Q. ...And I don't - - we don't know - - I don't know if Dr. Fauci ever responded, but did you end up on the February 1st conference call?

A. I did.⁸³

Dr. Andersen testified to what he presented on the February 1 conference call.

⁸¹ Transcribed Interview of Anthony Fauci, M.D., former Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, at 61-63 (Jan. 9, 2024) [hereinafter "Fauci TI 2"].

⁸² E-Mail from Mike Ferguson, Professor, University of Dundee, to Jeremy Farrar, Ph.D., *et. al.*, Dir., Wellcome Trust (Feb. 9, 2020, 12:00 PM).

⁸³ Transcribed Interview of Lawrence A. Tabak, D.D.S., Ph.D., Principal Dep. Dir., Nat'l Insts. of Health, at 133 (Jan. 5, 2024) [hereinafter "Tabak TI"].

Dr. Kristian Andersen (June 16, 2023)

Q. And what, to the best of your recollection, and briefly, what did you present on the call?

A. I presented the main findings I had, which was some of the features that I found to be unusual in the viral genome, including the receptor binding domain, the furin cleavage site, the damage, one site which is a restriction site, and also just outlining some of the research that have been ongoing at the Wuhan Institute of Virology. And I had a presentation, which you have as part of your exhibits too.

Q. Regarding the Wuhan Institute of Virology, what did you present?

A. Just in broad terms, the fact that they were culturing viruses from bats, or attempting to culture viruses from bats, isolate viruses from bat samples, which is not easy, in BSL-2; and, also, some of their chimeric work using WIV-1, for example, which is a common backbone that they are using; as well as just the general strategies around creating chimeric viruses, much of which I believe was done in BSL-2 and, as I mentioned, animal work in BSL-3. But those were my, sort of, concerns around the research and the reason, of course, for why we need to consider a potential lab leak as a scientific hypothesis, yes.⁸⁴

Dr. Andersen further testified that the primary participants on the call were himself, Dr. Rambaut, Dr. Holmes, Dr. Christian Drosten,⁸⁵ Dr. Ron Fouchier,⁸⁶ and Dr. Marion Koopmans.^{87, 88} Both Dr. Garry and Dr. Andersen testified about any comments made by Dr. Fauci or Dr. Collins on the February 1 Conference Call.

Dr. Robert Garry (June 9, 2023)

Q. Did [Dr. Fauci] say anything?

A. He didn't say a whole a lot.

Q. To your recollection - - what did he say?

⁸⁴ Garry TI, *supra* note 77, at 89-90.

⁸⁵ Dr. Christian Drosten: Professor, Deputy Coordinator Emerging Infections, German Center for Infection Research, DE.

⁸⁶ Dr. Ron Fouchier: Deputy Head of the Erasmus MC Department of Viroscience, Erasmus MC, NL.

⁸⁷ Dr. Marion Koopmans: Head of the Erasmus MC Department of Viroscience, Erasmus MC, NL.

⁸⁸ Andersen TI, *supra* note 55, at 98.

A. He just acknowledged that he was there, but the details are not really clear. He really didn't say much of substance. It was, you know -- I mean, Jeremy Farrar was clearly sort of introducing and ending the meeting. It was his call to make. Neither Fauci or Collins really had much to say, other than just, you know, maybe a point of clarification here or there.

Q. ...Was Dr. Collins on the call?

A. He was on the call. What I remember was is that he was basically on and off the call, because I think he was having some kind of a social event at the time. So, he did come on and off. But he, you know, he made his presence, you know, just I'm here, basically, known a couple of times.

Q. Was that - - to your recollection, was that the substance of his speaking role?

A. He really didn't offer anything scientifically.⁸⁹

Dr. Kristian Andersen (June 16, 2023)

Q. On the conference call -- we talked a little bit about it -- what do you recall Dr. Fauci saying, if he said anything?

A. I honestly don't remember Dr. Fauci, Collins -- I believe there might've been other NIH contingents on the call too. They probably had some questions, but I don't recollect that they -- they certainly didn't add anything of substance to the scientific discussion. Again, the discussions were: Jeremy said a few things to sort of set up the call and "here's what we're going to do," but, otherwise, the conversation was just between myself, Eddie Holmes, Andy Rambaut, Christian Drosten, Ron Fouchier in particular, so among the experts present on the call.

Q. Do you recall Dr. Collins saying anything on the conference call?

A. I do not, no.⁹⁰

⁸⁹ Garry TI, *supra* note 77, at 132.

⁹⁰ Andersen TI, *supra* note 55, at 96.

In a transcribed interview, Dr. Tabak testified he joined the call to discuss the presence of O-linked glycans and that the presence of these glycans does not indicate whether COVID-19 emerged as a natural spillover or via a laboratory related incident.

Dr. Lawrence Tabak (January 5, 2024)

Q. ...So kind of just the invitation just kind of fell into your inbox, and you went from there?

A. I had a specific reason for wanting to join the call.

Q. What was that?

A. Because I had one observation that I wanted to share with the group, and I did.

Q. Was it the O-linked glycans?

A. Correct.

Q. I appreciate it. I'm not a scientist at all, so, like, anything that I've learned is because I've just been listening to people like you. But the presence of the O-linked glycans themselves does not lean one way or another?

A. I don't think so.

Q. Okay.

A. I think you could argue it either way. I really do.⁹¹

The February 1 conference call was subsequently summarized in a memo.⁹²

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⁹¹ Tabak TI, *supra* note 83, at 134- 136.

⁹² E-Mail from Lawrence Kerr, Ph.D., Dir., Off. Of Pandemic and Emerging Threats, Off. Of Global Affairs, U.S. Dep't of Health & Human Servs., to REDACTED (Feb. 5, 2020 1:54 AM).

DRAFT PROPOSAL: WHO-Convened Discussion on Evolutionary Origins of 2019-nCoV

Since the release of the first full genome sequence of 2019-nCoV on January 10, 2020, the global scientific community has been rapidly and diligently analyzing the available sequence information and other data in order to learn more about the origins and properties of this newly emerging virus. Initial analyses have identified phylogenetic linkages to other betacoronaviruses from bats, and we anticipate learning more about the origins of this virus as additional sequences are released and further analyses are performed. However, the combination of the global spotlight on the outbreak, the speed at which the results of these analyses are being released (not all of which have been peer-reviewed), and the creation of rumors by multiple and varied interpretations of the results have fueled rumors and suspicion of potential intentional creation of this new virus. To address responsibly such rumors and more fully understand the potential future risk to human health from this and other coronaviruses of animal origin, we propose that WHO bring together scientific experts that are broadly representative of the global scientific community for the specific purpose of evaluating the evolutionary origins of 2019-nCoV.

On February 1, 2020, U.S. National Institutes of Health Director Francis Collins, U.S. National Institute of Allergy and Infectious Diseases Director Anthony Fauci, and Wellcome Trust Director Jeremy Farrar discussed emerging published analyses on potential evolutionary origins of the virus with several highly esteemed scientists with expertise in evolutionary biology. The group was unanimous in their assessment that the paper by an Indian research group pointing out that there are HIV gene sequences in the 2019-nCoV virus and thus indicating intentional insertion were not credible. However, several in the group noted that the sequences of published isolates of the nCoV included mutations in the virus that have never been seen before in a bat virus. Although there were some who felt such mutations could occur naturally, others felt that they were suggestive of intentional insertion, thus questioning the origin of the virus. Thus, the group agreed that it would be beneficial to gather a larger group of scientific experts broadly representative of the global scientific community convened by WHO to discuss the evolutionary origins of 2019-nCoV and its lessons for future risk assessment and understanding of animal/human coronaviruses.

Participants in the call included:

- Francis Collins, Director of the U.S. National Institutes of Health, U.S.;
- Anthony Fauci, Director of the U.S. National Institute of Allergy and Infectious Diseases, U.S.;
- Jeremy Farrar, Director of the Wellcome Trust;
- Patrick Vallance, U.K. Chief Scientific Adviser and Head of the Government Science and Engineering;
- Kristian Anderson, Director of Infectious Disease Genomics, Scripps Research Translational Institute, CA, U.S.;
- Christian Drosten, Director of Human Virology at the German Center for Infection Research at Charité – Universitätsmedizin, Germany;
- Edward Holmes, Professor of Viral Evolution at University of Sydney;
- Andrew Rambaut, Professor of Molecular Evolution, University of Edinburgh’s Institute of Evolutionary Biology, U.K.;
- Ron Fouchier, Deputy Head of Department of Viroscience, Erasmus Medical Center, NL;
- Robert Garry, Professor of Virology, Tulane University School of Medicine, Louisiana, U.S. ;
- Mike Ferguson, Professor of Life Sciences at University of Dundee, U.K.; and
- M.P.G. Koopmans, Head of Department of ViroScience, Erasmus Medical Center, NL.

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Both Dr. Andersen and Dr. Garry testified regarding if Dr. Fauci ever directed them to write a paper regarding the origins of COVID-19. Dr. Garry testified, “he never directed that to me.”⁹³ However, Dr. Garry clarified, “I’m not privy to all the communications that Dr. Fauci had with the other authors.”⁹⁴ Dr. Andersen testified that in addition to Dr. Fauci “suggesting” a paper about a potential lab leak on January 31, 2020, on the February 1 Conference Call, Dr. Fauci “encouraged to, you know, follow the scientific process on this which ultimately ends up in peer-reviewed publications.”⁹⁵ Dr. Andersen clarified that Dr. Fauci specifically mentioned drafting a peer-reviewed paper on January 31, stating, “he specifically mentioned that if I believed this was a lab leak, I should consider writing a peer-reviewed paper on it.”⁹⁶

When Dr. Andersen presented a draft of Proximal Origin to *Nature*, he stated it was “prompted” by Dr. Fauci and later stated the goal of Proximal Origin was to “disprove the lab leak theory.”⁹⁷

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⁹³ Garry TI, *supra* note 77, at 133-134.

⁹⁴ *Id.*

⁹⁵ Andersen TI, *supra* note 55, at 145.

⁹⁶ *Id.*

⁹⁷ E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Clare Thomas, Editor, *Nature* (Feb. 12, 2020, 23:09); E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Christian Drosten, Ph.D., Deputy Coordinator for Emerging Infections, German Center for Infection Research, *et. al.* (Feb. 8, 2020).

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

Dear Clare,

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

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

Best,
Kristian

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

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

P: [REDACTED]
C: [REDACTED]
T: [REDACTED]
E: [REDACTED]
W: [REDACTED]

Assistant: [REDACTED]

When asked about this e-mail, Dr. Garry testified:

Dr. Robert Garry (June 9, 2023)

Q. Did Dr. Andersen ever express this to you, the feeling that he was prompted by Dr. Farrar, Dr. Fauci, and Dr. Collins?

A. I mean, I think in the -- in the broad sense. Yeah, I'm not quite so sure how to answer that. I mean, you know, this is the first time I'm actually seeing this email, the way he wrote it here. So, I'm a little surprised that he wrote it that way. I probably wouldn't have written it this way. But, you know, I think you're probably going to have to ask Kristian what he thought about, you know, why he put it that

way. Maybe he was, you know -- I don't know. I really shouldn't speculate on that. You probably need to ask him.⁹⁸

When asked about this email, Dr. Andersen confirmed that he was referencing the January 31 phone call with Dr. Fauci.

Dr. Kristian Andersen (June 16, 2023)

Q. What did you mean by “prompted by Jeremy Farrar, Tony Fauci, and Francis Collins”?

A. I mean specifically that -- again, as I've already explained, is that they prompted us to the idea of seriously considering the origin of the virus and to consider producing a paper on that...*And, again, remember my first conversation with Tony Fauci, where he specifically suggests that if I think this came from the lab, I should consider writing a scientific paper on it.*

Q. So that's what the - - the prompt he was referencing - - that first conversation?

A. *Correct.*⁹⁹

The first draft of a report that would become Proximal Origin was completed by 7:40 p.m. on February 1—only hours after the conference call. While it may not have been the goal of the February 1 Conference Call, a written product of some sort was certainly discussed and contemplated on the February 1 Conference Call.

Dr. Robert Garry (June 9, 2023)

Well, you know, of course, we had the teleconference on February the 1st, 2020. And we had already, you know, had many discussions amongst ourselves, I mean. And by ourselves, I mean Kristian and Eddie and Andrew and I, with other people. So, you know, there were sort of notions and ideas circulating around.

And, you know, the possibility of the paper, we're scientists. We write papers. We communicate. We do, you know, we do science communication. That's the sort of the final stamp on a lot of work that you might do is to write up a paper. So, of course, I think that was in everyone's mind...

⁹⁸ Garry TI, *supra* note 77, at 166.

⁹⁹ Andersen TI, *supra* note 55, at 170.

And so, I think by, you know, by that February 1 teleconference, if you want to mark it there, I mean, it didn't take too many days after that.¹⁰⁰

The Stated Goals of Proximal Origin

First, on February 8, 2020, Dr. Andersen wrote, “[o]ur main work over the past couple of weeks has been focused on trying to disprove any type of lab theory, but we are a crossroad where the scientific evidence isn’t conclusive enough to say that we have high confidence in any of the three main theories considered.”¹⁰¹

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

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

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

As to publishing this document in a journal, I am currently not in favor of doing so. I believe that publishing something that is open-ended could backfire at this stage. I think it's important that we try to gather additional evidence - including waiting on the pangolin virus sequences and further scrutinize the furin cleavage site and O-linked glycans - before publishing. That way we can (hopefully) come out with some strong conclusive statements that are based on the best data we have access to. I don't think we are there yet.

Best,
Kristian

Second, on February 20, 2020, Dr. Andersen—in trying to defend the viability of Proximal Origin—wrote, “[u]nfortunately none of this helps refute a lab origin and the possibility must be considered as a serious scientific theory (which is what we do) and not dismissed out of hand as another ‘conspiracy’ theory. We all really, really wish that we could do that (that’s how this got started), but unfortunately it’s just not possible given the data.”¹⁰²

¹⁰⁰ Garry TI, *supra* note 77, at 130-131.

¹⁰¹ E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Christian Drosten, Ph.D., Deputy Coordinator for Emerging Infections, German Center for Infection Research, *et. al.* (Feb. 8, 2020, 22:15).

¹⁰² E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Claire Thomas, Ph.D., Senior Editor, Nature (Feb. 20, 2020, 17:48).

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

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

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

Best,
Kristian

According to Dr. Farrar, in addition to the specific goal of disproving the lab leak theory, Proximal Origin was to be a "go to scientific statement to refer to."¹⁰³ Further, Dr. Farrar e-mailed Dr. Daszak and stated the goal of Proximal Origin was to "effectively [put] to bed the issue of the origin of the virus."¹⁰⁴

From: Jeremy Farrar <[REDACTED]>
To: "Peter Daszak" <[REDACTED]> "Christian Drosten"
[REDACTED] "Michael RYAN" <[REDACTED]> "Bernhard F. SCHWARTLANDER"
Subject: COVID-19 issue
Sent: Wed 2/12/2020 9:34:49 AM (UTC-05:00)

Got a taxi to airport and on flight with Peter.

I hope there is a paper/letter ready this week to go to Nature (and WHO) which effectively puts to bed the issue of the origin of the virus.

I do think important to get ahead of even more discussion on this which may well come if this spreads more to US and elsewhere and other "respected" scientists publish something more inflammatory.

¹⁰³ E-Mail from Jeremy Farrar, Ph.D., Dir., Wellcome Trust, to Kristian Andersen, Ph.D., *et. al.*, Professor, Scripps Research (Feb. 8, 2020).

¹⁰⁴ E-Mail from Jeremy Farrar, Ph.D., Dir., Wellcome Trust, to Peter Daszak, Ph.D., Pres., EcoHealth Alliance, Inc. (Feb. 12, 2020, 9:34 AM).

The Possible Motives of Proximal Origin

The first possible motive to downplay the lab leak theory was an interest by those involved to defend China. This motive was expressed by numerous individuals including Dr. Farrar, Dr. Rambaut, Dr. Andersen, Dr. Fouchier. Similarly, Dr. Collins expressed concerns regarding “international harmony.”¹⁰⁵

1. Dr. Andrew Rambaut

On February 2, 2020, Dr. Rambaut, communicating over a private Slack channel with Dr. Andersen, Dr. Holmes, and Dr. Garry, wrote, “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 process.”¹⁰⁶

2. Dr. Kristian Andersen

In response to Dr. Rambaut’s message above, Dr. Andersen replied, “[y]up, I totally agree that that’s a very reasonable conclusion. Although I hate when politics is injected into science – but its impossible not to, especially given the circumstances.”¹⁰⁷

3. Dr. Ron Fouchier

Dr. Fouchier, in emails following the February 1 Conference Call, stated, “...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.”¹⁰⁸

4. Dr. Francis Collins

Dr. Collins, in emails following the February 1 Conference Call, stated, “...the voices of conspiracy will quickly dominate, doing great potential harm to science and international harmony.”¹⁰⁹

The second possible motive to downplay the lab leak theory was to lessen the likelihood of increased biosafety and laboratory regulations. Dr. Fouchier stated, “[t]his manuscript would be much stronger if it focused on the likelihood of the first 2 scenarios as compared to intentional or accidental release. That would also limit the chance of new biosafety discussion that would

¹⁰⁵ E-Mail from Francis Collins, M.D., Dir. Nat’l Insts. of Health, to Jeremy Farrar, M.D., *et. al.*, Dir. Wellcome Trust (Feb. 2, 2020).

¹⁰⁶ Message from Andrew Rambaut, Ph.D., Slack (Feb. 2, 2020, 11:53 a.m.).

¹⁰⁷ Message from Kristian Andersen, Ph.D., Slack (Feb. 2, 2020, 11:56 a.m.).

¹⁰⁸ E-Mail from Ron Fouchier, Ph.D., Deputy Head of the Erasmus MC Department of Viroscience, Erasmus MC, to Jeremy Farrar, Ph.D., Dir. Wellcome Trust, *et. al.* (Feb. 2, 2020, 8:30 AM).

¹⁰⁹ E-Mail from Francis Collins, M.D., Ph.D., Dir. Nat’l Insts. of Health, to Jeremy Farrar, Ph.D., Dir. Wellcome Trust, *et al.* (Feb. 2, 2020, 10: 27).

unnecessarily obstruct future attempts of virus culturing for research and diagnostic purposes for any (emerging/zoonotic virus).”¹¹⁰

Message

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

I am not in favor of publishing as is. I fail to see how the last of the three discussed scenarios (passaging) does not fall under the category of “laboratory manipulation”. There is no evidence that might hint to this scenario and hence it should be put aside just like the engineering option. As far as I am aware, no laboratory has worked on passaging the pangolin-origin virus, the bat-CoV RaTG13, or another closely related virus or had access to it prior to the outbreak. That nCoV-2019 could originate from a SARS-like virus in Chinese labs can also be excluded. This information could be added after reference 10 in the manuscript, to provide further argument.

If we assume passaging as a possible scenario here, we must assume it is also plausible for all outbreaks from the past, present and future. This manuscript would be much stronger if it focused on the likelihood of the first 2 scenarios as compared to intentional or accidental release. That would also limit the chance of new biosafety discussions that would unnecessarily obstruct future attempts of virus culturing for research and diagnostic purposes for any (emerging/zoonotic) virus.

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

With kind regards,
Ron

The Involvement of Dr. Fauci, Dr. Collins, and Dr. Farrar

Throughout the drafting process, the authors of Proximal Origin were keenly aware of the influence of Dr. Fauci, Dr. Collins, and Dr. Farrar.

It appears a draft of Proximal Origin did not leave the authorship group until on or around February 4 or 5. Dr. Andersen wrote to Dr. Holmes, Dr. Garry, and Dr. Rambaut, “[u]nless others have further comments, I’d say this is ready to go up the chain.”¹¹¹ Dr. Holmes responded, “[w]orks for me. Should I quickly check with Jeremy to see if he is happy for it to be circulated to the higher group?”¹¹² A few hours later, Dr. Holmes sent the first summary to Dr. Farrar.¹¹³

¹¹⁰ E-Mail from Ron Fouchier, Ph.D., Deputy Head of the Erasmus MC Department of Viroscience, Erasmus MC, to Jeremy Farrar, Ph.D., Dir. Wellcome Trust, *et. al.* (Feb. 8, 2020, 11:36 AM).

¹¹¹ E-Mail from Kristian Andersen, Ph.D., Professor Scripps Research, to Robert Garry, Ph.D., Professor, Tulane School of Medicine, *et. al.* (Feb. 5, 2020).

¹¹² E-Mail from Dr. Edward Holmes, Ph.D., Professor, University of Sydney, to Kristian Andersen, Ph.D., *et. al.*, Professor Scripps Research (Feb. 4, 2020).

¹¹³ E-Mail from Dr. Edward Holmes, Ph.D., Professor, University of Sydney, to Robert Garry, Ph.D., *et. al.*, Professor, Tulane School of Medicine (Feb. 4, 2020, 12:36 PM).

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

I've just passed to Jeremy.

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

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

Dr. Farrar immediately sent the draft to Dr. Fauci and Dr. Collins.¹¹⁴

From: Jeremy Farrar <[REDACTED]> (b) (6)
Sent: Tuesday, February 4, 2020 2:01 AM
To: Fauci, Anthony (NIH/NIAID) [E] <[REDACTED]> (b) (6); Collins, Francis (NIH/OD) [E] <[REDACTED]> (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

In response to the draft, Dr. Collins wrote, "...repeated tissue culture passage is still an option – though it doesn't explain the O-linked glycans" and "I'd be interested in the proposal of accidental lab passage in animals (which ones?)." Dr. Fauci responded, "?? Serial passage in ACE2-transgenic mice."

After Dr. Farrar received their responses, he recounted them to Dr. Holmes.¹¹⁵

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¹¹⁴ E-Mail from Jeremy Farrar, Ph.D., Dir. Wellcome Trust, to Anthony Fauci, Dir., Nat'l Inst. of Allergy & Infectious Diseases, Nat'l Insts. of Health, & Francis Collins, M.D., Ph.D., Dir., Nat'l Insts. of Health (Feb. 4, 2020, 2:01 AM).

¹¹⁵ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Robert Garry, Ph.D., Professor, Tulane School of Medicine, *et. al.* (Feb. 4, 2020, 2:59 PM).

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

Agreed. Timing is perfect.

Bob - a question from Jeremy:

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

Any thoughts?

Eddie

PROFESSOR EDWARD C. HOLMES FAA FRS

ARC Australian Laureate Fellow

THE UNIVERSITY OF SYDNEY

Marie Bashir Institute for Infectious Diseases & Biosecurity,
School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia

T [REDACTED]

E [REDACTED]

Around this time, the authors were awaiting new sequences, Dr. Holmes stated, “[s]hould I tell Jeremy to hold sending the summary out to the group while we investigate more or does that really matter? He did say that more wildlife needed to be studied. He’s sent it to the Bethesda Boys.”¹¹⁶ Dr. Rambaut responded, “[p]erhaps we say we are adding new information? See whether he wants to hold off. I suspect Bethesda will be sending it round already?”¹¹⁷ These are apparent references to Dr. Fauci and Dr. Collins.

Dr. Robert Garry (June 9, 2023)

Q. Who do you think the “Bethesda Boys” are?

A. I’m not 100 percent sure, but I think I can make an educated guess that this was Dr. Fauci and Dr. Collins.

Q. Is it your estimation that “Bethesda” also refers to Dr. Fauci and Dr. Collins?

A. Yes.¹¹⁸

Dr. Kristian Andersen (June 16, 2023)

Q. Who is Dr. Holmes referencing when he says, “Bethesda Boys”?

A. I don't know, but I assume he means the NIH folks and -- them, so that would be my best guess, yeah.

¹¹⁶ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Andrew Rambaut, Ph.D., *et. al.*, Professor, University of Edinburgh (Feb. 5, 2020).

¹¹⁷ E-Mail from Andrew Rambaut, Ph.D., Professor, University of Edinburgh, to Edward Holmes, Ph.D., *et. al.*, Professor, University of Sydney (Feb. 5, 2020).

¹¹⁸ Garry TI, *supra* note 77, at 174.

Q. Is it your same presumption that he's referencing NIH?

A. That's my assumption, yes.¹¹⁹

On February 7, 2020, Dr. Farrar said, “will share with TC [teleconference] group over the weekend...”¹²⁰ On February 8, Dr. Farrar forwarded a draft of Proximal Origin to the same participants of the February 1 Conference Call—further linking that call to the conception of Proximal Origin.¹²¹

Within hours of receiving the draft, Dr. Fauci, worried about the possibility of serial passage in animals in a lab, asked the whole group, “[w]ould serial passage in an animal in the laboratory give the same result as prolonged adaption in animals in the wild? Or is there something that is fundamentally different in what happens when you serial passage versus natural animal adaption?”¹²² Dr. Garry responded, “[i]t’s possible to fairly rapidly select for more pathogenic variants in the laboratory.”¹²³

In addition to Dr. Fauci’s and Dr. Collin’s involvement, Dr. Farrar led the drafting process and made at least one direct edit to Proximal Origin. Dr. Farrar, however, is not credited as having any involvement in the drafting and publication of Proximal Origin, when in fact he led the drafting process and made direct substantive edits to the publication.

On February 17, 2020, right before publication, Dr. Lipkin emailed Dr. Farrar to thank him for leading the drafting process of Proximal Origin, to which Dr. Farrar responded that he will “push” the publisher.¹²⁴

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¹¹⁹ Andersen TI, *supra* note 55, at 176.

¹²⁰ E-Mail from Jeremy Farrar, Ph.D., Dir. Wellcome Trust, to Edward Holmes, Ph.D., *et. al.* Professor, University of Sydney (Feb. 7, 2020).

¹²¹ E-Mail from Jeremy Farrar, Ph.D., Dir. Wellcome Trust, to Edward Holmes, Ph.D., *et. al.* Professor, University of Sydney (Feb. 8, 2020).

¹²² E-Mail from Anthony Fauci, M.D., Dir., Nat’l Inst. of Allergy & Infectious Diseases, Nat’l Insts. of Health, to Jeremy Farrar, Ph.D., *et. al.*, Dir., Wellcome Trust (Feb. 8, 2020).

¹²³ E-Mail from Robert Garry, Ph.D., Professor, Tulane College of Medicine, to Anthony Fauci, M.D., *et. al.*, Dir., Nat’l Inst. of Allergy & Infectious Diseases, Nat’l Insts. of Health (Feb. 8, 2020).

¹²⁴ E-Mail from Lipkin to Jeremy Farrar, Ph.D., Dir. Wellcome Trust (Feb. 17, 2020).

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

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

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

Jeremy,
Thanks for shepherding this paper. Rumors of bioweaponing are now circulating in China.

Ian

Further, Dr. Andersen testified that Dr. Farrar was the “father figure” of Proximal Origin.¹²⁵ In addition to leading the drafting and publication process, Dr. Farrar made at least one direct edit to Proximal Origin.¹²⁶

From: "Kristian G. Andersen" [REDACTED]
Date: Monday, 17 February 2020 at 18:11
To: Jeremy Farrar [REDACTED]
Cc: [REDACTED], "Garry, Robert F" [REDACTED], Edward Holmes [REDACTED], Ian Lipkin [REDACTED]
Subject: Re: Connections COVID-19

Sure, attached.

K

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

Sorry to micro-manage/microedit!

But would you be willing to change one sentence?

From

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

To

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

This evidence suggests that Dr. Farrar was involved in the drafting and publication of Proximal Origin and probably should have been credited or acknowledged for this involvement. Both Dr. Fauci and Dr. Collins testified they did not provide edits to Proximal Origin.

¹²⁵ Andersen TI, *supra* note 55, at 180.

¹²⁶ E-Mail from Jeremy Farrar, Ph.D., Dir., Wellcome Trust, to Kristian Andersen, Ph.D., *et. al.*, Professor, Scripps Research (Feb. 17, 2020, 10: 42 AM).

The Involvement of Dr. Lipkin

Dr Lipkin was the only author of Proximal Origin that was not on the February 1 Conference Call.¹²⁷ Dr. Lipkin confirmed he was not even invited to the February 1 Conference Call, and he had no prior knowledge of the call taking place.¹²⁸

Dr. Ian Lipkin (April 6, 2023)

- Q. When did you eventually learn of the call?
- A. Actually, I learned of it far more recently than you might expect - - I can't tell you precisely when, but I did not know about it in February of 2020.
- Q. The existence of the call or what was communicated on the call was not communicated to you during the drafting of Proximal Origin?
- A. That is correct.¹²⁹

Despite the authors completing the first draft of Proximal Origin by February 1, Dr. Lipkin was not invited to join and was not sent a draft until February 10.¹³⁰ In that email, Dr. Holmes stated, "I'll have to chat with Jeremy in a little while to see if I can get you more directly involved."¹³¹ It is unclear, why Dr. Farrar had approval over Dr. Lipkin's involvement.

Prior to being added as an author, Dr. Lipkin spoke to Dr. Holmes a few times. On at least one occasion, Dr. Lipkin raised concerns regarding the furin cleavage site. As Dr. Holmes recounted on February 10, "Ian Lipkin just called - very worried about the furin cleavage site and says that high ups are as well, inc. intel."¹³² Dr. Holmes later said, "I think Ian thinks it's from a lab."¹³³

After reading the draft shared with him, Dr. Lipkin responded:¹³⁴

¹²⁷ Lipkin TI, *supra* note 38, at 92.

¹²⁸ *Id.*

¹²⁹ *Id.*

¹³⁰ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Ian Lipkin, M.D., Professor, Columbia University (Feb. 10, 2023).

¹³¹ *Id.*

¹³² E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Andrew Rambaut, Ph.D., *et. al.*, Professor, University of Edinburgh (Feb. 10, 2020).

¹³³ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Kristian Andersen, Ph.D., *et. al.*, Professor Scripps Research (Feb. 11, 2020).

¹³⁴ E-Mail from Ian Lipkin, M.D., Professor, Columbia University, to Eddie Holmes, Ph.D., Professor, University of Sydney (Feb. 11, 2020, 9:01 AM).

On 11 Feb 2020, at 9:01 am, Ian Lipkin [REDACTED] 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

Dr. Garry testified that Dr. Lipkin "...made a nice authorship contribution" and that "he read the paper many times and made some good comments back and forth..."¹³⁵ Dr. Lipkin testified that he believed he was added to Proximal Origin because of his prior authorship of related papers.

Dr. Ian Lipkin (April 6, 2023)

Q. Why do you think Dr. Holmes invited you to join as an author?

A. I had written an article on why the risk of wild animal markets. I sent it to him, asked him to be a coauthor with me. He agreed. And my guess is that it was in that context that he invited me to join this paper.¹³⁶

However, this is not what the other authors discussed when considering whether to add him to the authorship group. According to Dr. Holmes, the authors added Dr. Lipkin as an author not necessarily for his expertise but for "safety in numbers" and "gravitas."¹³⁷

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¹³⁵ Garry TI, *supra* note 77, at 160.

¹³⁶ Lipkin TI, *supra* note 38, at 93.

¹³⁷ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Kristian Andersen, Ph.D., *et. al.*, Professor, Scripps Research (Feb. 12, 2020, 1:15 AM).

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

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

From Ian about the Feb 7 summary.

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

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

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

Dr. Garry testified that he agreed with Dr. Holmes, stating, “I mean, I think I must have agreed generally about it because I did concur with adding him as an author. I’m not sure I agree with every rationale there. I’m not sure that the GOF really adds much weight.”¹³⁸

Dr. Andersen testified that he agreed with Dr. Holmes, stating, “I think he is an -- you know, he has done important work and including collaborated with Chinese authors. He's a well-known individual within sort of the emerging infectious disease field. So, from that perspective, adding Ian as an author, yes, that helps add to the weight of the paper and the authors, and, like, look, these are really experts to have looked at this, yes.”¹³⁹

Proximal Origin’s Flawed Scientific Analysis

The conclusions of Proximal Origin rested on three main arguments: (1) the presence of a non-optimal RBD and that RBD appearing in other viral sequences—particularly pangolins, (2) the presence or furin cleavage sites in other coronaviruses, and (3) the concept that any laboratory manipulation would have used an already published viral backbone.¹⁴⁰ Each of these arguments was flawed and rested on unsupported assumptions.

1. The Receptor Binding Domain

“While the analyses above suggest that SARS-CoV-2 may bind human ACE2 with high affinity, computational analyses predict that the interaction is not ideal and that the RBD sequence is different from those shown in SARS-CoV to be optimal for receptor binding. Thus, the high-affinity binding of the SARS-CoV-2 spike protein to human ACE2 is most likely the result of natural selection on a human or human-like ACE2 that permits another optimal binding solution

¹³⁸ Garry TI, *supra* note 77, at 161.

¹³⁹ Andersen TI, *supra* note 55, at 163-164.

¹⁴⁰ Proximal Origin, *supra* note 41.

to arise. This is strong evidence that SARS-CoV-2 is not the product of purposeful manipulation.”¹⁴¹

As discussed in a May 26, 2020 Working Paper authored independently by DIA scientists entitled, “Critical analysis of *Andersen et al. The proximal origin of SARS-CoV-2*” [hereinafter “Working Paper”], this argument rested on assumptions rather than facts.¹⁴² Instead of relying on scientific data or evidence, Proximal Origin assumes a methodology and intent of a fictional scientist.¹⁴³ In essence, Proximal Origin argues that this fictional scientist would want to design the most optimal RBD possible, which COVID-19 does not possess.

Dr. Kristian Andersen (June 16, 2023)

We knew, based on, you know, much of the great research that Dr. Baric did with SARS-1 is that based on that were predictions of here's the optimal way in which a sarbecovirus will bind into the human ACE2 receptor. That is described in the literature, right? So, if you were to design a new receptor binding domain, presumably you would choose that, right? That would be the logical way to do it.

And SARS-2 doesn't have that at all. It has a completely different solution, right, which we had never seen before. Yet it still appeared to bind well to the human ACE2 receptor -- which we now know, yes, it does bind well to the human ACE2 receptor, but it binds well to a lot of other ACE2 receptors, right, not just human.

So, yeah, that's the idea behind, like, if you were to build this from scratch, you would take the solution that you already know works well. Because that's how science is done, molecular biology is being done.¹⁴⁴

The Working Paper outlined that a more common approach is to simulate nature in the lab by taking novel coronaviruses and simulating recombination events—even by inserting furin cleavage sites—instead of optimizing the virus.¹⁴⁵ This was explained further during a transcribed interview with an author of the Working Paper, CDR Chretien.

CDR Jean-Paul Chretien (June 29, 2023)

A. Well, they had pointed out that the receptor-binding domain would not have been predicted to be very good or optimal for infecting human cells. And for me that implied an assumption that if

¹⁴¹ Proximal Origin, *supra* note 41.

¹⁴² CDR Jean-Paul Chretien & Dr. Greg Cutlip, *Working Paper 26 May 2020: Critical Analysis of Andersen et al. The proximal origin of SARS-Cov-2*, DEF. INTEL. AGENCY (May 26, 2020) [hereinafter “Chretien & Cutlip Working Paper”].

¹⁴³ *Id.*

¹⁴⁴ Andersen TI, *supra* note 55, at 122.

¹⁴⁵ Chretien & Cutlip Working Paper, *supra* note 144.

SARS-CoV-2, whatever was in lab, that it probably would have come about in that way where one might have a priori designed a sequence to infect human cells. And that certainly is possible, but we showed examples of the literature of novel coronaviruses being developed in different ways, and what we -- what we found was more of an empirical approach where one might take a backbone virus, a coronavirus from one species and insert part of a coronavirus from another species to observe the effects, and all serving stated purposes of developing medical countermeasures or improving public health. But what we saw in scientific practice was much more of an empirical approach and not -- not an approach by design to achieve a specific function.

Q. So, the reality was scientists more taking an approach to try to mimic natural recombination to see what those viruses would do in a human population?

A. Yes.

Q. Not with a stated goal of making the most effective coronavirus possible?

A. That's right.¹⁴⁶

When asked if the arguments in Proximal Origin regarding the RBD rested on assumptions, Dr. Garry testified:

Dr. Robert Garry (June 9, 2023)

Q. Is that still resting on an assumption that that's not done, that they weren't testing suboptimal RBDs at some point?

A. I suppose, but why would you do that, you know? I mean, especially if you're thinking that this virus was somehow engineered to be a weapon or, you know, at least be a good pathogen, you wouldn't make a binding domain that was, you know, as poor as your computer predicted it would be for either one of those scenarios.¹⁴⁷

*"The finding of SARS-CoV-like coronaviruses from pangolins with nearly identical RBDs, however, provides a much stronger and more parsimonious explanation of how SARS-CoV-2 acquired these via recombination or mutation."*¹⁴⁸

¹⁴⁶ Transcribed Interview of CDR Jean-Paul Chretien, Program Manager, Biological Technologies Office, Defense Advanced Research Projects Agency, at 35 (June 29, 2023) [hereinafter "Chretien TI"].

¹⁴⁷ Garry TI, *supra* note 77, at 151.

¹⁴⁸ Proximal Origin, *supra* note 41.

Again, according to CDR Chretien, the discovery of a very similar RBD in a naturally occurring pangolin virus is largely irrelevant.

CDR Jean-Paul Chretien (June 29, 2023)

So one of the -- the scenarios we laid out as plausible, and I think would still be plausible, is to begin with a bat origin coronavirus, something along the lines of RaTG13 but more similar to the -- or very, very closely similar to SARS-CoV-2, and then -- and then evaluate the effects of inserting a receptor-binding domain from another species, such as a pangolin. And that's consistent with work that we've seen published from various coronavirus research labs and would be consistent with the observed SARS-CoV-2 as well.¹⁴⁹

Dr. Garry agreed that this scenario was an entirely plausible outcome.

Dr. Robert Garry (June 9, 2023)

Q. If I in theory were to take that particular pangolin spike protein and attach it to a backbone of some other virus, that product that I would have created, though, theoretically in a lab, would itself have had the six key amino acid mutations being discussed here, right? I know that's a - - hypothetical question.

A. The way you said it, hypothetically, sure.¹⁵⁰

Further, Dr. Garry testified that the pangolin sequences “are interesting, but they, you know, by themselves, don’t tell you that, the virus was natural or from a lab.”¹⁵¹

Dr. Robert Garry (June 9, 2023)

Q. What does this mean?

A. Okay. It means that, you know, the pangolin sequences are interesting, but they, you know, by themselves, don’t tell you that, the virus was natural or from a lab... You know, the pangolin viruses, by themselves you know, they have the similarity in the receptor binding domain, but, you know, there are other viruses out there like RaTG13 that is still, you know, a closer virus overall. None of the viruses that were known have a furin cleavage site, at least in these, you know, these close -- the ones that we're talking about here.¹⁵²

¹⁴⁹ Chretien TI, *supra* note 148, at 36.

¹⁵⁰ Garry TI, *supra* note 77, at 112.

¹⁵¹ *Id.*

¹⁵² *Id.*

When asked if Proximal Origin’s arguments regarding the RBD ruled out a lab origin, CDR Chretien testified, “[n]ot in my assessment.”¹⁵³ It is clear, the science and facts did not support Proximal Origin’s conclusion that COVID-19’s RBD “is strong evidence that SARS-CoV-2 is not the product of purposeful manipulation.”¹⁵⁴

2. *The Furin Cleavage Site*

“Polybasic cleavage sites have not been observed in related ‘lineage B’ betacoronaviruses, although other human betacoronaviruses, including HKU1 (lineage A), have those sites and predicted O-linked glycans. Given the level of genetic variation in the spike, it is likely that SARS-CoV-2-like viruses with partial or full polybasic cleavage sites will be discovered in other species.”¹⁵⁵

The central pillar of Proximal Origin’s argument is that science would eventually find a furin cleavage site in a related coronavirus. This is a clear assumption with no proof nor evidence. Further, as of December 4, 2024, there still has not been a furin cleavage site discovered in sarbecoviruses—the subgenus COVID-19 belongs to—despite years of searching.

Dr. Andersen confirmed the rarity of furin cleavage sites in sarbecoviruses, stating, “...the furin cleavage site itself, which we had not seen in sarbecoviruses before.”¹⁵⁶ Dr. Garry confirmed this, stating, “...SARS-Cov-2 so far is the only sarbecovirus that has a furin cleavage site.”¹⁵⁷ Further, Dr. Lipkin stated, “[s]o, amongst the SARS-like viruses, and there are many coronaviruses, that was the first time that we’d seen that furin cleavage type.”¹⁵⁸ When asked, “[h]ave there been any other SARS-related viruses...that has had a furin cleavage site?,” Dr. Farzan testified, “[n]o.”¹⁵⁹ Finally, when asked, “...has there been a furin site observed in any viruses in the sarbecovirus family other than COVID-19?,” CDR Chretien stated, “...not to my knowledge.”¹⁶⁰

“The acquisition of both the polybasic cleavage site and predicted O-linked glycans also argues against culture-based scenarios. New polybasic cleavage sites have been observed only after prolonged passage of low-pathogenicity avian influenza virus in vitro or in vivo. Furthermore, a hypothetical generation of SARS-CoV-2 by cell culture or animal passage would have required prior isolation of a progenitor virus with very high genetic similarity, which has not been described. Subsequent generation of a polybasic cleavage site would have then required repeated passage in cell culture or animals with ACE2 receptors similar to those of humans, but such work has also not previously been described. Finally, the generation of the predicted O-linked

¹⁵³ Chretien TI, *supra* note 148, at 36.

¹⁵⁴ Proximal Origin, *supra* note 41.

¹⁵⁵ *Id.*

¹⁵⁶ Andersen TI, *supra* note 55, at 95.

¹⁵⁷ Garry TI, *supra* note 77, at 119.

¹⁵⁸ Lipkin TI, *supra* note 38, at 70.

¹⁵⁹ Transcribed Interview of Michael Farzan, Ph.D., Professor of Pediatrics, Harvard Medical School (Apr. 21, 2023) [hereinafter “Farzan TI”].

¹⁶⁰ Chretien TI, *supra* note 148, at 37.

glycans is also unlikely to have occurred due to cell-culture passage, as such features suggest the involvement of an immune system.”

Again, according to the Working Paper, this argument rested on a false assumption that all research is published. Dr. Garry testified:

Dr. Robert Garry (June 9, 2023)

Q. Is it possible - - maybe not probable, but possible - - that scientists do experiments they don't publish?

A. Sure.¹⁶¹

Dr. Lipkin testified:

Dr. Ian Lipkin (April 6, 2023)

Q. Do you know of any researchers that don't publish everything they sequence?

A. Yes.¹⁶²

Dr. Farzan testified:

Dr. Michael Farzan (April 21, 2023)

Q. ...have you ever conducted or known someone to conduct an experiment that they did not publish or make public?

A. Sure.¹⁶³

Further, many involved in Proximal Origin, or the February 1 Conference Call believe that it is possible to manipulate a novel coronavirus in a lab to force the selection of a furin cleavage site. In an email, Dr. Garry wrote, “[b]ottom line – I think that if you put selection pressure on a Cov without a furin cleavage site in cell culture you could well generate a furin cleavage site after a number of passages...”¹⁶⁴

¹⁶¹ Garry TI, *supra* note 77, at 153.

¹⁶² Lipkin TI, *supra* note 38, at 70.

¹⁶³ Farzan TI, *supra* note 161, at 26.

¹⁶⁴ E-Mail from Robert Garry, Ph.D., Professor, Tulane School of Medicine, to Kristian Andersen, Ph.D., *et. al.*, Professor, Scripps Research (Feb. 4, 2020, 2:50 PM).

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

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

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

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

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

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

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

Via Slack, Dr. Garry stated, “you can synthesize bits of genes de novo with perfect precision then add them back in without a trace.”¹⁶⁵ This idea was reiterated by Dr. Fouchier, who stated, “[M]olecular biologists like myself can generate perfect copies of viruses without leaving a trace, eg the BAM HI site.”¹⁶⁶

Message

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

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

Ron

¹⁶⁵ Message from Robert Garry, Ph.D., Slack (Feb. 6, 2020, 7:09 p.m.).

¹⁶⁶ E-Mail from Ron Fouchier, Ph.D., Deputy Head of the Erasmus MC Department of Viroscience, Erasmus MC, to Andrew Rambaut, Ph.D., Professor, University of Edinburgh (Feb. 8, 2020, 2:50 PM).

Further, Dr. Garry testified that it would be possible to generate a furin cleavage site in a lab.

Dr. Robert Garry (June 9, 2023)

Q. But a novel coronavirus, if I just bring in a novel coronavirus, its still possible that I could create a furin cleavage site?

A. I mean, its possible. I - - you know, its possible.¹⁶⁷

Additionally, Dr. Garry testified that a scientist could conduct serial passaging of a virus in animals to generate a furin cleavage site and that this virus would be indistinguishable from a natural one.

Dr. Robert Garry (June 9, 2023)

Q. Would past evolutionary passage in an animal in a laboratory look the same as evolutionary passage in an animal in the wild?

A. In principle, yes. It's a very difficult experiment you are describing though.

Q. Are people capable of conducting that experiment?

A. They're capable of doing it. There would have to be a reason why they would want to do that. And just doing it on some random bat viruses is probably not something that most scientists would consider.

Q. Could you put enough laboratory selection pressure on a novel coronavirus to generate a furin cleavage site?

A. I mean, is it possible? It's in the realm of -- it's something -- I mean most everything is possible, right? Is it probable? Probably not, I would have to say. I mean, in principle, you know, lots of things can happen; you know, unexpected things can happen. But designing an experiment to actually make that happen, I'm not sure that there's any scientist that's really capable of doing that.¹⁶⁸

Dr. Andersen agreed when asked, “you could put enough pressure on a coronavirus to generate a furin cleavage site?” He responded, “I think as a hypothesis, I think it’s a good hypothesis.”¹⁶⁹

¹⁶⁷ Garry TI, *supra* note 77, at 34.

¹⁶⁸ Garry TI, *supra* note 77, at 32-33.

¹⁶⁹ Andersen TI, *supra* note 55, at 159.

No known SARS-related coronavirus or sarbecovirus—the subgenus that COVID-19 belongs to—has a furin cleavage site and none have been found since the beginning of the pandemic. Further, those involved with Proximal Origin believed it is possible to artificially create a furin cleavage site in the lab. When asked if the arguments regarding the furin cleavage site put forth in Proximal Origin ruled out a lab origin, CDR Chretien testified, “no, not in my mind.”¹⁷⁰

3. *The Novel Backbone*

“Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used. However, the genetic data irrefutably show that SARS-CoV-2 is not derived from any previously used virus backbone.”

The Proximal Origin authors are correct that COVID-19 does not derive from any published backbone, but they once again assume that all data has been previously published, a faulty assumption. As noted in the Working Paper, “[r]ecent technological innovations make it easier than ever for scientists to develop new reverse genetics systems.”¹⁷¹ When asked for more detail, CDR Chretien testified:

CDR Jean-Paul Chretien (June 29, 2023)

Q. So, it would be possible that there are novel backbones or novel reverse genetics systems that are out there but not published?

A. Yes.

Q. And even simpler than that, not necessarily a novel backbone, but is it possible that researchers just used an unsequenced or unpublished coronavirus as the backbone?

A. Yes.¹⁷²

Via Slack, the Proximal Origin authors rebutted their own argument. Dr. Andersen wrote, “[j]ust in case people think it is difficult to make a CoV reverse genetics clone from scratch – these guys did it in a week...”¹⁷³

Further, Dr. Andersen wrote, “[o]ne important thing I came across though – for the SARS GoF studies they created a reverse genetics system for their bat virus on a whim. So, Ron’s and Christian’s argument (which I found to be the strongest) about that not being feasible is not true – they were already creating those.”¹⁷⁴

¹⁷⁰ Chretien TI, *supra* note 148, at 39.

¹⁷¹ Chretien & Cutlip Working Paper, *supra* note 144.

¹⁷² Chretien TI, *supra* note 148, at 39.

¹⁷³ Message from Kristian Andersen, Ph.D., Slack (Feb. 21, 2020 9:05 p.m.)

¹⁷⁴ Message from Kristian Andersen, Ph.D., Slack (Feb. 2, 2020 6:48 p.m.)

The Proximal Origin authors did not believe their own arguments against a lab leak as written in Proximal Origin. This is exemplified by comparing the authors' contemporaneous Slack messages and e-mails, media reports, and interview transcripts with the two primary conclusions of Proximal Origin—"we do not believe that any type of laboratory-based scenario is plausible" and "[o]ur analysis clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus."¹⁷⁵

The Publication of Proximal Origin

On February 6, 2020, Dr. Farrar first suggested publishing Proximal Origin.¹⁷⁶

Message

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

From Jeremy.

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

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

Thoughts?

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T [REDACTED]
E [REDACTED]

On February 7, 2020, Dr. Farrar suggested possible journals for publication of Proximal Origin.¹⁷⁷

[REMAINDER OF PAGE INTENTIONALLY BLANK]

¹⁷⁵ Proximal Origin, *supra* note 41.

¹⁷⁶ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Kristian Andersen, Ph.D., et. al., Professor, Scripps Research (Feb. 6, 2020, 2:36 AM)

¹⁷⁷ E-Mail from Jeremy Farrar, Ph.D., Dir. Wellcome Trust, to Edward Holmes, Ph.D., et. al., Professor, University of Sydney (Feb. 7, 2020).

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

When can you update?

Lancet

Nature

NEJM

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

Can I help with any of the editors?

Who will be authors from your side?

Then, right before Proximal Origin was publicly released, it received the final publication push and approval from Dr. Collins. In an email from Dr. Holmes, he recounted Dr. Collins writing, “[t]his is really well done, and I would argue ought to be made public ASAP (Jeremy sent it this morning).”¹⁷⁸

Message

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

Just got this from Francis Collins.

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

Francis"

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

Cheers,

Eddie

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T [REDACTED]
E [REDACTED]

¹⁷⁸ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Robert Garry, Ph.D., *et. al.*, Professor, Tulane College of Medicine (Feb. 16, 2020, 3:06 PM).

Four hours later, according to Dr. Holmes, “[a]ll came together very quickly in the end. Jeremy Farrar and Francis Collins are very happy. Works for me.”¹⁷⁹

Message

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

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

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T [REDACTED]
E [REDACTED]

Proximal Origin Gets Rejected from *Nature*

On February 12, 2020, Dr. Andersen pitched Proximal Origin to *Nature*.¹⁸⁰ In his first pitch, as described above, he wrote, “[p]rompted by Jeremy Farrar [sic], Tony Fauci, and Francis Collins, Eddie Holmes, Andrew Rambaut, Bob Garry, Ian Lipkin, and myself have been working through much of the (primarily) genetic data to provide agnostic and scientifically informed hypothesis around the origins of the virus. We are not write finished with the writeup and we still have some loose ends, but I wanted to reach out to you to see if this might be potentially of interest? We see this more as a commentary/hypothesis, as opposed to a more long-form Letter or Article.”¹⁸¹

Senior Editor at *Nature* Clare Thomas responded, “Yes please!”¹⁸²

On February 17, 2020, Dr. Holmes, on behalf of Dr. Andersen, submitted a manuscript titled, “The Proximal Origin of SARS-CoV-2” to *Nature* for review.¹⁸³ Later that day, Dr. Andersen followed up writing, “[s]orry for contracting you again. The manuscript was put on Virological this morning, which has created some urgency from Wellcome, WHO, and

¹⁷⁹ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Kristian Andersen, Ph.D., *et. al.*, Professor, Scripps Research (Feb. 16, 2020, 6:59 PM).

¹⁸⁰ E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Clare Thomas, Editor, *Nature* (Feb. 12, 2020).

¹⁸¹ *Id.*

¹⁸² E-Mail from Clare Thomas, Editor, *Nature*, to Kristian Andersen, Ph.D., Professor, Scripps Research (Feb. 13, 2020).

¹⁸³ E-Mail from Clare Thomas, Editor, *Nature*, to Kristian Andersen, Ph.D., Professor, Scripps Research (Feb. 17, 2020).

others...this is an extremely rapidly evolving situation – which has unfortunately been amplified due to some recent “speculations” from parts of the US media.”¹⁸⁴

Ms. Thomas responded, “I have two reviewers looking at it already...”¹⁸⁵

The Proximal Origin authors, themselves, recommended reviewers. According to Dr. Garry, “[s]o as you know when you submit, you’ll need to suggest reviewers to include and exclude. Seems easy – there are some natural choices for both lists.”¹⁸⁶ Dr. Holmes responded, “[o]h, yes the reviewers are easy...I think this is a slam dunk.”¹⁸⁷ These comments raise serious bias concerns with both the review of Proximal Origin and the scientific peer review process generally. Neither Dr. Andersen nor Dr. Garry knew which suggested reviewers were included or excluded.

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

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

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

Sent from my iPhone

Message

From: Edward Holmes

Sent: 2/16/2020 2:38:46 AM

To: Garry, Robert F

CC: Ian Lipkin
Andrew Rambaut
[REDACTED], Kristian
G. Andersen
[REDACTED]

Subject: Re: Paper

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

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

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The University of Sydney | Sydney | NSW | 2006 | Australia

T
E [REDACTED]

¹⁸⁴ E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Clare Thomas, Editor, Nature (Feb. 17, 2020).

¹⁸⁵ E-Mail from Clare Thomas, Editor, Nature, to Kristian Andersen, Ph.D., Professor, Scripps Research (Feb. 18, 2020).

¹⁸⁶ E-Mail from Robert Garry, Ph.D., Professor, Tulane College of Medicine, to Edward Holmes, Ph.D., *et. al.*, Professor, University of Sydney (Feb. 16, 2020, 7:36 PM).

¹⁸⁷ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Robert Garry, Ph.D., *et. al.*, Professor, Tulane College of Medicine (Feb. 16, 2020, 2:38 AM).

On February 20, 2020, *Nature* officially rejected Proximal Origin for publication. Ms. Thomas stated, “[w]e’ve now obtained two ref reports on the paper (appended below), and I’ve had the opportunity to discuss them with our chief editor Magdalena Skipper. In the light of the advice received I am afraid we have decided that we cannot offer to publish in *Nature*.”¹⁸⁸ The primary reason for denial, as stated by Ms. Thomas, was, “...one of our referees raised concerns (also emphasized to the editors) about whether such a piece would feed or quash the conspiracy theories.”¹⁸⁹

Regarding the denial, Dr. Andersen testified:

Dr. Kristian Andersen (June 16, 2023)

Q. Did you ever get told why *Nature* originally rejected Proximal Origin?

A. They -- I think they rejected the paper because I think the reviewers felt that probably -- I mean, reviewer two was pretty critical about our conclusions of the paper and felt that they should have been stronger, and I think he had relayed those concerns to the editor, and I think that that would have been the reason.

Q. The conclusions that -- what do you mean?

A. Basically, that we -- because, again, we kept the possibilities of -- remember the submitted version to that was open-ended, agnostic as to whether it could have been a lab passage of the two versions of the natural origin that we discuss. And I think the editor probably felt that that was too open-ended. That was clearly what -- especially reviewer two pointed that out in their review, which we disagreed with.¹⁹⁰

Dr. Garry testified:

Dr. Robert Garry (June 9, 2023)

Q. What were the reasons for the rejection?

A. They -- well, I mean, you can read all the reviews of the paper. They thought that we came down too strongly on the side that the virus had been of possible lab origin. And some of the reviewers wanted us to take that out, and we didn't think that was appropriate.¹⁹¹

¹⁸⁸ E-Mail from Clare Thomas, Editor, *Nature*, to Kristian Andersen, Ph.D., Professor, Scripps Research (Feb. 20, 2020).

¹⁸⁹ *Id.*

¹⁹⁰ Andersen TI, *supra* note 55, at 186.

¹⁹¹ Garry TI, *supra* note 77, at 176,

After the denial, Ms. Thomas suggested submitting Proximal Origin to *Nature Medicine*.¹⁹²

Proximal Origin Gets Accepted at *Nature Medicine*

On February 27, 2020, Dr. Andersen submitted Proximal Origin to *Nature Medicine*.¹⁹³ In his submission, Dr. Andersen wrote:

I believe Clare over at Nature might have mentioned our commentary on the proximal origins of the hCoV-19 virus last week. We have been incorporating some critical changes to the reviewer's comments, so I just wanted to reach out to you to see if you're still interested in having a look at this manuscript? We're still incorporating a few changes but will have all of this wrapped up shortly as we're on a tight deadline - the media interest in this has been enormous and hasn't slowed down (we have refrained from commenting until formal publication). The public interest has also been very high, with more than 65,000 reads of the blog post version over the last week.¹⁹⁴

After having been denied by *Nature* for not downplaying the possibility of a lab leak strongly enough, the authors decided to make this submission stronger.

Dr. Kristian Andersen (June 16, 2023)

- Q. You, and correct me if I'm wrong, said something along the lines earlier that the line: We do not believe that any type of laboratory-based scenario is plausible was added at some point?
- A. Correct. That was added to the final version of -- this was added after it went over to Nature Medicine, yes.
- Q. Did Nature Medicine add the line?
- A. No.
- Q. How did that process play out? How did that line get added?
- A. That's based on our edits to the paper. Again, as the editor at Nature Medicine states, is that he thought that the paper had grown significantly since the one he had seen from Nature. We had to shorten it. You need to trim this back down, more or less, to the size

¹⁹² E-Mail from Clare Thomas, Editor, Nature, to Kristian Andersen, Ph.D., Professor, Scripps Research (Feb. 20, 2020).

¹⁹³ E-Mail from Kristian Andersen, Ph.D., Professor Scripps Research, to Joao Monterio, Editor, Nature Medicine (Feb. 27, 2020).

¹⁹⁴ *Id.*

of the Nature version while retaining the major changes in response to the reviewers. And some of the responses to the reviewers was that the reviewer felt that we could be more specific on, for example, that lab origins were less likely than we initially entertained, and I agreed with that. I think we all agree with that, and those were changes that we incorporated. So that includes that we don't believe that any type of lab origin is plausible. It's something that was added in response to the reviewers, our own thinking of the topic, and then getting it published in Nature Medicine, as opposed to Nature.¹⁹⁵

On March 5, 2020, *Nature Medicine* accepted Proximal Origin for publication.¹⁹⁶

The Anonymous Whistleblower to Jon Cohen

On July 25, 2020, an anonymous whistleblower emailed Mr. Jon Cohen, a reporter for *Science* magazine, and alleged that Proximal Origin plagiarized the arguments of others from the February 1 conference call.¹⁹⁷ The whistleblower also alleged that this was one of the reasons that *Nature* rejected the paper.¹⁹⁸ Mr. Cohen forwarded these claims to Dr. Andersen and Dr. Holmes and said, “[h]ere’s what one person who claims to have inside knowledge is saying behind your backs...”¹⁹⁹

Dr. Andersen and Dr. Holmes then drafted a response to Mr. Cohen and forwarded their draft to Dr. Fauci and Dr. Farrar for approval.²⁰⁰ In this email, Dr. Andersen expressed concerns about confirming that the February 1 Conference Call took place, stating, “[w]e need to reply back to Jon, which would include confirming that this meeting took did indeed take place with you and Jeremy present. Please let me know if you have any comments or concerns in this regard.”²⁰¹

In response to Dr. Andersen, Dr. Farrar replied, “[c]an we get the sequence of events right and agreed before a substantive reply goes back to Jon?”²⁰² Dr. Holmes, responded with a revised draft and wrote, “[f]or Tony’s benefit a revised draft of the email to Jon is pasted below.”²⁰³

While the identity of the anonymous whistleblower is still unknown, the Proximal Origin authors had their own suspicions. Dr. Holmes opined, “...I’m 100% sure it was Ron who leaked

¹⁹⁵ Andersen TI, *supra* note 55, at 186-187.

¹⁹⁶ E-Mail from Nature Medicine, to Kristian Andersen, Ph.D., Professor, Scripps Research (Mar. 5, 2020).

¹⁹⁷ E-Mail from Jon Cohen, Reporter, Science, to Kristian Andersen, Ph.D., Professor, Scripps Research, & Edward Holmes, Ph.D., Professor University of Sydney (July 25, 2020).

¹⁹⁸ *Id.*

¹⁹⁹ *Id.*

²⁰⁰ E-Mail from Kristian Andersen, Ph.D., Professor, Scripps Research, to Anthony Fauci, M.D., et. al., Dir., Nat’l Inst. Of Allergy & Infectious Diseases (July 28, 2020).

²⁰¹ *Id.*

²⁰² E-Mail from Jeremy Farrar, Ph.D., Dir., Wellcome Trust, to Kristian Andersen, Ph.D., et. al., Professor Scripps Research (July 28, 2020).

²⁰³ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Jeremy Farrar, Ph.D., et. al., Dir. Wellcome Trust (July 28, 2020).

it – he was the most angry – and I still think it was like Baric who emailed Jon Cohen.”²⁰⁴ Dr. Rambaut responded, “I agree – most likely Ron doing the leaking.”²⁰⁵

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

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

A

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

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

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

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

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Dr. Baric denied being the anonymous individual that e-mailed Mr. Cohen.

Dr. Ralph Baric (January 22, 2024)

Q. After the fact -- and then there's a reporter at Science Magazine named John Cohen.

A. I know him.

Q. He put out some emails after the fact of an anonymous person that claimed that the "proximal origin" authors plagiarized some ideas and went a little bit too far. Are you aware of those emails?

A. John contacted me.

²⁰⁴ E-Mail from Edward Holmes, Ph.D., Professor, University of Sydney, to Kristian Andersen, Ph.D., *et. al.*, Professor, Scripps Research (July 28, 2020, 3:58 PM).

²⁰⁵ E-Mail from Andrew Rambaut, Ph.D., Professor, University of Edinburgh, to Edward Holmes, Ph.D., *et. al.*, Professor, University of Sydney (July 28, 2020, 6:21 PM).

- Q. Were you the –
- A. No, I was not. I was not. I was building suspense.
- Q. So Dr. –
- A. And it worked.
- Q. It did. Part of it is because Dr. Holmes thinks you were the one that contacted John Cohen.
- A. Well, that's why he may say it. He and -- I'm forgetting his name, sorry -- Andersen. If that's what they thought, he may have been really irritated with me if he felt that it was me, but it was not.
- Q. What did Mr. Cohen contact you about?
- A. He was asking me the same question you asked me, was I the author of that statement? And I said, no, I was not.
- Q. Do you know who is?
- A. No, I don't.²⁰⁶

The Critical Reception of Proximal Origin

On February 19, 2020, Proximal Origin was cited in the letter in *The Lancet* titled, “Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19.”²⁰⁷ Proximal Origin was cited as proof “this coronavirus originated in wildlife.”²⁰⁸

On March 17, 2020, Dr. Andersen’s employer, Scripps Research, put out a press release regarding Proximal Origin entitled, “The COVID-19 coronavirus pandemic has a natural origin, scientists say.”²⁰⁹ Dr. Andersen is quoted in this release saying, “...we can firmly determine that SARS-COV-2 originated through natural process.”²¹⁰ Dr. Farrar’s organization, The Wellcome Trust, is also quoted in the release, stating, “they conclude that the virus is the product of natural evolution.”²¹¹

NIH and NIAID were keenly anticipating the release of Proximal Origin. On February 19, 2020, the NIAID Office of Communications spoke internally regarding the paper and stated,

²⁰⁶ Baric TI, *supra* note 39, at 124-125.

²⁰⁷ Charles Calisher, Ph.D., *et. al.*, *Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19*, THE LANCET (Feb. 19, 2020).

²⁰⁸ *Id.*

²⁰⁹ *The COVID-19 coronavirus epidemic has a natural origin, scientists say*, SCRIPPS RESEARCH (Mar. 17, 2020).

²¹⁰ *Id.*

²¹¹ *Id.*

“[t]he Office of Communications asked if we could alert them if this paper is accepted in a peer review journal. Do you know if the authors have submitted it to a journal?”²¹²

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

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

Thank you,

Amanda Coleman [C]
[REDACTED]

An NIH employee responded, “I reached out to Kristian and team...the text is submitted to Nature. Kristian suggests that the office of Communication can communicate directly with Chris Emery [Scripps Research].”²¹³

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

Hi Amanda,

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

REV0002496

Thanks,

Reed

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

*Best,
Kristian*

²¹² E-Mail from Amanda Coleman, Nat'l Inst. Of Allergy & Infectious Diseases, Nat'l Insts. Of Health, to Reed Shabman, Program Office, Nat'l Inst. Of Allergy & Infectious Diseases, Nat'l Insts. Of Health (Feb. 19, 2020, 1:21 PM).

²¹³ E-Mail from Reed Shabman, Program Office, Nat'l Inst. Of Allergy & Infectious Diseases, Nat'l Insts. Of Health, to Amanda Coleman, Nat'l Inst. Of Allergy & Infectious Diseases, Nat'l Insts. Of Health (Feb. 19, 2020, 3:30 PM).

On March 26, 2020, Dr. Collins wrote a blog post for the NIH regarding Proximal Origin.²¹⁴ Dr. Collins wrote, “[a] new study debunks such claims by providing scientific evidence that this novel coronavirus arose naturally.”²¹⁵ Dr. Collins concluded, “[e]ither way, this study leaves little room to refute a natural origin for COVID-19.”²¹⁶

On April 16, 2020, more than two months after the original February 1 Conference Call and a month after Proximal Origin was published, Dr. Collins emailed Dr. Fauci and expressed dismay that Proximal Origin did not successfully squash the lab leak theory. He stated, “I hoped the Nature Medicine article on the genomic sequence of SARS-CoV-2 would settle this...”²¹⁷ Then Dr. Collins asked Dr. Fauci, “[w]ondering if there is something NIH can do to help put down this very destructive conspiracy...Anything more we can do?”²¹⁸

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²¹⁴ Francis Collins, *Genomic Study Points to Natural Origin of COVID-19*, NAT’L INSTS. OF HEALTH (Mar. 26, 2020).

²¹⁵ *Id.*

²¹⁶ *Id.*

²¹⁷ E-Mail from Francis Collins, Dir., Nat’l Insts. Of Health, to Anthony Fauci M.D., Dir. Nat’l Inst. Of Allergy & Infectious Diseases, Nat’l Insts. Of Health (Apr. 16, 2020, 10:45 PM).

²¹⁸ *Id.*

From: [Fauci, Anthony \(NIH/NIAID\) \[E\]](#)
To: [Collins, Francis \(NIH/OD\) \[E\]](#)
Subject: RE: conspiracy gains momentum
Date: Thursday, April 16, 2020 10:45:00 PM

Francis:

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

Best,

Tony

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

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 that didn't get much visibility.

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

Francis

Dr. Collins testified that "Nature Medicine article" was in reference to Proximal Origin.²¹⁹ The next day, on April 17, 2020, Dr. Fauci cited Proximal Origin from the White House podium.

White House Press Conference (April 17, 2023)

Q. Mr. President, I wanted to ask Dr. Fauci: Could you address these suggestions or concerns that this virus was somehow manmade, possibly came out of a laboratory in China?

Dr. Fauci. There was a study recently that we can make available to you, where a group of highly qualified evolutionary

²¹⁹ Transcribed Interview of Francis Collins, M.D., Ph.D., former Dir., Nat'l Insts. of Health (Jan. 12, 2024) [hereinafter "Collins TI"].

virologists looked at the sequences there and the sequences in bats as they evolve. And the mutations that it took to get to the point where it is now is totally consistent with a jump of a species from an animal to a human. So, I mean, the paper will be available — I don't have the authors right now, but we can make that available to you.²²⁰

After the briefing, a reporter directly asked which paper Dr. Fauci cited and was then sent Proximal Origin. The reporter wrote, “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?”²²¹

On Apr 19, 2020, at 2:21 PM, Bill Gertz [Redacted] 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
National Security Correspondent
@BillGertz | direct [Redacted]
TheGertzFile.com
<twtlogo.jpg>
3600 New York Ave NE | Washington DC, 20002

Dr. Fauci responded, “[h]ere are the links to the scientific papers and a commentary about the scientific basis of the origins of SARS-Cov-2” and lists Proximal Origin.²²²

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²²⁰ Remarks by President Trump, Vice President Pence, and Members of the Coronavirus Task Force in Press Briefing, The White House (Apr. 17, 2020) [hereinafter “Remarks by President Trump April 17, 2020”].

²²¹ E-Mail from Bill Gertz, Correspondent, The Wash. Times, to Anthony Fauci, M.D., Dir. Nat’l Inst. Of Allergy & Infectious Diseases, Nat’l Insts. Of Health (Apr. 19, 2020, 2:21 PM).

²²² E-Mail from Anthony Fauci, M.D., Dir. Nat’l Inst. Of Allergy & Infectious Diseases, Nat’l Insts. Of Health, to Bill Gertz, Correspondent, The Wash. Times (Apr. 19, 2020, 9:25 PM).

On Apr 19, 2020, at 9:25 PM, Fauci, Anthony (NIH/NIAID) [E] <Redacted> wrote:

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

SSCP_NIH002046

National Institute of Allergy and Infectious Diseases

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Dr. Fauci later stated he may not have ever actually read Proximal Origin.²²³ This raises questions of why he would cite a paper, he did not even read, from the White House podium as proof COVID-19 was not the result of a lab leak.

Dr. Collins testified that despite his e-mail suggesting he desired more action to “put down” the lab leak hypothesis, he did not instruct Dr. Fauci to cite Proximal Origin from the White House.²²⁴ Dr. Fauci also testified that his statement at the White House was not in response to Dr. Collins’ e-mail.²²⁵

On January 9, 2024, Mr. Don McNeil, former science and health reporter for the *New York Times*, published “The Wisdom of Plagues: Lessons from 25 Years of Covering Pandemics.” In *Wisdom of Plagues*, Mr. McNeil recounted:

²²³ Megan Stack, *Dr. Fauci Could Have Said a Lot More*, THE N.Y. TIMES (Mar. 28, 2020).

²²⁴ See Collins TI, *supra* note 221.

²²⁵ See, Transcribed Interview of Anthony Fauci, M.D., former Dir., Nat’l Inst. of Allergy & Infectious Diseases, Nat’l Insts. of Health (Jan. 8, 2024) [hereinafter “Fauci TI 1”].

Far more serious errors occur when sources deliberately deceive reporters. In late July 2023, this book was almost in print when I learned, from emails and Slack chats [released] by the Congressional Subcommittee on the Coronavirus Pandemic and posted on *Public*, a Substack magazine, that I was the victim of deception in the pandemic's earliest days. In February 2020, four eminent scientists whom I respected had discussed with each other various ways to throw me off track when I asked whether it was possible that the virus had been manipulated in a lab or might have leaked from one. Their efforts affected how I viewed the controversy over Covid's origins and how the *Times* covered it. My publisher allowed me to quickly rewrite this chapter.²²⁶

Mr. McNeil also confirmed that the Proximal Origin authors' deception altered how the New York Times reported on COVID-19 origins.

²²⁶ Donald G. McNeil, Jr., *The Wisdom of Plagues: Lessons from 25 Years of Covering Pandemics* (Simon & Schuster, 2024).