Important documents regarding
THE ORIGINS OF SARS-CoV-2

The emails & other documents following this cover letter are from verifiable sources. Some of them were obtained through Freedom of Information Act (FOIA) requests to government agencies, and others were released by public figures.

☞ There are no anonymous sources here. This isn't a Q-Anon type hoax.
☞ All documents are *currently* available on the internet to the general public. Sources are indicated.

Documents in the public domain are not guaranteed to stay in the public domain: it's a fairly simple matter for government officials to take down websites, or force web-hosts to remove offending documents. For this reason, all the documents disclosed here are archived offline.

Please read the enclosed documents carefully, all the way through, so that you can discover information relevant to helping you make important decisions concerning your health and well-being.

The following documents are transcriptions of letters that were provided to Project Veritas. The author, Major Joe Murphy, USMC, is a real person who works in Naval Intelligence.

Originals are currently available for download HERE: https://assets.ctfassets.net/syq3snmxclc9/2mVob3c1aDd8CNvVnyei6n/95af7dbfd2958d4c2b8494048b4889b5/JAG_Docs_pt1_Og_WATERMARK_OVER_Redacted.pdf

The nature of the letters is self-explanatory.

From: Murphy, Joseph P Maj usmc DARPA DIRO (USA) [redacted]
Sent:
To:
Cc:
Subject:
Capt xxxxx,

Thanks for responding.

I'm reaching out to communicate some information relative to COVID that I don’t believe xxxxx or your director is aware of. You probably saw earlier this week that more official documents linking NIH and EcoHealth Alliance to the Wuhan Institute of Virology were published by Intercept. I came across additional incriminating documents and produced an analysis shortly after leaving DARPA last month. This report was routed to the DOD IG office.

I’m unsure whether the significance of what I communicated is understood by those that receive the report. Decisions with regards to vaccines do not appear to be informed by analysis of the documents. The main points being that SARS-CoV-2 matches the SARS vaccine variants the NIH-EcoHealth program was making in Wuhan; that the DOD rejected the program proposal because vaccines would be ineffective and because the spike proteins being inserted into the variants were deemed too dangerous (gain-of-function); and that the DOD now mandates vaccines that copy the spike protein previously deemed too dangerous. To me, and to those who informed my analysis, this situation meets no-go or abort criteria with regards to the vaccines until the toxicity of the spike protein can be investigated. There’s also information within the documents about which drugs effectively treat the program’s SARS-CoVs.

Thus why I’m reaching out. I’m trying to help aid leadership grapple with the vaccines and the mandate with as much information as is available. I wanted to push this information your way.

Several of the documents referenced in the IG report have since been downgraded.

Please reach out to me with questions.

V/R,

Major Joe Murphy USMC
Marine Program Liaison
Code 34 & 35
Office of Naval Research
Work: [redacted]
Cell: [redacted]
[redacted]

UNCLASSIFIED
DEFENSE ADVANCED RESEARCH PROJECTS AGENCY
675 NORTH RANDOLPH STREE
ARLINGTON, VA 22203-211 4

13 Aug 21

From: COMMANDANT OF THE MARINE CORPS FELLOW, DARPA
To: INSPECTOR GENERAL

Subj: SARS-CoV-Z ORIGINS INVESTIGATION WITH US GOVERNMENT PROGRAM UNDISCLOSED DOCUMENT ANAL YSIS

Ref:(l) Executive Slide HR0011880017 EcoHealth Alliance DEFUSE
(2) HROOllBSOO 17-PREEMPT-FP-019-PM Summary (Selectable – Not Recommended) Recommende
(3) PREEMPT Volume 1 no ESS HR00118S0017 EcoHealth Alliance DEFUSE
(4) PREEMPT Volume 2 EHA Final HR00118S0017 EcoHealth Alliance DEFUSE
(5) SF424_2_0-V2.0 HR00118S0017 EcoHealth Alliance DEFUSE
(6) WIV Budget packet HR00111880017 EcoHealth Alliance DEFUSE
(7) WS00094394-RR_KeyPersonExpanded_2_0-V2.0 HR001118S0017 EcoHealth Alliance DEFUSE
(8) W500094394-RR_Per sonalData_1_2-V1.2 HR001118S0017 EcoHealth Alliance DEFUSE

1. SARS—CoV-Z i s an American-created recombinant bat vaccine, or its precursor virus. It was created by an EcoHealth Alliance program at the Wuhan Institute of Virology (WIV) , as suggested by the reporting surrounding the lab leak hypothesis. Tyhe details of this program have been concealed since the pandemic began. These details can be found in the EcoHealth Alliance proposal response to the DARPA PREEMPT[ii] program Broad Agency Announcement (BAA) HR00118S0017, dated March 2018[iii] – a document not yet publicly disclosed.

The contents of the proposed program are extremely detailed. Peter Daszak lays out step-by-step what the organization intends to do by phase and by location. The primary scientists involved, their roles, and their institutions are indicated. The funding plan for the WIV work is its own document. The reasons why nonpharmaceutical interventions like masks and medical countermeasures like mRNA vaccines do not work well can be extrapolated from the details. The reason why the early treatment protocols work as curatives are apparent.

SARS-CoV-2's form as it emerged is likely as a precursor, deliberately virulent, humanized recombinant SARSr-CoV that was to be reverse engineered into a live attentuated SARSr-Cov bat vaccine. Its nature can be determined from analysis of its genome with the context provided by the EcoHealth Alliance proposal. Joining this analysis with US intelligence collections on Wuhan will aid this determination.

When synthesized with the EcoHealth Alliance proposal, US collections confirm EcoHealth Alliance was performing the work proposed. The analysts produce their reports in a vacuum, absent the context the proposal provides. As a fellow at DARPA, I could see both, and can do the synthesis. For instance, WIV personnel identified in intelligence reports are named in the proposal, these people use the lexicon of the proposal in the collections, and the virus variants proposed for experimentation are identical to those gleaned by collections. Moreover, I am also privy to information obtained by congressional office investigators and by DRASTIC [iv], which further collaborates that the program detailed in the BAA response was conducted until it was shut down in April 2020.

The purpose of the EcoHealth program, called DEFUSE[v] in the proposal, was to inoculate bats in the Yunnan, China caves where confirmed SARS-CoVs were found. Ostensibly, doing this would prevent another SARS-CoV pandemic; the bats' immune systems would be reinforced to prevent a deadly SARS-CoV from emerging. The specific language used is "inoculate bats with novel chimeric polyvalent spike proteins to enhance their adaptive immune memory against specific high-risk viruses." [vi] Being defense-related, it makes sense that EcoHealth submitted the proposal first to the Department of Defense, before it settled with NIH/NIAID. The BAA response is dated March 2018 and was submitted by Peter Daszak, president of EcoHealth Alliance.

DARPA rejected the proposal because the work was too close to violating the gain-of-function (GoF) moratorium, [vii] despite what Peter says in the proposal (that the work would not [viii]). As is known, Dr. Fauci with NIAID did not reject the proposal. The work took place at the WIV and at several sites in the US, identified in detail in the proposal. [ix]

The EcoHealth Alliance response to the PREEMPT BAA is placed along with other proposal documents in the PREEMPT folder on the DARPA Biological Technologies Office JWICS (top secret) share drive, address: Network/filer/BTO/CI Folder/PREEMPT

This folder was empty for a year. The files, completely unmarked with classification or distribution data, were placed in this folder in July 2021, which conspicuously aligns with media reporting, my probing, and Senator Paul's inquiry into NIH/NIAID gain-of-function programs. The unmarked nature combined with the timing signals that the documents were being hidden. No files at DARPA go unmarked in classification or distribution, including proprietary documents. Furthermore, PREEMPT is an unclassified program.

The files are now also held by Marine Corps Intelligence Activity (MCIA). They are identified in the reference block above.

2. SARS-CoV-2, hereafter refered to as SARSr-CoV-WIV, is a synthetic spike protein chimera engineered to attach to human ACE2 receptors and

inserted into a recombinant bat SARSr-CoV backbone. It is likely a live vaccine not yet engineered to a more attenuated state that the program sought to create with its final version. It leaked and spread rapidly because it was aerosolized so it could efficiently infect bats in caves, but it was not ready to infect bats yet, which is why it does not appear to infect bats. The reason the disease is so confusing is because it is less a virus than it is engineered spike proteins hitch-hiking a ride on a SARSr-CoV quasispecies swarm. The closer it is to the final live attentuated vaccine form, the more likely that it has been deattenuating since initial escape in August 2019.

The utility of certain countermeasures can be extrapolated from the documents:
The team selected for SARSr-CoVs that were most monoclonal antibody and vaccine resistant.
It is not practical to inoculate bats directly with shots, nor can bats get respiratory infections from droplets, so the team developed an aerosol to deliver the inoculations directly into the caves. To ensure it worked well, they developed the aerosol against masked civets.
The proposal notes that interferon, Remdesivir, and chloroquine phosphate inhibit SARSr-CoV viral replication.

Because of its (now) known nature, the SARSr-CoV-WIV's illness is readily resolved with early treatment that inhibits the viral replication that spreads the spike proteins around the body (which induce a harmful overactive immune response as the body tries to clear the spikes from the ACE2 receptors). Many of the early treatment protocols ignored by the authorities work because they inhibit viral replication or modulate the immune response to the spike proteins, which makes sense within the context of what EcoHealth was creating. Some of these treatment protocols also inhibit the action of the engineered spike protein. For instance, Ivermectin (identified as curative in April 2020) works throughout all phases of illness because it both inhibits viral replication and modulates the immune response. Of note, chloroquine phosphate (Hydroxychloroquine, identified April 2020 as curative) is identified in the proposal as a SARSr-CoV inhibitor, as is interferon (identified May 2020 as curative).

The gene-encoded, or “mRNA,” vaccines work poorly because they are synthetic replications of the already-synthetic SARSr-CoV-WIV spike proteins and possess no other epitopes. The mRNA instructs the cells to produce synthetic copies of the SARSr-CoV-WIV synthetic spike protein directly into the bloodstream, wherein they spread and produce the same ACE2 immune storm that the recombinant vaccine does. Many doctors in the country have identified that the symptoms of vaccine reactions mirror the symptoms of the disease, which corroborates with the similar synthetic nature and function of the respective spike proteins.
The vaccine recipient has no defense against the bloodstream entry, but their nose protects them from the recombinant spike protein quasispecies during “natural infection” (better termed as aerosolized inoculation).

Furthermore, the EcoHealth proposal states that a “vaccine approach lacks sufficient epitope coverage to protect against quasispecies of coronavirus.” [x] Consequently, they were trying to make vaccines work by “targeted immune boosting via vaccine inoculators using chimeric polyvalent recombinant spike proteins.”[xi] The nature of using a spike protein vaccine with one epitope against a spike protein vaccine with a quasispecies may explain the unusual (and potentially detrimental) antibody response among the vaccinated to the new COVID variants.[xii] Fundamentally, the knowledge the proposal provides signals that the risk of Antibody Dependent Enhancement (ADE) from vaccination should be evaluated with high priority, on top of the reality that single-epitope vaccines will have little effect against SARSr-CoV-WIV, as indicated in the proposal.

The potential for SARSr-CoV-WIV to deattentuate requires immediate attention. Live vaccines have been found to deattentuate in the past. If this is the case with SARSr-CoV-WIV, then the mass vaccination campaign actually performs an accelerated gain-of-function for it. Since it is designed for bats off of a human-susceptible SARS-CoV, vaccinating humans against it actually gains its function back towards a more deattenuated human-susceptible form. Improving the SARSr-CoV-WIV spike protein to gain robustness against monoclonal vaccines is one of the steps of the DEFUSE program. The mechanism to improve the SARSr-CoV-WIV spike protein (other than direct engineering) is to challenge it against animals that have spike protein-only antibodies. The intent was to perform this task against humanized mice and then “batified” mice. Instead, it was done with the world’s population.

SARS-CoV-WIV is not meant to kill the bats, but to immunize them. This nature may explain its general harmlessness to most people, and its harmfulness to the old and comorbid, who are in general more susceptible to vaccine reactions. The asymptomatic nature is also explained by the bat vaccine-intention of its creators (a good vaccine does not generate symptoms). Such effects would be expected of an immature vaccine, or a vaccine being reverse engineered from a more virulent form into an attenuated form. The spike protein effect on ACE2 receptors exacerbates the harmfulness in accordance with age and comorbidity. The nature of SARSr-CoV-WIV’s deattenuation will also indicate future virulence, though knowing its nature at last neutralizes the threat as effective treatments can be applied with confidence.

3.DRASTIC and other scientists will clean up my description of SARSr-CoV’s nature and progression within the DEFUSE program. This information is sufficient for an investigative report and more than enough to correct the existing pandemic strategy. Previously, the nation did not know itself, nor the adversary in the pandemic conflict. Now it knows both. The problem can be framed appropriately and specifically against a confirmed hypothesis. Limiting disease transmission can be dropped as the implied strategic end, as it is not the actual problem, nor is it actually feasible. The strategy will then align early treatment protocols and prophylaxis with the known curatives as ways and means. This course of action will achieve the strategic end of clinical resolution for those that are susceptible to the adverse effects from SARSr-CoV-WIV inoculation.

4. I will inevitably be asked how I figured this out and how I discovered the documents. The pandemic response became the predominant focus of my fellowship efforts. DARPA worked a number of pandemic innovations and much of its team was familiar with biodefense. I had the opportunity to “sit in the back row” per se and observe and listen-in on the government’s efforts. My obligation-light fellowship also allowed me to observe and read the field. This observation grew in scope to the point that it became a series of reports, like a military scout would prepare when tasked to investigate a problem.

These reports served as iterative thinking against the problem over many months. Eventually, I arrived at a hypothesis that what leaked from the WIV could be a bat vaccine or its precursor. It was feasible that the US would try to avoid a SARS-CoV outbreak by stopping it at its source, not by halting its infections amongst people, but by halting the infection amongst the bats. Americans are creative, even if imprudent, and technologically confident enough to try it. This concept seemed to fit within the PREEMPT program construct as well, and DRASTIC had discovered that some earlier specimens within the USAID PREDICT program were obtained in Africa and sent to the WIV. Moreover, the unusual nature and pathology of the virus hinted that it could be a vaccine or be vaccine-like.

A technological challenge as difficult as inoculating bats in China would be tried at DARPA first. The massive, “Manhattan Project”-level of information suppression executed by the government and the Trusted News Initiative indicates that it would be covered-up if something bad happened. The lab-leak hypothesis and squabbling between Senator Paul and Dr. Fauci indicated that the cover up was more localized. Further, an actual cover-up would be more disciplined with its paperwork. So I presumed that the unclassified files would be concealed on a higher network and found them where I expected them to be. I understood what they were and their content, pushed the files off-site, and compiled this report.

8/13/2021
Joseph Murphy
Major, US Marine Corps
Signed by: MURPHY.JOSEPH.PATRICK 1275023554

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[i] DARPA: Defense Advanced Research Projects Agency

[ii] PREEMPT: Preventing Emerging Pathogenic Threats

[iv] DRASTIC: Decentralized Radical Autonomous Search Team Investigating COVID-19. This collection of scientists and sleuths broke open the lab leak hypothesis into the mainstream and has picked apart Chinese and World Health Organization (WHO) reports on SARS-CoV-2’S origins in Wuhan.

[v] DEFUSE: Defusing Threat of Bat-borne Coronavirus

vi PREEMPT Volume 1 no ESS HR00118S0017 EcoHealth Alliance DEFUSE. Another description used: “We will develop recombinant chimera spike proteins from known SARSr-CoVs, and those characterized by DEFUSE, using details of SARS S protein structure and host cell binding, we will secrence, reconstruct, and characterize spike trimmers and RBDs of SARSr-CoVs, incorporate them into nanoparticles or raccoon poxvirus vectors for delivery to bats.”

vii Dr. James Gimbert, DARPA Program Manager states: “team’s approach does potentially involve GoF/DURC research (they aim to synthesize spike glycoproteins that may bind to human cell receptors and insert them into SARS-CoV backbones to assess capacity to cause SARS-like disease.”

viii “We will commercially synthesize SARSr-CoV S glycoprotein genes, designed for insertion into SHC014 OR WIV16 molecular clone backbones (88% and 97% S protein identity to epidemic SARS-Urbani). These are BSL-3, not select agents or subject to P3CO” (they use bat SARSr-CoV backbones which are exempt)”

ix Duke NUS Medical School, UNC, UGSG National Wildlife Health Center, Palo Alto Rsesearch Center, Kumning, Signapore, and Madison, WI.

[x] PREEMPT Volume 1 no ESS HR00118S0017 EcoHealth Alliance DEFUSE

xi PREEMPT Volume 1 no ESS HR00118S0017 EcoHealth Alliance DEFUSE

xii “For Delta, neutralizing antibodies have a decreasing affinity for spike protein, while facilitating antibodies have a “strikingly increased” affinity for spike protein.” Yahi, et al. “Infection-enhancing anti-SARS-CoV-2 antibodies recognize both the original Wuhan/D614G strain and Delta variants. A potential risk for mass vaccination?” Journal of Infection. August 9, 2021. https://www.journalofinfection/com/article/S0163-4453(21)00392-3/fulltext

End of document

The following letters were made available by their authors, Congressman James Comer and Congressman Jim Jordan, and are sitting on a congressional server at

https://republicans-oversight.house.gov/wp-content/uploads/2022/01/Letter-Re.-Feb-1-Emails-011122.pdf

The nature of the letters is self-explanatory.

Congreſs of the United States
Washington, DC 20515

January 11, 2022

The Honorable Xavier Becerra
Secretary
U.S. Department of Health and Human Services
200 Independence Ave., SW
Washington, D.C. 20201

Dear Secretary Becerra:

We write to request a transcribed interview of Dr. Anthony Fauci, Director, U.S. National Institute of Allergy and Infectious Diseases (NIAID). Excerpts of emails we are making public today (see enclosed Appendix I) reveal that Dr. Fauci was warned of two things: (1) the potential that COVID-19 leaked from the Wuhan Institute Virology (WIV) and (2) the possibility that the virus was intentionally genetically manipulated. It is imperative we investigate if this information was conveyed to the rest of the government and whether this information would have changed the U.S. response to the pandemic.

Despite Dr. Fauci claiming otherwise on multiple occasions, he was, in fact, aware of the monetary relationship between NIAID, the U.S. National Institutes of Health (NIH), EcoHealth Alliance Inc. (EcoHealth), and the WIV by January 27, 2020.[1] Dr. Fauci also knew that NIAID worked with EcoHealth to craft a grant policy to sidestep the gain-of-function moratorium at the time.[2] This new policy, designed by EcoHealth and agreed to by NIAID, allowed EcoHealth to complete dangerous experiments on novel bat coronaviruses—with very little oversight—that would have otherwise been blocked by the moratorium.[3] In January 2020, Dr. Fauci was also aware that EcoHealth was not in compliance with the terms of its grant that funded the WIV.[4] EcoHealth was required to submit an annual progress report to NIAID by September 30, 2019, and had not yet done so.[5] The Committee subsequently learned that EcoHealth failed to submit these reports presumably to hide a gain-of-function experiment conducted on infectious and potentially lethal novel bat coronaviruses.[6]

By January 27, 2020, Dr. Fauci knew NIAID had funded EcoHealth, the WIV was a subgrantee of EcoHealth, and EcoHealth was not in compliance with its grant reporting, in particular a grant that NIAID knew had gain-of-function potential on novel bat coronaviruses. It

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[1] Email from Greg Folkers to Anthony Fauci, et. al. (Jan. 27, 2020) (On file with Comm. Staff); Zachary Basu, *Fauci and Rand Paul clash over NIH funding for Wuhan Institute of Virology,* AXIOS (May 11, 2021).

[2] Sharon Lerner & Mara Hvistendahl, *NIH Officials Worked with EcoHealth Alliance to Evade Restrictions on Coronavirus Experiments,* INTERCEPT (Nov. 3, 2021).

[3] *Id.*

[4] Letter from Lawrence Tabak to James Comer (Oct. 20, 2021).

[5] *Id.*

[6] *Id.*

is unclear if Dr. Fauci reported any of these issues to his superiors. We need to know the entirety of what Dr. Fauci knew and when he knew it.

On February 1, 2020, Dr. Fauci, Dr. Collins, and at least eleven other scientists convened a conference call to discuss COVID-19.[7] It was on this conference call that Drs. Fauci and Collins were first warned that COVID-19 may have leaked from the WIV and, further, may have been intentionally genetically manipulated. Again, it is unclear if either Dr. Fauci or Dr. Collins ever passed these warnings along to other government officials or if they simply ignored them.

Only three days later, on February 4, 2020, four participants of the conference call authored a paper entitled "The Proximal Origin of SARS-CoV-2" and sent a draft to Drs. Fauci and Collins.[8] Prior to final publication in *Nature Medicine*, the paper was sent to Dr. Fauci for editing and approval.[9] It is unclear what, if any, new evidence was presented or if the underlying science changed in that short period of time, but after speaking with Drs. Fauci and Collins, the authors abandoned their belief COVID-19 was the result of a laboratory leak. It is also unclear if Drs. Fauci or Collins edited the paper prior to publication.

On April 16, 2020, more than two months after the original conference call, Dr. Collins emailed Dr. Fauci expressing dismay that the *Nature Medicine* article—which they saw prior to publication and were given the opportunity to edit—did not squash the lab leak hypothesis and asks if the NIH can do more to "put down" the lab leak hypothesis.[10] The next day—after Dr. Collins explicitly asked for more public pressure—Dr. Fauci cited the *Nature Medicine* paper from the White House podium likely in an effort to further stifle the hypothesis COVID-19 leaked from the WIV.[11]

Rather than be transparent with the Committee, HHS and NIH continue to hide, obfuscate, and shield the truth. By continuing to refuse to cooperate with our request, your agencies are choosing to hide information that will help inform the origins of the ongoing pandemic, prevent future pandemics, respond to future pandemics, inform the United States' current national security posture, and restore confidence in our public health experts. HHS and NIH's continued obstruction is likely to cause irreparable harm to the credibility of these agencies. The emails released today raise significant questions, including but not limited to:

1. Did Drs. Fauci or Collins warn anyone at the White House about the potential COVID-19 originated in a lab and could be intentionally genetically manipulated?

2. If these concerns were not shared, why was the decision to keep them quiet made?

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[7] Email from Jeremy Farrar to Anthony Fauci, et. al. (Feb. 1, 2020) (On file with Comm. Staff).
[8] Email from Jeremy Farrar to Anthony Fauci & Francis Collins (Feb. 4, 2020) (On file with Comm. Staff)
[9] Email from Kristian Andersen to Anthony Fauci, Francis Collins, & Jeremy Farrar (Mar. 6, 2020) (On file with Comm. staff).
[10] Email from Francis Collins to Anthony Fauci, et. al. (Apr. 16, 2020) (On file with Comm. Staff).
[11] John Haltiwanger, *Dr. Fauci throws cold water on conspiracy theory that coronavirus was created in a Chinese lab,* BLOOMBERG (Apr. 18, 2020).

3. What new evidence, if any, came to light about COVID-19 between February 1, 2020 and February 4, 2020 to alter the belief it originated in a lab?

4. Did Drs. Fauci or Collins edit the *Nature Medicine* paper entitled "The Proximal Origin of SARS-CoV-2"?

5. Would having this knowledge earlier have benefitted either vaccine or treatment development?

6. By February 1, 2020, were Drs. Fauci or Collins aware of the State Department's warnings about WIV safety?

7. Would this warning have changed the early response to the COVID-19 pandemic?

These questions are vital to understanding this and future pandemic responses. Unfortunately, thus far, HHS and its subordinate agency have hidden behind redactions to shield these emails from public scrutiny. We call on you to immediately lift these redactions and produce the email communications to Congress. Further, considering the import of the above questions, we request Dr. Anthony Fauci be made immediately available to sit for a transcribed interview. Please respond by January 18, 2022 to confirm.

Thank you for your attention to this important matter.

Sincerely,

James Comer

James Comer
Ranking Member
Committee on Oversight and Reform

Jim Jordan

Jim Jordan
Ranking Member
Committee on the Judiciary

cc: The Honorable Carolyn Maloney, Chairwoman
Committee on Oversight and Reform

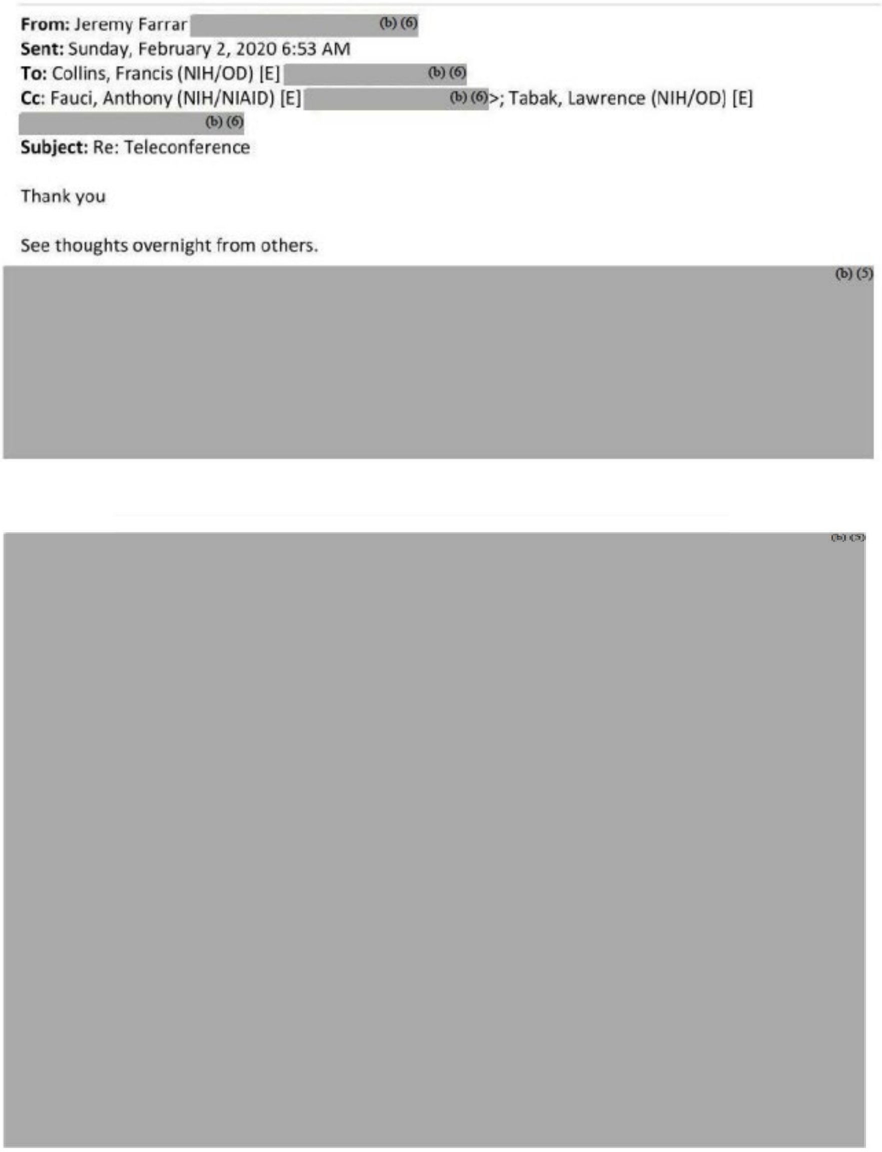
The Honorable Jerrold Nadler, Chairman
Committee on the Judiciary

Appendix I

These emails were originally produced redacted via the Freedom of Information Act and subsequently to Committee Republicans. At the request of Committee Republicans and pursuant to the Seven Member Rule, the Department of Health and Human Services made unredacted versions available for an *in camera* review but not available to the public. Committee staff, to the best of their ability, hand transcribed the contents of the emails and excerpts of those transcriptions are reproduced below. Unless otherwise noted, emphasis is added.

Notes from Participants on February 1, 2020 Conference Call

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



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

Thank you

See thoughts overnight from others.

[redacted] (b) (5)

[redacted] (b) (5)

From Mike Farzan (discoverer of SARS receptor):

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

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

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

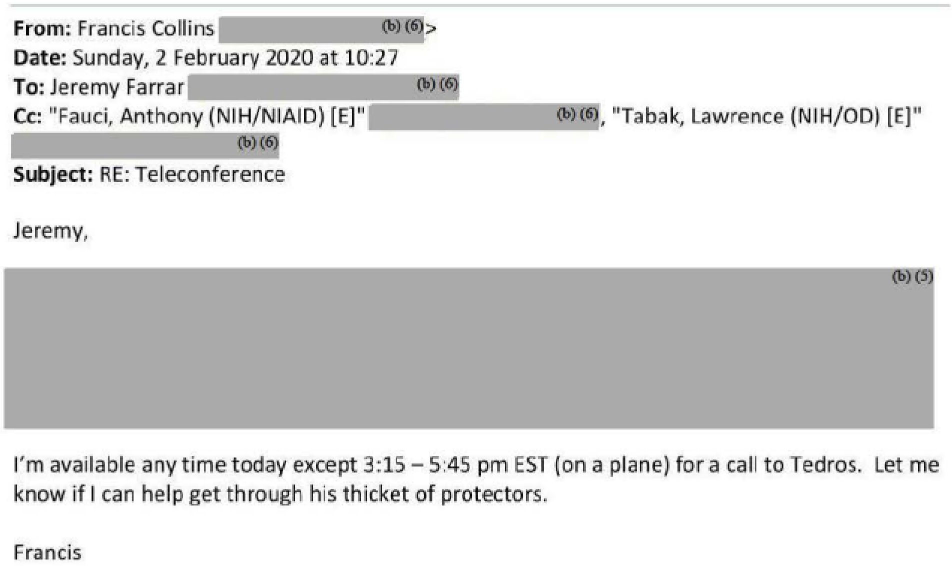
From Bob [Garry]:

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

That is the big if.

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

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



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

Jeremy,

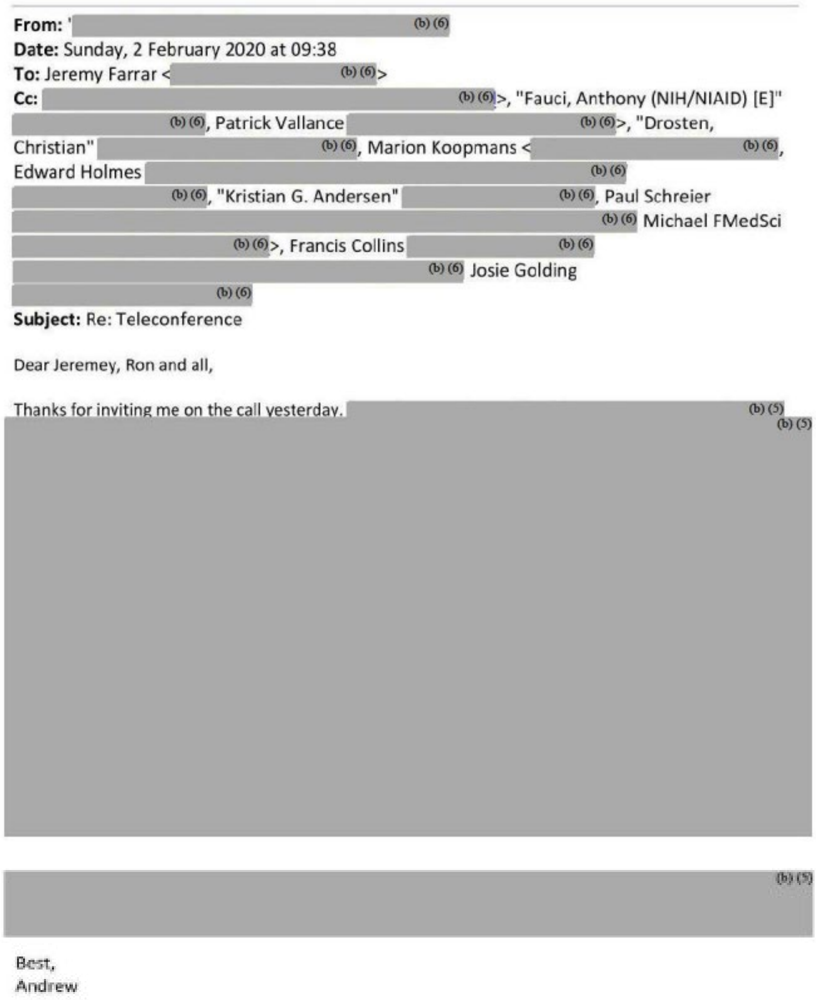
(b) (5)

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

Francis

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

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



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

Dear Jeremey, Ron and all,

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

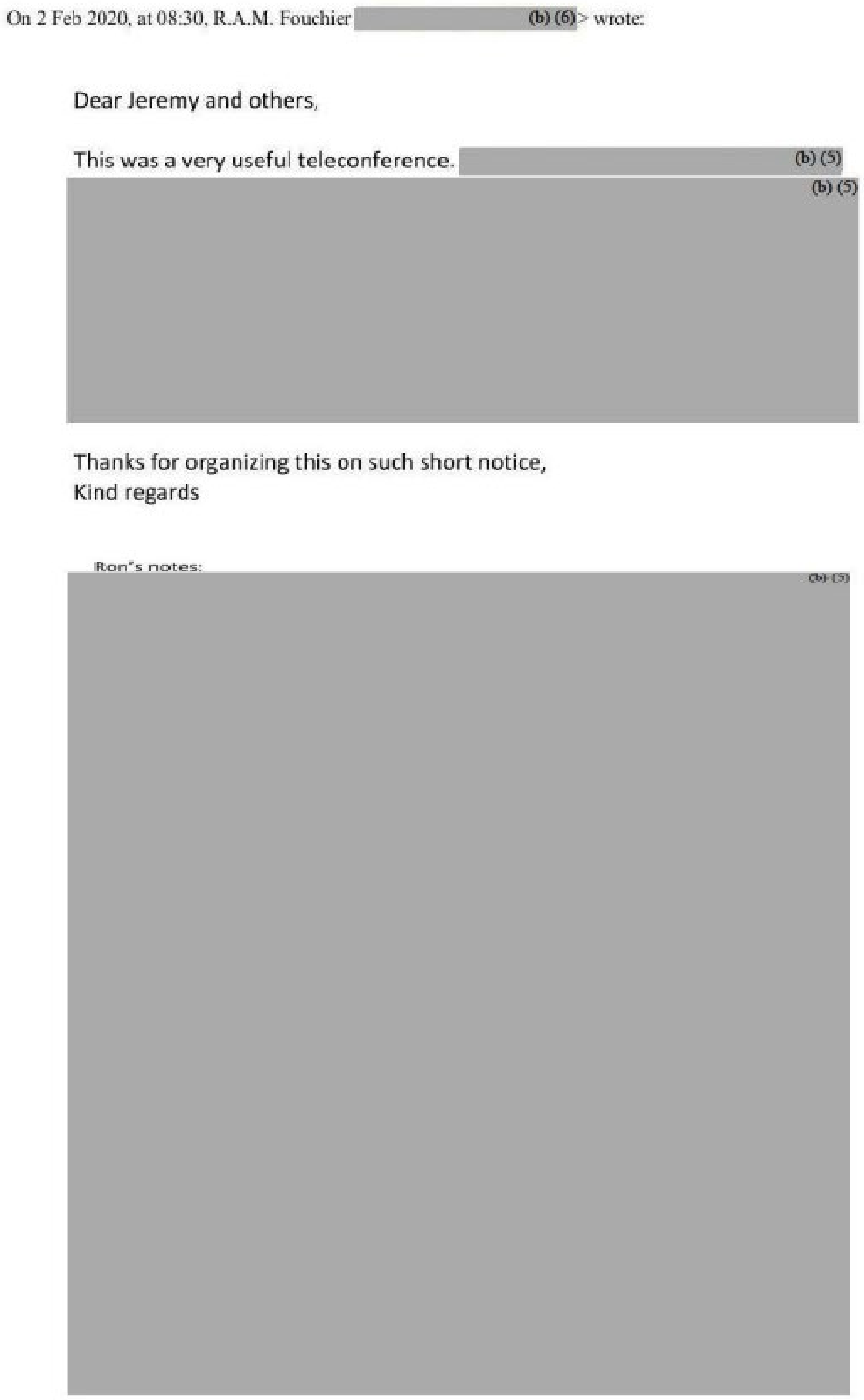
[redacted] (b) (5)

Best,
Andrew

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

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

4. Email from Dr. Ron Fouchier



On 2 Feb 2020, at 08:30, R.A.M. Fouchier [redacted] (b) (6)> wrote:

Dear Jeremy and others,

This was a very useful teleconference. [redacted] (b) (5)

[redacted] (b) (5)

Thanks for organizing this on such short notice,
Kind regards

Ron's notes:

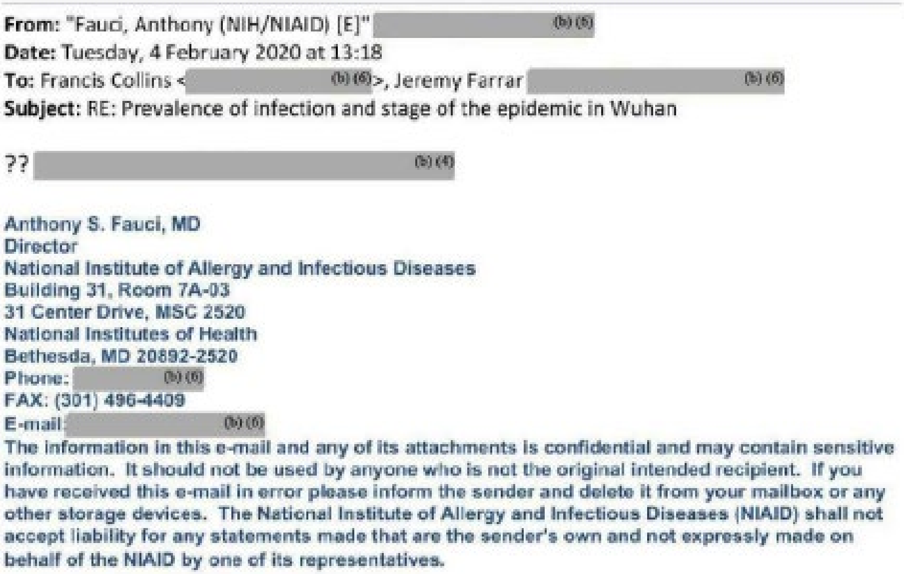
[redacted] (b) (5)

… Given the evidence presented and the discussions around it, I would conclude that a follow-up discussion on the possible origin of 2019-nCoV would be of much interest. However, I doubt if it needs to be done on very short term, given the importance of other activities of the scientific community, WHO and other stakeholders at present. It is my opinion that a non-natural origin of 2019-nCoV is highly unlikely at present. Any conspiracy theory can be approached with factual information.

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

Reaction to First Draft of *Nature Medicine* “The Proximal Origin of SARS-CoV-2”

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



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

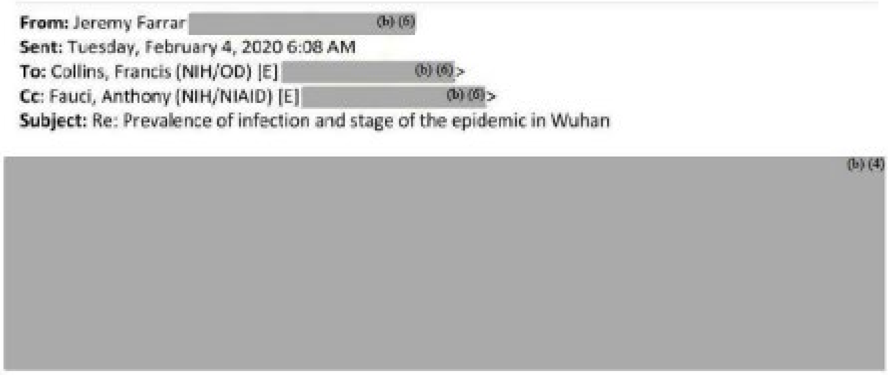
?? [redacted] (b)(4)

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

The information in this e-mail and any of its attachments is confidential and may contain sensitive information. It should not be used by anyone who is not the original intended recipient. If you have received this e-mail in error please inform the sender and delete it from your mailbox or any other storage devices. The National Institute of Allergy and Infectious Diseases (NIAID) shall not accept liability for any statements made that are the sender's own and not expressly made on behalf of the NIAID by one of its representatives.

…Serial passage in ACE2-transgenic mice

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

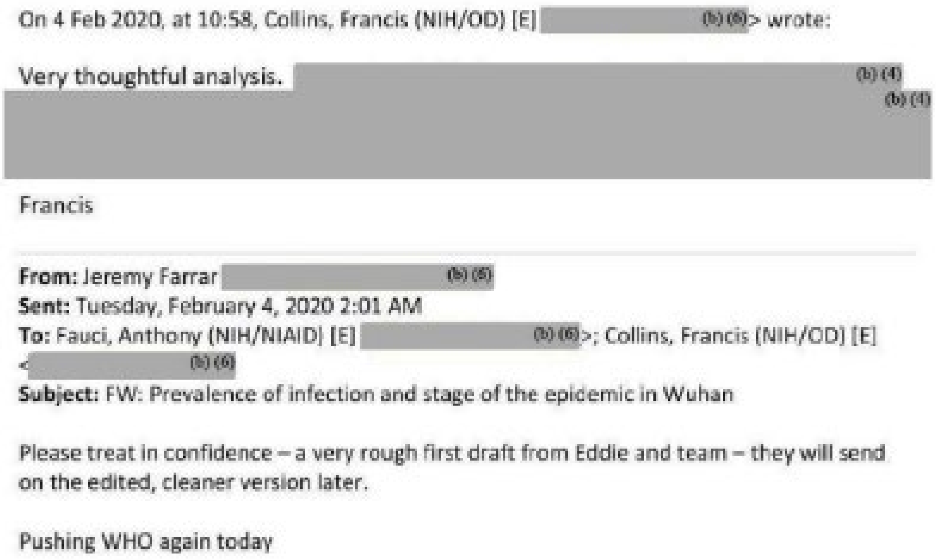


From: Jeremy Farrar [redacted] (b) (6)
Sent: Tuesday, February 4, 2020 6:08 AM
To: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

[redacted] (b) (4)

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

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



On 4 Feb 2020, at 10:58, Collins, Francis (NIH/OD) [E] (b) (6)> wrote:

Very thoughtful analysis. (b) (4)
(b) (4)

Francis

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

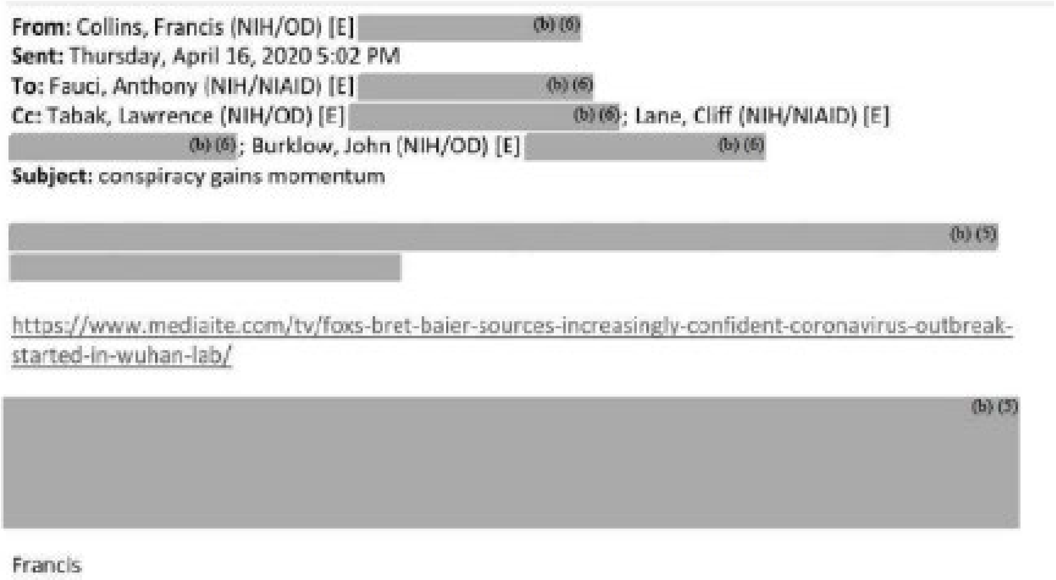
Please treat in confidence – a very rough first draft from Eddie and team – they will send on the edited, cleaner version later.

Pushing WHO again today

> …[Eddie Holmes] arguing against engineering but repeated passage is still an option…

Government Official Attempts to Stifle the Lab Leak Hypothesis

1. Email from Dr. Francis Collins to Drs. Anthony Fauci, Lawrence Tabak, Cliff Lane, and Mr. John Burklow



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

[redacted] (b) (5)

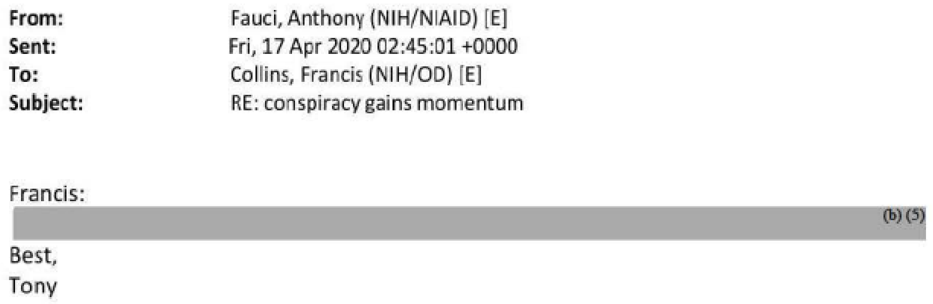
https://www.mediaite.com/tv/foxs-bret-baier-sources-increasingly-confident-coronavirus-outbreak-started-in-wuhan-lab/

[redacted] (b) (5)

Francis

> Wondering if there is something NIH can do to help put down this very destructive conspiracy, with what seems to be growing momentum:
>
> https://www.mediaite.com/tv/foxs-bret-baier-sources-increasingly-confident-coronavirus-outbreak-started-in-wuhan-lab/
>
> I hoped the Nature Medicine article on the genomic sequence of SARS-CoV-2 would settle this. But probably didn’t get much visibility.
>
> Anything more we can do? Ask the National Academy to weigh in?
>
> Francis

2. Email from Dr. Anthony Fauci to Dr. Francis Collins



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

Francis:

(b) (5)

Best,
Tony

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

End of document

The following are samples of some of the emails obtained by a reporter named Jason Leopold via a FOIA (Freedom of Information Act) request, and made available to the public HERE:

https://www.documentcloud.org/documents/20793561-leopold-nih-foia-anthony-fauci-emails

One of them was written by the lead author of a white paper published by Nature claiming that the preponderance of evidence is against a lab origin for the SARS-CoV-2 virus. Immediately prior to an emergency meeting organized by Anthony Fauci and Francis Collins, he had expressed the opinion that parts of the SARS-CoV look engineered. The evening after the meeting, he started work on the white paper expressing a very different opinion.

Another is from Anthony Fauci congratulating the author for getting the paper published. Fauci had convened an emergency meeting with 4 of the 5 authors the same day they started work on the paper.

Another is from Peter Daszak of EcoHealth Alliance thanking Fauci for referring reporters to that paper, to get them off the trail leading to Peter Daszak's gain-of-function project at the Wuhan Institute of Virology.

Fauci had a conflict-of-interest in promoting this paper, and even more so, helping to write it.

Here is some background information about the investigative reporter who obtained and released the emails, copied verbatim from his Wikipedia entry:

Jason Arthur Leopold (born October 7, 1969)[1] is an American senior investigative reporter for BuzzFeed News.[2] He was previously an investigative reporter for Al Jazeera America[3] and Vice News.[4] He worked at Truthout as a senior editor and reporter, a position he left after three years on February 19, 2008, to co-found the web-based political magazine The Public Record, Leopold's profile page on The Public Record now says he is Editor-at-Large.[5] Leopold returned to Truthout as Deputy Managing Editor in October 2009 and was made lead investigative reporter in 2012[6] before leaving Truthout in May 2013.[7] He makes extensive use of the Freedom of Information Act to research stories.[8]

Leopold was the journalist who forced the release of all of Hillary Clinton's emails through the Freedom of Information Act. He was identified by the Transactional Access Clearinghouse as "by far the most active individual FOIA litigator in the United States today."[9] He has written stories on a many subjects including in the past decades on BP, Enron, the California Energy Crisis, the Bush administration's torture policies, and the Plame affair. His pieces have been published in The

Guardian,[10] Asia Times,[11] the Los Angeles Times, The Wall Street Journal, CBS MarketWatch,[12][13][14] The Nation, and Utne Reader. He has also written about foreign and domestic policy online for publications such as The Guardian,[10] Alternet, CounterPunch, Common Dreams, The Huffington Post, Political Affairs Magazine, The Raw Story, Scoop, ZNet and others.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 18:43:31 +0000
To: Kristian G. Andersen
Subject: RE: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Thanks, Kristian. Talk soon on the call.

From: Kristian G. Andersen [redacted] (b) (6)>
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Jeremy Farrar [redacted] (b) (6)>
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

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

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

Best,
Kristian

On Fri, Jan 31, 2020 at 18:47 Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)> wrote:

> Jeremy/Kristian:
> This just came out today. You may have seen it. If not, it is of interest to the current discussion.
> Best,
> Tony
>
> ---
>
> **From:** Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6)
> **Sent:** Friday, January 31, 2020 8:43 PM
> **Subject:** Science: Mining coronavirus genomes for clues to the outbreak's origins

From: [redacted] (b) (6)
Sent: Sun, 8 Mar 2020 09:23:28 -0400
To: Kristian G. Andersen
Cc: Jeremy Farrar;Collins, Francis (NIH/OD) [E];Robert Garry;Edward Holmes;Andrew Rambaut;Ian Lipkin;Chris Emery
Subject: Re: SARS-CoV-2 article to be published in Nature Medicine

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

> On Mar 6, 2020, at 4:23 PM, Kristian G. Andersen [redacted] (b) (6)>wrote:
>
> Dear Jeremy, Tony, and Francis,
>
> Thank you again for your advice and leadership as we have been working through the SARS-CoV-2 'origins' paper. We're happy to say that the paper was just accepted by Nature Medicine and should be published shortly (not quite sure when).
>
> To keep you in the loop, I just wanted to share the accepted version with you, as well as a draft press release. We're still waiting for proofs, so please let me know if you have any comments, suggestions, or questions about the paper or the press release.
>
> Tony, thank you for your straight talk on CNN last night - it's being noticed.
>
> Best,
> Kristian
>
> **Kristian G. Andersen, PhD**
> Associate Professor, Scripps Research
> Director of Infectious Disease Genomics, Scripps Research Translational Institute
> Director, Center for Viral Systems Biology
>
> **The Scripps Research Institute**
> 10550 North Torrey Pines Road, SGM-300A
> Department of Immunology and Microbial Science
> La Jolla, CA 92037
>
> [redacted] (b) (6)

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 19 Apr 2020 03:29:42 +0000
To: Peter Daszak
Subject: RE: Thank you for your public comments re COVID-19's origins

Peter:
Many thanks for your kind note.
Best regards,
Tony

From: Peter Daszak [redacted] (b) (6)
Sent: Saturday, April 18, 2020 9:43 PM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6); Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)>
Cc: Stemmy, Erik (NIH/NIAID) [E] [redacted] (b) (6)>; Erbelding, Emily (NIH/NIAID) [E] [redacted] (b) (6)>; Aleksei Chmura [redacted] (b) (6)
Subject: Thank you for your public comments re COVID-19's origins
Importance: High

Tony (cc'ing David so that you might pass this on to Tony once he has a spare second)

As the PI of the R01 grant publicly targeted by Fox News reporters at the Presidential press briefing last night, I just wanted to say a personal thankyou on behalf of our staff and collaborators, for publicly standing up and stating that the scientific evidence supports a natural origin for COVID-19 from a bat-to-human spillover, not a lab release from the Wuhan Institute of Virology.

[redacted] (b) (7)(A)

From my perspective, your comments are brave, and coming from your trusted voice, will help dispel the myths being spun around the virus' origins.

Once this pandemic's over I look forward thanking you in person and let you know how important your comments are to us all.

Cheers,

Peter

End of document

The following letter was posted as-is by Dr. Andrew Huff on his Twitter account. The date, and to whom the letter was addressed are presumed missing, possibly to protect whoever his government contact is, but in any case, he intended the rest of it to be an open letter.

His Twitter account is here: https://twitter.com/AGHuff

Dr. Andrew Huff is a real person. His name and position within the company are copiously mentioned in numerous documents distributed by EcoHealth Alliance itself, before his apparent falling-out with his boss.

In late October 2021, I came forward as a material witness and whistle blower related to numerous unethical and criminal behaviors that took place at EcoHealth Alliance, the organization that established the relationship with the Wuhan Institute of Virology and funded the development of SARS-COV2, more commonly known as COVID-19.

- EcoHealth Alliance engaged in fraud against the US government (Timecard fraud, and contract reimbursement fraud). After I identified and learned about these serious issues, I brought them to the attention of Dr. Peter Daszak, Dr. Aleksei Chamura, and CFO Harvey Kasdan. After raising these issues at the meeting, Harvey Kasdan went home from work, had a heart attack, and died.

- Dr. Peter Daszak disclosed to me in late 2015 and early 2016 that he was working with the CIA. I also have documents in my possession, and which have been posted to Twitter and shared with several journalists that prove EcoHealth Alliance was working with the intelligence community. These documents include the InQTel pitch deck authored and presented by Dr. Daszak, and the IARPA report that I wrote.

- The executive team openly discussed the gain of function work and research in China where I was opposed to it for numerous obvious reasons (mainly training the CCP in bioweapons and intellectual property theft).

- EcoHealth Alliance, and foreign laboratories, did not have the adequate control measures in place for ensuring proper biosafety, biosecurity, and risk management in place, ultimately resulting in the lab leak at the Wuhan Institute of Virology. In fact, I raised these concerns at an executive project planning meeting, where Dr. Daszak quickly dismissed my concerns. This information is also validated by cables between the US Consulate in China and the State Department. Although, this is not limited to China.

- EcoHealth Alliance was working with the Wuhan Institute of Virology and gain of function work with Dr. Ralph Baric at the University of North Carolina **<u>before</u>** NIH NIAID and Dr. Anthony Fauci funded the work there. I have released the documents that prove this claim on Twitter and to the press.

- EcoHealth Alliance, as do most of the best scientists in the world, **work before of receipt of the funding to complete the work**. This is commonplace throughout academia, and this is how the best scientists collect the necessary "preliminary data" to obtain funding on highly competitive grants. Often, the first year of work is mostly or completely completed, before the funding is awarded. At EcoHealth Alliance we always worked ahead of the work. This is an important fact because the DEFUSE grant proposal sent to DARPA by EcoHealth Alliance specifically describes the gain of function work that would lead to an accidental or intentional release of SARS-COV2, by the Chinese, beginning in September of 2019. Suggesting, that there is a high likelihood that the work in the DARPA DEFUSE proposal written and submitted by EcoHealth Alliance was well underway before an award determination by DARPA was made.

- Dr. Peter Daszak could be a double agent working on behalf of the Chinese government. This is based on my observations of his behavior and the nature of statements related to working with the Chinese (did not see risks, concerns, or other obvious problems) related to conducting gain of function work or other high risk laboratory work, in China. Which is completely absurd given what a CEO's duties and responsibilities are to the board of directors, the company, and its employees.

I look forward to testifying under oath to these unfortunate factual statements and I am at your service.

Sincerely,

Andrew Huff, PhD, MS

End of document

End