COMMITTEE ON OVERSIGHT AND ACCOUNTABILITY,

SELECT SUBCOMMITTEE ON THE CORONAVIRUS PANDEMIC,

U.S. HOUSE OF REPRESENTATIVES,

WASHINGTON, D.C.

INTERVIEW OF: ROBERT F. GARRY

Friday, June 9, 2023

New Orleans, Louisiana

The interview in the above matter was held at Tulane University Medical School, Hutchinson Building, 1430 Tulane Avenue, New Orleans, Louisiana, commencing at 8:57 a.m. Central Time.

Appearances:

For the SELECT SUBCOMMITTEE ON THE CORONAVIRUS PANDEMIC:

MITCH BENZINE, STAFF DIRECTOR

MADELINE BREWER, COUNSEL

PETER SPECTRE, PROFESSIONAL STAFF MEMBER

GIANCARLO PELLEGRINI, MINORITY CHIEF COUNSEL

JOSEPH ROMERO, MINORITY COUNSEL

For TULANE UNIVERSITY:

SHARON COURTNEY, VICE PRESIDENT FOR GOVERNMENT AFFAIRS

DAVID STEIN, SENIOR ASSOCIATE GENERAL COUNSEL

For ROBERT F. GARRY:

MARY M. GARDNER

RONALD JACOBS

Venable LLP

600 Massachusetts Avenue, NW

Washington, D.C. 20001

Mr. Benzine. This is a transcribed interview of Dr. Robert F. Garry, Jr., conducted by the House Select Subcommittee on the Coronavirus Pandemic. Under the authority granted to it by House Resolution 5 and the rules of the Committee on Oversight and Accountability. This interview is requested by Chairman Brad Wenstrup as part of the select subcommittee's oversight of the Federal Government's response to the coronavirus pandemic. Further, pursuant to House Resolution 5, the select subcommittee has wide-ranging jurisdiction but specifically to investigate the origins of the coronavirus pandemic, including but not limited to the Federal Government's funding of gain-of-function research.

Can the witness please state his name and spell his last name for the record?

Dr. Garry. Robert F. Garry, G-a-r-r-y.

Mr. Benzine. Thank you. Dr. Garry, my name is Mitch Benzine, and I am the staff director for the majority staff of the select subcommittee. I want to thank you for coming in today for this interview. The select subcommittee recognizes that you're here voluntarily, and we appreciate that.

Under the select subcommittee and Committee on Oversight and Accountability's rules, you are allowed to have an attorney present to advise you during this interview. Do you have an attorney representing you on a personal capacity today?

Dr. Garry. Yes.

Mr. Benzine. Will counsel please identify themselves for the record.

Mr. Jacobs. Sure. Ronald Jacobs.

Ms. Gardner. Mary Gardner.

Mr. Benzine. Dr. Garry, are there any other attorneys present representing your employer?

Dr. Garry. Yes.

Mr. Benzine. Will counsel please identify themselves for the record?

Mr. Stein. Hi. My name is David Stein, senior associate general counsel for Tulane University.

Mr. Benzine. Will the other from Tulane, please?

Ms. Courtney. Sharon Courtney, vice president for government community relations.

Mr. Benzine. All right. Thank you. For the record, starting with the majority staff, any additional staff members in the room, please introduce themselves with their name, title, and affiliation.

Ms. Brewer. Madeline Brewer, counsel for majority.

Mr. Spectre. Peter Spectre, personal staff member for majority.

Mr. Pellegrini. Giancarlo Pellegrini, minority chief counsel.

Mr. Romero. Joseph Romero, counsel for the minority.

Mr. Benzine. Okay. Thank you, all. Dr. Garry, before we begin, I would like to go over the ground rules for the interview. The way this interview will proceed is as follows: The majority and minority staff will alternate asking you questions one hour per side per round until each side is finished with their questioning. The majority staff will begin and proceed for an hour, and then the minority staff will have an hour to ask their questions. We will then alternate back and forth in this manner until both sides have no more questions. If either side is in the middle of a specific line of questioning, they may choose to end a few minutes past the hour to ensure completion of that specific line of questioning, including any pertinent followups. In this interview, while one member of the staff of each side may lead the questioning, additional staff may ask questions.

There's a court reporter taking down everything I say and everything you say to make a written record of the interview. For the record to be clear, please wait until the staffer questioning finishes each question before you begin your answer, and the staffer will wait until you finish your response before proceeding to the next question. Further, to ensure the court reporter can properly record this interview, please speak clearly, concisely, and slowly. Also, the court reporter cannot record nonverbal answers, such as nodding or shaking your head, so it is important that you answer each question with an audible verbal answer.

Exhibits may be entered into the record. Majority exhibits will be identified numerically. Minority exhibits will be identified alphabetically. Do you understand?

Dr. Garry. I do understand.

Mr. Benzine. We want you to answer our questions in the most complete and truthful manner possible. So we will take our time. If you have any questions or do not fully understand the question, please let us know. We will attempt to clarify, add context to, or rephrase our questions. Do you understand?

Dr. Garry. I do understand.

Mr. Benzine. If we ask about specific conversations or events in the past, and you are unable to recall the exact words or details, you should testify to the substance of those conversations or events to the best of your recollection. If you recall only a part of a conversation or event, you should give us your best recollection of those events or parts of conversations that you do recall. Do you understand?

Dr. Garry. I do.

Mr. Benzine. Although, you are here voluntarily, and we will not swear you in, you are required, pursuant to title 18, section 1001, of the United States Code, to answer questions from Congress truthfully. This also applies to questions posed by

congressional staff in this interview. Do you understand?

Dr. Garry. I do understand.

Mr. Benzine. If at any time you knowingly make false statements, you could be subject to criminal prosecution. Do you understand?

Dr. Garry. I understand.

Mr. Benzine. Is there any reason you are unable to provide truthful testimony in today's interview?

Dr. Garry. There's no reason.

Mr. Benzine. The select subcommittee follows the rules of the Committee on Oversight and Accountability. Please note that, if you wish to assert privilege over any statement today, that assertion must comply with the rules of the Committee on Oversight and Accountability. Pursuant to that, committee rule 16 (C)(1) states: For the chair to consider assertions of privilege over testimony or statements, witnesses or entities must clearly state the specified privilege being asserted, and the reason for the assertion on or before the scheduled date of testimony or appearance. Do you understand?

Dr. Garry. I understand.

Mr. Benzine. Ordinarily, we take about a 5-minute break at the end of each hour of questioning, but if you need a longer break or a break before that, please let us know, and we will be happy so accommodate. However, to the extent that there's a pending question, we would ask that you finish answering the question before we take the break. Do you understand?

Dr. Garry. I understand.

Mr. Benzine. Do you have any other questions before we begin?

Dr. Garry. No more questions.

EXAMINATION

BY MR. BENZINE:

Q All right. Thank you. I want to thank you again for appearing voluntarily for this interview and your work over the years in the field of science. I want to go through your education and experience first. Where did you attend undergraduate school?

A Two schools; Indiana University in Bloomington, and then I finished at Indiana State University in Terre Haute, Indiana.

Q And what degree graduate with?

A Bachelor of science in biology.

Q Where did you get your doctorate?

A University of Texas at Austin.

Q Is your doctorate in a specific discipline?

A Microbiology.

Q And who is your current employer?

A Tulane University School of Medicine.

Q And what is your current job title?

A I'm a professor and also an associate dean.

Q Can you elaborate more on, I guess, the day-to-day for both of those? What's your professorial role, and what's the dean role?

A Well, I do scientific research. I train graduate students. I give lectures occasionally. Not so much anymore. And the associate dean title is for biomedical sciences. So I had our graduate program for Ph.D. and master's students.

Q Can you briefly go through your career up until now?

A It's fairly straightforward. After the Ph.D. at University of Texas, I came

here as an assistant professor in 1983. I started working on what I've been working on for a long time: virology. And so I moved through the ranks and, you know, wouldn't want to be doing anything else.

Q You've been at Tulane your entire career?

A I have. We had my 40th anniversary last -- a couple weeks ago.

Q That's impressive. Congratulations.

A Thank you.

Q Do you currently hold or have you previously held any honorary positions?

A Oh, gosh. Well, I mean, you know, I'm a member of a lot of scientific societies, and, you know, I do other things in the scientific world. I'm not exactly sure. I'm the president of the Viral Hemorrhagic Fever Consortium. I think that would be the one I would bring forward first. I'm also the cofounder of a company called Zalgen Labs. Those two things are probably the titles I would point you to.

Q So that goes to kind of my next question. Do you currently hold, or have you previously held any positions on boards of companies, nonprofits, or otherwise?

A Well, that would be the Zalgen Labs, but I have done that for other companies, too, over the years.

Q Too?

A Oh, there's a company called Autoimmune Technologies, and just, you know, various informal consulting roles for a lot of companies over the years.

Q Can you explain those Zalgen Labs a little bit more?

A Zalgen Labs is a company that was founded by two of my ex students here at Tulane University. They were a little older than average students and had a lot of experience in the biotechnology industry already before they came to Tulane for their doctoral degrees. So Luis Bronco started his branch of Zalgen Labs in Maryland; and

Matt Boisen started his branch in Denver, Colorado, or outside of Denver. Dr. Bronco works on monoclonal antibody therapies. And Matt Boisen does immunoassays and assay development. And the company's been pretty successful so far.

Q Does Zalgen Labs receive any -- monoclonal antibodies was a common treatment for COVID-19. Did Zalgen Labs receive any contracts or purchase agreements from the Federal Government?

A They did not. We work on monoclonals for other viruses like Lassa virus and Ebola virus.

Q Thank you. In addition to academic virology, have you had any experiences with emerging disease outbreaks prior to COVID-19?

A I have. It's been practically my entire career. Of course, I started working on AIDS and human immunodeficiency virus, which was, of course, an emerging virus, you know, back in the eighties, maybe even before that. And I spent about 20 years doing that work, working in the field of, you know, basic science but touching onto translational work where you developed assays, immunoassays, things like Western blots. I did some work on that. Also, I worked on basic questions about how HIV causes its pathology; so how it interacts with cells. In the course of doing that, I learned a lot about the viral glycoproteins; the spikes on the surface of HIV that, you know, all unblocked viruses have. And so some of that I translated into, you know, working on emerging viruses, particularly after the 9/11 incident and the anthrax attacks, and things. There were funds shifted to work on emerging viruses, biothreat agents. And so I kind of shifted some of my emphasis from HIV to these emerging viruses, like Lassa virus and Ebola virus.

Q Can you explain a little bit more like the work on anthrax and bio threats?

A I didn't work on anthrax.

Q Okay.

A But, at that time, you know, the government and other people were interested in basically all, you know, infectious agents that could potentially be used as bioweapons. And so they called for proposals to basically do some work on some of these understudied viruses. And it was an opportunity for me to work on a virus called Lassa virus, which causes a hemorrhagic fever in West Africa. So, for the past 15, 16 years, I've been working mostly on Lassa virus, you know, all the way from just developing diagnostics, which I had background in from the HIV days to, you know, now we're currently working on countermeasures, which would be diagnostics and vaccines and other things like that. So.

Q We're understanding that you've primarily worked on Lassa. Were coronaviruses at all involved in this?

A I did work on Ebola virus -- on coronavirus too. First SARS in 2002, '3, and '4. You know, emerging virus is interesting to me. Some of the work that I did initially on that virus was to look at its glycoprotein, the spike protein which is famous now. We all know about it. But, you know, the first SARS had a similar protein, and so, just as soon as the sequence for that virus was published, we did some analysis. "We" being a, you know, team of people that I have worked with over the years, but looking at that protein to see basically how it was put together and, you know, what its functions might be.

Q Thank you. Over the course of your career, have you received grants or contracts from the Federal Government?

A The NIH has been very generous to me, so I've, you know, been grateful for that support, yes.

Q What topics have usually been --

A Virology. So HIV, I had grants, you know, for about 20 years to work on

those basic science aspects I mentioned. And then, since then, we've been funded to do work on Lassa and Ebola and some other emerging viruses.

Q Do you have any current grants?

A Yes.

Q Which ones? Briefly, if there are a lot.

A There is a list, yes. Let me, just the highlights. I'm a -- one of the principal investigators on a project called -- the main program is CREID, which is the Center for Research in Emerging Infectious Diseases. Another grant that I'm on is a systems biology grant. So studying, basically, you know, viruses using big -- Big Data and big computers, and things like that. So that's a center for systems biology and viruses. And I, you know, have some RO1 grants on vaccines and monoclonal antibodies for Lassa virus.

Q Thank you. The CREID one, your other PI is Dr. Andersen --

A That is correct, yes. And also Pardis Sabeti at Harvard.

Q Thank you. I'm going to go down a long list of names, and I just want a yes or no if you have spoke with, emailed, texted, communicated with any of these people regarding COVID-19 or the origins of COVID-19 between late December 2019 and present. Dr. Francis Collins?

A Yes.

Q Dr. Anthony Fauci?

A Yes.

Q Dr. Lawrence Tabak?

A Yes.

Q Dr. Hugh Auchincloss?

A Yes.

Q Dr. Cliff Lane?

A I am going to have to say I don't remember specifically. I do suspect he was on some of the emails.

Q Okay. Dr. David Morens?

A Yes.

Q Dr. Ping Chen?

A Again, I don't know all the names of all the people who are on all the emails. It's possible, but I don't recall specifically.

Q Dr. Ian Watson?

A Same answer. I don't know.

Q Dr. Andrew Pope?

A I am going to have to go same answer.

Q Dr. Victor Dzau?

A Again, the same answer.

Q Dr. Robert Redfield?

A No.

Q Dr. Michael Lauer?

A Again, I'm not sure. It's entirely possible, but I don't know for certain.

Q Dr. David Christian Hassell?

A I don't recall his name specifically now.

Q Dr. Jeremy Farrar?

A Yes.

Q Dr. Kristian Andersen?

A Yes.

Q Dr. Michael Farzan?

A Yes.

Q Dr. Eddie Holmes?

A Yes.

Q Dr. Ian Lipkin?

A Yes.

Q Dr. Andrew Rambaut?

A Yes.

Q That's helpful going further.

A Yes.

Q That was yes?

A It is yes.

Mr. Pellegrini. I have a question. Is this regarding the origin of COVID or anything related to COVID?

Mr. Benzine. Both.

Mr. Pellegrini. Both.

BY MR. BENZINE:

Q Dr. Christian Drosten?

A Yes.

Q Dr. -- I'm going to butcher it again -- Ron Fouchier?

A Yes. I can see your thing.

Q Doctor, I think I need 16-point font so I can read it. Dr. Marion Koopmans.

A Yes.

Q Dr. Peter Daszak?

A Yes.

Q Dr. Aleksei Chmura?

A I don't recall.

Q Dr. Kevin Olival?

A It's possible. I just don't recall specifically.

Q That's okay. Thank you. Dr. Michael Worobey?

A Yes.

Q Dr. Jonathan Pekar?

A Yes.

Q Dr. Florence Debarre?

A That's right. It's yes.

Q Dr. James LeDuc?

A I think yes is the answer, the proper answer to that. I'm sure we've been on a couple of emails together.

Q Dr. Shi Zhengli?

A Yes.

Q Dr. George Dzau?

A Yes.

Q Dr. Ralph Baric?

A Right. I am going to have to say I'm not exactly sure. There probably have been emails, but I don't know for certain.

Q I want to ask you the same kind of question, just any interactions not with -- any interactions with people at or the institution itself about the origins of COVID or COVID-19 generally but probably more specifically the origins from December to now at the Wuhan Institute of Virology?

A Minor, but yes.

Q The Wuhan Centers for Disease Control and Prevention?

A No.

Q The Chinese Centers for Disease Control and Prevention?

A No.

Q Wuhan University?

A Well, to the extent that the Wuhan Institute of Virology is part of that, I guess I'd probably have to say yes, but not specifically with the university per se.

Q Okay. The Chinese Academy of Sciences?

A I think that's the same answer. It's part of the Wuhan -- it's a part of that. So.

Q The Academy of Military Medical Sciences?

A No.

Q The Fifth Institute under the National Defense Ministry of China?

A No.

Q You said it was minor, what was the level of the communication with anyone at the Wuhan Institute of virology?

A There was a paper that appeared in one of the American Chemistry Society Journals that made some specific accusations against Dr. Zhengli Shi. And there were several virologists that basically responded and wrote a letter to the editor saying that that paper was not very scientific and probably didn't belong in the journal. And so I was happy to sign that because I don't think that's the way that the scientific literature should be used.

Q I am going to go back through some of the names. Some of them we'll get into more detail. What was the level of communication you had with Dr. Auchincloss?

A I believe he was on an email. He might have even been on one other of the conference calls that I had with Fauci and Collins. But, again, I'm not sure -- I'm not sure

of all people that were on those calls. I'm pretty sure he was on the original email list, though.

Q All right. I appreciate it. And then what's the -- we'll get into this in a little bit, too. What's the level of communication with Dr. Morens?

A Morens? I think I have been on a few email chains with him.

Q What about -- I assume, well, I won't assume. What's the level of communication with Dr. Shi?

A Very minor.

Q Was it regarding that letter?

A It was in regard to the American Chemical Society paper.

Q What about Dr. Dzau?

A Just some minor communications here. You know, you asked me about shared emails, and I'm sure I've been on a few with him. Some of the people that I was co-author on with the Proximal Origins paper are, you know, they know Dr. Dzau; they went to school with him. So there was some joint communications --

Q Did you ever have an individual phone call with Dr. Dzau?

A Not an individual phone call. I did listen to a seminar that he gave one time and asked him a question after the seminar was over.

Q Okay. Thank you.

Mr. Benzine. I want to introduce what we will mark first as majority exhibit 1.

[Garry Majority Exhibit No. 1

Was marked for identification.]

Mr. Jacobs. Mitch, can I ask a quick clarifying question --

Mr. Benzine. Yes.

Mr. Jacobs. -- about one of the questions you asked, which when talking about

the NIH funding, the "we" there, Dr. Garry, is that you personally, or is that the -- going back to Mitch's question about NIH, the funding doesn't come to you personally, does it?

Dr. Garry. No, sir, it doesn't. It comes to the university.

Mr. Jacobs. Thanks.

Dr. Garry. We write the grants. The grant is funded through the university, and we do the work.

Mr. Benzine. Thank you. I appreciate it.

Mr. Jacobs. Sure.

BY MR. BENZINE:

Q So this will be marked majority exhibit 1. It's an email from Dr. Morens to Dr. Daszak, and you're on the CC line as well. It's Bates marked Garry, G-a-r-r-y 0001774. And, for clarity in the record, the document has some redactions done by the majority staff to protect personally identifiable information. So we already talked about Dr. Morens a little bit. Who is he? What's his job title, are you aware?

A He works with Dr. Tony Fauci. I'm not exactly a hundred percent sure there, you know, of his precise job title, but he is a long-time colleague with Fauci.

Q At the National Institute of Virology --

A That's correct.

Q I want to read two specific lines from the email. The first one is the first line after the salutation. It read: As you know, I try to always communicate on gmail because my NIH email is FOIA'd constantly.

And then, at the bottom, it says: Don't worry, just send to any of my addresses, and I will delete anything I don't want to see in The New York Times.

Did you often communicate with Dr. Morens over gmail?

A You know, honestly, I probably wouldn't have looked and see which email

account he was using, so I don't know how to answer that question, you know, within any --

Q Did you ever speak with Dr. Morens about official business about NIH work, grant funding, NIH-funded papers?

A I mean, I think, you know, I was definitely on email chains that Dr. Morens was involved in. And, also, I think he may have been on those -- some of those teleconferences. So the answer to that is yes.

Q I want to go through some of the names before and ask a more specific question to the best of your recollection understanding they are emails from years ago, and you may not look at the "to" line, if you have communicated with any of the following people via personal email or personal cell phone. Dr. Francis Collins?

A Could you repeat that? I'm not sure if I understand the question.

Q Yes. So asking if you have communicated with any of the following individuals on a personal email, so an email that doesn't end in dot.gov --

A Okay.

Q -- or a personal cell phone?

A Okay. Got it.

Q Dr. Francis Collins?

A No.

Q Dr. Anthony Fauci?

A No.

Q Dr, Lawrence Tabak?

A No.

Q Dr. Hugh Auchincloss?

A No.

Q Dr. Cliff Lane?

A No.

Q Dr. David Morens?

A No.

Q This is his gmail, just so you know.

A Oh, okay. That -- oh, okay. Okay. Thanks. I appreciate that.

Q I didn't want you to get --

A Well, no, because you've got it blocked out.

Q At the bottom, it's got his gmail. I wasn't going to --

A Oh, okay. So apparently the answer to that is yes.

Q Dr. Ping Chen?

A Well, now I'm wondering, but I'm thinking no.

Q To the best of your recollection?

A Not that I'm aware of, to the best of my recollection.

Q Dr. Ian Watson?

A No.

Q Dr. Andrew Pope?

A No.

Q Dr. Victor Dzau?

A No.

Q Dr. Robert Redfield?

A No.

Q Dr. Michael Lauer?

A No.

Q Or Dr. David Christian Hassell?

A No.

Q All right. Thank you. Switching gears talking, we can move down to exhibit 1.

Mr. Jacobs. Can I ask a clarifying question on that?

Mr. Benzine. Yeah.

Mr. Jacobs. Dr. Garry, if you had been on a group email with a lot of different people than the ones that were just read through, would you necessarily have noticed if it was a personal email versus a government email?

Dr. Garry. Unlikely. Yeah.

Mr. Benzine. I appreciate it.

Dr. Garry. Yeah. I mean, like I -- yeah, I probably should have answered "I don't know" for all of those, but yeah.

BY MR. BENZINE:

Q To the best of your recollection, we're good. So some baseline, moving on to kind of baseline questions on the origins of COVID-19. Yes or noes to these, and we can dive in further. Is investigating the origins of COVID-19 important?

A It is.

Q Is discovering the origins of COVID-19 important?

A It is.

Q Why is that?

A Well, I think I'll give you an answer that a lot of people give. You know, we need to know how this pandemic started so that we can help, you know, put into place measures so that it doesn't -- something like that doesn't happen again.

Q What does the origins of an emerging virus, any virus not just COVID-19, tell you in preparation for a future pandemic?

A Well, if you know the mechanism by which it spilled over, then you can look at those spillover events and try to mitigate them, try to ensure that, you know, people don't get exposed to those viruses in that way.

Q So, after going back to once before SARS and MERS that were zoonotic from wildlife trade, what would a prevention strategy be for a zoonotic spillover?

A Well, you could regulate the wildlife trade better than it is currently being regulated. You could monitor the animals, you know, don't allow illegal wildlife trade. You know, monitor the farms and other places where these wild animals are kept and test them for viruses. There are ways that you can do it.

Q How would you go about regulating the wildlife trade?

A Well, you'd have to have some sort of a government intervention there. They would have to have people that would inspect the farms and probably take samples from the animals and monitor the people that are in contact with the animals to, you know, see what they have been exposed to.

Q Were systems like that put in place in China after SARS-1?

A I'm not an expert on that area, but my understanding from looking into it is that they were pretty minor.

Q What were they, to your understanding?

A Well, they temporarily shut down some of the wildlife farms after the first SARS outbreak in 2002. There were actually several outbreaks that happened around that same time. But I -- you know, my impression is and, you know, it's backed up by, you know, people in the scientific literature that pretty much reverted to what it had been before, which is more or less not a very well-regulated industry. It's not like our beef industry or the farming here in the U.S., But that -- in that, you know, the illegal part of that trade, you know, which is informal and, you know, basically trapping wild animals

and bringing them in for sale, pretty much went back to the way it was before.

Q And those animals that are -- it's animals, raccoon dogs, common animals that could transmit infectious disease?

A There were many animals in that wildlife trade that are susceptible to SARS-CoV-2, yes.

Q Do you think, in your opinion, we'll know for sure where COVID-19 came from?

A I do think that we know where the outbreak started in Wuhan; where it came from before that I doubt that we'd ever really find out the answer.

Q In your opinion, is the origin of COVID-19 still unsettled science?

A It's settled science, as far as I'm concerned. Other people may disagree, but we know to a pretty high degree of confidence that the outbreak started in a seafood market in the city of Wuhan.

Q So, not just the epicenter, you believe the origin was the seafood market?

A I do.

Q Okay. Can you explain briefly why -- and we'll get into more why later, but --

A Well, yes. There's a lot of evidence, okay, that it started in that seafood market. I can start with the epidemiology of the early cases. And, you know, much of this is documented in our published papers in the scientific literature, the peer-reviewed papers in science, and so, and some of the nature journals. So the early cases, including cases that were early on linked to the market and cases that weren't epidemiologically linked, they happened all clustered around the market, okay, within that same neighborhood. So that wouldn't happen if the virus had, for example, leaked from the Wuhan Institute of Virology.

We also looked at the -- followed genetics of the virus early on. That was actually our first paper, the Proximal Origins paper, where we looked at the genetics of the virus and its relationship to other coronaviruses. And what some of the features that we initially thought may be unusual turned out to actually have the counterparts in natural viruses. So nothing unusual about the genome that was suggested that, you know, had anything other than a natural origin. That was backed up in two thousand -- after the pandemic started with an isolation of the virus from a bat in Laos, a bat called Bengal 2052 (ph), which is actually very similar to SARS-CoV-2, particularly, at the amino acids -- not the nucleotides so much but the amino acids, the proteins themselves, are extraordinarily similar. In fact, this is a virus that, you know, had we isolated it not in the context of the pandemic, we'd probably would have called this another strain of SARS-CoV-2. So it's a very similar virus. So, if there's a virus like that in nature, there's no reason to think that anybody assembled it or put it together. There's more. Okay.

After the outbreak started in the city of Wuhan, the Chinese CDC collected samples, environmental samples from the market. Okay. They sampled a lot of surfaces and, you know, things inside of freezers, and the like. That data we analyzed independently from the Chinese CDC and found that the samples that ultimately tested positive for SARS-CoV-2 all clustered in one particular area of that seafood market, the Southwest corner of the market. And so it turns out that's not an insignificant finding because that is actually where the part of the market where they sold these wild animals, some legally, some illegally. So it's not just the clustering of the early patients, the ones from December, you know, before the virus was widespread in the city, but it's also inside the market, too, where you find the SARS-CoV-2, right where you have the wild animals. Again, and I'll probably repeat this several times, that's not consistent with the virus

having leaked from a lab 20 kilometers away from that market. You just can't construct any like reasonable -- you know, you can say, oh, is it possible, yes, but you can't construct any reasonable or plausible mechanisms by which the virus entered in precisely that location, if it had leaked from the lab.

There are other things that the genetics of the virus can tell us. Okay. There are actually two lineages of the virus that were present in Wuhan early in the pandemic. This is the Pekar et al paper. Those lineages are called lineage A and lineage B. Okay. So both of those lineages, it turns out, were present in those environmental samples at the market. This is really deep down into the, you know, the phylogeny of this virus early on. And I won't go through the details. We can go through Pekar et al if you'd like, but basically what we know is, is that lineage B spilled over first in the market, okay, in the market. Okay. Because most of those early cases in the market were of this lineage B virus. But there's a lineage A virus there, too. And the particular importance of lineage A is that that lineage is closer to the original bat coronaviruses. Okay. There's several mutations that make us believe that that is deeper in the phylogeny than lineage B viruses. But the analysis there that we did in Pekar et al showed that the lineage A virus spilled over second, a week, 2 weeks later in the market.

So, if your scenario is that somehow or other somebody from the lab introduced that, then you have to think, okay, they introduced it twice because if they had introduced, you know, -- the only really -- the only logical way to explain this is that the virus was in the animals that were in the market. They were lineage A and lineage B viruses. It doesn't make any sense to think that a human introduced that based on that analysis of the phylogeny.

Q Two followup questions. So my understanding -- and please correct me if I'm wrong -- is that the early cases used in your papers were from the WHO report about

the origins?

A That's where we first saw it, but yes. The actual locations of the patients, their home addresses were from the WHO report. That's correct.

Q Do you have any ascertainment bias concerns on the WHO's case definition for links to the market?

A I don't.

Q Why?

A Well, they described pretty clearly how those cases were ascertained in that WHO report. I don't see any red flags there. It seems like they were perfectly -- they were competent epidemiologists. They didn't introduce anything that I would call bias. They basically looked at all the hospitals, all the cases in the entire city of Wuhan. And there's no reason for me to believe that they somehow or purposely threw out cases here and there so that they would, you know, implicate the seafood market there, which it doesn't make any sense. The data stands up to that kind of scrutiny. No ascertainment bias, in my opinion.

Q The U.S. intelligence community believes that COVID was circulating probably in November of 2019. Does that affect that calculation that there might have been cases prior to the WHO's?

A It does not. Our phylogenetic analysis, it's called the Time to Most Common Recent Ancestor Analysis, suggests that, you know, mid-November is a perfectly plausible time when it could have spilled over.

Q Okay.

A That's also consistent with the seafood market being the source, basically.

Q Do you have any knowledge of the experiment, any experiments being conducted at the Wuhan CDC?

A I don't have any knowledge.

Q Okay. We have had interviews with Dr. Lipkin and Dr. Farzan. And, when asked if the origin of COVID-19 is unsettled science, Dr. Lipkin said, "In my mind, it is," and Dr. Farzan said, "Probably, yes, unsettled." So you would disagree with both of them?

A I disagree with both of them.

Q Thank you. I want to talk a little bit about when kind of you first heard of COVID-19, the process and some of the science behind it. It appears -- and I think everyone agrees at this point -- that the first report of what would eventually become COVID-19 was on PubMed on December 30th, 2019. Can you describe what PubMed is.

A PubMed is basically a series of databases. It's organized by the NIH or probably more technically Health and Human Services. But it's where, for one thing, all, you know, a lot of scientific papers are basically aggregated on that site. You can go to the site. You can access the papers. But they do other things, too. That site, in general, you know, keeps databases of viral genetic sequences, other sequences. You know, it's a pretty massive effort that the government is undertaking there with that.

Q Is it common that they post emerging disease notifications?

A So I am not sure if you've got it exactly right. There's another data -- there's another website called ProMED-mail.

Q All right.

A And that would be the -- probably the one that you're thinking about.

Q Uh-huh.

A And that's where -- it's run by an entirely different group of people. It's not -- I don't know exactly how -- who manages it or controls it, but it's a kind of a go-to site where virologists, epidemiologists, other people that are interested in emerging diseases can go because they scan news sites and the internet and the like to find out, is

there a disease emerging somewhere in the world? And then they'll post a little notice and maybe a link to whatever information that they have about that. So ProMED-mail is, I believe, probably what you're referring to there.

Q That's fair. There's a lot of websites. I'm not a virologist.

A Yeah, okay. Yeah.

Q So that report on ProMed then said: Undiagnosed pneumonia in China, Hubei.

Hubei is the province containing Wuhan. China first officially reported this unexplained virus the next day, on December 31st, 2019. Is that when you first learned about the emerging disease?

A The date you have is December 31st there?

Q It's when China reported it.

A You know, I'm not sure that I personally knew about it exactly on that date, but it's New Year's Eve, right?

Q Right.

A So, you know, I didn't know. I was getting, you know, questions about it and, you know, calls from people. It was sort of being generally discussed, you know, somewhere around. But I think it would have been more after the new year --

Q Early January?

A -- when I had learned about it, yeah.

Q I want to talk about when the sequence of the virus first became available. Do you recall when you first saw the sequence of --

A Well, I knew about the sequence on January the 10th, because that's when my colleague, Eddie Holmes, had, you know, had convinced people to release it. And it was released on a website called Virological.org, which is actually run by Andrew

Rambaut. On January 10th, I didn't really have a chance to look at it that closely. I was at a -- I remember all these events, right, because they're significant, and they're important to me. I was at a study section, an NIH study section. We were reviewing grants on tick-borne emerging viruses, and so I was at that. So these are events that take place all day and, you know, into the evening usually. And so I just didn't have any time to actually get down and look at that sequence, although I was interested in it. We've done some similar analysis on the original SARS virus, and I was interested to see how closely, you know, some of the sequences lined up, how the proteins looked, were they the same. When I did finally get around to, you know, quiet time sitting at the computer and I was able to download the sequence and look at it, the first thing I looked at was the spike protein, and I found that it had a furin cleavage site, which was of note and interesting. You'll come back to furin --

Q There are lots of conversations about furin cleavage sites.

A Okay.

Q We'll come back to that. So you kind of answered my next question of who made the sequence publicly available. It was Dr. Holmes. Do you recall who he made it available on behalf of?

A Oh, gosh. Some of the colleagues in China that he was working with. Dr. Zhang I believe is the name that comes to mind, but I'm not a hundred percent certain about that.

Q The next day, according to Dr. Farrar, Dr. Zhang's lab was shut down for recertification. Do you know what that means?

A I don't have any idea.

Q Have you had a lot of -- so you said you only had minor communication with the Wuhan Institute of Virology and Dr. Shi. Have you done any other significant work

with Chinese virologists or with the Chinese Academy of Sciences or --

A I have not.

Q Okay. Can you explain the importance of the sequence of a virus?

A Well, it's very similar to the significance of any genome or our own DNA, for that matter. It's what directs the coding of all of our proteins and other molecules in our body, or if you are a virus, the proteins in the virus. The genomes can tell you a lot about, you know, what the -- if you're a virologist, that you can look at the sequence of the virus and derive some information. It's a little bit of a niche area, you know. Not everybody, you know, can tell a lot from just looking at the protein sequence, but it's something that I've been studying for a while, so.

Q Yeah, I've seen sequences now that I never thought I would. And I don't know how you guys read it, so more power to you.

A Thank you.

Q And it is impressive. You said it can tell you things about how the virus will behave. What different --

A Well, it can't tell us everything, right? It can tell us a few things. And so, when you get the nucleotide sequence of the virus, then you can pretty quickly translate that into the amino acid sequences. Okay. And, from those sequences, you can tell a few things. And I was able to tell a few things like the fact that it had this, you know, pretty similar structure to other spike proteins of coronaviruses. There's nothing particularly unusual or out of the way about the SARS-CoV-2 spike. So organized in the same way. It has, you know, some features that, you know, if you've been looking at them for 20-odd years, you can probably figure out, you know, what they are. And then one of these features was that furin cleavage site. But it's right at the point in the virus protein where we expect it to be. And, you know, we can look at the sequences up and

the sequences down and, you know, pretty much tell that it's pretty much a typical coronavirus spike protein.

Q Would just looking at the sequence be able to tell you it's infectivity, transmissibility, or whether or not it can be transmitted asymptomatically?

A Absolutely not. You wouldn't be able to tell anything like that. You know, even if you had done the analyses that I was able to do, you couldn't tell can it affect a person, can it affect, you know, another animal, or a bat, or whatever. You wouldn't be able to tell that.

Q All right. Thank you. So you've touched on it, and I want to talk about it a little bit. One of the, I guess, semi-unique features of COVID-19 is the furin cleavage site. Can you explain what a furin cleavage site does generally?

A Well, the spike protein of SARS-CoV-2 sits on the surface of the virus, the virion, the virus particle. It mediates a lot of important things for the virus. It's the protein that your immune system recognizes because it's just right there on the surface. So what your immune system then tries to do is to stop that spike protein from doing its job. And its job is to get the virus genome into the cell. So the spike protein binds to the surface of the cell. In this case, the SARS-CoV-2 spike binds to a protein we call ACE2. Okay. It interacts pretty specifically with that cellular protein, the cellular protein or cellular receptor that we call it. After that binding, there's a whole series of events. But the main event for the virus at least is to fuse the envelope, the lipid-containing part of the virus, the membrane of the virus, if you will, with the membrane of the cell. Okay. And so, to do that, you need to break down some energy barriers. Putting two lipids together; they're both hydrophobic. They don't come together that easy. But viruses have evolved these surface glycoproteins, the spike protein for coronavirus, that is able to do that job. The spike is basically a machine that

fuses the viral membrane with the cell membrane. Okay. So, to do that, the spike protein has to be cleaved to expose another part of the viral spike protein. But it's a fusion peptide. It's able to interact with the lipid molecules and to bring the two membranes together and to start the process of the virus and the cell fusing so you can get that genome inside.

But the virus has -- you know, the virus has a -- the reason the virus does it this way is because it has a problem. Okay. If it were to expose that fusion peptide just generally, then the virus will just start fusing with everything, including the cell that it had come out of where it was being produced. Okay. So you don't actually want that -- the virus doesn't want that to happen because it would not allow it to, you know, become an infectious particle and to get to the place that it really wants to get, which is another cell so it can infect it. So it uses this sort of triggering mechanism. And the trigger is basically the cleavage of the protein.

Now, a furin is not the only enzyme that can do that. It just happens to be one that, you know, that this virus likes to use. But it clips the protein, exposes that fusion peptide, and lets it start that, you know, that next important step of replication.

Q And you've touched on this, but you can tell if there's a fusion cleavage site based solely off the genomic sequence?

A Not the genomic sequence --

Q Okay.

A -- but once you translate it into proteins, there's a particular series of amino acids that make it a furin cleavage site.

Q Is there a way to tell if a virus gained a furin site via natural or laboratory passage?

A Just from the sequence, no.

Q Is there a way to tell not from the sequence?

A I mean, you can do a series of analyses like we did where you look at the phylogeny of the virus and see if this is a, you know, if there's anything unusual about the site that makes you think that it was inserted. And we did that analysis. We looked at these sequences and the related viruses; looks to me like it was just a perfectly natural event that, you know, led to the insertion of that furin cleavage site. Other related viruses, like common cold viruses that, you know, we probably all have been infected with, that are also beta coronaviruses in the same genus of SARS-CoV-2 have furin cleavage sites. It's a site that is very often mutated, changed in coronaviruses. They like to -- they seem to like to play around with that because of, you know, a central role in the way the virus replicates. And so we know that, you know, other viruses have gained and lost these sites over evolutionary time. It's exactly what it looks like has happened with SARS-CoV-2.

Q But you can't tell directly from the sequence; you would have to do the further analysis?

A That's correct.

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.

Q But you could actually conduct serial passage to speed up evolution and create a furin cleavage site?

A In principle, yes, you could, you know. Why would you do that? I'm not sure why anybody would actually do that, but.

Mr. Benzine. I would like to introduce what would be majority exhibit 2.

[Garry Exhibit No. 2
Was marked for identification.]

Dr. Garry. Do I keep these? Are you wanting these back?

BY MR. BENZINE:

Q We'll have them back at the end. But, if you want to keep it for now, you can.

A That's okay.

Q So this is an email from you to Dr. Andersen, Dr. Holmes, Dr. Rambaut, and Bates marked Garry, G-a-r-r-y 0000100. And your email is written on the page. At the bottom of your email, you say: Bottom line -- I think that if you put selection pressure on a COV -- meaning a coronavirus -- without a furin cleavage site in cell culture, you could well generate a furin cleavage site after a number of passages. 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.

Is this what you were just describing, that it is possible to put enough laboratory

pressure to create a furin cleavage site?

A So, yeah, I think I need to put, you know, this in context, though. The, you know, an experiment like you described was done with influenza virus. So maybe in influenza viruses -- they had to passage it about a hundred times to get the furin cleavage site. The second thing to put in context is, is that we have additional studies now on SARS-CoV-2 that were done after the pandemic, of course. And people have tried to -- have grown the virus, of course. And one thing that is observed is, is that the virus actually loses its furin cleavage site on passage in cells. So it's actually the opposite of what we thought maybe at the time might be possible and might be going on. So it loses the furin cleavage site instead of gaining it. It's so volatile, it goes away. There was, you know, some data, apparently from SARS-CoV-2, the Ron -- was Ron Fouchier, that -- where he suggested that this might happen, but that must have just been a rumor. I have never seen the data that anything like this might have happened.

Q Dr. Fouchier was the one that conducted the influenza experiment, right?

A Yeah. That's right.

Q And that experiment led to the gain-of-function moratorium in the United States?

A It did, yes.

Q So you said that COVID-19 while put through selection pressure loses its furin site. But a novel coronavirus, if I just bring in a novel coronavirus, it's still possible that I could create a furin cleavage site?

A I mean, it's possible. I -- you know, it's possible.

Q Okay.

Mr. Pellegrini. Could I ask for clarification, just this email exhibit 2, that is not the entire email, right? This is one page from a larger chain?

Mr. Benzine. Correct, the rest of the email --

Mr. Pellegrini. Is the context --

Mr. Benzine. No, I'm happy to -- yes.

Mr. Pellegrini. Sure.

Mr. Benzine. All right. Thank you. We can move on from exhibit 2. A few more questions before my hour is up. I'm going to introduce what will be the majority exhibit 3.

[Garry Majority Exhibit No. 3
Was marked for identification.]

BY MR. BENZINE:

Q This is a page out of Dr. Farrar's book titled "Spike." Have you read his book?

A You know, I thumbed through it. I did not sit down and read it cover to cover.

Q So, right in the middle of the page, the highlighted portion, it says: Eddie -- I'm assuming, if you're willing to assume, too, that's Eddie Holmes -- has screen shots taken from social media in China about the coronavirus sequence. They suggest the full genome was known by a genomics company in China by 27 December 2019. It was reported to both China CDC and the hospital who provided the sample on 27 and 28 of December. Were you aware of any Chinese genomics company having a sequence prior to Dr. Holmes' release of it on January 10th?

A I certainly wasn't aware at the time. I mean, I have heard these stories, but, you know, I can't verify any of them. So I don't know.

Q Did Dr. Holmes share this information with you?

A I'm sure that we talked about the whole release of the genome. It's, you

know, something that I'm sure there are emails and exchanges that we had about it. And this does seem to come up before, yeah.

Q Okay. Do you have any knowledge or rationale why they would have been delayed in its release?

A I can't speculate on that.

Q We can move on from that one. On January 3rd of 2020, ProMed came out with another update that said the number of cases in Wuhan was rising, and there were new cases in Hong Kong. Does that imply human-to-human transmission by that point?

A It does.

Q On January 14th, the World Health Organization said there was no clear evidence of human-to-human transmission of the novel coronavirus. Why do you think they would have said that?

A I can't speculate. Obviously, they were wrong.

Q One of the dangerous aspects of the virus is asymptomatic spread. On March 11th, 2020, Dr. Redfield, he was then Director of the U.S. CDC, testified in front of our committee and said asymptomatic spread is possible.

By March 11th, did you think asymptomatic spread was possible?

A You know, I did think it was possible, you know, at the time, but, you know, I wanted to see the evidence for it, because obviously that's an important aspect of a virus that, you know, would make it much more difficult to get the outbreak under control.

Q Looking at the data, when did you first think asymptomatic spread might be occurring?

A It was later than that when actual studies had been done where they currently looked at patients to see when the virus was being shed from their, you know, from their respiratory tract. And, you know, they found that, yeah, it was shed long

before they started to show any symptoms and, of course, some people not showing any symptoms of SARS infection at all.

[9:57 a.m.]

BY MR. BENZINE:

Q On June 8th, the WHO said asymptomatic spread is very rare.

Was that an accurate statement?

A We know it's not now, yes.

Q Thank you.

Ms. Gardner. Can we clarify? 2020.

Mr. Benzine. June 8th, 2020.

We are 5 minutes away from my hour. So we're going go off the record right now and can take a 5- or 10- minute break, whichever one you would prefer.

[Recess.]

Mr. Pellegrini. We can go back on the record.

EXAMINATION

BY MR. PELLEGRINI:

Q Dr. Garry, my name is Giancarlo Pellegrini. I'm the chief minority counsel. Ask you a few questions today.

All the guidelines that you discussed with my colleague about the previous hour will also apply to our conversation.

Does that make sense?

A It makes sense.

Q Great.

A I understand.

Q Great. Well, we appreciate you coming in today. We appreciate your time.

So I'd like to do a little bit of fast-forwarding with respect to the events that I think sort of have brought us here today. Just to lay a very basic foundation for our conversation, there is a big conference call that occurred on February 1st of 2020. There is, subsequent to that, the Proximal Origin paper of which you are a coauthor.

You are, of course, familiar with both the conference call and the paper. Is that right?

A That's correct.

Q I imagine you would be at this point.

I'd like to talk a little bit about the broad topic of who organized the conference call and who subsequently sort of led the paper.

And I want to be clear. I'm not suggesting that there's anything untoward or nefarious about the call or about the paper, but there has been a substantial amount of attention devoted to the question of who organized those events and why.

It's been, I think, suggested that Dr. Anthony Fauci and/or Dr. Francis Collins maybe had sort of a leading role in those events. And there have been various suggestions as to why those folks might have organized these events. Maybe it was to suppress a certain amount of scientific evidence in support of a lab origin theory.

To be candid with you about our perspective on the minority side, we're a little confused about that storyline. For us, when we look at documents that we've received from yourself and elsewhere, it does not look to us like any of that is the case.

What it looks like is that Dr. Jeremy Farrar sort of arranged the initial conference call -- and we can talk about what seems to have been his thinking for that -- and played sort of an organizing, shepherding, quarterbacking role with respect to the rationale for somebody writing a paper in the first place and then specifically the Proximal Origin paper and the process by which the paper was written, where it was published, and all that sort

of thing. That's our impression just as an initial matter.

I think, just as a threshold matter, is it your recollection that Dr. Farrar played a role similar to the one I just described?

A I generally agree with what you said.

Q Yeah, just from a general point of view --

A Yeah.

Q -- we're talking about --

A I generally agree with what you said. It was Dr. Farrar who initially organized that teleconference.

Q Is it your general recollection that Dr. Anthony Fauci or Dr. Francis Collins played the same kind of role in this story?

A The same kind of role --

Q Did they --

A -- you just mentioned?

Q Did Dr. Fauci or Dr. Collins arrange the conference call? Was it their conference call?

A To my knowledge they did not arrange the conference call.

Q Was either Dr. Fauci or Dr. Collins involved in the nitty-gritty of your drafting process, whether that's suggesting line edits or making specific suggestions about who should be a coauthor, where the paper should go, things of that nature? Our impression is that Dr. Farrar played that role, not Dr. Fauci or Dr. Collins.

A And actually neither one of them played that role.

Q Okay. So what I think would be useful is if we walked through a number of emails that we've got that you're on -- none of them will be a surprise -- and just describe the extent to which the emails are consistent with what we're sort of talking about here

or inconsistent potentially.

Mr. Pellegrini. So I'd like to introduce minority exhibit A.

[Garry Minority Exhibit No. A
Was marked for identification.]

BY MR. PELLEGRINI:

Q And I'll give you a moment just to glance as it and for it to work its way around our conference room here.

All right. And it's got a back side. It's double -- double-sided.

A Okay.

Q So, if I can just discuss this email for a moment, this is pretty early on, I think, in our story. This is February 1st. And this appears to be Dr. Farrar organizing the logistics of the conference call in question.

And so I think, if I could, just sort of direct your attention to a few components of the email, I think, just starting in the middle of that first page, this document is Bates stamped Garry 6 with a number of zeros in the middle there.

Dr. Farrar appears to be distributing to yourself and a large group of other folks dial-in details. Is it fair, I think, to infer that those are the dial-in details for the February 1st conference call?

A They are.

Q All right. Great. And I note that the dial-in number starting with plus 44, does that appear to you to be a United States phone number?

A It's not. It's a London number.

Q It's a London. And Dr. Farrar, where is he from or where is he located?

A I believe he's from London.

Q Okay.

A At least he was at the time.

Q Okay. So it seems perhaps fair to infer that Dr. Farrar's sending this London number, and being in number, that it's either Dr. Farrar is the one arranging the number or his organization over there in London.

On the second page, it looks like -- these emails run in reverse chronological order. So the email you're seeing on the second page is earlier in time than what we just looked at.

A Okay.

Q We have an email from Dr. Farrar, again, to what I take to be the participants on the conference call and describing, it seems, like parameters of the call. And there are a few aspects of that. The first is that he distributes what appears to be an agenda there in the middle of the second page.

Do you see that?

A I do.

Q Great. And I think it's correct to say that J.F. is Jeremy Farrar. And so it looks like Dr. Farrar has assigned himself a couple of roles here on the call. He has assigned himself the introduction, the focus of the call, the desired outcomes of the call, the summary, as well as next steps of the call.

Does that look right to you, as well?

A The beginning and the end.

Q Yes.

A That's correct.

Q All right. And then a little bit above that in bold, Dr. Farrar says: I will be on email throughout. Email Paul or I, Paul, if any problems.

And do you know who Paul is by any chance? I take it to be the only "Paul" on

the cc line, which is Paul Schreier@wellcome -- do you have any different understanding?

A I don't have any different understanding.

Q All right. And so assuming that it is Mr. Schreier, that's a colleague, it would appear, of Dr. Farrar. Is that right?

A Yes.

Q Okay. And Dr. Farrar continues: If you cannot make it, I will phone you afterwards to update.

Okay. So just sort of taking this email on its face, we have Dr. Farrar sharing the dial-in details for the call on a British line, sharing the agenda for the call, assigning himself the role of introducing everybody, defining the scope of the call, defining the focus and desired outcomes of the call, the summaries can come from Dr. Farrar, next steps come from Dr. Farrar. And Dr. Farrar is there to troubleshoot for anybody who can -- is having technical problems and Dr. Farrar will call anybody who missed the call afterwards.

Does that sound to you like it was Dr. Farrar's call?

A It does. It was Dr. Farrar's call.

Q Is that consistent with your recollection of the call?

A It is.

Q Is there anything on here suggesting that it was Dr. Fauci's call?

A No.

Q Certainly Dr. Fauci was an attendee on the call -- we see him in the cc line but nothing in the substance of the email to suggest that Dr. Fauci played the type of organizing role that we're seeing from Dr. Farrar. Is that right?

A That is correct.

Q And I presume it would be a similar impression for Dr. Collins, nothing here

suggesting that it was Dr. Collins' call.

A That's correct, too.

Q And is that consistent with your recollection of the call?

A It is.

Q Okay. You can put that one away.

There may be a certain degree of repetition here.

A That's okay.

Q I appreciate your patience.

A No problem.

Mr. Pellegrini. I'd like to introduce minority exhibit B, as in "boy."

[Garry Minority Exhibit No. B

Was marked for identification.]

BY MR. PELLEGRINI:

Q I'll give you a moment to glance that over.

So this is just a continuation of the email that we started with. You can see the agenda, you know, on the back pages. This document, I should note for the record, is the first page is Bates stamped Garry 25.

What I'd like to focus your attention on is the first page of the email labeled "Garry 25," specifically this email from Dr. Farrar, starting in the middle of the page.

And it seems -- and I wonder if this is your impression -- that this is an email Dr. Farrar sends after the call occurs, sort of a summing-things-up email. I see there in his first long paragraph: This call was very helpful.

Is that -- is that your impression of what this email is?

A It is.

Q Okay. And specifically in Dr. Farrar's third paragraph, the long one that

starts with "we on this call" halfway through that paragraph, I'm just going to read a few sentences out loud, if that's okay.

He says: In order to stay ahead of the conspiracy theories and social media, I do think there's an urgency for a body to convene such a group -- something he was talking about earlier -- and commission some work to draft, quote, To understand the evolutionary origins of 2019-nCoV, end quote, important for this epidemic and for future risk assessment and understanding of animal, slash, human coronavirus.

He continues: In other words, a completely openminded and neutral question, bringing in the best minds.

I'll pause there. It sounds like -- and I would appreciate your views on this -- this is sort of the beginning of a thought process from Dr. Farrar where he's thinking there would be a broader value or usefulness in somebody writing and publishing a paper about the origins of SARS-CoV-2.

Is that also your impression?

A Well, I think that could be incorporated into that. But specifically here I think he's pointing to another body, somebody like the WHO he was thinking about, that would convene a conference and discuss these issues amongst a broader group of scientists.

Q No doubt about it, a project with the aim I just described or really Dr. Farrar described.

A Uh-huh.

Q But it sounds like for him at this early stage he envisions that more as flowing through the WHO.

A That's correct.

Q Yeah. Okay. And it does sound like in his view he wants whatever that

endeavor ends up being to be, quote, completely openminded and neutral, just from reading his email.

Do you tend to agree?

A That was my impression of his -- what he wanted, as well.

Mr. Pellegrini. Okay. Put that one away.

I'd like to introduce minority exhibit C as in "cat."

[Garry Minority Exhibit No. C

Was marked for identification.]

Mr. Pellegrini. I'm just going to let it work its way around.

BY MR. PELLEGRINI:

Q So this is a pretty long email chain with all sorts of technical substance, which at this moment I am not going to really get too far into. I'm sure I or my colleague will later. I really just wanted to touch on the first page of this document which is Bates labeled Garry 45.

And so this is February 2nd now and so still pretty soon after the call, the next day. And looks like this is an email from Dr. Farrar where he is sort of, again, assigning himself a number of to-do items and among them in his words: I will be in contact with WHO today. I contacted them last night and will speak with them today and set up a broader call with them as soon as possible.

And then a little further down: I believe the best way forward is for a body like WHO to ask or commission a group of scientists from around the world to ask the neutral question, quote, to understand the evolutionary ay origins of 2019-nCoV, end quote, important for this epidemic and for future risk assessment.

And I'll just pause. So is this consistent with what we were really just discussing, which is Dr. Farrar starts to sort of look at the landscape out there and think to himself:

Hey, there would be a value in somebody tackling, somebody respected, tackling the question of evolutionary origins of 2910-nCoV? And, for him at this point in the process, that logically would make sense as emanating from the WHO.

A That's correct.

Q That's all -- that is all consistent with your recollection, as well as with the email --

A It is.

Q -- correct?

We'll get to this a little bit. But is it -- is it right that in the days that followed, whether it's that the WHO just didn't necessarily act with the speed that Dr. Farrar was looking for or whether they weren't exactly on the same page -- I don't know -- but this is the beginning of a thought process on his part that in the coming days started to shift over to you-all, you and your coauthors, which would eventually kind of become proximal origins?

A I'm not sure those two things are mutually exclusive.

Q Okay.

A I think that there, you know, was still, you know, a value in having a group like WHO take a look at the question.

You know, I think that, you know, there were probably several people in the room that were thinking about, you know, the question. And logically the thing then would be to do would to put your thoughts together in a publication of some sort.

Q Great. Thank you. You can put that one away, as well.

Mr. Pellegrini. So I'd like to introduce minority exhibit D.

[Garry Minority Exhibit No. D

Was marked for identification.]

BY MR. PELLEGRINI:

Q So this is another sort of longer chain with substantive discussion. And, again, I really am just going to focus with you on the very first page of that chain. There are other issues in there that I'm sure will get attention later.

I'll just give you a moment --

A Yeah, yeah.

Q -- to look at it?

A Yeah.

Q Great. The top email on the first page of that chain is from Dr. Eddie Holmes, and I'm just going read a couple of sentences that are pertinent.

He says: Kristian -- that's Kristian Andersen, correct?

A Correct.

Q All right: Kristian, I think you are right that a careful report is the way to go. No need to super rush. Pass to Jeremy and let decide where to share it, perhaps to the WHO group.

And then he later says: I'll let Jeremy know what we are up to.

Okay. Is it fair to say that this is the beginning of what would become the Proximal Origin paper?

A I'm not sure that the concept there was as fully formed yet but, I mean, it -- you could construe it that way, yes.

Q The --

A Yeah.

Q -- the very beginning of the beginning.

A Yeah.

Q Okay. And we have Dr. Eddie Holmes.

And could you describe just for a moment the connection between Dr. Holmes and Dr. Farrar? They have an existing, preexisting relationship?

A Well, they're both English.

Q Uh-huh.

A They know each other. I mean, Jeremy Farrar is the -- was the head of the Wellcome Trust. So, I mean, he was a well-known figure in, you know, in the UK, a scientist himself, epidemiologist, virologist in one sense.

So I don't know precisely where they came in contact. It was -- it -- but Eddie Holmes was trained in London and, you know, spent a lot of time there before he moved to Australia. So I'm certainly -- certain they traveled in the same circles of, you know, fairly high levels of science in the UK.

Q Okay. Great. Thank you.

And so okay. Dr. Holmes says, with respect to a then nascent, careful report, he says: Pass to Jeremy and let decide where to share it.

And then again: I'll let Jeremy know what we are up to.

Is that consistent with the idea that Dr. Farrar sort of started to take on a role where he was either involved with or -- or I don't want to say had a decisionmaking role but had some degree of decisionmaking over, for example, where this paper would ultimately go, where it would be shared?

A So let -- I mean, I'll answer it to say, you know, obviously, other people were in contact with -- with Dr. Farrar. I myself wasn't. So I don't really know exactly what the, you know, the level of conversation was going on there between some of my coworkers and Dr. Farrar.

I never actually spoke with him about the paper. I was kind of digging into the science bits and stuff at that time myself. So I can't really answer your question with

any --

Q That's all --

A -- any authority.

Q I certainly appreciate that. And so, to an extent, because of that, we may be limited by just what --

A Uh-huh.

Q -- the email says.

A Uh-huh.

Q But, at the very least, in terms of what the email says, when Dr. Holmes says, a careful report is the way to go, pass to Jeremy and let decide where to share it, that sure does sound as if Jeremy will be making the decision about where to share it. Is that fair?

A I think in general he was -- he was set up to play an advisory role, you know, in having started the teleconference and other things.

Q Sure.

A So yeah.

Q Do you see anything in that email indicating that Dr. Anthony Fauci or Dr. Francis Collins were making decisions about where to share the paper?

A No.

Q Do you have any recollection of Dr. Fauci or Dr. Collins making decisions about where to share the paper?

A They didn't convey anything to me along those lines.

Q Okay. Thank you.

Mr. Pellegrini. I'd like to introduce Minority Exhibit E.

[Garry Minority Exhibit No. E

Was marked for identification.]

BY MR. PELLEGRINI:

Q So this document is Bates stamped Garry 146. It's a few days later here, February 6th. And, again, it's a longish chain with a lot of discussion of pangolins, which I imagine we will also be discussing at some point.

But I would like to focus your attention specifically on the page labeled "148" --

A Okay.

Q -- if I could.

And, in the middle of that page there's an email from Dr. Holmes, and Dr. Holmes appears to copy and paste an email or a communication of some kind from Jeremy, which I think we can assume is Dr. Jeremy Farrar. I think I've been putting the wrong emphasis on the wrong syllable there on his last name. So we'll say Farrar from here on in.

A Okay.

Q And that says, from Dr. Holmes, it says, "From Jeremy," and then, in quotations: 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, end quote.

So it seems -- and is this consistent with your recollection -- that at this point Dr. Farrar has received either a first draft or some form of the paper that you and your coauthors had been working on? At this point, it's referred to as a report, it sounds like.

A Yes, certainly by the 6th of December -- of February, we had put -- put some thoughts on paper.

Q Okay.

A Yeah.

Q And we seem to have Dr. Farrar asking for sort of a specific, not necessarily a line edit but a specific thematic change. He asks: Is it possible to dampen down further the conspiracy idea and make it totally neutral?

That seems for us pretty consistent with the idea that Dr. Farrar played sort of a substantive -- "oversight" might be too strong of a word but quarterbacking role with respect to this paper. Would you tend to agree with that?

A I mean, I would say it was more of a general advisory role --

Q Uh-huh.

A -- I mean, just general, you know, 30,000 kind of foot of this thing. You know, in terms of the nitty-gritty and writing the paper and the like, he didn't have any -- any of that kind of input.

Q Sure.

A But, you know, from an advisory role, sure, I think he's a trusted and respected scientist and a good friend of Eddie Holmes. So --

Q To some extent it seems, as a reader, unique though in the sense that in this example, for example, we have the email from Dr. Farrar specifically --

A Uh-huh.

Q -- not from three people of which Dr. Farrar is one. Is that fair?

A Sure.

Q Okay.

A Fair.

Q And it sounds like Dr. Farrar, as well as Marion -- are you familiar offhand with who Marion is?

A Marion would be Marion Koopmans --

Q Okay.

A -- a Dutch scientist, a Dutch virologist who was on the original teleconference.

Q Great. And so Dr. Farrar and Marion are both wondering whether actually publishing this sooner but ruthlessly on the science is worthwhile.

So, again, to us, that reflects the degree of substantive involvement for Dr. Farrar with the path of the paper. Is that fair?

A That's fair.

Mr. Pellegrini. Okay. I'd like to introduce minority exhibit F.

[Garry Minority Exhibit No. F
Was marked for identification.]

BY MR. PELLEGRINI:

Q So this is an email chain with yourself and your coauthors. The chain spans February 7th and 8th. And, again, there is a lot of substance here. But I just want to focus your attention on a few discrete parts of the email, starting with the very last page. That last page is Bates stamped Garry 201. The first page for the record is Garry 194.

But, on that last page, Garry 201, in the middle of the page, we've got Dr. Farrar, and his email says: When can you update, question mark. Lancet, Nature, NEJM.

Do you know offhand what NEJM is?

A New England Journal of Medicine.

Q Okay. Great.

Will all review immediately after quick QC. Will share with WHO. Can I help with any of the editors?

What is your impression of what Dr. Farrar was sort of communicating there?

A So, when you're writing a scientific paper, one of the first things you have to decide is: Who are you going to write it for? Which journal are you going to submit it

to?

So this looks to me like he's making a suggestion of three possible journals, all high-level scientific journals, the best in the field actually. And so it looks like the suggestion is go for the top.

Q And what is your perception of what he is suggesting, although it's, I suppose, fairly self-evident, with "can I help with any of the editors"?

A So, you know, these journals -- Lancet, Nature, New England Journal of Medicine -- get a lot of submissions. Okay?

So it's not unusual for scientists to contact the editors ahead of time and, you know, even have others contact the editors on -- on their behalf to sort of say: Okay, I -- you know, would you be interested in such a paper? You know, so you don't waste your time, you know, writing a -- you know, something that is tuned to these journals -- they're all a little bit different. You know, you would write a paper differently for The Lancet as opposed to the New England Journal of Medicine or Nature. So it's just a way to sort of facilitate the process.

Q And, when Dr. Farrar says "will all review immediately, after quick QC, will share with WHO," you're limited simply by what you're reading. And I understand that.

A Uh-huh.

Q But does it sound as if he may have already spoken with folks at those various journals?

A I don't know that for sure.

Q Okay.

A Yeah.

Q All right. So if I could ask you on the page labeled Garry 199, down towards the bottom of that page is an email from Dr. Holmes. And the first line of that email

from Dr. Holmes reads: Jeremy wants us to publish our report somewhere. Thoughts?

And is it fair that the Jeremy there is Dr. Farrar?

A Yes. That's correct.

Q All right. So is it fair for me to have the impression there that Dr. Farrar was sort of affirmatively making his desires known as to the paper that you all were working on and whether it should be published?

A I think that's a fair assumption, yes.

Q Okay. And, then working our way towards the front of this document, if you go to Garry 195, towards the top of that page -- well, let's start in the middle. Let's go in the correct order here.

Dr. Holmes, in the middle of the page, says: Had a chat with Jeremy and Andrew.

And Andrew is very likely Dr. Rambaut. Is that right?

A That's correct.

Q And I've only now pronounced that correctly because I learned from the rest of you in the last hour. I would have sounded just the same as you, had it not been for that.

So had a chat with Jeremy and Andrew, and we agreed that Jeremy should then the doc to the other group members.

I think -- don't know if you agree -- is the inference the word "then" there should perhaps say "send." Do you have a similar impression?

A I have a similar impression.

Q Okay.

And then a little bit higher up on this page, Dr. Rambaut says, quote: Jeremy is pushing us to get a paper ready to go. Probably Nature.

So putting those two emails together, at the very least reading them now, is it your impression that Dr. Farrar was pushing you all to get a paper ready to go and also serving as sort of an intermediary where the draft would be sent by him onto that larger group?

A First part, yes.

Q Okay.

A Second part I -- I -- I don't recall that.

Q Okay.

A So I don't think that would be actually the way that it would be done. I mean, the authors would submit the paper to the journal. It wouldn't go through an intermediate like that.

Q Sure. Do you think it's possible that when we refer to "sending," the word says "then" --

A Yeah.

Q -- but I think it's probably --

A Send.

Q -- "send," the doc to the other group members, that is not referring to the journals? It's referring to the larger group of folks who are on that conference call.

A That's correct.

Q Okay. Then, on the first page of this email chain, numbered 194, an email from Dr. Holmes towards the top says: Things moving fast. Suggestion is to redraft the doc to make it more of a letter and come down more on the natural origin, given the pangolin and the glycan stuff.

Did I pronounce "glycan" correctly?

A You did.

Q That's a lucky guess. That's great.

This is difficult, and it may be that you would not be able to say you have any personal knowledge of this.

But, as a reader, when Dr. Holmes says that the suggestion is to redraft the doc, is it a reasonable inference that that suggestion is coming from Dr. Farrar, understanding that you would not know personally?

A It's certainly a possibility.

Q A possibility.

A But I don't know for sure.

Mr. Pellegrini. Okay. All right. I'd like to introduce minority exhibit G.

[Garry Minority Exhibit No. G
Was marked for identification.]

BY MR. PELLEGRINI:

Q My Gs look like 6s. I apologize for that.

Okay. So this is a short one, just one page. And this is February 8th now. And we have Dr. Farrar sending an email to what looks like the broader group that were on that February 1st conference call. And what he appears to be doing is sharing the latest draft of what would then become the Proximal Origins paper.

Is that also what it looks like to you?

A Yes. That's all correct.

Q Okay. And Dr. Farrar has in his email -- this is soliciting inputs. It says interested in your -- I'll give it a pause.

He says: Interested in your views?

And some of the things he would like to know is whether the paper is reasonably balanced, is there anything anyone disagrees with, advice on whether the paper should

be published.

So is that all consistent with the idea that Dr. Farrar acted as an intermediary for you-all in terms of socializing the paper with the broader group?

A I think that's an accurate description, yes.

Q Would this email on its face be consistent with the idea that Drs. Fauci or Collins somehow played a similar role?

A It would be inconsistent with that.

Q Do you have any recollection of Drs. Fauci or Collins playing that sort of intermediary role?

A I have no personal recollection of that.

Q Okay.

Mr. Pellegrini. I'd like to introduce minority exhibit H.

[Garry Minority Exhibit No. H
Was marked for identification.]

BY MR. PELLEGRINI:

Q So this is a chain amongst yourself and your coauthors, and there's some substantive discussion here about Dr. Ian Lipkin and whatever it is that he thinks at the time. I'm really only focused on first page which is labeled Garry 265.

A Okay.

Q And at the top of that page is an email from Dr. Holmes, and in the last paragraph of Dr. Holmes' email, it says: Jeremy still wants us to write something.

Is that consistent with the idea that, at that point, Jeremy, Dr. Farrar, still wanted you to write something?

A It is.

Q All right. Is it consistent with the idea that Dr. Fauci or Dr. Collins had any

particular opinions at that point about whether or not you'd write something?

A It says nothing about Dr. Fauci or Collins.

Q Nothing in here suggesting any kind of similar role for Dr. Fauci or Dr. Collins.

A That is correct.

Q Okay. Don't worry. There's a second binder.

A Okay.

Q Yeah.

A All right.

Mr. Pellegrini. I'd like to introduce minority exhibit I.

[Garry Minority Exhibit No. I

Was marked for identification.]

Mr. Pellegrini. For the record, this is a document Bates stamped Garry 283.

BY MR. PELLEGRINI:

Q So this is now a few days later. We're up to February 14th. It's a chain between yourself and your coauthors. And we're going to walk through a few different parts of it, if we could start all the way at the back on page 286, down at the bottom of that page.

A Okay.

Q We have an email there from Dr. Holmes, and I'm just going to read a sentence out of his second paragraph where that says: I said I would send -- sent -- send Jeremy a draft to read Saturday morning while he is on a train from Munich to Salzburg.

The email above that from yourself, at the end of your email, says, you're discussing, I think, data or figures of some kind, and you say: Feel free to include those to Jeremy, as well, if you like, or not.

Is that consistent with the idea that Dr. Farrar was playing sort of a unique role in

his involvement with your paper at this point?

A I mean, he --

Q That's not unusual but clearly distinctive.

A It's true. He was playing an advisory role.

Q Okay. If we could continue to flip through that document to the page Garry 284, towards the top of that page is an email from Dr. Holmes that says:

I'll check with Jeremy. I'm now about as tarnished as Ian.

My inference, and you can correct me if you think I've got it wrong, is that there's some kind of discussion here about some sort of data or information. There's a debate about whether or not to include that in the paper.

And Dr. Holmes feels like: If you include it, I have to recuse myself.

And then that all culminates in Dr. Holmes saying: I'll check with Jeremy.

If you'd like, I can give you a moment to kind of scan the traffic to see if that's consistent. Or if your memory's so good that you recall that, that's fine, too.

A Well, I do kind of remember the exchange but not the specific details, so, yeah, just a second maybe --

Q Sure.

A -- to -- uh-huh.

Okay. Is there a specific question now?

Q Well, the question is whether -- it seems to a reader, but is this consistent with how you read it that ultimately the question of whether or not to include this information and the correlated question of whether or not to recuse Dr. Holmes, Dr. Holmes ultimately said: You know what, I'm just going to check with Jeremy Farrar.

Is that -- am I reading that correctly?

A I believe so, yes.

Q Okay.

A I mean, the general discussion's about a paper that had come out that was subsequently retracted.

Q Uh-huh.

A It was a paper by the author Xiao and Xiao, and it had to do with the Wuhan CDC.

Q Okay.

A Yeah.

Q Great. And then, on the first page here, Garry 283, at the bottom, very bottom, is an email from yourself, saying: Maybe I missed it. Did Jeremy nix Ian, or is he still on?

Do you recall what you meant by that or what you likely meant by that?

A I think that -- I think it was Eddie Holmes was asking if we should -- asking advice to Dr. Farrar about whether we should include Ian Lipkin on the paper or not. It was just a question.

Q Sure. The -- the -- the phraseology though, "did Jeremy nix Ian," reads as if Dr. Farrar had some degree of decisionmaking power over the question of whether or not Dr. Lipkin --

A Well, I'm not sure if I actually meant that. I -- I -- I don't think that we would have ceded that kind of decisionmaking to somebody that wasn't going to be an author on the paper. It's just I probably was using the word nix in more general terms. You know, did he say -- tell us anything that would have, you know, led us or precluded us from including Ian on the paper.

Q Sort of an advisory nixing as opposed to an official nixing?

A Correct.

Q Okay.

A Well put.

Q The plain meaning of the word in a vacuum, though, does suggest a certain amount of veto --

A Okay.

Q -- power.

A It is true, but we would -- I mean, we would were not taking that. We would have just -- we would have taken it as advice and probably gone our own way if we had decided otherwise.

Q All right. So this chain in its totality, some of the things that seem to exist within it are drafts of the paper are being sent to Dr. Farrar to read but specifically to Dr. Farrar and only Dr. Farrar. There's debate about whether to include certain information or, ultimately, there's a solicitation of Dr. Farrar's point of view and a separate discussion of the extent to which Dr. Farrar has either nixed, whatever that word means, Dr. Lipkin's participation as a coauthor.

That looks to me as if Dr. Farrar is playing some degree of quarterbacking role here with respect to the paper. Would you tend to agree with that impression?

A Yeah, in the sense that, yes, he was providing advice to us.

Q Sure.

A Yeah.

Q Is there anything in this email chain that you've seen or that we've discussed that suggests that Dr. Tony Fauci or Dr. Francis Collins were playing any sort of similar role at this time?

A There's not.

Mr. Pellegrini. Okay. I'd like to introduce minority exhibit J.

[Garry Minority Exhibit No. J

Was marked for identification.]

BY MR. PELLEGRINI:

Q So this chain is now February 15th. And it looks like the paper is almost finished, and this is a discussion amongst yourself and your coauthors.

I think what I'd like to just look at for a moment is -- the document itself is Bates stamped Garry 288. I'd like to look at the second page of the document, which is Garry 289, and towards the top of that page, Dr. Holmes sends an email that says: I will send through a final version that everyone can formally agree to later today. I'll also pass to Jeremy.

Okay. And then, on first page of the email, labeled Garry 288, also from Dr. Holmes, at the top of that page, Dr. Holmes says: I'll pass to Jeremy to see if he has any final comments or wants to be acknowledged.

So it seems as if Jeremy, Dr. Farrar, and specifically and only Dr. Farrar is receiving final drafts, being asked if he has any final comments.

Is that consistent with the idea that Dr. Farrar played, I think as you said, an advisory role, whatever adjective you choose, whether that's leading or advisory? Is this consistent with the idea he was playing that role with respect to this paper?

A It's consistent with that, yes.

Q Would this email be consistent or inconsistent with the idea that Drs. Tony Fauci or Francis Collins played any kind of similar role with respect to the paper?

A Yes.

Q I think it was binary consistent or inconsistent with the idea that --

A It would be inconsistent --

Q Okay.

A -- with that.

Q Thank you. I appreciate it.

Mr. Pellegrini. I'd like to introduce minority exhibit K.

[Garry Minority Exhibit No. K
Was marked for identification.]

BY MR. PELLEGRINI:

Q So this is February 16th. It seems as if the process of the paper is wrapping up. The first page is Bates stamped Garry 306. I'm only going to discuss one little snippet here, which is on the second page, numbered Garry 307.

Towards the top of that page, I think we have an email from yourself. And the second line of that email says: Jeremy, Dr. Farrar, has been amazing leader. Should be author.

Is that email consistent with the idea that Dr. Farrar was a leader on this paper?

A It is.

Q Okay. Is that email consistent or inconsistent with the idea that Drs. Fauci or Collins were leaders on the paper?

A It's inconsistent.

Q Okay. Do you have any recollection of Drs. Fauci or Collins being leaders on the paper?

A I have no personal recollection -- no personal recollection of that at all.

Mr. Pellegrini. Okay. Mitch, it's possible that I'm within 5 minutes of approaching my hour. Would it be okay if I took an extra 5 minutes to wrap this up?

Mr. Benzine. Yeah.

Mr. Pellegrini. Thank you. I appreciate it.

I'd like to introduce minority exhibit L.

[Garry Minority Exhibit No. L

Was marked for identification.]

BY MR. PELLEGRINI:

Q This document is Bates stamped Garry 492, and I'm only going to ask about the first page of the document at the top. You're welcome, of course, to flip through it. So, on the first page there, numbered 492, at the top, we have an email from Dr. Farrar to yourself and your coauthors. And that reads: Sorry to micromanage, micro edit. 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"?

Is that email consistent with the idea that Dr. Farrar either made or asked for line edits to the paper?

A He made this one change.

Q Yeah.

A It's consistent with that one line edit, yes.

Q Would this email be consistent or inconsistent with the idea that Drs. Fauci or Collins were suggesting specific line edits to the paper?

A It would be inconsistent with that.

Q Do you have any personal recollection of Drs. Fauci or Collins requesting specific line edits to the paper?

A I don't have any personal recollection of that.

Q Okay.

Mr. Pellegrini. I'd like to introduce minority exhibit M.

[Garry Minority Exhibit No. M

Was marked for identification.]

BY MR. PELLEGRINI:

Q So this document is Bates stamped Garry 541. And it's sort of a long chain, but my interest starts on page Garry 543 at the very bottom of that page.

So it seems as if the context here, February 17th, is that the paper is just about ready to go. And so we have Dr. Farrar asking you all at the bottom of that page: Any idea when likely to be released on preprint server?

And, then following into the subsequent page, he says: Thinking about the publicity of it.

And I'd like to read just a few other emails from him in this discussion. I think they're all related to each other. Towards the top of page 543, that same page, Dr. Farrar, I think picking up his own thought, says: Reason I ask about when to post is to coordinate press briefings, et cetera, et cetera, to make sure the key message are reasonably reported.

And then all the way to first page, Garry 541, Dr. Farrar at the top of that page says: As soon as the institutions or other that have to approve a press statement are back, it would be very important to coordinate the lay messages from the piece, preferably before the narrative gets written and broadcast by others.

So is it fair to say that Dr. Farrar was playing certainly a coordinating role with respect to the messaging of the paper?

A Well, he was playing a role. I'm not so certain it was the major role because, at that point, we'd already written the paper, and it was kind of in our hands. But he was certainly playing a role in that respect.

Q But how about a material role in the messaging of the paper?

A Yes, sir.

Q Okay. Is there anything in this email chain indicating that Drs. Fauci or Collins played a similar role in the messaging of the paper? That's a difficult question.

A It's a long chain.

Q It's a long email chain.

A It's a long chain.

Q I won't ask you to read everything, so I -- yeah.

A They did not --

Q Okay.

A -- play any role in that respect.

Mr. Pellegrini. All right. I should have asked you, as well. Is it okay if I take an extra?

Mr. Jacobs. That's fine.

Mr. Pellegrini. Thank you. I appreciate it.

Mr. Garry. No problem.

Mr. Pellegrini. I'd like to introduce minority exhibit N.

[Garry Minority Exhibit No. N

Was marked for identification.]

BY MR. PELLEGRINI:

Q So this chain is Bates stamped Garry 779, and it takes place a lot later. We're in July of 2020 now. And it's a discussion between yourself and your coauthors, I think with the exception of Dr. Lipkin.

And one sort of administrative thing I want to note for the record, which is on the third page of this document, Bates stamped 781, you can see that the format of this email as produced is such that there's one letter on each line.

And so as a result of that, I have not included that portion of this chain because it

would have required printing 800 pages. So I hope you don't mind that, but I did just want to mention it for you.

So, having noted that, I think, although you're welcome to glance through it to refresh your own recollection, the context here perhaps is you've gotten, you-all as a group, have sort of gotten your sort of first outreach from a journalist with respect to the events that we just talked about back in February of 2020.

And there's sort of a discussion of what level of detail will be included in responding, things of that nature.

But what I'm particularly interested in is the email at the top of the first page, page 779, from Dr. Holmes. And the first line of his email says: No. Sorry. Not doing that. Jeremy started this. That's the truth.

Is that email consistent with the idea that Jeremy started this and that's the truth?

A So I think this is about something else actually, not the -- not the proximal -- I mean, it's about the Proximal Origins paper, per se. But it's too late -- it's too late in the process. This is -- this is another -- this is another issue that arose later on about the Proximal Origins paper, about the teleconference, and other things like that.

So could you repeat the question, though? I --

Q Sure.

A I think I'm going have to answer "no" to it because -- just because it doesn't really apply to the, you know, the media conversation of the Proximal Origins paper, because that paper was published in March. There was quite a bit of attention to it paid in March.

Q No doubt about it. My impression of the context of the email --

A Yeah.

Q -- is that somebody within your group --

A Yeah.

Q -- had received some sort of inquiry from John whose last name, we can see the reference to John at the bottom of 779, who I think is from Science magazine.

A It's true. That's John Cohen --

Q John Cohen.

A -- a reporter from Science Magazine, yes.

Q And this is where it's difficult with the formatting of this particular chain.

A Right.

Q But I think it says John Cohen had received some sort of information from somebody, making a particular spin claim with respect to what that anonymous person thinks happened back in February.

A That is -- that is correct.

Q Okay.

A Yes.

Q And so I think there's a discussion amongst the rest of you about the shape that a response might take and for whatever reason the -- Dr. Holmes' "no, sorry, not doing that," not totally clear with respect to the exact context of that. But it does seem as if, when Dr. Holmes says, "Jeremy started this, that's the truth," the context of that is the broader question of how these events of February 2020 sort of were set into motion. That's our impression.

A Yes, I -- you know, I'm not exactly sure what Dr. Holmes was thinking then --

Q Okay.

A -- with this email.

Q Certainly. Fair enough.

A To be honest about it, I don't -- I don't remember the context.

Q At the very least, does the email seem to suggest that Dr. Holmes thought at this time that Dr. Farrar was sort of at the center of the events that were being discussed?

A Yeah, I don't know what was precisely on Eddie Holmes mind at this point in time --

Q Sure.

A -- with that particular email. So I can't really speak for him about that but yeah.

Mr. Pellegrini. Great. I've got one last document. I'll be brief, and I'll try to wrap up as quickly as I can, appreciating the extra time that you all have given me.

This document is -- I'm going to label that minority exhibit O.

[Garry Minority Exhibit No. O
Was marked for identification.]

BY MR. PELLEGRINI:

Q So this is an excerpt for the second time today from Dr. Jeremy Farrar's book "Spike," which I believe you said last time around you had flipped through perhaps but not really sat down and read cover to cover.

And, for the record, the excerpt we're looking at here is from page 64 of the hard copy of "Spike." It appears as page 62 here due to Amazon, Kindle printing challenges, so we're all aligned.

But the paragraph of interest to me occurs, if I could direct you to first paragraph after what appear to be three small virus images, which is consistent with the title of the book, because we can see the little spike of proteins there, I'm going to read just a couple of sentences from that paragraph out loud. Quote: My overriding concern was to get to the bottom of the origins of the virus as quickly, calmly, and scientifically as possible. The first task was to discreetly gather panel of top-class scientists to ponder aloud about

what we were dealing with. I set up a conference call.

Is that last sentence consistent with the perception that Dr. Farrar set up the conference call?

You're welcome to scan the couple of paragraphs after that to confirm.

A No, it's consistent with that.

Q Okay. Is that sentence where he says "I set up a conference call," consistent or inconsistent with the idea that Dr. Tony Fauci set up the conference call?

A It is inconsistent.

Q How about Dr. Francis Collins?

A Inconsistent with him setting it up, as well.

Q Is Dr. Farrar's sentence here consistent with your recollection to the extent you recall who set up the conference call?

A It is consistent with that.

Q All right. Great. I'm going to ask a couple of yes/no, questions, which I think will go quickly. And then we will take a break.

Putting all of those documents together, to the extent you recall, did Dr. Farrar organize the conference call?

A Yes.

Q Okay. Did Dr. Farrar play a substantive advisory role in the paper?

A Yes.

Q Okay. Did Dr. Tony Fauci organize the conference call?

A No.

Q Did Dr. Fauci, as far as you were able to see, play a substantive advisory role in the paper in the way that Dr. Farrar did?

A No.

Q Okay. Did Dr. Francis Collins organize the conference call?

A No.

Q Did Dr. Francis Collins play a substantive advisory role in the paper the way that Dr. Farrar did?

A He did not, no.

Q Did Tony Fauci or Francis Collins ever threaten you or bully you or intimidate you into concealing or altering the findings of your paper or in any other way?

A No.

Q Okay. Did Drs. Fauci or Collins ever threaten to revoke or withhold Federal funding from you in any way?

A No.

Q Are you aware of any efforts by Drs. Fauci or Collins to suppress scientific inquiry into the origins of the virus?

A No.

Q Is there any version of this question that I haven't asked you yet to which the answer would somehow be yes?

A There is not.

Q Okay. And, to be really clear, Dr. Jeremy Farrar, I know he played an advisory role in the paper, set up the conference call. But did he -- he ever at any point threaten you or bully you into taking a particular point of view with respect to the virus' origins?

A No.

Mr. Pellegrini. Okay. That is all I have. I appreciate the extra time. Thank you.

And we can go off the record, yeah.

[Recess.]

[11:30 a.m.]

Mr. Benzine. I think we are at a quorum. We can go back on the record.

BY MR. BENZINE:

Q Dr. Garry, I want to go back to our conversation and shift a little bit generally to how novel viruses can appear. There are, I guess, two viable pathways: a zoonotic event or a research-related event.

Can you describe a zoonotic event?

A A zoonotic event is where an animal has a virus and transmits it to a person.

Q What in your estimation would be considered a laboratory or a research related with that?

A Where a virus in a laboratory is transmitted to a person in that lab who then spreads it to other people.

Q So would a researcher intentionally manipulating viruses and then subsequently getting infected be a laboratory event?

A It would be.

Q What about a researcher conducting serial passage on a naturally occurring virus and getting infected?

A Well, you said it was a natural virus, so I would categorize that as more sort of a hybrid kind of thing going on.

Mr. Pellegrini. I'm sorry, Dr. Garry, could you just project for me.

Dr. Garry. I'm sorry. So you said it was a natural virus. So I would categorize that more as kind of a hybrid event, that they were working with a virus that was in nature and then it infected the person in the lab who spread it from there.

BY MR. BENZINE:

Q Does your --

A So it involves a lab, but it also involves a natural virus. But no manipulation of the virus, I think that's the way you specified the question and that's how I'd answer the question.

Q So you would categorize serial passages as not manipulating a virus?

A Serial passage is manipulating the virus, yeah.

Q All right. That was the question, whether research was conducted in a serial passage --

A So you're kind of in a natural virus.

Q -- and getting infected in a laboratory.

A Okay. That would be a laboratory event, yes.

Ms. Gardner. Dr. Garry, make sure you let him finish his question before you answer.

Dr. Garry. Oh, sure.

Ms. Gardner. The court reporter's going not like that --

Dr. Garry. Okay. All right. Okay. Sorry.

BY MR. BENZINE:

Q What about a laboratory researcher strictly working with a naturally occurring virus in the lab and getting infected? That would be the hybrid event that --

A It would be, yes.

Q What about a researcher getting infected by a novel virus during field work and bringing it back to the lab?

A Again, I would categorize that as a hybrid event because they were basically, you know, just happened to be a person working in a lab. I mean, that's an area of if it was, say, just any member of the public would certainly be considered a natural event.

So, yeah.

Q Have laboratory or research-related accidents happened before? Have there been infections related to a laboratory accident?

A None that have created a pandemic.

Q But there have been?

A Certainly. You know, mistakes happen.

Q Is it important to -- in an emerging disease, is it important to investigate both possible pathways thoroughly, both the lab and a zoonotic event?

A It is.

[Garry Majority Exhibit No. 4
Was marked for identification.]

BY MR. BENZINE:

Q I would like to introduce what will be majority exhibit 4. It's long and hefty, and I apologize.

This is the final publication from the Lancet Commission on lessons learned for the future of COVID-19.

We'll do it Giancarlo's way. I'll just hand it to you, so you can figure it out from there.

Are you aware of this publication?

A I am.

Q The chairman of the Commission was Dr. Jeffrey Sachs. Do you know Dr. Sachs?

A I have never personally met Dr. Sachs. Of course, I know who he is.

Q I want to actually, I'm sorry, take a step back. Have you read the Lancet Commission report?

A I have.

Q And you answered my next question. Have you ever met Dr. Sachs?

A Not personally, no.

Q Have you ever communicated with Dr. Sachs?

A Yes.

Q What were the nature of those communications?

A He asked me to serve on a panel to discuss the origins of SARS-CoV-2.

Q At Columbia University or --

A I'm not exactly sure where they were going to do it. I think it was intended to be a ZOOM meeting.

Q Did you sit on that panel?

A I declined.

Q Okay. Why did you decline?

A I didn't think that the panel would be balanced, scientifically, so I had no interest in really arguing with people about this we -- yeah. Good enough answer.

Q Thank you. Are you aware of who else was invited?

A Yes.

Q Can you name them?

A There were -- let's see, one of the persons was Alina Chan. Another person was Jesse Bloom. And there were possibly -- maybe -- I think -- I'm not sure whether or not Richard Ebright was invited to that particular one, but possibly, yeah.

Q And which of those three did you think were -- didn't provide balance, or all three?

A You know, probably Jesse Bloom would have been okay. He's actually, you know, a scientist. The other two have taken distinctly nonscientific views on the origins

of SARS-CoV-2, so I had no interest in doing a public debate with them.

Q Great. Thank you.

I want to turn to -- I don't know the actual page number in the document I handed you, but it's page 1,232 as labeled at the bottom left-hand corner of the page.

A What was the number again? I'm sorry.

Q 1,232.

A 1,232. All right.

Q On the left-hand column is a bolded title of a section called The origins of SARS-CoV-2. Do you see that?

A I do.

Q I want to read some passages and just ask if you agree with the passage or not.

Identifying these origins -- referring to the origins of COVID-19 -- would provide greater clarity into not only the causes of the current pandemic but also vulnerabilities to future outbreaks and strategies to prevent them.

Do you agree with that?

A I do.

Q More than 2 years into the pandemic, the search for the origin of COVID-19 remains incomplete and inconclusive.

So this was published September of 2022. Do you agree with --

A I don't agree with that statement.

Q Okay. And the third one: The hypothesis about both natural and laboratory spillovers are in play and need further investigation.

Do you agree with that statement, at that time, September of 2022?

A Can you point me to it on the document? I'd like to read exactly what it

says.

Q Yes.

Mr. Jacobs. The last sentence of the first paragraph?

Mr. Benzine. Yes.

BY MR. BENZINE:

Q The last sentence of the first paragraph: Independent experts consulted by the Lancet COVID-19 Commission shared the view that hypothesis about both natural and laboratory spillovers are in play and need further investigation.

A I disagree with that statement.

Q So the last two you disagreed with. Can you explain why?

A I do not believe the laboratory origin of the virus is in play anymore.

Q I want to introduce what will be majority exhibit 5.

[Garry Majority Exhibit No. 5

Was marked for identification.]

Mr. Pellegrini. I'm sorry, Mitch. I thought this was 5. Oh, it's 4. Okay. Thank you.

BY MR. BENZINE:

Q This is an email chain with you on it and a couple of other scientists, and it is Bates numbered Garry 0001964 through Garry 0001968. At the bottom of the page marked 1964, there's an email from you, and you appear to be referencing majority exhibit 4, the Lancet COVID-19 Commission report that we just introduced. Is that true?

A It is, yeah.

Q In this email you described the Lancet report as being hijacked by an American-hating narcissistic conspiracy theorist driven by a cabal of grifters. Do you recall writing that?

A Now that you've pointed it out to me, I do remember it, yeah.

Q Can you explain that statement?

A I believe that I'm referring to Jeffrey Sachs here and the other people that he had asked me to debate with. And it's colorful language, but I stand by it.

Q Can you elaborate more on why, why are you referring to Dr. Sachs in that way?

A Well, we'll just start with the America-hating term, I think he said several things not just related to origins that makes me think that he has a problem with the United States of America. And he's accused us of doing some things that -- like, for example, starting the Ukraine war, that I just don't believe are correct. So I stand by my term there.

Narcissistic, I mean, I'm not a psychiatrist, but in my opinion that fits. Conspiracy theorist, yes. He is advancing a lot of different conspiracies, not just those related to COVID-19. The cabal of grifters part, I don't mind telling you that I believe that refers to Alina Chan and Richard Ebright, who are pressing their own agendas about the COVID origins. So cult language, that I stand by it. Luddites, of course is antiscientific, which I also stand by.

Q The Lancet was listed in a previous exhibit as -- and you, I believe, testified that it's one of top three most prestigious medical journals. Why would they pick Dr. Sachs to lead this commission?

A You know, I don't really know.

Q Were you asked to be on the Commission?

A I was not.

Q We can move on from that one.

I want to spend a little bit of time talking about laboratory's biosafety levels in the

Wuhan Institute of Virology. Can you explain the various biosafety levels and the type of research that each would apply to? So going from BSL-1 to 2 to 3 to 4.

A Sure. BSL-1 is, you know, I think you might describe it like a high school biology lab. No particular personal protective equipment. You know, no high-risk experiments going on. Just this room could serve as a biosafety level 1 lab. There's no restrictions going in and out or anything like that.

Biosafety level 2 goes up quite a bit, actually, because at a biosafety level 2 you can work with infectious pathogens, like HIV, for example. No restrictions about going in and out of the labs. Much more -- you know, it's possible that you, depending on the experiment that you were doing, you would have to wear personal protective equipment. And it's just not a situation that we would have the general public moving in and out of.

Biosafety level 3 and 4 are actually not that terribly different. They are distinguished by the types of pathogens that you work on in those laboratories. So the biosafety level 3 containment, for the most part, is directed at risk toward pathogens, like influenza, SARS-CoV-2, and -- you know, and a few other pathogens that don't quite make it to the level where you have to have the space suits, the individual air supplies, and things like that. But 3 is a pretty high level of containment.

Biosafety level 4 is the level that you, you know, often see depicted in movies about, you know, viruses that escape and cause a pandemic. So it's a lab where people, you know -- it requires a lot of training just to work the equipment, to use the equipment. People are in pressurized suits so that, you know, their air supply is outside the building, outside the -- outside the, you know, the room that they're working in. It's a high-containment lab. Suitable for working with, you know, very highly infectious and pathogenic viruses, like Ebola, for example.

Q And correct me, is one of the suggestions for a biosafety level 4 pathogens

that don't have a cure or a treatment for?

A That's one of the considerations that people use to, you know, put viruses into categories that require different levels of containment. But, you know, even the biosafety 2 pathogen, HIV is a pretty serious virus that you don't want to get.

Q Where would you work with novel viruses, not knowing their pathogenicity or lethality? Or is it better to risk on the side of higher biosafety or --

A I mean, that's a difficult question. I mean, we're -- I would need a lot more context to answer that. I mean, any unknown virus, I mean, the odds that it's going to be a potential pandemic pathogen are extraordinarily low. You know, if they're known pathogenic viruses, then you can make a reasonable assessment about, you know, what level they need to be worked on. So there are just too many variables. I can't really answer it based on, you know, on that.

Q Moving to the Wuhan Institute of Virology. Have you ever professionally collaborated with the Wuhan Institute?

A On science, no. I did mention that one letter that I had signed off on with Zhengli Shi.

Q But you had never had a subgrant or any kind of --

A No, no scientific kind of -- no, no.

Q Okay.

A Sorry. I interrupted you. I didn't mean to do that.

Q No, no problem.

A Yeah.

Q Have you ever been to the Wuhan Institute of Virology?

A No.

Q We talked about your communications with Dr. Shi a little bit. Have

you -- outside of that letter, have you ever professionally collaborated with Dr. Shi?

A No.

Q Have you ever met Dr. Shi?

A I can't say yes or no. I've been to a lot of virology conferences over my time. I'm pretty sure we were probably at a similar con -- or the same conference at once. I do not remember, personally recall having -- ever having a conversation with her at such a conference.

Q All right. Thank you.

[Garry Majority Exhibit No. 6
Was marked for identification.]

BY MR. BENZINE:

Q I want to introduce what we'll mark as majority exhibit 6.

This is a fact sheet about the activity at the Wuhan Institute of Virology. It was published by the U.S. Department of State on January 15th, 2021.

Were you aware of this document before I just showed it to you?

A I was. I am, yes.

Q Have you read it?

A I've read it at one point in time, yes.

Q All right. On page 2 of the printout, it starts going through various points. The first point says, Illnesses inside the Wuhan Institute of Virology. And the first bullet under that says: The U.S. Government has reason to believe that several researchers inside the WIV became sick in autumn of 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illness.

Putting aside whether or not you believe that statement to be true, would an outbreak of a virus inside a lab be a data point suggesting a laboratory accident?

A Can you repeat the question? I missed the first part, but I believe that the -- the qualification I didn't quite get.

Q The qualification of putting aside whether or not you believe what the State Department put out is accurate, would an outbreak of a virus inside a lab be a data point suggesting that there was a laboratory accident?

A Yes.

Q Okay. Thank you.

Keep this one close by, but I'm going to also introduce majority exhibit 7.

[Garry Majority Exhibit No. 7
Was marked for identification.]

BY MR. BENZINE:

Q This is an email chain between a number of scientists, including yourself, from August of 2021. It is Bates numbered Garry 0001694 through Garry 0001703. On the first page, the one ending in 1694, it's about three-quarters of the way down the page, a paragraph that starts with "I'm also."

A Okay.

Q And reads: I'm also going to be looking closely at the comments on the supposed three sick researchers at WIV. Danielle Anderson, and Australian virologist who was at the WIV at the time, basically said that they did not exist. The three sick workers narrative was pushed at the end of the Trump admin by David Asher, who worked outside the IC -- meaning intelligence community, I assume. Is that correct?

A That's correct.

Q -- to generate intel regarding the lab leak. I do not find it credible.

I want to talk about this a little bit. Are you referencing majority exhibit 6, the January State Department fact sheet, when you're talking about the three sick

researchers?

A I mean, that's where that originally came from, but I was actually referencing the -- President Biden's Intelligence Committee report, that I was interested in seeing what they -- what comments they made about this document 6.

Q I believe in the report they said it's not dispositive. It doesn't prove that it came from a lab. Is that your recollection too?

A Of the --

Q Of the IC report?

A Of the IC report. Generally speaking, I think that's my recollection, sitting hearing at the moment, yeah.

Q Who is Danielle Anderson? You say she's an Australian virologist. Can you elaborate a little bit more on who she is?

A She is a Australian virologist now. She spent some time at the Wuhan Institute of Virology. I don't know her personally, but I read her -- some of her accounts, you know, in the popular press. And that's what this paragraph is basically based on there.

Q So she didn't communicate it to you; it was through press reporting?

A No. No, this is through press reporting, yes.

Q To your recollection, what was the press reporting that she said? So, obviously, she said she was at the Wuhan Institute and there weren't any sick researchers.

A She said there was no sick -- there was no outbreak of anything at the time, at the time that she was there, yes.

Q Do you -- a little bit further down, you say the narrative was pushed at the end of the Trump admin by David Asher. Do you stand by that? Do you think the sick

researcher narrative is a political one?

A It's my understanding of the facts that went down, yeah.

Q What -- can you elaborate a little bit more what is the basis for that understanding?

A So David Asher has been on the news a lot talking about the origins of COVID -- SARS-CoV-2, and he did work in the Trump administration at the end, and this was his task. I know he was involved in several meetings and discussions and, you know, I -- it's just -- this is an accurate reflection, I think, of my understanding of what his position was about those three sick workers.

Q Did you ever meet with her or talk with Dr. Asher about the origins?

A I did not.

Q Do you have an active security clearance?

A Not currently.

Q When did your security clearance lapse?

A Oh, I had a security clearance to discuss the HIV outbreak.

Q So a while before the COVID-19 pandemic elapsed?

A Yeah, many years.

Q After President Biden was sworn into office, State Department officials said of the fact sheet, of majority exhibit 6, quote: There wasn't significant or meaningful disagreement regarding the information presented in the fact sheet. No one is disputing the information, the fact that these data points exist.

So you would disagree with that statement?

A I think it's factually inaccurate, yes.

Q I'm going to move on and introduce majority exhibit 8.

[Garry Majority Exhibit No. 8

Was marked for identification.]

BY MR. BENZINE:

Q This is a cable from the U.S. Department of State, dated January 19th, 2018, entitled, China Opens First Biosafety Level 4 Laboratory. And for the record, the document is marked unclassified.

Were you aware of this? Had you been aware of this document before just now?

A I have not.

Q Would you like a moment to skim?

A Sure.

Q Okay. I'm going to primarily focus on one line in the summary. On the first page, the last line reads -- or second to the last line: Ultimately, scientists hope the lab will contribute to the development of new antiviral drugs and vaccines, but its current productivity is limited by a shortage of highly trained technicians and investigators required to safely operate a BSL-4 laboratory and a lack of clarity in related Chinese Government policies and guidelines.

What does that mean? How do you interpret that sentence?

A I think it says what it means. They hope to use the lab for productive work and they don't have enough people that are highly trained to do that yet.

Q Is having higher trained technicians important in -- under BSL-4 conditions?

A It is.

Q What is some of the training that you go through in order to operate a BSL-4?

A You learn how to work the equip -- you learn how to work in the suits, basically. That's the major step. It's not -- you know, it's not something -- you have to

put them on properly. You have to be able to go in and out. You have to understand what, you know, what happens inside the suit and outside the suit. And, you know, there are a lot of other challenges in that lab that, you know, working in a big clunky thing like that makes it difficult. But, you know, it's more than that.

I mean, you know, you're working with very dangerous pathogens that, you know, if you don't work the suit right and work your in-and-out right of the laboratory, you can create problems on yourself or for other people. So it takes a lot of training.

Q Do you -- to your knowledge and recollection, was, not necessarily at this time but over the last 5 years, pre- and current pandemic, was the Wuhan Institute of Virology working with novel SARS-like coronaviruses?

A They have published papers in the scientific literature on viruses that are related to SARS-1. So the answer to that question is yes.

Q Do you know what biosafety level they were conducting the research under?

A I do not have personal knowledge of that, no.

Q Do you know whether it has been reported?

A It's been reported that it was biosafety level 2 and 3, depending on the experiment.

Q Okay. Is that consistent with how you would operate on those types of pathogens?

A At the time they were doing the experiments, that would be the same rules that we would have in place in the U.S., biosafety level 2. But a lot of investigators said that wasn't high enough. They should be at 3. And so I would concur with that. It should have been done at 3. But, you know, it would have been consistent with our guidelines as well to work with some of those novel viruses at 2.

Q So you would say that it should have been done at BSL-3 regardless of the

guidelines. So --

A Yes.

Q -- I'm implying from that statement that maybe our guidelines should be strengthened a little bit too. Is that correct?

A That is correct.

Q Okay. Who else -- you mentioned a few other investigators think they should have been operating at BSL-3. Do you recall who you're thinking of when you said that?

A Just a lot of -- I mean, I -- I do run in the virology circles, right, so a lot of people who I talk to, I mean, I -- you know, it's probably not necessary for naming any particular names, but I think most people have reached a consensus that that is probably what we should be doing, is working with these novel bat viruses at biosafety level 3.

Q Was one of them Dr. Lipkin?

A I'm not sure if I've had a specific conversation with him about that, but just based on what I know and understand, I'm pretty sure he would concur with that.

Q Okay. So, generally, not specific to the Wuhan Institute, not specific to COVID-19, operating and understanding too that it's consistent with the U.S. guidelines, operating at a lower than optimal biosafety with fewer and a shortage of highly trained technicians would pose dangers. Is that correct?

A I mean, hypothetically, sure, of course, I mean, the way you set it up. I mean, I think I have to caveat that by saying that, you know, just isolating random bat viruses is not likely to expose you to the next pandemic pathogen. So I think that is the basis for the -- you know, for our current guidelines here in the U.S., but that should be changed. But the idea is, is that, you know, it takes a special -- takes a lot of special properties for a virus to become a pathogen that can spread and, you know, infect people

all around the world than just randomly picking a virus out of the millions of viruses that are out there. You're not likely to do that.

Q Does going beyond just isolating or sequencing the novel viruses to creating chimeric viruses increase that risk?

A In principle, it does. But, again, there's, you know, a very low likelihood that any scientist could actually design a chimera that would spread and cause a pandemic. We just don't know enough about virology to sort of intentionally do that. You know, is it possible? I mean, in the general sort of thing that, you know, we could -- that that could happen during the course of an experiment, yeah, it's possible. Is it likely or even plausible? It's highly unlikely and I would say almost impossible that that could potentially happen.

Q Okay. Thank you.

I want to shift gears a little bit, talk about gain-of-function research, as it's colloquially known, as it's known postmoratorium, and then some questions about the health alliance.

I'll go ahead and introduce exhibit 9.

[Garry Majority Exhibit No. 9
Was marked for identification.]

BY MR. BENZINE:

Q For the record, this is a printout of the NIH's website. And on the very last page you can see last reviewed July 12th, 2021. For the record, it's a printout from October 19th, 2021. And the second paragraph on the first page defines gain-of-function research as: The term gain-of-function research describes a type of research that modifies a biological agent so that it confers new or enhanced activity to that agent.

Would you agree with that definition?

A I would.

Q Is there a difference between gain-of-function research and experiments with an enhanced potential pandemic pathogen?

A Well, not all experiments with enhanced potential -- with ePPPs are gain-of-function research, but --

Q So the U.S. Government further regulates research with enhanced potential pandemic pathogens. Can something meet the definition of gain of function while also not meeting the definition of that further scrutiny?

A Yes.

Q Okay. There are benefits and concerns to gain-of-function research. You know, I hear from the, like, agriculture community about their -- how they make our strawberries better, and various kinds of things. Can you run through how in virology what benefits gain-of-function research has?

A Well, again, it depends on your definition. So there are so many definitions of gain-of-function research out there that, you know, you have to --

Q We'll use the NIH's.

A Yes. So the NIH's are actually pretty restricted, okay. So making a strawberry taste better, you know, with genetic engineering probably wouldn't necessarily -- would not fall into gain-of-function research, okay. But, you know, potentially gain-of-function research can tell you about how a pathogen acquires what we would call virulence factors, the ability to become more pathogenic. It could also show you what features it acquires to become more transmissible.

So both of those are sort of inherent, you know, what we consider important for pandemic pathogens. They have to be transmissible. They have to have some level of

virulence. And so gain-of-function research, in principle, can give virologists insight into those two features, which I believe are important to learn more about.

Q You used the term "in principal." Why did you choose to caveat it that way?

A Well, I mean, I -- you know, I don't think that we've seen any gain-of-function research that has given us such great, you know, insights into these things. But two experiments that are actually often held up that led to the moratorium in 2014, you know, gave us some important information, but, you know, not the sort of, you know, important information that would allow us to go out and design something that would stop a virus, the next virus like that.

So, you know, the -- in fact, those experiments, you know, gave you some viruses that could spread easier but were less pathogenic. So no real insight to how, you know, a virus can acquire all those, you know, necessary features that, you know, really become -- you know, and tell us about pathogenesis. We know viruses that do that, obviously. A virus like SARS-CoV-2 did, between the 1918 flu virus, but we don't understand everything about the viruses yet. So, you know, those are important things to figure out.

Q Some scientists say gain of function can lead to vaccines and therapeutics. To your knowledge, have there been any vaccines or therapeutics designed off the back of a gain-of-function experiment?

A Yes, but it depends on your definition of gain of function. So if you use a looser definition than the NIH does, a gain-of-function experiment would be to adapt a virus to a new species. So in the example of SARS-CoV-2, initially that virus would not grow well in mice. So some researchers adapted the virus to grow well in mice. That is, in a looser sense of gain of function, a new -- you know, it's a new function for the

virus, it can now grow into a new species, which, you know, a laboratory mouse is important in the model. And a lot of early studies were done on these lab-adapted SARS-CoV-2s that, you know, gave us insight into the virus. So that was important. It got us further along. That was closer to, you know, understanding more about the virus.

Now, turns out that SARS-CoV-2 actually gained that function on its own, but, you know, that's another story.

Q Using the NIH's definition, so intentionally modifying a biological agent to confer newer enhanced activity to that agent --

A Yeah.

Q -- are you aware of any of those types of experiments that have resulted in a therapeutic or a vaccine?

A No. But, I mean, again, this is a very strict definition here of gain of function. If you loosen up that definition and just, you know, more broadly talk about, you know, adapting viruses to new hosts and things like that, then, yeah, they certainly have led to vaccines and therapies and things like that.

Q Do you have any concerns publishing experiments that fall under the NIH's definition of gain of function?

A Well, it would depend on the outcome of the experiment, okay. I mean, if there was any scientists that was actually successful in doing it, I can see where, you know, some of that information might be sensitive, you know, because it might, you know, give virologists insight that we currently don't have into how to make a virus, you know, more pathogenic or more transmissible.

So, yes, I can see where that information -- you know, you might want to consider how that was distributed.

Q Would -- you said it could provide virologists more information. Could it --

A Or people that are -- virologists that don't have everybody's interest in their best --

Q So could publishing one of these experiments result in a terror group getting more knowledge than they previously had and could result in a biological or a chemical weapon?

A Well, it's a hypothetical. But, you know, hypothetically, if, you know, somebody actually did figure this out or, you know, something like that, it -- yeah, it could help those types of people, yeah.

Q Thank you. I want to shift gears a little bit, but keep the -- keep exhibit 9 close by. We'll come back to it.

A Okay.

Q But I want to talk about EcoHealth and Dr. Daszak a little bit. So you talked earlier that you had communicated with him about COVID-19. I think that's everything from the emails as well.

Have you ever professionally collaborated with EcoHealth Alliance before?

A No.

Q Have you met Dr. Daszak?

A I met him for the first time at a conference middle of last year.

Q Okay. How did you get to know -- you were obviously communicating with him before then. How did you get to know him or get introduced to him?

A Well, I hadn't had that much contact with him. I mean, those emails that are in the record now are basically those emails. And I think the first contact was he, you know, saw me on some news program and complimented me, you know, for effective science communication. It's just a cordial email.

Q In February of 2022, Dr. Drosten gave an interview in a Driven magazine

regarding the origins of COVID-19. Are you aware of that interview?

A Vaguely.

Q Okay. We'll introduce majority exhibit 10.

[Garry Majority Exhibit No. 10

Was marked for identification.]

BY MR. BENZINE:

Q So this is an email chain, along with lots of people on it, including yourself, and Bates numbered GARRY0001935 through GARRY0001946.

On the page that ends in 1937, there's an email from Mary Marshall that -- in the email which we'll go further down to -- includes an English translation of the interview Dr. Drosten gave.

First, you testified earlier that you have spoken to Dr. Drosten, who was on the first -- February 1st teleconference. Do you know him personally beyond that?

A I don't know him personally. I'm certain we've been at virology conferences together. In fact, he was at a conference I was at just a few weeks ago.

Q Do you know his work?

A Yes, I know his work.

Q Do you respect his work?

A Absolutely. He's a great scientist.

Q Okay. This email from Ms. Marshall, do you know who Mary Marshall is?

A I do.

Q Who is she?

A I believe she is a former employee of ProMED-mail, which came up earlier.

Q Okay. Going to the page that is marked 1939, the top of the page says, "Here's the English translation." And then it appears to be the English translation of the

German article that we talked about earlier.

Does this recollect you reading this article before?

A I mean, I'm pretty sure I read this. I mean, it was early last year, about a little more than a year ago now. I mean, I don't have a really firm recollection of, you know, all the details, obviously.

Q Okay. Going to the page that ends in 1940, there's a question, and it says, "Which ones?" And I want to start there. It's Dr. Drosten talking about experiments -- beginning to talk about experiments conducted at the Wuhan Institute of Virology with EcoHealth Alliance. And there's a lot of questions about furin cleavage sites, and Dr. Andersen's first email, which we'll get to eventually. And then flipping over to 1941 --

A Uh-huh.

Q -- the question: Did the intervention make the virus more dangerous? And Dr. Drosten says -- oh, I'm sorry. I'm going back up to the first paragraph.

So in response to, In your view, are there any new findings on the origin of the virus in the meantime? -- meaning since the February 1st conference call -- at the end of the second line Drosten answers: Another thing also surprised me: Project reports became public showing that the Institute of Virology in Wuhan had indeed conducted so-called gain-of-function experiments in a project of the U.S. NGO EcoHealth Alliance. In these experiments, bat viruses were given new spike proteins by means of genetic engineering. It turned out that the viruses constructed in this way were able to reproduce better. It also became known that there were plans to insert furin cleavage sites, but this was to be done in an American laboratory and the project was not funded.

I want to read a longish segment from EcoHealth's year five progress report. And I tweaked a few of the words so that the record is clear.

EcoHealth writes: In year five, we continued in vivo infection experiments of diverse bats, SARS-related coronaviruses on transgenic mice, expressing human ACE2. Mice were infected with four strains of SARS-related coronaviruses with different spike proteins, including full-length recombinant virus of SARS-related Wuhan Institute of Virology 1 and 3 chimeric viruses with the backbone of Wuhan Institute of Virology 1 and spike proteins from three other bat coronaviruses. All of the four viruses caused lethal infection in human ACE2 transgenic mice, but the mortality rate vary among four groups of infected mice. Fourteen days post-infection, five out of seven mice infected with Wuhan Institute of Virology 1 remained alive, while only two out of eight mice infected with one of the full-length chimera survived. These results suggest that the pathogenicity of the chimera is higher than the others.

Does this sound like the experiment that Dr. Drosten is referencing in this interview?

Mr. Pellegrini. I'm sorry. Is there a copy of that that I can see or that Dr. Garry can see?

Mr. Benzine. I can still print the 500-page progress report if you want me to.

Ms. Gardner. Would you mind if he just read like -- I know it's your notes, but --

Dr. Garry. I can answer the question. I don't know for sure.

BY MR. BENZINE:

Q Okay.

A I would be speculating if I gave you a definitive answer.

Q That's fine.

Does that experiment that I just read, creating full-length chimeric viruses with new spike proteins that result in a higher lethality in humanized mice, constitute gain of function?

A I would have to really know more about the context of the experiment to know and to answer your question accurately from a scientific point of view. In the U.S. guidelines, you know, they specifically exclude experiments with natural bat viruses, okay. It only -- the gain of function they're talking about is, you know, basically known pathogens.

So it just depends on your definition of gain of function. If you have a loose definition, then, yes, that would fit the criteria. If you have the definition that the NIH uses and other, you know, that we use in our regulations here, then, no, it wouldn't.

Q So you testified earlier that a project could be gain of function without being under the further scrutiny of ePPP regulations.

A Uh-huh.

Q Under the NIH's definition of gain of function, research that modifies the biological agent so that it confers newer enhanced activity to that agent, would EcoHealth's experiment qualify?

A I can't -- I just don't have proper context to give you a professional answer on that. I'd have to really know more about -- you know, more than just, you know, hearing that paragraph read to me to be able to make an evaluation there.

Q Okay. I would like to now introduce what will be majority exhibit 11.

[Garry Majority Exhibit No. 11
Was marked for identification.]

BY MR. BENZINE:

Q This is a letter from Dr. Tabak to at the time Ranking Member James Comer, who is now chairman of the Committee on Oversight and Accountability, from October 20th, 2021. And it outlines the fifth and final progress report for the RO1 grant that EcoHealth did in conjunction with the Wuhan Institute of Virology.

The letter states -- let me find it so I can point you to the correct paragraph. In the fourth paragraph it describes the experiment.

The limited experiment described in the final progress report provided by EcoHealth Alliance was testing if spike proteins from naturally occurring bat coronaviruses circulating in China were capable of binding to human ACE2 receptor in a mouse model. All other aspects of the mice, including the immune system, remained unchanged. In this limited experiment, laboratory mice infected with the SHC014 WIV1 bat coronavirus became sicker than those infected with the WIV1 bat coronavirus.

Does that sound like they created a virus with enhanced -- well, does that sound like it would meet the NIH's definition of gain-of-function research?

A Well, again, I need more information to really make a -- I haven't read the entire 500 pages of that progress report. I mean, I'm going ahead and read the name paragraph, and it said the NIH determined it did not fit the definition --

Q They said it didn't fit the definition of ePP standards.

A Right, right.

Q We've already established that an experiment can be gain of function --

A Right.

Q -- and fit the definition of gain of function without ePP.

Modifying a biological agent so it confers new or enhanced activity is the definition. They modified WIV1, right, making it SHCO14 WIV1, and those mice became sicker, sicker than WIV1. That's enhancing the transmissibility or virulence of that virus. Does this describe a gain-of-function research experiment?

A I mean, well -- again, I mean, it's the context of everything, right, that's important. You know, what were the precise pathogens and all of that. So, you know, I have, you know, taken a look at some of the original data and the experiments and

things like this, and I didn't think it fit the definition. But, you know, I mean, if I had gotten more information and more details, you know, I might change my mind. I just don't have enough context to really give you, you know, a virologist, you know, professional opinion on this.

Q Okay.

A Yeah.

Q The letter also states -- let me find it so I can point you in the right direction. It's on the bottom of the last page.

The analysis attached confirms -- which we don't have, but it's not relevant to the question -- that the bat coronaviruses studied under the EcoHealth Alliance grant could not have been the source of SARS-CoV-2 and the COVID-19 pandemic.

You testified at the beginning that you've received Federal grants before. Is that correct?

A That's correct.

Q Did those grants involve collecting sequencing viruses?

A Yes. Some did, not all.

Q Under the ones that did involve --

A Most did not.

Q Okay. Under the ones that did involve collecting sequencing viruses, were the sequences published?

A You know, we haven't gotten quite that far. I'm talking about this Centers for Research in Emerging Infectious Diseases grant. And we got a little sidetracked with the SARS-CoV-2 pandemic to actually go out and try to find some new ones, so --

Q In your professional experience, have you ever personally seen a federally funded or any kind of research project where they didn't publish every sequence that

they collected?

I'll rephrase it.

A Yeah. Maybe rephrase it because, I mean, I --

Q Is it possible that while doing viral sequencing research that you do not publish every sequence you come across?

A I mean, that's possible.

Q Okay.

A Yeah.

Q In your experience with grants, if the grant application is denied by the Federal Government, are there other avenues for funding?

A Sure.

Q And in your experience, is it common for an organization to begin some of the work proposed prior to submission of a grant proposal?

A It is.

Q Why is that?

A You need plenary results to usually run the application. You have to establish that you have, you know, the capability, the experience, the track record to do the experiments that you're proposing. And one good way to do that is to show them that you've already done some similar experiments. So, yeah.

Q While collaborating on a grant, if an actual experiment is done in one lab, are the collaborators taught about how to conduct that experiment or are they fire-walled off?

A I'm sorry, I didn't quite catch that last part.

Q So I'll phrase it specifically. Are you aware of the proposal submitted to DARPA, the defused proposal that was denied?

A I'm aware of it in general terms, yeah.

Q Are you aware of what was proposed?

A I mean, only in general terms. I haven't scrutinized the document.

Q Can you explain what your awareness of it is?

A It's really just in very broad terms. I mean, I think they were proposing to study bat coronaviruses just in general and to, you know, understand what the diversity was in nature.

Q Was there a proposal to insert furin cleavage sites into these background viruses?

A I've seen that paragraph and I've read it because it's, you know, been the topic of a lot of discussion. So the answer to your question is yes.

Q Where was that work proposed to take place?

A At the University of North Carolina.

Q Was the Wuhan Institute of Virology a proposed collaborator on that grant?

A They were.

Q Would the University of North Carolina not tell the Wuhan Institute of Virology that they were doing that work?

A I don't know. It's speculation.

Q Okay. Thank you.

Mr. Benzine. We are close to the end of the hour. We can go off the record and take a break.

Mr. Jacobs. Actually, before we do that --

Mr. Benzine. Yeah.

Mr. Jacobs. -- can I just ask a couple of quick clarifying --

Mr. Benzine. Yes.

Mr. Jacobs. Dr. Garry, you have not read the fifth progress report on the EcoHealth Alliance grant that's referred to in this letter?

Dr. Garry. I have not, no.

Mr. Jacobs. That's all.

Mr. Benzine. Okay. We can go off the record.

[Recess.]

[1:10 p.m.]

Mr. Pellegrini. Okay. So we can go back on the record.

BY MR. PELLEGRINI:

Q So, Dr. Garry, I'd like to talk a little bit about the proximal origin paper itself, if we could. And so I will start by introducing that paper as minority exhibit P.

[Garry Minority Exhibit No. P
Was marked for identification.]

BY MR. PELLEGRINI:

Q And that's just so -- I know you're familiar with it, but it's just so we have it at hand in the event that that becomes useful. But I expect this to be a little bit more dialogue. I will not run you through 50 emails out of a binder this time.

A Okay.

Q So, if we could, I'd like to start by just talking a little bit about the context, broader context, at the time that this paper was written.

As I understand it, there were various theories floating around about possible origins of SARS-CoV-2. There may have been something related to HIV. There was a general discussion of bioweapon engineering.

Could you just talk for us a little bit about that context and how it affected sort of the broader importance of this work?

A We tried to make those kinds of theories that were floating around in the sort of the nonscientific sphere irrelevant to our analysis. What we were intent on focusing on was the actual data that we could derive from the prior scientific literature, from the genome itself that, you know, had been published, new information that was coming through, like pangolins and pangolin coronaviruses and the other things like that.

So to directly answer your question, you know, of course, we're all humans, right. I mean, these things are percolating in the background, but we did the best we could as professional scientists to try to ignore those influences and just focus on the science.

Q What were those theories? I mean, I recall that one of them was linked to HIV. Do you recall what that particular --

A I do recall that one.

Q -- theory was?

A I'm sorry.

Q No, please.

A I didn't mean to interrupt you.

Q The coffee went down the wrong pipe here.

A Yeah. So there was a theory that was circulating that HIV and SARS were somehow combined -- or some SARS-like virus was combined to make SARS-CoV-2. It was actually a preprint in the -- you know, on a -- on a server. Preprints are just, you know, preliminary versions of paper that -- papers that people will put out.

And this particular one had garnered a lot of attention. It appeared, you know, probably very close to around the time of that February 1st teleconference that we've talked about. So, I mean, that was out there.

The preprint was eventually withdrawn because it was flawed. It was fatally flawed. There's no evidence whatsoever that, you know, HIV sequences were put into SARS-CoV-2. That just didn't happen.

Q And the bioweapon theory?

A I mean, the bioweapon theory, you know, was something that we considered in the proximal origins paper, you know. And there, again, is just really no evidence that -- that this virus was constructed as a bioweapon, had been manipulated in

any way. We couldn't -- couldn't find any evidence for that in the sequence itself or anywhere else.

Q Okay. So turning to the substance of paper and the different categories, the way that the paper breaks the different possibilities down --

A Uh-huh.

Q -- first, could you just give us a little bit of context on the emergence of past viruses that you might be familiar with, whether that's SARS-1 or MERS, sort of what that path of emergence has looked like in the past?

A The one that's most relevant to the emergence of SARS-CoV-2 is the first SARS that happened in China in 2002, '03, and '04. And I think one of the important aspects of that is, is that there were multiple spillovers of that virus from animals to humans. Some of the first people that were infected with SARS-1, I'll call it just to keep it -- keep them straight, were people that actually worked in the wildlife trade. And so the -- the biggest -- the biggest spillover, the one that led to the most cases, was also linked back to the wildlife trade.

So that's the most relevant thing. The first SARS was -- and I think, you know, you might -- you'll probably find some people that will dispute it. But, you know, I think the scientific opinion is, is that was most definitely a spillover that involved animals that were, you know, sold at markets and things like that.

Q And is there anything about the city of Wuhan specifically -- and we talked a little bit about it earlier -- whether that relates to particular animals that are concentrated in one place or concentration of early cases that influences the way that you assess what is likely or not likely with respect to SARS-CoV-2?

A Well, I mean, we got into looking at those aspects after the proximal origins paper, that that -- those -- the topic you just mentioned is more relevant than some of

our later papers that we've -- we've put together and published.

And so -- but just, you know, to sort of answer your question more broadly out of the context of proximal origins, yeah, it's a large city, okay. And, you know, one thing that we have come to the conclusion is, is that, yeah, a large city is important for getting a pandemic started. You need to have people in close contact with each other so it can be spread. You know, if it's a rural area where there's a spillover, you know, the chances are that that virus is going to die out before it hits a population center. So a big city like Wuhan is expected in that -- in that way.

Now, another aspect of Wuhan that's important to note, I think, is that there were only four places in the city that were selling these types of animals that are susceptible to SARS-CoV-2. And the largest one, the one that had sold the most animals, was the seafood market.

Q That's the market we were discussing earlier?

A It is, yes.

Q Okay. So it seems as if the paper itself breaks out zoonotic origin into a couple of different categories. There's natural selection in an animal host before zoonotic transfer, and then separately there's natural selection in humans following zoonotic transfer.

Could you just talk a little bit about what those two categories are, what they represent --

A Uh-huh.

Q -- some of the things you might look for when trying to judge what might be more or less likely between them?

A Sure. So, I mean, it's generally -- I mean, we generally assumed in writing the paper that, you know, this was a virus that had ultimately come from a bat, okay.

And, you know, that's the origin of a lot of coronaviruses. You know, the bats have coronaviruses. Sometimes they spill over.

But the question is, you know: What makes them good human pathogens as opposed to, you know, viruses that replicate in bats? So two possibilities there that we discussed in the paper. The -- I don't know if it's the first or the second, but, yes.

Yeah, the first one was, you know, selection in an animal host. So a bat virus would then -- would spill over into an animal and then circulate in that animal and pick up properties that, you know, enable it to replicate better in a nonbat animal.

What actually appears to have happened in the case of SARS-CoV-2 is that it picked up the ability to replicate in a lot of different kinds of animals, unfortunately, including humans, okay.

So the second possibility that we discussed in the paper was is that the -- you know, that humans picked up some progenitor of SARS-CoV-2 and then it passed from human to human, maybe in a slightly, you know, a different form, or, you know, maybe it didn't have the furin cleavage site or something like that, a less transmissible, less pathogenic form.

But in the course of transmitting between humans at this low level, it picked up additional properties that eventually, when it showed up in Wuhan, led to the spread of the virus. So we don't think that second possibility is, you know, as likely at all now.

Q Got it. First one seems more likely.

A It does.

Q Okay.

A Yes.

Q Great.

A Based on all the extra data and evidence that we have accumulated.

Q I appreciate it.

What I'd like to do is turn to some components of the paper that are more focused on possible lab-based theories.

A Uh-huh.

Q And there will be just a certain amount of terminology setting. I profess I do not have a scientific background. So if I misuse any terms, just jump in and correct me.

But it seems as if the broad category of lab-based scenario sort of breaks out into a few subcategories within this paper. I'm going to try to characterize those and we'll see if I get it right.

There's, first, a broad idea of whether or not the virus is a laboratory construct or purposefully manipulated. And then, separately, there's discussion of other lab-based scenarios which seems to be primarily be about passage in a lab. Is that fair?

A Fair.

Q Okay. Great. That's an accomplishment for me.

I'd like to explore that first category first, if I could, the idea of whether or not the virus is a lab construct purposefully manipulated. And a point on terminology, I've seen the term "genetically engineered" --

A Uh-huh.

Q -- sort of being used in that same context. I understand those three phrases to be, to some degree, interchangeable. Is that generally right?

A That's fair enough, yeah.

Q Fair enough. Okay. Great.

A Yeah.

Q And I understand that to be referring to deliberate and direct modification of

genetic material. That might occur by a few different techniques and it might leave a marker or a trace or it might not. But in any case, it is deliberate and precise in a way that, for example, passage would not be. Is that still fair?

A That's -- that's very fair. That's correct.

Q Okay. Great. So as a reader of the paper, it seems as if the paper makes two basic arguments in support of the idea that the virus is not engineered or a laboratory construct.

There's an argument related to receptor-binding domain mutations and the predicted binding affinity of those mutations. And there's a separate point about the use or lack thereof of a known viral backbone.

If I could touch first on the receptor-binding domain issue. And I think, if for nobody's sake but my own, I need to establish that I understand the concept correctly. So I'm going to give it another shot and we'll see if I can get this one right.

There's a portion of the virus' spike protein referred to as the receptor-binding domain, sometimes called RBD.

Good so far?

A Good so far.

Q Great. And within the receptor-binding domain, which being a protein, is made up of chains of amino acids, so within the RBD, we have six particular amino acid residue sites that are either the key or a large part of the key in determining the binding affinity for the virus to the human ACE2 receptor or any ACE2 receptor. Is that correct?

A That is correct.

Q Great. And so the argument existing, I think in the paper, if I understand it correctly, is the idea that, okay, this virus has mutations at these six key residue sites, as compared to SARS-1, as a baseline. And those mutations allow the virus seemingly to

bind quite well to ACE2.

However, computational models based on what was known at that time would not really have predicted that. The models would have predicted that the virus' binding affinity was suboptimal. And, therefore, if somebody were designing a receptor-binding domain, this particular design would not have been rational because it would have been predicted to be suboptimal in its binding affinity.

Is that -- have I characterized it correctly?

A You have characterized it exactly correctly.

Q All right.

A Very well done.

Q Great. I'm excited about that.

So I understand, I think, the premise of that argument. I think a question that would be helpful for us to understand a little more about is what, if anything, does that argument tell us about the possibility of work involving naturally occurring viruses? Is there an extent to which that argument depends on the idea that a human being was choosing, themselves, the particular mutations?

A Well, I think the argument goes like this. You know, the -- if a human had set out to design this receptor-binding domain, they would have used one of these computer programs to predict the interactions between the amino acids and the ACE2 receptor that -- that you mentioned. And they would have come up with a solution for that binding that is entirely different than what the virus actually came up with.

It just means that nature is much better at doing that kind of -- and evolution of the virus is much better at arriving at a good binding solution than any human in a lab sitting down at the computer could have come up with.

So it -- it really is -- it comes down to what you said, I think very nicely, is that, you

know, if a human had set out to do it, they would have designed it entirely differently.

Q Is there an extent to which it is possible that if a human, rather than doing that, were taking components of different naturally occurring viruses and attaching them to each other, that this point about predicted binding affinity would have a little bit less relevance?

A Well, at the time we wrote the paper, we -- we had just learned about the pangolin coronavirus. And, in fact, that pangolin coronavirus has the receptor-binding domain, the RBD, that's very similar to SARS-CoV-2. So that told us that nature had already selected such a binding solution in another coronavirus. So it made the idea that SARS came by that, you know, what initially looked like kind of an unusual solution, a perfectly natural one.

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 --

A And the way --

Q -- hypothetical question.

A The way you said it, hypothetically, sure.

Q Okay.

A Yeah, uh-huh.

Q That's plenty on receptor-binding domains.

The concept of a known virus backbone, could you -- I mean, I think I could possibly pull it off. But if you don't mind, would you mind explaining what a backbone is?

A Okay. So the idea if you're, you know, looking at the possibility of modifying a virus in the lab, requires that you have something that's close, okay. I mean, the genome of SARS-CoV-2 is about 30,000 nucleotides. Those bases, A, T, C, U. And then -- A, U, C -- never mind this one. Okay. So it's 30,000 nucleotides to deal with.

And so, you know, the closest virus we know about now is a virus called Bengal 2052. It's about 96.8 percent similar to SARS-CoV-2. That's about a thousand of those nucleotides different.

So, you know, the laboratory and that you were hypothesizing may have created SARS-CoV-2 in the lab, would have had to have had a virus that was much closer than that, much closer than any of the viruses that we even know about now, to get from, you know, this hypothetical virus to SARS-CoV-2.

Nobody's going to be able to sit down in, you know, a lab with, you know, a virus that's only 97 percent similar and design it in a way that you could get to, you know, such a, you know, very efficient pathogen with SARS-CoV-2.

Q There -- can you just talk a little bit why you would expect somebody doing that kind of hypothetical work to use a known published backbone?

A It -- you know, it just comes down to, you know, you work -- you know, the scientists in the laboratory are trying to figure out about how these viruses replicate and, you know, what their features are that make them do what they do, you know, make them transmissible, make them pathogenic. The idea that you'd spend a whole lot of time on just some random virus from a bat doesn't really make much sense from a scientific standpoint, you know. It's not something that's very likely at all. In fact, it's very unlikely to give you any very -- any useful information.

Why would you just -- you know, there are millions of viruses out there, literally

more than that. You know, just picking one and saying, okay, we're going to do this, kind of very detailed, intense, expensive kind of work on it really doesn't make any sense.

Most virologists, if they're studying viral pathogenesis, will at least start from something that's sort of known, that we know that this virus, for example, or one of its relatives causes an important human disease.

Q Is there any extent to which somebody might want to examine the emergence potential of viruses that are not yet known human pathogens?

A Well, sure, they would. The -- and that -- and that's important to do. We've not sampled, you know, nearly enough coronaviruses out in nature to know, you know, the extent of the -- the extent that this virus, these -- this virus family, you know, varies. How many different variants are there of these SARS-like viruses? That would be important to know because the next one may, you know, be that next pandemic threat.

But having said that, you know, the idea that you would just sort of randomly pick one of those or even a dozen of those and start, you know, doing complex manipulations in a lab, it's just not what -- you know, it's just not a very productive line of research. You probably wouldn't find out very much about it.

You know, once you've found the virus, done the genetic sequences, find out where they fit in the tree and that kind of analysis, you know, actually going in there and trying to manipulate it, why would somebody do that? There's just -- it just doesn't make any sense to us that somebody would pick a random virus like that to do this kind of work.

Q I know that you would not have personal knowledge of this. But is it your understanding that the Wuhan Institute of Virology possessed bat virus sequences that were not published in their totality, that we, the world, were not -- we're not in

possession of 100 percent of bat viruses at WIV?

A I mean, I've heard that being alleged. I don't have personal knowledge of what sequences they had or --

Q Sure.

A -- you know, didn't have and published, didn't publish. There would be no way for me to really know that. I've just heard what you've heard.

Q The -- well, certainly that's all I know as well.

But the RaTG13 virus, as an example, I think was published in 2020 as the pandemic was picking up speed, but I think is understood to have been collected by Wuhan Institute some number of years earlier.

A That's what the 13 means.

Q Oh.

A 2013.

Q That's a light bulb going off in my head. Great.

For the transcript.

Thank you.

Okay. If we could talk about the idea of passage and culture in a lab. And if I just understand what passaging is, grow a virus in cells, allow it to replicate for some period of time, transfer that virus to other cells, and repeat the process and just keep doing it. And eventually you start to see, I guess, evolution in a sense, changes. And you can make inferences about the selective pressure on the virus.

Is that an accurate description?

A That's extremely accurate.

Q Okay. Extremely accurate. Great.

And is it right that passage can occur in vitro, essentially in a test tube or Petri

dish, or also can occur in live animals? Is that right?

A It's been done both ways.

Q Done both ways. Okay. Great.

Trying to sort of separate the distinct arguments in the paper that cause one to view passage as a less likely origin. I think I track three of them. And you can correct me if there are more or less. One being the idea that the pangolin has identical RBD mutations in the six key sites; the second relating to the existence of the furin cleavage sites and the specific conditions under which that had previously been observed in passage; and the last being O-linked glycans.

I think those are the three in the paper related to passage. Does that sound right?

A That does sound right, yes.

Q All right. Great.

A I'll just not shake my head.

Q I appreciate it.

A Yeah.

Q I'm sure she appreciates it.

A Yeah.

Q So taking them each in turn, the pangolin receptor-binding domain. I know I mentioned it. You mentioned it earlier. Can you just describe for us the significance of the pangolin RBD?

A Well, it has, you know, sort of a temporal significance because the sequence of that virus really came available to us, you know, while we were writing this paper. And it's very similar to the SARS-CoV-2 RBD.

I mean, that part -- I mean, the viruses themselves are different in a lot of ways.

But in this one particular feature of the spike protein, the receptor-binding domains are very similar. So that told us that this particular RBD or something like it had already evolved in nature. So it was there.

And, you know, knowing how coronaviruses evolve and sometimes exchange genetic material with each other in nature, this showed us a very natural pathway to get to a virus like SARS-CoV-2 that had an RBD that, you know, really hadn't been seen before and that seemed to have unique binding properties. But it told us that that part of the virus was very likely natural.

Q Great. And then I suppose I have a similar question to -- to previously with respect to the RBD, which is: Is there an extent to which it is possible that if somebody were to perform passage, and starting out with a naturally occurring virus, that for the purpose of the hypothetical has a receptor-binding domain identical to -- a hypothetical -- identical to the pangolin, that that possibility is not necessarily foreclosed by the fact that the receptor-binding domain has its original origins in nature? Is that fair?

A If you're -- I -- I mean, I don't really --

Q That was a --

A I don't want to speculate on what you're asking me. But, I mean, I think it's unlikely that it -- that if you passed any virus like in a cell culture system, that you would end up with that particular binding solution. I don't see how you could really do it.

It takes a lot of time, you know. And there's just not enough time in the lab to really put that much pressure on the virus to come up with all those changes. The virus would likely just not grow into cultures that -- or something along those lines. You'd really have to -- it just is very unlikely to happen, in my opinion.

Q But would it be possible to start with this particular receptor-binding

domain? I understand there's no factual --

A Oh. To -- you mean --

Q Yeah.

A -- and get it to grow in its culture? Yeah, you could do that.

Q If we could talk about the furin cleavage site.

A Uh-huh.

Q You've already explained what a furin cleavage site is, which I appreciate it. Why was it considered notable or unusual at the outset that SARS-CoV-2 had a furin cleavage site?

A It's suppressive. We know, you know, virologists know that there are avian influenza viruses that start out as low pathogenicity viruses. If somehow -- and there are several different pathways for this -- they acquire a furin cleavage site or a polybasic cleavage site, whatever you want to call it, they can become much more pathogenic and better able to transmit in people and cause disease.

So the presence of a furin cleavage site gave people like me who have studied viruses for a while a little bit of pause.

Q To what extent had furin cleavage site previously been observed in similar coronaviruses in the subgenus or in the genus level?

A Okay. So at the genus level, we're talking about beta coronaviruses. There are beta coronaviruses of -- that infect people, that cause the common cold. One of them is called OC43. The other one's called HKU1, or Hong Kong University 1. They both -- they're one of four common cold coronaviruses. They're both beta coronaviruses, so in the same genus of coronaviruses as SARS-CoV-2. And they both have furin cleavage sites. In fact, they have even better furin cleavage sites than SARS-CoV-2 does. SARS-CoV-2 has what we call a minimal furin cleavage site. Those

other two viruses I mentioned have better, more efficient furin cleavage sites.

At the subgenus level, we're talking about sarbecoviruses. Okay. And SARS-CoV-2 so far is the only sarbecovirus that has a furin cleavage site.

I mean, after looking through this and looking at the literature and figuring this out, we decided that wasn't such a big deal. You have to have something about a virus like SARS that's spreading so easily in the human population that make it unusual. So that's probably the furin cleavage site. So you'd expect it to be a little bit different than its, you know, immediate, you know, most closest family members, the sarbecoviruses.

But just to put that in a little bit more context, I mean, sarbecovirus is a subdivision of a genus. It's like, you know, okay, your -- you know, your brothers and sisters but not your cousins, right. I mean, it's a very -- they're all -- you know, there are betacoronaviruses that have furin cleavage sites. So it's not unusual for the family.

And we also know that that site, that place in the virus is very highly variable amongst all the different viruses in the coronavirus family. So furin cleavage sites come and go in these viruses. There are actually four subgenuses of the betacoronaviruses, and we know that four out of five now have viruses that have furin cleavage sites.

Q Got it. Thank you. That's very helpful.

And in the paper, I think, there are two distinct sort of points made. One relates to the previous observation of furin cleavage sites after prolonged passage of low pathogenicity avian flu viruses.

A Right.

Q And then the other one is that in order to develop this particular furin cleavage site passage, you would have had to isolate a progenitor virus that nobody has described doing.

On the avian flu point, just for my own understanding, is it that that -- it's not

necessarily that is the sole condition under which a furin cleavage site could develop in passage, right? It's that that is where it --

A No. It happens in nature too. And it often happens in situations where the avian flu virus gets into, like, chicken flocks and has a lot of opportunity to pass from bird to bird in that. I mean, it's not really a natural situation. It's a, you know, a chicken farm. But, you know, you get a lot of this animal-to-animal passage, and that can give you a furin cleavage site.

So I guess, you know, just to add, the other point I'd make about SARS-CoV-2 is that, you know, when we wrote the paper, we thought, okay, that's a possibility of how it picked it up. But it turns out we know something more about the furin cleavage site now. When you actually pass SARS-CoV-2 in cell culture to sort of redo that same thing with the actual virus, it loses the furin cleavage site.

So it's kind of the opposite of what we predicted. The furin cleavage site goes away when you try to pass it on normal cells like Vero cells that people use to grow coronaviruses.

Q Is there any thought as to why that is?

A It doesn't need it, subculture. Okay. It can grow perfectly well without the furin cleavage site. It has other ways to activate the spike.

Q Okay. On the -- on the point that to develop this particular furin cleavage site in culture, you would have had to isolate a progenitor virus, that work has not previously been described.

Is there an extent to which that implies a certain degree of human trust? And that -- that is not strictly speaking fully a scientific argument, right? Depends on folks telling each other what they're doing. Fair?

A Fair enough.

Q Okay. The O-linked glycans, if you could just describe what those are for us, please.

A Okay. So that was actually one of the things that I did on the paper -- for the paper --

Q Right.

A -- was just the interest that I had about these O-linked glycans.

So there's -- glycan means sugar, okay, basically. And these are sugar molecules that are put on the surface of -- are put on the surface proteins of viruses, so like the spike protein of SARS-CoV-2.

For the virus, they are -- they act like a shield. So the virus has evolved glycans on its surface basically to protect itself from the immune system of a human or the animal, whatever, you know, they find themselves in.

So SARS-CoV-2 has on the spike protein many of these glycans. I believe the number is 27 of this one particular type called N-linked glycans.

Well, I was interested in -- if you read back through some of those emails, I saw one of those -- some of those this morning. We were talking about that, you know. And it actually turns out that I had an interest in the O-linked glycans, which are a minor class.

But I was surprised to find, you know, pretty shortly after, you know, looking at the sequence initially and finding the furin cleavage site, that I put it through this other computer algorithm. And it predicted that right at that very site where the furin cleavage site is are three predicted O-linked glycan attachment sites. Okay.

So -- and that was really the first time that anybody had actually thought to look at that, I think. And wouldn't have thought to look at that except for the SARS-CoV-2, but we did.

Subsequently, I looked at other viruses like some of these avian influenza viruses and other viruses that have similar surface glycoproteins. Many of them actually also have that modification. They put these -- this one particular type of sugar, or glycan, right around the furin cleavage site. Okay. So that implies that, you know, that -- two things. The O-linked glycans are probably part of that glycan shield that I talked about, because the furin cleavage site or the cleavage site, if it's not a furin cleavage site, is a vulnerable part.

In other viruses we know that that site is often attacked by the immune system. You know, an antibody goes there and binds and keeps the virus from cleaving it, from -- from -- it keeps furin out of there and keeps the virus from being activated. It's a good way to neutralize the virus. So these O-linked glycans could help to protect that site.

But we also think that the O-linked glycans are in some way regulating the efficiency of that cleavage too. We now know that those -- that the virus actually does put O-linked glycans on there. We're very careful in the paper to say that those are just predicted sites, that they haven't been shown. But people with the proper experience and techniques, you know, have gone and looked. And, yes, the O-linked glycans actually are present in that site. So they do exist. So they're involved in regulating the efficiency of the cleavage too. So it's a natural process.

And why that was significant for the paper, you know, no -- you know, what -- nobody knew about them before. How would you engineer a site that actually by chance just happened to have them? Seems very unlikely.

Q And the significance of the presence of an immune system --

A Uh-huh.

Q -- what is that significance?

A So that goes to the whole glycan shield part. You know, presumably viruses evolve these glycans to help protect the virus from the immune system. That wouldn't happen in a cell culture experiment, right. The cell cultures don't have an immune system to put that kind of pressure on.

So if you were doing cell passage, which is what we were talking about there, without an immune systems, why put the sugars there? It just probably wouldn't happen.

Q Got it. Okay. Great.

So you answered one of my questions before I asked it, which is the distinction between predicted glycans or confirmation that they are present. It has since been confirmed that they are present.

A Yes, that's true.

Q Great. And with the understanding that they are present, does that reflect a 100 percent certainty that they represent the presence of an immune system, or is it something less than 100? The strong likelihood, where on the scale does that fall?

A It's less than 100. I mean, it's a pretty good indication. I mean, scientists are sort of trained not to try to put, you know, those kind of percentages on things. That's why you'll very often see, you know, scientists write about a piece of data that they say that that suggests that this happened without really quantifying it.

Q Sure.

A Yeah.

Q For my own ability, to the extent that we know the glycans are there, we will posit that they reflect the involvement of an immune system. Would that fact in and of itself tell us anything about the possibility of serial passage in animals?

A Well, I mean, obviously the animals are going to have an immune system,

and they would put pressure on it. So in principle, yeah, you could passage a virus that didn't have a furin cleavage site through animals, a lot of animals, and potentially generate one.

Those are really hard experiments, though, and expensive and time-consuming. Like, you have to -- when it was done in influenza viruses, you know, they did it actually in eggs, embryonated eggs, but it took something like 50 passages. So that's a very tedious and long-term experiment that you have to really be committed to. And the idea that you would do that with just some random virus that you may have collected out in the field doesn't make a whole lot of sense really.

Q Great. Zooming out for a moment, could you talk a little bit about the evolution, so to speak, of your own views on the origin question --

A Uh-huh.

Q -- and whether that's from the first time you saw the sequence or --

A Uh-huh.

Q -- through the writing of this paper, through the market data, or up until present day? What has been the path of your own views on this?

A Well, you know, when we first set out with just having the sequence, I think -- and we decided that, you know, it was worth taking a hard look at this origin question, I would say that I was open to the possibility that it might have come from the laboratory.

As we -- as we and I dig deeper in -- dig deeper into the data and, you know, the likelihood that it was a natural virus just got more and more likely.

More recently over the past several years, I think we've accumulated a lot of data involving the seafood market and the phylogenetics, the two lineages of the virus.

Even more recently, the fact that, yes, we actually have DNA from raccoon dogs

and civets and other susceptible animals right in the place in the market where we believe the spillover occurred, all that data has, you know, led me to a place where, you know, I don't see how it's even possible that, you know, one could consider lab origin anymore. It's just, you know, too many things point to the natural origin.

Q And as you said, for you, this is a settled question from a science point of view.

A Myself and I think quite a few other scientists.

Q Great. When we think about preventing the next pandemic, so the -- the subcommittee is all about preventing the next pandemic and being able to react and prepare in a way that reflects lessons learned from the previous pandemic. You have touched on this a little bit previously. Could you sketch for us some steps that you think would be useful for us to take that reflect thought about laboratory safety and wildlife-related issues and any other issue that you think is pertinent?

A I can, sure. First of all, I think that we should separate those two issues, okay. I mean, laboratory safety, biosafety, biosecurity, bioweapons, that's all a very important and, you know, thing that we should deal with, you know, as a, you know, not only just in the United States but as a global community. We need to look at that. We need to rethink some of the things that have been done in the past and that we will do going forward.

But I'd really like to see that separated from the origin question, because there's -- there's -- you know, there's no evidence that, you know, this is anything that was manipulated in a laboratory. So let's have the conversation about, you know, lab safety. That's great.

I'm a virologist. That kind of thing affects me every day. I have students and colleagues and, you know, people I care about that work with these viruses that, you

know, if there was an accident, you know, there's a good chance that the person could die. There's a good chance that, you know -- I mean, I work with them too. So, you know, we're very careful about it.

It's a very personal thing to me, this issue of biosafety and biosecurity. And I think it is for -- you know, for all people that work with viruses that, particularly at, you know, biosafety level 3, biosafety level 4.

So, you know, let's talk about that. But, you know, let's separate it, I would hope, from, you know, these other issues, which, you know, are really in that sense kind of a distraction from actually getting to where we need to be on biosafety and biosecurity.

In terms of the wildlife trade, I mean, there are a few obvious things that we could do. I think I touched on some of these things before. I mean, I personally think that that trade needs to be more highly regulated. There are things that we could do. I mean, and it's not just in China. It's in other countries. I mean, there are wet markets in -- you know, in cities all over the world. Even right here in Louisiana we have markets that sell animals that are trapped in the wild. And, you know, that needs to -- you know, we need take a look at that, you know, from the potential of that being a place where, you know, viruses from these animals can spill over to people.

So let's look at that. Let's see what the, you know, what the risk factors are. There's some science that can be done at that animal-human interface. We need to know, you know, what viruses are there. We need to set up systems where, you know, people that interact with wild animals are, you know, at least surveyed, find out what viruses are out there.

And the wildlife trade itself needs to be better regulated. I mean, we can -- I mean, I'm not going to say that we need to totally shut it down. There are people that

will say that it does need to be shut down. But it's, you know, it's part of people's culture.

So let's not -- you know, let's see what can be done on a, you know, on a regulatory level, monitoring these farms, probably shutting down the illegal trade of the animals, because that is a higher risk, and monitoring the places where these animals are sold to see that, you know, if the humans and the animals are getting sick and, if they are, what are they getting.

Mr. Pellegrini. I appreciate it. Thank you.

We can go off the record. That's all I have.

[Recess.]

Mr. Benzine. We can go back on the record.

BY MR. BENZINE:

Q So I want to shift gears and talk a little bit about what minority staff has been asking you about, the conference call and the drafting of the paper of proximal origins.

I'm going to -- it's likely I introduce exhibits that are similar to what you've already seen, if not exactly the same. So we'll just -- we'll keep running. But when I reference it, it will be referenced in a majority exhibit number.

So I'm going to go ahead and introduce majority exhibit 12.

[Garry Majority Exhibit No. 12
Was marked for identification.]

BY MR. BENZINE:

Q So this is a long email chain. The first one, which we're not going to pay a lot of attention to, is between Dr. Farrar, Dr. Fauci, and Dr. Tabak. It is Bates numbered SSCP_NIH0759 through SSCP_NIH000768.

And I want to flip to the last page, 768. They're double-sided, so you can just flip it on over.

A Oh, okay.

Q And as has already been discussed a little bit, this is the agenda and roster for a teleconference taking place on February 1st, 2020. Your name is listed on the roster. But just for the record, were you on this call?

A I was.

Q How were you invited to the call?

A I believe I received an email from Jeremy Farrar.

Q Okay. Was -- to the best of your recollection, what day was that?

A Probably the day before or --

Q Okay.

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

Q Were there any subsequent calls involving this group regarding the origins of COVID?

A If there were this particular group, I wasn't invited to them.

Q Okay. Were there subsequent calls with various delineations of people in this group about the origins of COVID?

A Well, yes, I had multiple interactions with Kristian Andersen, Eddie Holmes, and Andrew Rambaut. We wrote the proximal origins paper.

Q But no follow-up calls or teleconferences or Zooms that included Dr. Collins, Dr. Fauci, or Dr. Tabak?

A No, not that I was invited to.

Q We're going to keep this handy, but -- actually, no, we're going to stay right here and move to page 761. And in the middle there it says -- this is an email from

Dr. Farrar to Dr. Collins, Dr. Fauci, and -- or excuse me. It's an email from Dr. Farrar, yeah, to Dr. Collins, Dr. Fauci, and Dr. Tabak. And it includes notes from various people on the conference call.

It says on the middle of the page there, "From Bob." Is that you?

A That's me.

Q So, obviously, this is kind of a compilation of your notes. I note from other emails I think this is two emails that Dr. Farrar pushed into one. But to the best of your recollection, is -- are these your words?

A What follows from "From Bob"?

Q Uh-huh.

A I mean, they're at least a very close approximation, yes.

Q Okay. It's not Dr. Farrar going off on a limb and putting your name on it?

A No.

Q Okay. I want to keep this one out but turn to discussing the genesis drafting and publication of proximal origins of SARS-CoV-2 of which you are a coauthor with Dr. Andersen, Dr. Lipkin, Dr. Holmes, and Dr. Rambaut.

For the record, this has been one of the most influential papers on origins of COVID-19 that's been published. By a few days ago, it's been accessed over 6 million times, cited in other publications 3,000 times. It's the second most influential article of a similar age across all topics and all journals, and it is the most influential article of a similar age across all topics published in Nature Medicine.

Can you briefly describe the origination of the idea for drafting a paper and who first had that idea?

A I'm trying to -- I mean, ever since the sequence appeared in -- on Virological on January the 10th, you know, there were virologists that were looking at that sequence

and thinking the same question that a lot of people were thinking is: Where did this virus come from?

And, of course, you know, I have my circle of people that I collaborate closely with, including Kristian Andersen and other people here in New Orleans.

So the idea of taking a deep dive into the whole topic and maybe writing a paper on it probably emerged fairly early in the whole process, because these are interests that -- that I've had for a long time. You know, viruses, you know, how do they evolve? The spike proteins and various things like that, these are -- we had done some of the similar types of work with the original SARS spike. And, you know, so these were things that we were thinking about and talking about just, you know, with a new opportunity, a new virus.

When did the idea of proximal origins coalesce? I think that was the second part --

Q Uh-huh.

A -- of your question. 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. But I think if you go through some of the emails, you'll see there's questions about timing and appropriateness and when would this be done and by whom and all that kind of thing that were all considerations.

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. A few things happened. You know, the pangolin coronavirus sequence came out. You know, the teleconference itself, you know, got us thinking. And, you know, we were consulting with some of the best, you know, scientific minds on the planet there, thinking about this.

And so, you know, the idea of writing a paper just became more and more, more viable over time. And at some point, you know, I think the consensus of those four people -- Eddie, myself -- Eddie Holmes and Kristian Andersen, Andrew Rambaut, myself -- was, yeah, we probably have enough to write a pretty decent paper that, you know, would be important and impactful and, you know, at least set some of the boundaries of, you know, of the discussion about where this virus may or may not have come from.

Q Was the idea of publishing something, a paper, a report, however you want to characterize it, discussed on the February 1st conference call, or was it coalesced with you four afterwards?

A You know, honestly, I don't remember the details. I don't know if the idea -- I can't say one way or the other whether the idea of writing a paper came up or not because I just don't remember that level of detail of the conversation.

Certainly, you know, in the days that followed that conference, the four people that I mentioned -- Eddie Holmes, Andrew Rambaut, Kristian Andersen, myself -- I said, well, this is a group that could probably do something along those way -- along those lines. And, you know, we have the expertise, you know, different areas of expertise but enough to probably at least consider it.

Q On the conference call, the roster has -- I believe it's just Dr. Fauci on it.

A Uh-huh.

Q Was Dr. Fauci actually on the call?

A He was.

Q Did he say anything?

A He didn't say a whole lot.

Q To your recollection --

A To my recollection.

Q -- what did he say?

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 So that was my next question. Dr. Collins is not on the roster. 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.

Q While -- while the idea of a paper or some other kind of published work was coming to -- coming to fruition, did you communicate about it over any sources other than email?

A We eventually set up a Slack channel.

Q Okay. In --

A I mean, just to be complete, you know, we set up a Google Doc to actually write the paper --

Q Uh-huh.

A -- which is another way to communicate.

Q Was there extensive communication over Slack? I saw Slack referenced in the emails a little bit. Were there things -- what was the difference in the communication between the Slack channel and the email communication?

A I mean, there was probably more on the Slack channel than on email just because it's a, you know, it's a more efficient way to communicate than email. Email's a little clunky.

Q Yeah. Sticking with kind of like how the paper came to be in a little bit on the call, in a January 2022 Intercept article, after the Oversight Committee released a letter with the unredacted versions of these emails, you gave a quote that said: The major feedback we got from the February 1st teleconference was, number one, don't try to write a paper at all. It's unnecessary. Or, number two, if you do write it, don't mention a lab origin, as that will just add fuel to the conspiracists.

For clarification, you added after publication: One thing that could be misconstrued is that neither Dr. Fauci or Dr. Collins suggested in any way that we not write the proximal origin paper. Likewise, neither one suggested that we not mention the possibility of a lab origin. These were comments from others in emails after the call.

I'm just going to run through a couple of quick questions.

To your recollection, did Dr. Fauci ever direct either explicitly or implicitly you and your coauthors to draft a paper regarding the origins of COVID-19?

A He never directed that to me. Okay. So I -- he never said, Bob, write the paper. I never got that communication. I'm not privy to all the communications that

Dr. Fauci had with the other authors.

Q Okay.

A But for me, no. And I never heard of any other communications.

Q To your knowledge and recollection, did Dr. Collins ever direct either explicitly or implicitly you and your coauthors to draft a paper regarding the origins of COVID-19?

A So basically same answer. He never directed me to do it. I never heard that he had done that from any of the other coauthors, but I'm not privy to all their conversations.

Q Same one, one more time. To your knowledge and recollection, did Dr. Farrar ever direct or -- ever direct either explicitly or implicitly you and your coauthors to draft a paper regarding the origins of COVID-19?

A Well, I suppose how you would construe that, he did advise us that, you know, it probably would be a good idea to write one. Did he -- you know, he doesn't have the capacity to order us to do that or anything like that. But, you know, as a scientist, as a friend of some of the authors, he said, Hey, look, this is something you guys should probably do and do it well. So why not go ahead and do it? But did he order us? Did he offer us grants? No.

Q Were any of your coauthors hesitant to publish the paper?

A I mean, you know, it's -- for one, it's a fairly big undertaking and it's already turning into sort of a contentious area. So I think, you know, various people, you know, Kristian Andersen, Eddie Holmes, Andrew Rambaut, myself, I mean, you know, we're all careful scientists, right. But, you know, it's -- sometimes, you know, wading into an area like this might, you know, be time-consuming, and we're doing other things, so maybe a little hesitancy there. And I do believe that, you know, at least initially, you know, for at

least a week or so after the call, it was really uncertain whether we should or shouldn't, you know.

And I think during that period of time it really came down to what data was available, what information we thought we could piece together. And I didn't -- I'd mentioned this a couple of times, that we got that pangolin sequence, which I think really was the sort of the impetus to say, okay, well, here, you know, we've got -- probably got enough that we can make a, you know, a reasonable contribution.

Q Was -- was there any hesitation after it was drafted? Not just leading up, not like the work product, but was there any hesitation about publication after it was drafted?

A Not to my recollection but, you know, I mean, you're always -- I mean, you know, people second-guess themselves sometimes. But I don't recall that happening in this case.

Q So your comment to the Intercept, is that on the call? That --

A Uh-huh.

Q -- granted, not Dr. Fauci or Dr. Collins, but people on the call suggested do not write a paper, it's unnecessary. And maybe the same or others said, if you do write it, don't mention a lab origin as that will just add fuel to the conspiracists.

Do you recall who said writing a paper was unnecessary?

A Some of the most strong advocates of the natural origin on the call that had already sort of made up their minds based on, you know, their own reading of the situation. So I would say that would include Christian Drosten, Ron Fouchier, and Mary Koopmans.

I don't recall exactly who said what, you know. I do just recall that, you know, there was a consens -- that those -- amongst those three, they said it's not necessary.

This is clearly a natural virus. And I don't actually recall which one of them said the second thing about the fueling the conspiracists, but it was one of those three.

Q Okay. So it was a combination --

A I mean, we're on a vid -- we're not on a Zoom call or anything like that. You can't tell who it is. So, you know, it could have been one of the males. It could have been Marion. I don't know.

Q All right. But one of those three --

A Yeah.

Q -- some combination therein for those two comments?

A Yeah.

Q Okay. Thank you.

A It was probably either Christian or Ron Fouchier, because Marion wasn't on the entire call.

Q And then --

A She also had a social thing going on. It was a Saturday, if you recall.

Q Yeah. And that's Christian Drosten, not Kristian Andersen.

A Correct.

Q Correct. Okay.

Mr. Benzine. I'd like to introduce majority exhibit 13.

[Garry Majority Exhibit No. 13
Was marked for identification.]

BY MR. BENZINE:

Q It should look very familiar to you. It is a copy of the final publication entitled, "The proximal origin of SARS-CoV-2."

A I'm just going to sign it for you. Oh, it's not a pen. Oh, okay. I need one

with an autograph pen. Sorry.

Q And we'll need -- we'll need exhibit 12 throughout this conversation. So we'll be kind of going back and forth.

A Okay.

Q So like I said, this is the final published paper entitled, "The proximal origin of SARS-CoV-2," in Nature Medicine.

Can you very briefly -- and we'll get into more details -- describe the process of drafting this paper.

A I can. The first draft was made by Kristian Andersen. And it was made somewhere around -- you know, I mean, actually it started before that February 1st teleconference. Some notes and things were jotted down. I mean, exactly when it sort of coalesced into something that, you know, might be considered the progenitor of this paper probably happened a few days later or so. But by February 4th, we had a fairly robust draft or Kristian at least had written some notes and things down into something that was started to look like a report of some kind.

Q Had the pangolin RBD sequences come out by February 4th?

A Somewhere around that time we knew that they existed. I'm not sure that we actually got the sequences until a few days later.

Q Okay. First, the paper eliminates a laboratory construct or a purposefully manipulated virus. Is that correct?

A I think the wording is very unlikely or --

Q "Clearly show."

A -- "clearly show." Okay. Okay.

Q "Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus."

A I agree with that.

Q Do you stand by that statement?

A I do.

Q Does that -- that would include genetic engineering, correct?

A Yes.

Q Okay. I would like to introduce what is going to be majority exhibit 14.

[Garry Majority Exhibit No. 14

Was marked for identification.]

BY MR. BENZINE:

Q This is an email chain between yourself and others, including Dr. Collins and a couple of others. The -- I want to flip to the page marked 223, all the way on the -- oh, this got printed backwards. So the front page is actually the back page.

A Oh, okay.

Q So we'll just have to creatively work around the staple.

A Okay.

Q But it is Bates marked Garry 000223 through Garry 000226. And at the bottom of what is the first page, 22 -- or at the top, 223, there's an email from Dr. Rambaut. And the last paragraph says: The sequence data clearly and unambiguously rules out any form of lab construct or engineering of the virus.

Do you agree with that statement?

A Okay. So you're talking about the paragraph at the top, the first --

Q I'm sorry. The last paragraph on the page, it starts with, "I disagree with Ron."

A Okay.

Q The second sentence says: The sequence data clearly and unambiguously

rules out any form of lab construct or engineering of the virus.

A I mean, I think that is correct.

Mr. Jacobs. Mitch, I'm sorry. Can you -- this looks like it's kind of broken mid -- like as if 222 might be another --

Mr. Benzine. No, this is the first page of this one.

Mr. Jordan. Is it? Okay.

Mr. Benzine. Yeah. It's just stapled back --

Mr. Jacobs. No, I realize it's stapled backwards, but it just seems like that email subject to the "Re" would get a reply. I just didn't know if they --

Mr. Benzine. It's on the next page.

Mr. Jacobs. That's 224.

Mr. Benzine. Can we go off the record for just a second?

[Discussion off the record.]

Mr. Benzine. We can go back on the record.

BY MR. BENZINE:

Q I'll re-ask the question. So at the bottom of page marked 223, there's an email from Dr. Rambaut. And in the last paragraph, he says: The sequence data clearly and unambiguously rules out any form of lab construct or engineering of the virus.

Do you agree with that statement?

A I do agree with that statement.

Q The next email up, this time from Dr. Fouchier, he says: I do not understand Andrew's argument, "The sequence data clearly and unambiguously rules out any form of lab construct or engineering in the virus." Molecular biologists like myself can generate perfect copies of viruses without leaving a trace. The arguments for and against passaging and engineering are the same if you ask me.

What does he mean by molecular biologists can generate perfect copies of viruses without leaving a trace?

A I mean, he's simply just stating that the technology's evolved to the point where you can basically synthesize any gene that you want to sequence, whatever sequence you want. You can program the machine to synthesize those nucleotides in the order that you want.

So, I mean, it's a little bit of a non sequitur. I don't -- I mean, I don't agree with, you know, the sort of the general principle there. I do think that there are other arguments that we were using to rule out the possibility that this was a lab construct or a genetically engineered virus.

So, you know, I mean, it's a little hard in the context of all things. I mean, Ron Fouchier's obviously a very, you know, strong scientist. I'd probably agree with most things that he said. I just, in this context, I don't think he's fully understanding what we were trying to get across with that -- with that statement that it was paraphrased at least and similarly -- or at least something similar appears in the manuscript.

Q But -- so Dr. Fouchier's argument is that you can't just look at the sequence of the virus to know that it's -- to rule out genetic engineering?

A Again, I wouldn't want to put words into his mouth. I think, you know, you have to take what he said here. He's making a true statement. You can't actually synthesize things. But he also goes on to say that, you know, that there are arguments against passage and engineering. He's just basically saying that, you know, they're all the same. So maybe he -- I don't really want -- you know --

Q Uh-huh.

A -- I can't put words into his mouth. I think he's basically agreeing with us but maybe for other reasons.

Q Okay. I would also now like to introduce what will be 15 and hopefully stapled better so that we --

[Garry Majority Exhibit No. 15
Was marked for identification.]

BY MR. BENZINE:

Q So these are some of the mentioned Slack communications between you and your coauthors.

Flipping to the page marked REV0002876 --

A Okay.

Q -- there's a message from -- and this is a Slack conversation dated February 7th, 2020. There's a message from you first at the bottom: I'm thinking mostly about the PRRA to generate the furin site.

What is PRRA?

A Proline-Arginine-Arginine-Alanine. It's the amino acids that are encoded by -- at least partly encoded by the 12 nucleotide insertion into the area that we call the furin cleavage site --

Q Okay.

A -- at least in the gene level, like the nucleotide level.

Q And then you said: Relatively easy to drop 12 bases in.

What does that mean?

A It means that you could -- there are various methods of genetic engineering or actually just synthesizing the sequences that could allow you to modify a genome and put 12 nucleotides anywhere you want to.

Q Your -- another message on this chain from a little bit earlier is, you say: You can also synthesize bits of the genes de novo with perfect precision then add them

back in without a trace.

Is that similar to what Dr. Fouchier was talking about?

A It's similar, yeah.

Q What is -- what do you mean by "synthesize bits of the genes de novo"?

A You can now -- there are machines that exist and services, scientific companies that are built around the idea that you can just type out a nucleotide sequence, and then that machine will add the sequences, make you little bits of the RNA synthetically.

Q And --

A And more than a little bit; you know, like thousands of nucleotides actually.

Q What do you mean by "without a trace"?

A So it's referring to the -- sort of the old way, old way in a sense that one might do this, which is using other cloning methods.

So in the old days we didn't have these fancy machines that could just synthesize nucleotides. You had to use a technique called polymerase chain reaction to synthesize, you know, those kind of nucleotides and put them together. And you used old sort of methods to kind of stitch the sequences together, so restriction enzymes that cut sequences at different places and a lot more involved than what is -- you know, what's possible to do these days.

Q So prior to this new technology, genetically engineering or inserting bits of genes de novo would leave a trace?

A I mean, yes, and most likely it would, yeah. If you really knew what -- you know, how this was done, you could probably figure it out, yeah.

Q And but now you could do it without anyone knowing.

A Potentially.

Q So how would you be able to rule out genetic engineering based off the sequence on its own?

A Well, not -- not by looking for those traces of, you know, of the engineering, the splicing or putting together, but other methods which involve looking at similar other viruses, you know, seeing that site, you know, had its natural -- or, you know, the different parts of the genome had similar sequences in other viruses, and looking at the phylogenetics of the virus, you know, understanding that that -- you know, which, you know, we were able to do by comparing them, that that site is very frequently modified and changed in other viruses.

I've said it before a couple of times but the, you know, the cleavage sites change and come in and out of these viruses all the time during evolution. So this looked like that had happened in the case of SARS-CoV-2.

Q Would it be possible -- just in summary, would it be possible to generate a furin site in a lab, insert it into a virus without anyone but the laboratory technician knowing?

A Yes.

Q Thank you.

As minority counsel has talked about, going back to majority exhibit 13, the published version of proximal origins, there were kind of three -- and you can correct me if I'm wrong, as one of the named authors -- but three kind of primary reasons you came to the conclusion that COVID-19 was a naturally emerging virus: The presence of a nonoptimal receptor-binding domain, the presence of -- and that receptor-binding domain subsequently showing up in other virus sequences; the presence of furin cleavage sites in related coronaviruses; and the thought that any manipulation would have used a preexisting backbone.

Do you agree with that characterization?

A I -- we -- I agreed with it then and I agree with it now, yeah.

Q Okay. I want to talk about each of these and kind of how your thought process evolved and changed.

So the receptor -- for the receptor-binding domain, the paper said that it was not ideal. It was suboptimal. It wouldn't have been what, in essence, like a perfect RBD would be. Is that correct?

A Not precisely. I think that would be the computer predictions, okay. If they took that sequence and ran it through their binding algorithms, that would have been predicted not to be a very good binder. But, in fact, the amino acid sequences is a very good binder. It binds to the ACE2 very well.

So, you know, computers or a scientist working in a lab would have, you know, seen that -- you know, they wouldn't have thought that it would align that site because their computers would have told them it's not going to work very well.

Q Would there be a reason to design a suboptimal site?

A Not that I can think of.

Q Okay. We're going to do some flipping back and forth to majority exhibit 12.

A Is that the Slack?

Q No, it's the notes from after the conference call.

A Oh, okay. All right.

Q Going back to your section of the notes on the page marked 761 --

A Okay.

Q -- you start with: Before I left for the ball, I aligned nCoV with the 96 percent bat CoV sequence 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.

I think you said this before, but just for the record, this was during Mardi Gras season. That's the ball that you're referencing?

A It was. It was the Nyx ball. So, I mean, that Nyx comes up again, right, except this is N-y-x.

Q Is the nCoV referenced in here SARS-CoV-2 or COVID-19?

A It is. That's what we call the backbone.

Q NCoV being novel coronavirus?

A That's right.

Q Is the bat CoV at the WIV you referenced RaTG13?

A It is.

Q Can you kind of explain your thought process in the statement and what went through your mind with the RBD and the S protein being essentially identical outside of the furin sites?

A Sure. So let me put it into a little bit of context. I mean, this was, you know, during, you know, some -- I mean, there are probably Slack messages that correspond to that time, I would guess. But, you know, we're having discussions back and forth. And in this email I was basically playing the devil's advocate for, you know, was the furin cleavage site engineered or not.

And so I think you have to put this -- you know, these paragraphs which I typed up on my little iPhone there, into context and realize I was sitting at this Mardi Gras ball in the evening with an open bar. And so, you know, I was basically just saying, look, it looks unusual if you just look at it, you know, in that context. Twelve nucleotides, you know, it looks like it's just kind of popped in there if you only compare it to the RaTG13

sequence and, yeah, you could probably do it, you know. And then I, you know, went on to say that, you know, it doesn't seem likely that you'd use an existing clone of SARS-CoV-2 or of SARS or MERS.

And as, you know, Ron Fouchier said, you know, the techniques exist now. You can -- you know, you can put any mutations where you're interested in. So, you know, this was sort of my putting on the, you know, okay, maybe it did come from a lab hat and trying to make that argument, which we were basically stress testing, you know, for the paper.

Q Was your first blush of the receptor-binding domain that it was unique or interesting?

A Only because of the fact that there wasn't an analogous one in any coronavirus yet that, you know, was in this sort of subfamily.

Q What was the new science or data that changed your mind?

A So that happened over time. But, you know, immediately to this was the pangolin coronavirus, which had a receptor-binding domain that was very, very similar, especially in those critical amino acids.

Mr. Benzine. I want to introduce majority exhibit 15.

Ms. Gardner. Sixteen.

Mr. Benzine. Sixteen. Thank you. It's usually Giancarlo that catches my --

Mr. Pellegrini. I like to give other people the opportunity.

[Garry Majority Exhibit No. 16

Was marked for identification.]

BY MR. BENZINE:

Q So these are peer review questions and answers regarding the proximal origin paper from Dr. Andersen. Have you ever seen these before today?

A I have.

Q Did you help craft the answers to the questions?

A I did.

Q Both referees bring up the pangolin sequences in their questions.

A Uh-huh.

[2:47 p.m.]

BY MR. BENZINE:

Q The one on the first page.

Question 6: "There are two recent reports about coronaviruses in pangolins. The authors might want to comment on these."

And the response is that "... we should point out that these additional pangolin CoV sequences do not further clarify the different scenarios discussed in our manuscript. There is nothing in these reports that changes our statements regarding a potential role of pangolins."

What does that mean?

A So we had already included the pangolin coronavirus -- a pangolin coronavirus sequence in the manuscript. It was already in Figure 1, I believe. And there were a few other pangolin sequences that came out while this manuscript was being reviewed. And all we're pointing out is that, you know, additional sequences don't change our original thinking about the importance of those pangolin sequences.

Q Okay.

Going to Referee No. 2, starting on page 3 and going to page 4 -- just a moment. I lost my spot.

Excuse me. Back to page 3. There's the first question.

A Okay.

Q The first question from Referee 2 brings up the pangolin sequences again.

And the beginning of the second paragraph reads, "Unfortunately, the newly available pangolin sequences do not elucidate the origin of SARS-CoV-2 or refute a lab origin. To clarify, while the RBD from the Guangdong pangolin CoVs is the closest to

that found SARS-CoV-2, they are more divergent in the remainder of the viral genome...and do not possess the polybasic cleavage site insertion. Hence, there is no evidence on present data that the pangolin CoVs are directly related to the COVID-19 epidemic."

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, you know, the virus was natural or from a lab.

I mean -- and I don't think that we -- you know, I think we leave both of those possibilities open in the manuscript, the "Proximal Origins" paper, the way it was written. I mean, yes, we say that the lab origin is not very likely, or words to that effect, but, you know, we don't totally rule it out.

So, you know, I think what we're saying is that the reviewer is basically putting words into our mouth that we didn't actually say, so we're trying to correct that.

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.

And so we just make the fairly obvious statement, I think, that, you know, the pangolins are probably not, you know -- at least these coronaviruses that we know, they didn't touch off the COVID-19 pandemic. That's all we're trying to say.

Q It reads -- and I don't want to put words in your mouth --

A Right.

Q -- that the pangolin data doesn't eliminate the chance that the RBD is

laboratory-generated.

A By itself, it does not.

Q How do you eliminate laboratory origination for the receptor binding domains and if not for the use of the pangolin sequences?

A Well, I mean, we've talked about a few things about the receptor binding domain, I mean, one of them being that, you know, it's a pretty good binder, but, you know, computationally you would predict that that wouldn't be a good binder. That was one thing that we talked about.

I mean, the fact that you have a similar RBD in another coronavirus, this time from a pangolin, that is also very similar, points to natural origin. But there's -- I think all we're just pointing out is that we're trying to accumulate data here, and no one piece is data is going to, you know, touch the complicated topic, you know, one way or the other.

Q Can you explain one more time the RBD computer generation aspect?

A Sure.

So, you know, when two proteins come together -- my two fists are coming together now; I know that won't show up in the transcript -- but, you know, they are contact points. And those contact points are different amino acids. So there are different amino acids on the spike protein and different amino acids on the receptor, which in this case is a protein known as ACE2.

So the computer can calculate how well those amino acids interact with each other and make, you know, a generalized prediction about how well these two proteins will bind, how tightly they'll bind. I mean, what they're really calculating -- and this is really down in the weeds a bit, but, you know, they're calculating how much energy it would take to pull them apart, okay?

So, when you do that with the ACE2 protein and the SARS-CoV-2 protein, you

predict that it'd be easy to pull them apart, okay? When, in fact, when you do the actual experiment and measure that, they bind very tightly. So the computer prediction is not very good.

Q So the argument would be that, because the computer prediction is bad, scientists in a lab wouldn't want to use that situation?

A Wouldn't want to design the SARS-CoV-2 sequence -- you know, make that sequence and use it in their artificial virus.

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.

Q We can move on a little bit.

So the second data point that the paper uses is the furin cleavage site. And, just for the record, it's in some of the emails and notes to use "polybasic cleavage site" and "furin cleavage site" interchangeably?

A We did.

Q Okay.

A I mean, they can be. I mean, the arginines that are in that consequence, the RRAR, those are all basic amino acids. So "polybasic" means there's more than one.

Q And, in the paper, you say that it's likely SARS-CoV-2-like viruses with partial or full polybasic cleavage sites will be discovered in other species.

What does that mean?

A I think we were doing a little speculation there, but the speculation was that

eventually you might find a SARS-like virus that had a polybasic cleavage site.

Q Has one been found?

A No.

Q Um --

A Well, there has been one that's been found.

Q Is it COVID-19?

A It is.

Q Okay.

Back to majority exhibit 12, your notes again, on page 761, again, welcome you putting it in context.

You write -- it's three lines down in your notes -- "I really can't think of a plausible natural scenario where you get from the bat virus or one very similar to it to [novel coronavirus] 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 assume that's the junction. "I just can't figure out how this gets accomplished in nature. Do the alignment of the spikes at the amino acid level -- it's stunning. Of course in the lab it would be easy to generate the perfect 12 base insert that you wanted."

Can explain this one?

A Sure.

My thinking evolved. I've learned more about these sites, and by looking at other viruses in the, you know, coronavirus family, I've found out that, you know, this is a sequence or a place in the viral genome, in the spike protein, that is very volatile. It changes all the time.

And so that just made it -- you know, that fact makes it much more plausible that,

you know, these viruses are changing these sequences out all the time. There are lots of them that you can look at that clearly have been generated by, you know, similar processes that generated SARS-CoV-2. There's insertions, there's deletions, there's all kinds of changes that happen.

With the new variants of SARS-CoV-2 that have arisen, you know, we've got a lot of sequences from SARS viruses. I mean, there are 12 base -- 12 nucleotide insertions that have shown up in, you know, some of these variants of SARS-CoV-2. So it's not an unusual process.

Q But still no SARS-Co-Virus (ph) other than COVID-19 with a furin cleavage site?

A That is true.

Q Also in the paper -- and this was read by minority counsel as well -- you say, "Furthermore, a hypothetical generation of SARS-CoV-2 by cell culture or animal passage would have required prior isolation of a progenerator virus with very high genetic similarity, which has not been described."

Does that rest on an assumption that all of published science has been described?

A In part. But it's still, in my mind, a pretty good assumption. People have been looking for, you know, similar viruses, and none have shown up yet, so --

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

A Sure.

Q So that's possible.

The third major data point in "Proximal Origins" is the preexisting -- not using a preexisting backbone.

The paper states, "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."

Can you explain that a little bit?

A Well, people have been publishing on reverse-genetic systems, which is, you know, a way to change coronavirus sequences. Some of it's old technology, but, you know, these sequences have been manipulated in the past in other laboratories.

You know, there was no evidence that this is how SARS-CoV-2 was generated, though. None of those common features of those reverse-genetic systems were present in the virus. So restriction enzyme sites and things that, you know, might be used to swap pieces of a genome, none of that was present.

Q Does that contradict Dr. Fouchier's and your previous statements that you could create these insertions without a trace?

A It just says that, you know, the common way that this would've been done doesn't appear to have been done. You could use -- you could completely synthesize a brand-new genome, which I think was the point that Dr. Fouchier was making.

But it wouldn't be the way that, you know, for example, the Wuhan Institute of Virology was swapping sequences in and out. They weren't completely de novo synthesizing, you know, whole viruses or whole stretches of viruses. They were using the old cloning technique to do their recombination-type experiments.

Q Do you know if they had the capability?

A To sequence and create a virus completely --

Q Not necessarily a whole synthetic virus, but the capability to create an insert.

A Yeah, most certainly they do.

Q Okay.

Going back to the notes after the conference call, in your left hand, at the very bottom of your section, you write, "You were doing gain of function research you would NOT use an existing clone of sars or mersv. These viruses are already human pathogens. What you would do is clone a bat virus that had not yet emerged. Maybe then pass it in human cells for a while to lock in the rbs" -- is that supposed to be "RBD"?

A It probably is.

Q Okay.

A Yeah.

Q "... then you reclone and put in the mutations you are interested -- one of the first a polybasic cleavage site."

What does this statement mean?

A Again, I think I need to put it into the context that this was like: Okay, Bob, what would you do if you were actually cloning this virus? And this is the response.

I mean, I think that, you know, SARS itself already, you know, had, like, a 10-percent mortality rate; MERS coronavirus, the Middle Eastern respiratory syndrome virus, about a 30-percent mortality rate. So you wouldn't use those viruses. They're already -- you know, they're already quite capable pathogens.

But if, you know, you were a terrorist, you might pick a virus that hadn't been known. Because if you picked a known one, there are already countermeasures to it. So you might pick an unusual one, and then, you know, try to do something nefarious with it.

That's all I was saying. I mean, it's pretty common. I mean, this is what people in the biodefense area think about, you know.

Q Does the argument that COVID-19 would've used a previously used backbone, does that rest on an assumption, as well, that all viral backbones are

published?

A It does.

Q Okay.

We are 5 minutes before the hour. We can take a 5-minute break. I don't know if Giancarlo has any more questions.

Mr. Pellegrini. I have a few questions after a 5-minute break. It will not be close to an hour, but I would appreciate the 5 minutes in between, if that's okay.

Mr. Benzine. Perfect.

We can go off the record then.

[Recess.]

Mr. Pellegrini. We can go back on the record.

BY MR. PELLEGRINI:

Q So, Dr. Garry, I just want to ask a couple of clarifying questions about items that we have previously discussed. We previously discussed a State Department document that made reference to the possibility of illnesses at the Wuhan Institute of Virology. We discussed the plausibility of that claim, one way or the other.

What I did just want to do is take a look at the declassified intelligence community origins assessment, which I will introduce as minority exhibit Q, I believe.

[Garry Minority Exhibit Q
Was marked for identification.]

BY MR. PELLEGRINI:

Q This is a 17-page document. I will not ask you to read from the document. Are you generally familiar with it or have you seen it before?

A I have seen it before. I'm generally familiar with it.

Q Great.

If I could just take you to page 8 of that document. And in the upper right-hand corner of page 8, there is a box of text related to the illnesses. And if I could, I'll just read that box out loud.

It says, with a header, "WIV Illnesses in Fall 2019 Not Diagnostic": "The IC" -- intelligence community -- "assesses that information indicating that several WIV researchers reported symptoms consistent with COVID-19 in autumn 2019 is not diagnostic of the pandemic's origins. Even if confirmed, hospital admission alone would not be diagnostic of COVID-19 infection."

So I think my colleague, the majority counsel, did allude to this, but I just wanted to confirm: Do you share my understanding, when reading that, that this report is taking the position that, even if it were known to be true that these illnesses occurred and even if those illnesses resulted in hospital admission, that in and of itself would still not tell us whether or not the virus originated in that particular laboratory?

A That's my understanding.

Q Okay. Great.

That's all for that document.

If I could ask you to look at minority exhibit C that was previously handed out. I'll give you a moment.

A Okay.

Mr. Jacobs. That's at GARRY 45, right?

Mr. Pellegrini. It is.

BY MR. PELLEGRINI:

Q And so, for recollection, this is an email chain with attendees on the February 1st conference call.

And if I could direct your attention to the page that's Bates stamped GARRY 47.

That's the third page of the document.

A Got it.

Q So there's a long email that really takes up most of that page by Dr. Ron Fouchier, who we discussed a little bit.

And the context I'd like to set for my question is: There was previously a discussion about the extent to which attendees on that call may have suggested, "Well, I don't think you need to write a paper, and if you do write a paper, I don't think you should talk about lab origin" and various reasons that folks may have said that.

If I recall, I think from your end, you had said, well, here are three different folks who may have sort of made comments along those lines. I think one of them was Dr. Fouchier, if I recall correctly. Is that right?

A That's correct.

Q Great.

So, in this email that Dr. Fouchier sends -- I think what I'll do is just read an excerpt of it. In the middle of the page, the paragraph under the header "Ron's notes," I'll just read that paragraph.

"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 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. At present, the arguments that nCoV-2019 could have emerged from an animal source is much stronger than other possibilities."

Is it possible that that remark from Dr. Fouchier is what we're thinking of when we

think that folks, either during the call or after the call, may have said, "Hey, you shouldn't talk about a lab origin," that that might be part of what that recollection is?

A It's certainly part of it. Obviously, we didn't follow this advice, because in "Proximal Origins" we wrote about the potential for a lab origin.

Q Right. Right. And, to be clear, Dr. Fouchier -- I don't know if I'm pronouncing that correctly.

A "Fouchier."

Q "Fouchier."

A Yeah.

Q Okay. Where is he from?

A He is from Erasmus Medical Center in -- I guess that's the Netherlands.

Q Is he Dutch?

A He's Dutch.

Q Okay. So not American. Certainly not associated with the NIH in any manner. In other words, he doesn't work at the NIH?

A That's true.

Q All right.

I think that's all we had for this round, and we can go off the record.

[Recess.]

Mr. Benzine. Okay. We can go on the record.

BY MR. BENZINE:

Q So I want to talk about Dr. Lipkin and Dr. Farzan for a little bit.

A Okay.

Q Do you know or recall how Dr. Lipkin got added as an author?

A Only vaguely.

I think, when we were writing the paper, somebody said, maybe we need, you know, another set of eyes on this paper just to make sure that we've got, you know, all of our facts correct, somebody that, you know, knew the coronavirus literature pretty well.

I believe it was Eddie Holmes, who's a friend of Ian Lipkin, who suggested him. And, you know, there was some discussion -- I think you've seen some of the email back and forth -- about that, but I think the consensus was, sure, he would be a good person. He's written some nice papers about coronaviruses before, especially MERS coronavirus, so let's invite him on to take a look.

And he did. He came on. He read the paper many times and made some good comments back and forth and, you know, certainly made a nice authorship contribution.

Q Was Dr. Lipkin on the conference call?

A No.

Q Do you know -- and just if you know -- do you know Dr. Holmes' and Dr. Lipkin's current relationship?

A I don't know.

Q Okay.

I would like to introduce majority exhibit 17.

[Garry Majority Exhibit No. 17
Was marked for identification.]

BY MR. BENZINE:

Q This is an email chain between yourself, Dr. Holmes, Dr. Andersen, and Dr. Rambaut. It's Bates numbered GARRY0000272 through GARRY0000274.

And I want to turn attention to page 273. Dr. Holmes, at the email at the bottom page from Dr. Holmes, writes about Dr. Lipkin, "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" -- meaning "gain of function" -- "I think it adds weight. Happy to be over-ruled though."

Do you agree generally with that statement, that -- adding him for gravitas and his involvement in gain of function?

A 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 if I agree with every rationale there. I'm not sure that the GOF really adds much weight.

But, you know, I think, I mean, overall, I thought it was a perfectly reasonable thing to do, to add him as an author. And, you know, having somebody else with expertise in the area to look at the paper was certainly a good thing.

Q Flipping to 272, the first page, the very top email, you say, "Yes very interesting -- publish! I predict Kristian will soon have better dN/dS data to add productively to the mix as well. Stay agnostic...hope Ian can as well."

What did you mean by that?

A We had discussed many times about the need to examine all this data without being influenced by all the, sort of, chatter and noise that was going on, all the conspiracy theories that were being bandied about and to just focus on the data. And so that's what this comment represents.

Q Did you have any reason to believe that Dr. Lipkin wasn't agnostic or leaning to one way or another?

A I think I was just making a general comment that, you know, he would go along with, sort of, our approach to the whole paper and not bring other extraneous things into it. We were trying to focus on the actual science.

Q Okay.

I want to go ahead and introduce majority exhibit 18.

[Garry Majority Exhibit No. 18

Was marked for identification.]

BY MR. BENZINE:

Q This is another email chain between you, Dr. Holmes, Dr. Rambaut, and Dr. Andersen, Bates numbered GARRY0000263 through GARRY0000264.

On the back page, the very bottom email from Dr. Holmes reads, "Ian Lipkin just called -- very worried about the furin cleavage site and says that high ups are as well, inc. intel. Also saw the restriction site."

Keeping that email in mind, flipping back over to the top email from you, the second line is, "But if Lipkin says higher ups are concerned and Intel involved it's consistent with all we know too."

Who do you think the higher-ups are that you, Holmes, and Lipkin are referencing?

A I'm not sure about the other two. You know, I don't want to speculate on who their higher-ups were. But, I mean, I was aware that there were people that were discussing the potential origins and, you know, a possible lab origin at, you know, different government agencies.

Q This was after the conference call. Did the higher-ups include Dr. Fauci and Dr. Collins?

A I don't think that's who I was thinking about here. I think it was people at other places.

Q Can you explain a little bit more?

A Well, for one, I knew that, you know, there was discussion in the White House about where this virus had come from.

Q How did you know that?

A You know, I -- I mean, I'm fairly well-known in the virology field. I think I had gotten some calls from some folks. But I don't recall the exact details.

Q Who in the White House called you?

A I don't recall the exact details.

Q Okay.

And both Dr. Lipkin -- and you said, "Intel involved it's consistent with all we know too." What does that mean?

A Well, I mean, I think there were a lot of people that were discussing this, like I said. I'm not sure if I'm referring specifically in this email to "intel" as in, like, the intelligence community or not. I mean, I guess it's possible I was.

But, I mean, there was a lot of chatter and things going on. As I've said several times now, we were trying to keep some of that -- most of that out of our scientific evaluation of, you know, the genomes and other data that we had.

Q By February 10th, were you aware of any intelligence community involvement in the origins?

A Was I aware by February 10th? I mean, I think not directly. But I think that I had indications indirectly that that possibly was going on.

Q What were those indications?

A I mean, just for example, the call that I got from somebody at the White House. I can't remember exactly who it was or what they were doing, but it seemed to imply that there were other folks looking into this.

Q We can move on from those and move to Dr. Farzan. We'll go back to majority exhibit 13, which is the actual published version of "Proximal Origin."

A Okay.

Q On the last page, in the "Acknowledgments" section, it says, "We thank M.

Farzan for discussions." Is it your recollection that that's Michael Farzan?

A That's who it is, yes.

Q Okay. When asked during a transcribed interview if Dr. Farzan was aware that Dr. Andersen, you, Dr. Rambaut, and Dr. Holmes were going to acknowledge him at the end of the paper, he responded, "I was not aware of that prior to publication."

Did you know prior to publication that Dr. Farzan was going to be acknowledged on the paper?

A I signed off on the paper. I mean, he's not a direct colleague of mine. He's a colleague of Kristian Andersen. They're at the same institution, so --

Mr. Pellegrini. I'm sorry, Dr. Garry. Can you speak up a little bit?

Dr. Garry. I'm sorry. He's not at my institution. He's at Scripps Research, which is where Kristian Andersen is. So I didn't think too much of it when the acknowledgment was put in.

BY MR. BENZINE:

Q For the record -- and you would have probably no way of knowing this -- Dr. Farzan doesn't work at Scripps Research anymore. He works at Boston Children's Hospital.

A Oh, okay. Great. He did work there.

Q Yes, he did.

A Okay.

Q He did during this time. He worked at Scripps.

A Okay. All right. Great.

Q Did you have any discussions with Michael Farzan while drafting "Proximal Origin"?

A I did not.

Q Is it common practice to acknowledge people without their knowledge or permission?

A It's not common practice.

Q Okay. Do you have any knowledge of why Dr. Andersen would've done it in this case?

A I have no knowledge.

Q Is Dr. Farzan influential in coronaviruses and specifically SARS-related coronaviruses?

A He is. He discovered the receptor was ACE2 for the first SARS. Yeah.

Q Is it possible that Dr. Andersen, much like with Dr. Lipkin, wanted to add gravitas to the paper by acknowledging Dr. Farzan?

A I mean, you'd have to ask Dr. Andersen about that, but, you know, in the sense that anything's possible, it's possible, yeah.

Q I want to move on to the publication process of the paper and introduce majority exhibit 19.

[Garry Majority Exhibit No. 19
Was marked for identification.]

BY MR. BENZINE:

Q This is an email chain primarily -- I think entirely between Dr. Andersen and Clare Thomas from February 13th of 2020 and is Bates numbered REV0000266 through REV0000268.

Have you ever seen this email before -- these emails?

A I have not seen the emails, no.

Q Clare Thomas's email is at nature.com. Do you know what Ms. Thomas's role is?

A She's an editor.

Q Is she who you would send a paper to to be approved for publication?

A Well, you'd send it through the Nature submission system, and eventually it would probably get to her, yes.

Q Okay.

Flipping to the page marked 267, at the very top, bad grammar and spelling aside, Dr. Andersen writes, "Prompted by Jeremy Farrar, 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."

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.

Q Is that how you would read it, that the end of the "prompted" clause is after "Dr. Collins"? So it would read, "Prompted by Jeremy Farrar, Tony Fauci, and Francis Collins," space, "Dr. Holmes, Dr. Rambaut, Dr. Garry" --

A Yes, I'll concur with that. I probably would not have written it this way because -- yeah.

Q Okay.

A But, yeah, Kristian is -- go ask --

Q It's confusing grammar, but I --

A -- go ask him. Yeah. Yeah.

Q No, absolutely.

I now want to introduce majority exhibit 20.

[Garry Majority Exhibit No. 20

Was marked for identification.]

BY MR. BENZINE:

Q This is an email out of a very large FOIA production. That's why it's cut off.

A Uh-huh.

Q In the middle is an email from Dr. Andersen on February 8, 2020. And in the middle of the middle paragraph, there's a sentence that starts with "Our main work."

And it says, "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 we have high confidence in any of the three main theories considered."

What does "disprove any type of lab theory" mean?

A Well, for background, I probably have to go really deep into the scientific method here. And so, basically, we were testing the hypothesis that the virus may have leaked from the lab.

So, you know, in the scientific method, you don't really go out to try to prove something; you try to falsify a hypothesis. That's really the only thing you can do. Proof is a mathematical concept. We're virologists; we don't really do, you know, that type of mathematical proofs and things. But we do use the scientific method. And so that means that, you know, you make a hypothesis and then you try to disprove it.

So this is -- I mean, I know it sounds a little out of sync, but, you know, this is what we were trying to do. We were trying to falsify the lab leak hypothesis.

Q Was similar work conducted to try to disprove a market theory or a zoonotic theory, or was it just the lab theory?

A I would say, yes, that, you know, we were trying to collect all the data and see where it led us, you know. And if we had found data that falsified the market origin or a natural origin, we certainly would've followed that lead too.

Q What was -- so you said that you have a hypothesis and you try to disprove it.

A Yes.

Q Was the hypothesis of proximal origin that COVID-19 leaked from a lab and you were trying to disprove it? Or was it more information gathering to try to point to the most likely origin?

A I would say the latter rather than the former. I mean, it's not a formal kind of proof paper. It's not a mathematical paper. We were just laying out the possibilities and, you know, trying to discuss them to the best of our ability, you know, make the interpretations of the science the way we felt it was going.

Q Okay.

I want to -- we're just going to keep rolling through exhibits. I want to go to majority exhibit 21.

[Garry Majority Exhibit No. 21

Was marked for identification.]

BY MR. BENZINE:

Q This is another email chain, between yourself and Dr. Holmes, Dr. Lipkin, Dr. Rambaut, and Dr. Andersen and Bates numbered GARRY0000306 through 0000310.

On the first page, on the page numbered 306, there's an email from you in the middle. Do you see that?

A Yeah.

Q And it's to this group and says, "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."

And then Dr. Holmes responds, "Oh yes, the reviewers are easy...I think this is a slam dunk."

Who are the reviewers that you wanted to include on your paper?

A Oh, gosh. I don't remember who we picked. It's been -- it's been 3 years.

Q Okay.

A I don't recall.

Q Do you remember who the reviewers were that you wanted to exclude?

A I don't recall that either. Sorry.

Q We've talked a little bit about this --

A I wasn't the corresponding author of the paper, if you remember, so it wouldn't have been something that I would've necessarily, you know, committed to memory. I didn't write the cover letter, I didn't do any of those kind of things, so --

Q Is the choice of reviewers solely of the corresponding author? Would Dr. Andersen have been the one who --

A He is the one that would probably have suggested them. But, ultimately, the choice of the reviewers is up to the editor.

Q You've touched on this a little bit, and so I apologize for the redundancy. Can you go back through how you viewed Dr. Farrar's involvement in the "Proximal Origin" process?

A Dr. Farzan?

Q No, Farrar.

A Farrar. Oh, okay.

Well, he was the person that, you know, initiated the teleconference. And he was a good friend of Eddie Holmes and, you know, was, I think, keen to have a group of scientists, or groups of scientists, examine this question of where the, you know, SARS-CoV-2/nCoV might have come from.

And, you know, it's -- you know, he's a -- you know, he is an epidemiologist. You know, he is very interested in public health. I think this was just, you know -- and he's very much connected with the Government of the United Kingdom. So all these things, you know, made him, you know, an interested player in the whole process.

Q So you were asked about that earlier, and I'll provide a summary, and you can just tell me if it's in line with your recollection: that Dr. Farrar suggested various journals, coordinated with Dr. Holmes, suggested the direction and scope of the papers, suggested drafting changes, coordinated some press and messaging, and made at least one line-by-line edit.

Does that sound like an appropriate summary?

A Yes.

Q Why wasn't Dr. Farrar credited on the paper?

A Well, we asked if he wanted to be acknowledged, and he declined.

Q Do you have any knowledge of why he declined?

A No. I don't know.

Q In your professional experience, should he have been acknowledged?

A Not if he didn't want to be. So --

Q Is --

A -- you know, it's something that you would, you know, give the person an opportunity to say yes or no.

Q Is that common, that someone could have that level of advisory role and if they don't want to be with the paper they don't have to be?

A It might be a little unusual, but, you know, we had to respect his wishes.

Q Does that, in your opinion, pose any transparency concerns, that the reader wouldn't know who was --

A Who was dir- --

Q -- who was directing the paper?

A I mean, we intended the paper to basically stand on its own, to stand on the science. And, you know, I think we did our best to make sure that we were presenting the science the best way it could be presented. I mean, those are the considerations that we had.

You know, I think the paper has sort of taken on a life of its own, as we might all acknowledge here. And so, you know, those kinds of things about transparency and all that, I don't think they would've entered into our mind. I don't think we were going to think that this paper was gonna quite, you know, end up as the sort of focal point for a lot of discussion that it actually has, so --

Q In the past, would someone of that level of involvement been an author or been acknowledged?

A I mean, I think it could've gone either way, you know, the acknowledgment. I mean, you know, I think we all thought that he definitely deserved an acknowledgment, and we asked him, and he said, well, maybe not. So --

Q You were also asked a lot about whether or not Dr. Fauci or Dr. Collins had a role similar to Dr. Farrar in this kind of oversight advisory role, and you said you didn't

know and didn't have a recollection of those two having that kind of role.

Is that a fair summary?

A They certainly never contacted me and, you know, gave me advice about writing the paper or, you know, anything that even came close to the level of what Dr. Farrar did. So, you know, I can't speak for the other authors, but, you know, for myself, none of those -- neither of those people, you know, did anything really to influence the paper in any way.

Q Do you have knowledge of any communications between Dr. Farrar and Dr. Fauci or Dr. Collins regarding "Proximal Origins"?

A Not personally. They didn't -- I mean, only the ones that were included on email chains, which are, you know, relatively minor, I think.

Q Were you -- these answers after that are kind of self-explanatory, but for the record, were you on every phone call that Dr. Farrar had with Dr. Fauci and Dr. Collins?

A I certainly don't think that I was.

Q Were you on every email that Dr. Farrar had with Dr. Fauci and Dr. Collins?

A I don't think that I was, no.

Q And were you on every text message that Dr. Farrar had with Dr. Fauci and Dr. Collins?

A I think that's very unlikely.

Q Thank you.

You were also asked if drafts of "Proximal Origin" were being sent to Dr. Fauci or Dr. Collins. Do you recall that question?

A Did I ask that question?

Q Minority counsel asked that question.

A Oh. I think some of the drafts, at least one or so, were circulated to the

entire group, which would've included Fauci and Collins.

Q Do you know if any were sent just directly to them?

A I'm not aware of that, no.

Q Okay.

To your knowledge and recollection, did Dr. Fauci ever provide comments or edits to any draft of the "Proximal Origin" paper?

A He did not provide them directly to me. I can't really speak for the other authors.

Q Okay.

To your knowledge and recollection, did Francis Collins ever provide comments or edits to any draft of the "Proximal Origin" paper?

A He didn't provide any comments to me. I can't speak to the other authors.

Q And to your knowledge and recollection, did Dr. Jeremy Farrar ever provide comments or edits to any draft of the "Proximal Origin" paper?

A He did change -- or, suggested a change in one word in one sentence.

Q Was that his only edit?

A As far as I know, yes.

Q Okay.

I'd like to introduce majority exhibit 22.

[Garry Majority Exhibit No. 22

Was marked for identification.]

BY MR. BENZINE:

Q This is an email chain with yourself, Dr. Holmes, Dr. Rambaut, and Dr. Andersen, Bates numbered REV0002866 through REV0002873.

And I want to draw your attention to the page that ends in 2872. It's the last full

page.

A Okay.

Q And about halfway through, there's an email from Dr. Holmes. Do you see that one?

A Uh-huh.

Q The second paragraph says, "Should I tell Jeremy to hold on 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."

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 All right.

The next email up, from Dr. Rambaut, said, the first line, "Perhaps say we are adding new information? See whether he wants to hold off. I suspect Bethesda will be sending it round already?"

Is it your estimation that "Bethesda" also refers to Dr. Fauci and Dr. Collins?

A Yes.

Q Thank you.

[Garry Majority Exhibit No. 23
Was marked for identification.]

BY MR. BENZINE:

Q Moving to majority exhibit 23, this is another email chain, with yourself, Dr. Holmes, Dr. Rambaut, and Dr. Andersen, Bates marked GARRY0000608 through GARRY0000612.

Starting on the page that ends with 611 is an anonymous email to Jon Cohen.

We've talked about this earlier, but who is Jon Cohen?

A Jon Cohen is a reporter for Science magazine.

Q Are you aware of this email?

A I am.

Q Can you tell us a summary of the email or what the anonymous individual was alleging?

A He's basically saying that -- which I believe is going to be consistent with my testimony -- that the original authors of "Proximal Origins" each, to varying degrees, were open to the possibility that the virus had leaked from a lab.

Q He also talks about, in the third paragraph, "But, incredibly, Andersen et al. turned around and submitted the Proximal paper to Nature with the exact opposite claim, that the virus was NOT human engineered. They used (without acknowledgment, of course) all the arguments provided by the coronavirologists on the initial call in which they had tried to raise the human-engineered alarm."

What does that mean?

A I don't know. I don't know who this author was, and I'm not sure exactly what he's trying to insinuate here.

But I think my interpretation is, this is a bit of sour grapes about, you know, how widespread and how well-received the "Proximal Origins" paper was. And he's just saying that, well, you know, other people that they talked to, you know, they had influenced the way they wrote the paper and that, by the way, these guys, you know, first started out thinking that it may have leaked from a lab.

And that is certainly a true statement, you know, based on, you know, all the back communication that we've talked about. You know, certainly Andersen and Holmes, for two of us, probably were more than 50/50 that it might've come from the lab to start

with.

Q Uh-huh.

Moving to the page marked 612 -- it's the last page -- in the middle of the top paragraph, or at the end, it says, "Thomas," referring to Clare Thomas, the editor at Nature, "was quickly apprised of the situation and Nature rejected the paper."

Was "Proximal Origin" initially rejected by Nature?

A "Proximal Origin" was rejected by Nature, but not for the reasons that are outlines here in this.

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.

Q And then you submitted it to Nature Medicine and it was accepted?

A Well, I mean, it was transferred to Nature Medicine, okay? They basically looked at the same reviews and said, this is fine for our journal.

Q Is Nature Medicine a subsidiary of Nature?

A They both are Nature publications. Both are very prestigious journals.

Q Why would one have different standards than the other?

A I -- you know, I mean, it's just a different way of viewing it.

Q Okay.

I want to go to majority exhibit 24.

[Garry Majority Exhibit No. 24

Was marked for identification.]

BY MR. BENZINE:

Q It's again another email chain from yourself, Dr. Holmes, Dr. Rambaut, Dr. Andersen, Bates numbered GARRY0000600 through GARRY00000607.

I want to turn your attention to page 602. And towards the bottom of the page, there's an email from Dr. Holmes. And the middle sentence is, "Despite this, I am 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."

Do you agree that this statement is about the anonymous email that --

A I'm sorry, I'm not -- it's about the anonymous email, but I'm missing which paragraph you're referring to.

[3:58 p.m.]

BY MR. BENZINE:

Q At the bottom of 602.

A Oh, okay. I was looking on the wrong page. Okay. Right here. So --

Q It's about the Cohen email.

A Yeah. I mean, so -- I mean, these are Eddie Holmes's words. They're not my words. I mean, I think that I, you know, probably -- I agree with the sentiment. I'm not sure that he's got the right people or not. Like, I don't know that. I'm not sure that Eddie would say that he knows that. So I think it's speculation in, you know, what I believed would be considered a private conversation. But, you know, here we are, talking about it.

You know, I don't know. I mean, I personally don't know who the person was that wrote that anonymous letter to Jon Cohen. I just don't know.

Q In your estimation, is the "Ron" Ron Fouchier?

A I'm pretty sure that's who he's talking about here, but --

Q And "Baric" is Ralph Baric?

A That would be Ralph Baric, yeah.

Q And he's a professor at the University of North Carolina?

A That is where he's at, yes.

Q Thank you.

I want to go finish up "Proximal Origin" with two questions just asking if you still agree with their -- those statements.

The first one we've already kind of talked about. "Our analyses clearly show that COVID-19 is not a laboratory construct or a purposefully manipulated virus."

Do you stand by that statement?

A I do.

Q The next one is: "However, since we observed all notable COVID-19 features, including the optimized RBD and polybasic cleavage site, in related coronaviruses in nature, we do not believe that any type of laboratory-based scenario is plausible."

Do you stand by that statement?

A I do.

Q We can go off the record for one second.

[Discussion off the record.]

Mr. Benzine. We can go back on the record now.

BY MR. BENZINE:

Q On June 22, 2021, Dr. Jesse Bloom posted a preprint paper regarding early-2020 COVID-19 sequences that were removed from the NIH sequence database.

Are you aware of this paper?

A I am.

Q Are you aware of Dr. Bloom?

A I do know Dr. Bloom.

Q Have you ever met or spoken with Dr. Bloom?

A I don't believe we've ever actually met in person, but I have spoken to him on a Zoom call I'm pretty sure we're gonna talk about.

Q Do you have any personal feelings about Dr. Bloom?

A I'm a person, so I probably have some feelings about him, but I'm not sure they're relevant to this discussion.

Q Okay.

I would like to introduce majority exhibit 25.

[Garry Majority Exhibit No. 25

Was marked for identification.]

BY MR. BENZINE:

Q This is an email chain between yourself, Dr. Peter Daszak, Dr. Zhengli Shi, and Dr. Linfa Wang, Bates numbered GARRY0001239 through GARRY0001249.

A Uh-huh.

Q In the middle of page 1248, there's an email from you to Dr. Wang, Dr. Daszak, and Dr. Shi. And it says, "You might be aware of this preprint from Jesse Bloom (released today). It is already getting a lot of attention in the US press." And the date on that email is June 22nd.

Is that the same paper, the deleted sequence one?

A It is.

Q Why did you email it to those three scientists?

A I thought that they might know about, you know, possibly where these sequences were generated and had they been submitted to a Chinese database or not.

Q Going through onto page 1245, there's an email from you in response to an email from Dr. Shi. And the blue, I believe, are your words, and Dr. Shi's words are in black.

A Uh-huh.

Q So Dr. Shi said, "The lead author told me that because the sequences they got are not full-length genome and the quality is not good enough."

Is that your understanding of why the sequences were removed from the database?

A It is, yes.

Q And you write that "that's a reasonable explanation."

Is that a reasonable explanation?

A It is.

Q In the Dr. Bloom paper, he writes that there is no plausible scientific reason for the deletion. So you would disagree with that statement?

A I would.

Q Dr. Bloom continues, "It therefore seems likely sequences were deleted to obscure their existence." You would disagree with that statement?

A Yes.

Q On page 1245, the same page, you write in blue, "NIH did not send the sequences to Bloom. Bloom hacked the system and recovered the sequences himself from the cloud archive. NIH was surprised Bloom did this."

What do you mean by Dr. Bloom "hacked the system"?

A He basically got them from the Wayback Machine and, you know, some archives that NIH doesn't pay attention to. That's where they were at.

Q How did you know that NIH was surprised that Bloom did this?

A Well, I'm not sure exactly about the timing, because, you know, we did have a teleconference with Dr. Fauci, Dr. Collins, and Dr. Bloom and a few other scientists. So --

Q The teleconference was on June 20th. So it could've been at the teleconference?

A It was after the teleconference then.

Q Okay.

A There were people from the NIH archives, the databases, that were on that call. And I think I made a fair statement, that they were surprised that he had done this.

Q In Dr. Bloom's paper, again, he writes that, quote, "Understanding the spread of COVID-19 in Wuhan is crucial to tracing the origins of the virus, including identifying events that led to infection of patient zero."

Do you agree with that statement?

A I mean, in principle, yes, but, you know, finding such sequences is not what he did in his paper, and I don't think those sequences actually exist. So --

Q With your knowledge of Dr. Bloom's paper, is it a fair characterization that it discusses evidence and data related to the origins of COVID-19?

A I don't think it's a fair statement. I think those sequences reflected too light to really, you know, tell us much about where the virus had come from.

Q Okay.

I would like to shift to majority exhibit 26.

[Garry Majority Exhibit No. 26
Was marked for identification.]

BY MR. BENZINE:

Q This is another email chain. It includes yourself. It also has a number of other scientists, including Dr. Collins, Dr. Tabak, and Dr. Fauci, on it. And it's Bates numbered GARRY0001149 through GARRY0001153.

I'd like to turn your attention to 1152. It's an email from Dr. Collins. It's to Dr. Andersen, yourself, Sergei Pond, Rasmus Nielsen, Trevor Bedford, and then has CC'ed Dr. Fauci, Dr. Bloom, Dr. Embry, and Dr. Tabak, and is inviting you to join a teleconference regarding Dr. Bloom's paper on Sunday, June 20, 2021.

Did you end up attending this teleconference?

A I did.

Q To the best of your recollection, can you describe the rationale for the

teleconference and what happened?

A Well, they had gotten this preprint. I think that it was sent to them -- "they" being Dr. Collins and Dr. Fauci -- had gotten a preprint from Jesse Bloom.

There were some things in the paper that still ended up in the final version of the paper, but some other things that they were concerned about, particularly some of the language that they felt, and I concurred, were not really appropriate for a scientific paper, but they were in there anyway.

And so this teleconference was called. And it was, you know, a pretty spirited discussion about, you know, the paper and recovered sequences and things like that. So, you know --

Q Okay.

I would like to introduce majority exhibit 27.

[Garry Majority Exhibit No. 27
Was marked for identification.]

BY MR. BENZINE:

Q This is a memo prepared by Dr. Bloom providing his account of that teleconference. For the record, Dr. Bloom notes that these notes are not contemporaneous but written 6 months later.

Are you aware of this memo?

A I am aware of this memo. I think it was communicated by a Vanity Fair reporter, if I'm recalling that correctly.

Q That is correct. Have you read the memo before?

A I have. Yeah.

Q Okay.

At the bottom of the first page, Dr. Bloom writes, "At that point, the meeting

became extremely contentious. Kristian Andersen strongly objected to my pre-print, and said he found it deeply troubling."

Did the meeting -- was this a contentious meeting?

A Not to my recollection. I mean, you know, the people were clearly in disagreement about some of the points, but I think, you know, "extremely contentious" may be overstating the case. But, you know, I mean, it was -- you know, there were clearly disagreements about, you know, what, you know, the paper said and how it was stated.

Q In that same paragraph, Dr. Bloom continues to outline three objections that Dr. Andersen posed during the teleconference.

The first one, he says, "Kristian contended that if the Chinese authors had decided to delete their data, it was unethical for [Dr. Bloom] to analyze it further."

Do you recall Dr. Andersen stating that objection?

A I don't recall it having been stated that way. But I didn't make the statement myself. You'd probably have to ask, you know, Kristian exactly what he said and what he meant.

Q Do you agree that it's unethical to analyze deleted data?

A Well, I'm not sure exactly what Dr. Bloom was inferring in that either, so I'd have to get some clarification on that.

I mean, in principle -- I mean, there wouldn't even be a principle. I don't know. I mean, you know, I think you can analyze data, you know, wherever. So, you know, if you had the data, you should probably analyze it.

Q Okay.

A So was it deleted or not? You know, I -- in some ways, this is almost sort of -- you know, I think it's picking a point that, you know, probably doesn't need to be

picked at. I mean, you know, the data existed, and people were welcome to analyze it, as far as I'm concerned.

Q The next objection, as outlined by Dr. Bloom, says, "Second, Kristian contended that the phylogenetic analyses in the pre-print were not interesting because there was nothing unusual about the phylogenetics of early SARS-CoV-2 sequences in Wuhan."

Do you recall Dr. Andersen stating an objection along those lines?

A I mean, along those lines, I think, yes. I think the phylogenetic analysis in that preprint at the time was flawed, and, you know, what ended up in the paper was flawed. But, you know, I mean, it's science, it's data, you know. There are certainly -- you know, the record can be corrected.

Q After this objection, Dr. Bloom writes, "This point was strongly disputed by Rasmus Nielsen."

First, who is Dr. Nielsen?

A He's an evolutionary biologist, virologist. I don't really -- I mean, I'm not -- I mean, that's not exactly my field. So, I mean, I know that, you know, he's a scientist in that field, that's part of his expertise. But I don't really know the great details about, you know, his level of expertise or --

Q Dr. Bloom continues, "My strongest memory of the meeting is Kristian and Rasmus yelling at each other over Zoom."

Do you remember Dr. Andersen and Dr. Nielsen yelling at each other?

A Actually, I don't remember that. I don't know what individual people would characterize as yelling, but I don't think that -- you know, were voices raised? Maybe a bit. But is that yelling? I don't know. I, myself, personally, wouldn't have characterized it that way.

You know, it was a spirited discussion, but, you know, was it yelling? Were they, you know, screaming at each other like kids on a playground? I don't think that's a fair characterization of it.

Q The third objection that Dr. Bloom recalls is -- he states, "Finally, Kristian objected to my pre-print because he said that there was already intense criticism of scientists such as himself, he needed security outside his house, and my pre-print would fuel conspiratorial notions that China was hiding data and thereby lead to more criticism of scientists such as himself."

Do you recall Dr. Andersen stating an objection along those lines?

A I mean, again, it's been a while in vague terms, and I wasn't making the comments. You know, I mean, was something said along those lines? You know, I can't dispute it; I can't confirm it either.

You know, certainly, that is a true statement, that, you know, Kristian's had to have security outside of his house. That is a true statement.

Q Do you -- we touched on this earlier in the realm of gain of function, but would you agree in not publishing data because it might fuel conspiratorial notions about China or lead to criticism of scientists?

A I would not agree.

Q Dr. Bloom goes on to recount that Dr. Andersen -- this is now the third paragraph on the second page that starts with "Kristian Andersen."

A Uh-huh.

Q "Kristian Andersen then said that he was a screener at bioRxiv, and so he could delete the pre-print or revise it in a way that would leave no record that this had been done."

Do you recall that?

A I don't recall it because that's not what happened, actually. So he didn't say that he could delete it. And I believe that the person that actually runs the website clarified that. And he is -- Kristian is a screener for bioRxiv, but he doesn't have the power or the capability to delete a preprint.

Q What is your recollection of that situation then?

A I think that Kristian and all the people -- well, several of the people on the call, including myself and Dr. Fauci, suggested to Dr. Bloom that he might want to revise some of the language in his preprint. But that was pretty much the extent of it.

Q Dr. Bloom continues, in the middle of that paragraph, "At that point, both Anthony Fauci and Francis Collins clarified their views by each saying something to the effect: 'Just for the record, I want to be clear that I,'" meaning Dr. Fauci and Dr. Collins, "'never suggested you delete or revise the pre-print.'"

Do you recall that happening?

A I do recall that happening, and that is an accurate characterization of what those two people said.

Q Why would they have to say that if the offer wasn't made?

A They just wanted to make it clear to Dr. Bloom that they weren't trying to influence his, you know, ability or right to publish whatever he wanted to.

Q Okay.

Dr. Bloom continues after that sentence, "Kristian continued to press the point that he could use his capacity as a screener at bioRxiv to upload a revised version of pre-print. At that point, one of the NIH attendees (I think it was Francis Collins but I am not certain) said something to the effect: 'Kristian, if he's already submitted the pre-print, it's better if you don't pressure him to revise it.'"

Do you recall any of that?

A Well, you know, I wasn't sitting in the same chair that Dr. Bloom was, so he probably has a clearer recollection of that than I do, but I don't, you know, precisely recall these words from Dr. Collins, you know.

But, I mean, the consensus was to the effect that if he wanted to go ahead and publish his preprint, that he could certainly do that.

Q For clarity in the record, at this meeting or in any communications that you have knowledge or recollection of, did Dr. Andersen ever offer to -- or pressure Dr. Bloom to delete, revoke, edit, revise, or otherwise alter his preprint about the deleted COVID-19 sequences?

A I think Dr. Andersen and others on the call suggested to Dr. Bloom that he should revise some of the language in his preprint. So edit it, change it, revise it, yes, all those things happened.

Q Was there ever a suggestion to not publish it?

A There was -- not to my knowledge.

Q Okay.

You were correct; this memo was reported by Vanity Fair. And in as brief a statement as you could possibly provide to Vanity Fair, you said that Dr. Bloom's recount of the meeting was nonsense.

I assume, based off the last 3 minutes of testimony, that you would stand by that statement?

A I would.

Q Okay.

I have 2 more minutes.

One final question about the science. After all the testimony that you've provided today, do you believe it is at all possible that COVID-19 was the result of a

laboratory or a research-related incident?

A No.

Q I want to talk about the intelligence community a little bit, and then we can wrap up.

You testified a little bit today, but I'm going to ask the questions. The intelligence community has been investigating the origins of COVID-19 since early 2020.

Are you aware of these efforts?

A I am aware.

Q On May 26, 2021, President Biden announced that he directed the intelligence community to redouble their efforts to investigate the origins of COVID-19 and deliver an assessment in 90 days.

Are you aware of that announcement?

A I am.

Q On August 27, 2021, the Office of the Director of National Intelligence released an unclassified summary of that assessment.

Are you aware of that summary?

A I am.

Q Have you read that summary?

A Yes.

Q And on October 29, 2021, the Office of the Director of National Intelligence released a full declassified assessment.

Are you aware of that assessment?

A Yes.

Q Have you read that assessment?

A Yes.

Q At any point during any of these reviews, were you contacted by anyone in the intelligence community to assist in these assessments or investigating of the origins of COVID-19?

A Yes.

Q Which agencies?

A The CIA and the FBI.

Q When did those agencies contact you?

A Well, I don't recall the exact dates. But I did have an interview with agents from both of those agencies I just mentioned.

Q Generally, was it post-President-Biden-announcement or was it in 2020?

A It was during the 90 days.

Q During the 90-day review?

A Uh-huh.

Q What did those interactions look like?

A They looked like this room, practically. There were CIA agents and an FBI agent in there and somebody from the local FBI office. And, you know, we talked about the scientific data. They were both Ph.D. scientists from CIA and FBI that were pretty knowledgeable about the science and the data, and we had a day-long conversation.

Q Were the meetings together? Meaning, did you meet with the CIA individually and --

A There were -- yeah, there were three intelligence officers there, one from the CIA and two from the FBI. So they were all together, yeah.

Q Was it just one meeting?

A One meeting, all day.

Q Okay. Can you summarize what you told them? Does it line up with your

testimony here today?

A It does.

Q The FBI Director came out publicly and said the FBI's position is, with moderate confidence, that COVID-19 leaked from a lab.

Do you disagree with that assessment?

A I do.

Q Other than this interaction, do you keep or maintain any other relationship with any component of the intelligence community?

A No.

Q Have you had relationships with the intelligence community in the past?

A Yes.

Q Can you explain those a little bit?

A You know, occasionally, somebody will call up and want some advice about viruses, and, you know, I talk to the people on the phone. Yeah.

Q Okay. I don't want to dig too much in because we might get in trouble.

A Yeah.

Q That is all I have. We can go off the record.

[Recess.]

Mr. Pellegrini. All right. We can go back on the record.

BY MR. PELLEGRINI:

Q Dr. Garry, I'm going to ask just a few more questions, which will be clarifying questions based on documents we just saw in the previous hour.

And the first one of those questions relates to majority exhibit 19. I'll give a moment for that to be found. It's the one that starts with Bates number REV 266.

We're drowning in paper.

A Okay.

Q And, if you could, turn to the second page, which is numbered 267.

A Okay.

Q And at the top of that page, there's a paragraph -- this is an email from Dr. Kristian Andersen. There's a paragraph that starts with the words "Prompted by Jeremy Farrar, Tony Fauci, and Francis Collins," et cetera, et cetera.

Do you recall discussing this particular paragraph in the previous hour?

A I do.

Q Great.

Just a couple of questions about that. The first is, just to be really clear, this email was written by Dr. Kristian Andersen. You have no personal knowledge of what Dr. Andersen meant when he wrote it. Is that fair?

A That's fair.

Q Great.

I suppose, in the sense of possibilities and speculation, do you think it is possible -- because this is an email from Dr. Andersen to Clare Thomas, who's an editor at Nature magazine -- that's right, right?

A Correct.

Q Okay. Is it possible that Dr. Andersen is perhaps seeking to boost the gravitas of the paper as he tries to, I think, essentially sell it to Nature magazine? Is that a possibility?

A Yes, that's a possibility.

Q Okay.

In any event, the description of Dr. Andersen here, that the paper was "prompted by Jeremy Farrar, Tony Fauci, and Francis Collins," phrasing it that way and including

those three individuals, I think, is it fair to say that that is not consistent with your recollection of the paper, as a co-author?

A I think it overstates particularly the role of Fauci and Collins.

Q Okay.

Okay. If we could take a look at majority exhibit 20. And that does not have a Bates number on it, but -- well, I'll just pause there and see if I can help identify it.

Actually, I'm sorry, Counsel. Twenty-one. Apologies. And that does have a Bates number. That's GARRY 306.

So we discussed some of the emails on the first page here, which go to the process by which reviewers are selected for publications. And there's an email from yourself in the middle of the page: "As you know when you submit you'll need to suggest reviewers to include and exclude." And "there are some natural choices for both lists."

Just for those of us who might not be familiar with the process, the authors' suggesting reviewers to include and exclude, that certainly is not in order to get an easier peer review or somehow reduce the level or quality of scrutiny that your paper gets. Is that correct?

A That's correct.

Q And is the -- what is the purpose, I should say, of offering suggestions?

A The purpose is to identify some individuals who might have the expertise that would be appropriate to give a fair peer review.

Q Thank you. You can put that one away.

This one is not based on the documents; it's just in the abstract. But there was a brief discussion of the extent to which, if any, Dr. Fauci or Dr. Collins offered comments on the paper. And putting aside the question of to whatever extent those folks did or did not, I just want to ask, based on your recollection -- I don't have a document for

it -- but: Was it case that a number of people commented on the paper?

The paper was distributed to this larger group of attendees on the conference call -- Patrick Vallance; Ron Fouchier, who we've talked about; somebody named Mike Ferguson. All these various people, I think, commented on the paper. Is that right?

A I mean, not the paper per se, but, you know, the sort of whole discussion that we had had about the origins. And, yes, a couple of times, there were reports that, you know, hadn't yet coalesced into a paper yet that were circulated, and there was certainly feedback and discussion about that.

So what you stated about, yes, a lot of people commented, that's true.

Q So, to the extent that any one person commented on earlier drafts of the paper, or if we call it a report, that in and of itself would not put them in any position as distinguished from anybody else who was on that conference call, which is an attendee of the conference call and a reader of the draft. Is that fair?

A I'm sorry. I didn't quite get it.

Q No, I know. To offer comments on the draft --

A Yeah.

Q -- in and of itself, does not suggest anything more than what it is, which is offering comments on a draft?

A Right. No. Just normal scientific discussion.

Q It does not indicate any sort of central planning role with respect to the project itself?

A It does not.

Q Okay.

If I could ask you to look at majority exhibit 22. And that is Bates numbered REV 2866. And there was some discussion related to page 2872, towards the back of that

document.

A Okay.

Q There are two things I just wanted to highlight.

One is, in that the middle-of-the-page email from Dr. Holmes, we talked about the part of that email where Dr. Holmes says he, I think referring to Dr. Farrar, sent the paper to the Bethesda boys. And we established a reasonable assumption that that refers to Drs. Fauci and Collins.

I just want to confirm, you would not have personal knowledge of other people to whom Dr. Farrar sent the paper. Is that right?

A I would not.

Q Okay.

And in the email above that, when Dr. Rambaut says, "I suspect Bethesda will be sending it round already," am I perceiving correctly that Dr. Rambaut's comment is not based on his own personal knowledge; it's a suspicion of his? Does that seem fair?

A Seems fair.

Q Okay. And then, certainly, heading out one additional degree of separation, you would not have any personal knowledge of whatever it is that Dr. Rambaut suspects. Is that also fair?

A I would not.

Q Okay.

If I could ask you to look at majority exhibit 27. These are Jesse Bloom's notes.

A Okay.

Q So, two questions.

One is: We discussed that there may have been suggestions for Dr. Bloom to revise his preprint. To the extent that you recall, would the revisions have been for

portions of the paper going to, sort of, assumptions of mal-intent on the part of whomever it was that deleted this data, as opposed to revisions that would have deleted the central point of the paper itself, which is the removal of this data?

Does anybody suggest a revision that would have eliminated the information contained in the paper, or was it things like the word "surreptitious"?

A Nobody wanted to delete the scientific data or the discussion about the science. It was the what some of us considered unscientific language in the paper that, as you stated, you know, suggested malcontent on the part of any author. It's just not the typical thing that one would do in a scientific paper.

Q Great.

And I think the previous discussion was pretty clear on this point, but I will be extra clear. To your recollection, on that call, certainly neither Dr. Fauci nor Dr. Collins suggested that Dr. Bloom should delete his preprint. Is that correct?

A That's correct.

Q And Dr. Bloom's notes, it appears to us as readers, is consistent with that assertion. Is that correct?

A That's my reading of his notes, yes.

Q That's all we have, and we can go off the record.

Mr. Benzine. We're good to go. Thank you.

Dr. Garry. My pleasure.

[Whereupon, at 4:45 p.m., the interview was concluded.]

Certificate of Deponent/Interviewee

I have read the foregoing ____ pages, which contain the correct transcript of the answers made by me to the questions therein recorded.

_____

Witness Name

_____

Date