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INTERVIEW OF: CDR JEAN-PAUL CHRETIEN

Thursday, June 29, 2023

U.S. House of Representatives

Select Subcommittee on the Coronavirus Pandemic

Committee on Oversight and Accountability

Washington, D.C.

The interview in the above matter was held in Room 2157 of the Rayburn House Office Building commencing at 9:58 a.m.

Appearances:

For the COMMITTEE ON OVERSIGHT AND ACCOUNTABILITY:

MITCHELL BENZINE, Staff Director, Majority Staff

JACK EMMER, Majority Counsel

[redacted], Minority Chief Counsel

[redacted], Minority Counsel

[redacted], Department of Navy,
Office of Legislative Affairs, Counsel

[redacted], Department of Navy,
Office of Legislative Affairs, Counsel

[redacted], Office of the Secretary of Defense,
Legislative Affairs, Advisor

[redacted], DARPA, Chief of Legislative Affairs

[redacted], Defense Intelligence Agency,
Office of General Counsel

[redacted], Defense Intelligence Agency,
Congressional Affairs

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Office of General Counsel, Attorney-Adviser

P R O C E E D I N G S

Mr. Benzine. We can go on the record. This is the transcribed interview of Commander Jean-Paul Chretien 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 was 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?

CDR Chretien. Jean-Paul Chretien, C-H-R-E-T-I-E-N.

Mr. Benzine. Thank you. Commander Chretien, my name is Mitch Benzine and I'm 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 are 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 in a personal capacity with you today?

CDR Chretien. No.

Mr. Benzine. Is there an attorney present representing your agency with you today?

CDR Chretien. Yes.

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

[redacted]. My name is [redacted] with DOD OGC -- Office of General Counsel.

Mr. Benzine. Will the other agency staff please identify themselves for the record?

[redacted]. So [redacted] with DARPA, Legislative Affairs.

[redacted]. [redacted] with OSD, Legislative Affairs.

[redacted]. [redacted], counsel, Navy Office of Legislative Affairs.

[redacted]. [redacted], Legislative Affairs from Navy as well.

[redacted]. [redacted], Defense Intelligence Agency, Office of General Counsel.

[redacted]. [redacted], Defense Intelligence Agency, Congressional Affairs.

Mr. Benzine. All right. Thank you. Again for the record starting with the remainder of the majority staff, can the additional Congressional staff members please introduce themselves with their name, title, and affiliation?

Mr. Emmer. Jack Emmer, counsel, majority staff.

[redacted]. [redacted], minority counsel.

[redacted]. [redacted] chief minority counsel.

Mr. Benzine. Thank you.

Commander Chretien, before we begin I'd like to go over the ground rules for this interview. The way this interview will proceed is as follows. The majority and minority staff will alternate asking you questions one half hour per side per round until each side is finished with their questioning. The majority staff will begin and proceed for a half hour and then the minority staff will have a half hour to ask 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 questions, they may choose to end a few minutes past the half hour to ensure completion of that specific line of questioning, including any pertinent follow-ups. In this interview, while one member of the staff of each side may lead the questioning, additional staff may ask questions.

There is 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 you 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?

CDR Chretien. Yes.

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?

CDR Chretien. Yes.

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?

CDR Chretien. Yes.

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?

CDR Chretien. Yes.

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

CDR Chretien. Yes.

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

CDR Chretien. No.

Mr. Benzine. The Select Subcommittee follows the Committee's -- follows the rules of the Committee on Oversight and Accountability. Please note that if you wish to assert a 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 specific privilege being asserted and the reason for the assertion on or before the scheduled date of testimony or appearance." Do you understand?

CDR Chretien. Yes.

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

CDR Chretien. Yes.

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

CDR Chretien. No.

Mr. Benzine. We will start the majority's first 30-minute round of questioning.

EXAMINATION

BY MR. BENZINE:

Q Again, I want to thank you for taking part in this interview voluntarily and your work over the years, and

start briefly with your education and experience and get more into substance later. Where did you attend undergraduate school?

A I attended the Naval Academy.

Q And what degree did you graduate with?

A Political science.

Q Do you have any other graduate or doctorate degrees?

A Yes.

Q And what are those?

A A medical degree from Johns Hopkins School of Medicine, a PhD in genetic epidemiology from Johns Hopkins School of Public Health, and a master's in biostatistics, also from the School of Public Health.

Q And who is your current employer?

A I'm a naval officer assigned to DARPA.

Q Can you elaborate the acronym on the record?

A Apologies. Defense Advanced Research Projects Agency.

Q And what is your current job title for DARPA?

A I'm a program manager in the Biological Technologies Office.

Q Can you elaborate briefly on what your role and responsibilities are?

A Yes. As a program manager, we propose new

ideas for technologies. In my case, biological technologies or biomedical technologies that would serve a national security purpose and that would be revolutionary. And also take on programs started by previous program managers who have finished their tour and manage those programs as well.

Q Can you go through your career up until now? What other kind of major roles have you had?

A Yes. After I graduated from medical school and graduate school, I served an internship in internal medicine at what's now the Walter Reed Military Medical Center. I then served for four years in the Department of Defense global emerging infections system. I then went back into training and did a residency in preventive medicine at the Walter Reed Army Institute of Research. I did a postdoctoral fellowship in informatics back at Johns Hopkins.

I then served with the Marines for two years. I was with the Second Marine Expeditionary Force in North Carolina for a year, and then we deployed and I was with the Second Marine Expeditionary Force forward in Afghanistan. I came back from that and went to the Armed Forces Health Surveillance Center, now part of the Defense Health Agency.

And then I served a detail to the Office of Science and Technology Policy at the White House -- I was a senior policy advisor for biodefense -- and then to the Defense Intelligence Agency National Center for Medical Intelligence

for three years, and then to my current role at DARPA.

Q Can you -- specifically your last two roles, can you walk through your role and responsibilities while at OSTP?

A Yes. So I was the senior policy advisor for biodefense in the National Security and International Affairs Division, and my portfolio included pandemic preparedness and preparedness for and response to infectious disease outbreaks. And that was the bulk of my assignment there.

Q Can you also walk through your roles and responsibilities while at NCMI?

A Yes. At NCMI I served in a billet that my community -- Navy medical community maintains there, which is called the clinical consultant. So it's my role to advise analysts and leadership across the center on intelligence assessments that they are making and provide a clinical medical perspective on the range of topics that the center covers.

As a collateral duty, I was also the lead for the pandemic warning team.

Q Can you go into a little bit more detail on that one, the pandemic warning team?

A Yes. The -- a pandemic is one of a number of so-called "warning problems" that the intelligence community maintains. NCMI has the lead for the pandemic warning

problem. And without getting into classified information, my job was to work with representatives of agencies across the IC to provide early warning of pandemics.

Q While at these roles there have been various emerging disease outbreaks that have covered. Can you explain how you interacted -- and I'm just going to throw out, like Zika, Ebola, a couple have come up over your career. Can you explain kind of your experiences in reacting to those or working those various outbreaks?

A Yes. I served in different capacities when some of those outbreaks you mentioned came about. So, for example, in one of the earlier Ebola outbreaks I was serving at the Armed Forces Health Surveillance Center and we worked with interagency partners to develop models that might help us forecast how the outbreak would play out and might be useful for the response.

During the Zika outbreak I was at the Office of Science and Technology Policy, and we convened an interagency group to provide advice on scientific studies that might be undertaken to better understand how the outbreak was unfolding and better respond to the outbreak. And we worked -- my office at OSTP worked closely with the National Security Council on -- certainly on large-scale disease outbreaks, so we advised in a more immediate kind of response capacity for that.

And then while at the National Center for Medical Intelligence, I participated in those responses essentially as -- as an intelligence analyst and again providing a medical perspective for the other analysts there.

Q I'm going to shift to talking about the COVID-19 pandemic, both kind of where it began and then some of your work. You're clearly an expert on medicine and intelligence and various things. What does studying the origins of an emerging virus tell us to help us prepare for a future pandemic?

A I think understanding the origins of an emerging virus is very important for preparedness for future outbreaks. If we understand the natural reservoir and how that pathogen ended up in humans in the case of a naturally emerging outbreak, that may give us ideas about how to prevent those spillover events and those earlier stages of human-to-human transmission in the future.

And on the other hand, if a pathogen were to be the result of laboratory manipulation, then that would also be very useful to know from a laboratory biosafety standpoint.

Q So you touched on kind of the two viable pathways for a new virus to emerge; zoonotic or laboratory research related. Briefly can you explain what a zoonotic event is?

A Yes. A zoonotic event is a pathogen that

originates in an animal but is able to infect humans. It may have already always had the ability to infect humans. It may adapt to humans through spillover events over time, but at some point may acquire the ability to not only infect humans, but to spread among humans, and may have the ability to spread efficiently from human to human. So this is how influenza pandemics have come about in the past, for example.

Q Are there kind of, like, standard detection strategies for this kind of event?

A The foundation of preparedness for events like that is public health surveillance, which is monitoring populations for medical symptoms and diagnostic test results that may indicate that such an event has occurred.

There's also the potential for surveillance in animal populations as well, and the thinking there is that perhaps identifying these pathogens in animals may -- before they infect humans may give us a jump on those -- on those pathogens.

Q And then are there kind of standard countermeasures to try to slow down or prevent a zoonotic event?

A There are standard prevention measures that are designed to prevent that spillover in the first place, and that is largely limiting exposure to humans of animals that are known to harbor pathogens that may infect humans or

that may infect those pathogens. And then there also are strategies to monitor human populations that are in close proximity to animals that may harbor these viruses. And so that may give you an early indicator that a spillover event has occurred.

Q And the other side of the coin, what would you consider a laboratory or research-related event?

A A laboratory event could come about in a number of ways. It could be that a -- researchers at a laboratory take a sample from an animal in nature, bring that sample back to the laboratory and could accidentally infect themselves while working with that pathogen. In an example like that, there may be no manipulation of the pathogen at all. It may be a pathogen that occurred in nature that infects the laboratory workers.

It's also possible that in the course of doing experiments and in trying to understand the pathogen from a -- from the standpoint of developing medical countermeasures, for example, that a worker could infect themselves or potentially bring that pathogen from the laboratory and people outside of the lab could be infected.

Q What are common laboratory mitigation measures to try to prevent that kind of event?

A It's a couple of things. It's preventive measures and standard safety practices to reduce the risk of

laboratory worker infections. And the specifics of what those measures are depends on the types of pathogens the laboratory is working with and can be -- and may be very stringent for pathogens that cause severe disease, have no good treatments.

And then -- and then there's also the surveillance, health monitoring of laboratory workers and encouragement of them to seek -- to seek diagnosis and care if they become ill.

Q Would it include -- so you mentioned operating at the proper biosafety levels. Would it also include proper training of laboratory technicians?

A Certainly.

Q Moving on to specific to COVID-19, you were at your previous post at NCMI when COVID-19 emerged; is that correct?

A Yes.

Q How did -- when did you first hear about what became COVID-19?

A In December of 2019.

Q Through the Chinese reporting -- that was reported on PubMed, right?

A It was -- yes, there were reports in PubMed. And without getting into classified information, we did have other indications besides public reporting.

Q Did you have indications prior to December 31, 2019?

A I don't recall the exact date.

Q But early --

A But December -- certainly in December, sometime in December of 2019, yeah.

Q Is it safe to assume it was prior to December 31 if you were having indications that weren't on the Chinese -- the Chinese reported it on December 31, if --

A Right. Yes. So we did have earlier indications, not -- not of something that we knew at that point was this is coronavirus, but these were -- these were reports of people becoming sick.

Q Without -- if you can, without getting into the classified space, how did you first hear about it? How did those reports make it to you?

A We monitor a number of open source and -- we monitored when I was there a number of open source and classified systems for -- for indicators and warnings of outbreaks that may have pandemic potential. And so -- and so part of this is looking for clusters of human disease that may be consistent with a pathogen that has the ability to spread from person to person. And so our first indicators were from one of these systems.

Q Were those indications reported up the NCMI

chain to the White House or anything?

A I don't know what happened beyond NCMI. I just can't speak to that.

Q You touched on it a little bit. And again, not getting into anything classified here. Can you explain more the structure of the pandemic warning team at DIA? Is it all domestic? Is it international? What -- how does that look like?

A Yes, this was a function that NCMI had the lead for, and so it involved the various technical divisions within NCMI and also involved a larger community of interest, which involved other -- other members of the intelligence community. And we met virtually periodically, regularly between potential pandemic events to share information on what types of information we were monitoring, how we can improve our ability to get an early indicator of a pandemic.

And then during an event, which the COVID outbreak was the only such event during my time there when we were on an enhanced pandemic warning footing where we exchanged information more frequently. And we -- and we focused exclusively internationally.

Q What -- so after you got the indications of a kind of emerging illness in China, what actions did the pandemic warning team take? What was -- what were next steps?

A We assessed the information channels. We monitored for corroborating or complementary information. We shared information across agencies within our community of interest, and we wrote reports which were circulated in the -- in the usual way that reports are within this warning function within the intelligence community.

Q I want to go through some names of certain individuals, and just a "yes" or "no" if you communicated with them, briefed them, e-mailed with them about COVID-19 or origins of COVID-19.

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 Dr. Ping Chen?

A No.

Q Dr. Andrew Pope?

A No.
Q Dr. Victor Zhao?
A No.
Q Dr. Robert Redfield?
A No.
Q Dr. Michael Lauer?
A No.
Q Dr. David Christian Hassell?
A No.
Q Dr. Gray Hadley?
A No.
Q All right. Thank you.
We're just rolling through. This might be shorter than we thought.
Very -- yeah, we'll go ahead and get started on it. We're going to have to cut it off, though, at some point. I'm going to go ahead and introduce the two majority exhibits. They will be marked Exhibits 1 and 2.
(Exhibits 1 and 2 were identified for the record.)
BY MR. BENZINE:
Q Exhibit 1 the final published version of, "The proximal origin of SARS-CoV-2," written by Dr. Kristian Andersen. And Exhibit 2 -- we'll use them in tandem -- is an unclassified working paper published or drafted on May 26,

2020, and you are listed as one of the coauthors.

I want to start with Exhibit 2 and then work back to Exhibit 1, and kind of in the remaining time for my half hour go through maybe, like, the providence and structure of the working paper and then get into the details in the next half hour.

So first, is this working paper, I guess, real? Can you verify the authenticity of this document?

A Looking through the version in front of me briefly now, yes, this does accord with my recollection of what we wrote.

Q Okay. And you were a coauthor on this with Dr. Greg Cutlip; is that correct?

A Yes.

Q Who is Dr. Cutlip?

A Dr. Cutlip was also an analyst with NCMI at the time.

Q Do you know where he is now?

A Last I communicated with him, he was at the Institute for Defense Analysis.

Q Going to kind of how the working paper came to be, how did you make the determination to draft this paper?

A NCMI and other members of the intelligence community at the time were looking at the origins of the COVID-19 virus. And so this was a topic that we were

following in intelligence reporting and in open source literature and scientific literature.

The first exhibit, the paper by Andersen and colleagues, had come out recently and had provided evidence for a natural origin of the virus. The analysts that we worked with were very interested in that paper, and so we drafted the second exhibit, this working document, as a resource for them and provided our assessment of the evidence provided in the Andersen paper based entirely on scientific literature and not any intelligence reporting.

Q So it was -- I guess were you directed or told to draft the paper, or was it in assistance of other efforts at NCMI?

A Yes, it was to support other efforts, not a direct tasking.

Q And you eventually transferred the paper to the analysts for their use?

A We did circulate it within NCMI.

Q Did it get circulated outside of NCMI?

A I don't know.

Q Who is your -- did it get sent beyond the analysts? Did it get sent to your direct report or the director of DIA or anybody else?

A I don't know whether it went beyond NCMI or who beyond NCMI may have seen it. I do recall sharing it

with other analysts, and I -- but that's -- that's the best that I can recall now.

Q Was there any follow-up from any of the analysts? Did they just take it and say thank you or were there any briefings or questions or anything further?

A We did. A number -- a number of analysts did follow up and we had conversations and talked in more detail. And we did hold a briefing within NCMI as well.

Q And that briefing just kind of outlined what you put in the paper?

A Yes.

Q Did it go any further? Not into classified information, but did it go into any further -- any other assessments of the available evidence or science regarding the origins of COVID?

A No. We focused on the topics in the paper but provided more detail and scientific background.

Q Okay. I'm going to, like, jump ahead in the time and then we're going to work our way back. Did -- to your knowledge, did it go anywhere outside the government?

A I don't have any knowledge of that.

Q At any point in time, did anyone tell you to stop pursuing the origins investigation?

A No.

Q At any time did anyone tell you to stop

pursuing this particular work on proximal origin?

A No.

Mr. Benzine. We're at five minutes until the half hour, so we'll just break here and --

[redacted]. Sure.

Mr. Benzine. -- go off the record.

(Recess.)

[redacted]. We can go back on the record.

BY [redacted]:

Q Commander Chretien, thank you for coming in today. My name's [redacted]. I'm the chief minority counsel. Just want to ask a few questions. All the same guidelines that you discussed with my colleague earlier also apply to our conversation. And we appreciate your service to the country over the years.

I just wanted to ask a few questions about the scientific concepts, just picking out a few discrete concepts from the working paper if I could. And it looks like you have it in front of you, right?

A Yes.

Q Great. So just sort of working through it starting on the first page, I just want to focus on -- there's the second paragraph of the paper and the first sentence of that paragraph -- I'll read it out loud. "Here, we do not advance a particular SARS-CoV-2 origin scenario or

take issue with Andersen et al.'s conclusions." I just kind of wanted to break down both parts of that sentence. Am I right to presume that that first part means what it says? In other words, this working paper does not purport to take a particular position on the origin of SARS-CoV-2; is that right?

A That's correct.

Q Okay. And the second part I was a little curious about. In other words, is it it's that the working paper does not take issue with the conclusions that Andersen reached, but maybe takes issue with the way that he got there? Is that it?

A What we -- or at least what I had in mind there was their overarching conclusion that this virus was likely of natural origin. And so it was not -- it was not that conclusion that we were arguing against. We were assessing the evidence that they were using -- some of the evidence they were using to support that conclusion.

Q And this is sort of a fault of lawyers sometimes. I hate to overly parse the words, but is it not taking issue with the conclusion in the sense of I sort of agree with the conclusion, or I'm really just not taking a position either way and I'm not objecting to the conclusion, I'm just talking about his path?

A Yes, we -- we did not explicitly address their

conclusion that this was natural origin. And the reason for that is that that assessment would require a whole lot of additional information beyond what we looked at in this paper.

Q All right. There is some discussion on the bottom of page 1 and it flows into page 2 about furin cleavage site, or I think it's referred to here as a cleavage site for furin or polybasic cleavage site. I think that's all talking about the same thing. I just wanted to pin down -- and we've had to sort of learn as we go here because we don't necessarily have the scientific background, but the bottom of page 1, okay, "For a coronavirus to infect host cells" -- it's in the middle of that last paragraph -- "the spike protein must be activated by enzymes supplied by the host." And then at the top of page 2 there's a description of how that process in SARS-CoV-2 is affected by the furin cleavage site, if I understand that basic concept correctly. Good so far?

A Yes. Yes.

Q All right. I just wanted to -- it's just a really discrete narrow question, but is it correct that it is -- a furin cleavage site is not necessary in order for coronavirus spike proteins to be activated in a general sense? Like SARS1, for example, did not have a furin cleavage site; is that correct?

A Correct.

Q And the conclusion I draw from SARS1 not having a furin cleavage site is also correct, which is furin cleavage site not necessary in order for this process to occur in coronaviruses?

A Yes, for coronaviruses to infect human cells, not necessary.

Q Great. There's -- we've heard perhaps more than I ever wanted to hear elsewhere about furin cleavage sites. Something that we've heard about the SARS-CoV-2 furin cleavage site is that it is not ideal from an efficiency point of view, that it's been inserted out of frame. And I have not yet mastered exactly what that means. It has something to do with codons, as I understand it. But that -- and the specific amino acids within it, the PRRA, are not what -- if you were trying to design the ideal furin cleavage site, it would not be this. That it's inefficient in a sense. I don't know whether you, since writing this, have followed that line of argument or have any views on that.

A Well, this -- this was one of the arguments in Andersen's paper, not specifically on that -- on that sequence, but the receptor-binding domain more generally, that this would not have been predicted to be optimal for infecting human cells.

So if one were to use the tools that were available to scientists and to try to design the optimal sequence for human infection, one probably would not have come up with this. And that's an argument they advanced, and I don't disagree with that.

Q Yes. So for the amino acid mutations in the receptor-binding domain, right, Andersen makes that argument in the paper. You address it in this working paper. But separately from that, I think since proximal origin was written there's been a discussion amongst the scientific community about the extent to which the furin cleavage site and its sequence is or is not ideal or ideally efficient. And there seems to be a view that it is not ideal or ideally efficient, and I'm wondering just whether you've followed that conversation; and if you have, what, if anything, that indicates to you on this broader topic.

A I have not followed the science on that.

Q Okay. This is a similar question. We've heard elsewhere that the literature -- since this proximal origin was written, since your working paper was written, there has been literature indicating that the furin cleavage site in SARS-CoV-2 when put through the process of serial passage in human-like cells, if I understand it, tends to go away, which folks have suggested to us indicates perhaps that it's sort of the opposite of what you would expect if you

were starting from a theory that it arose in passage. I'm wondering if you're familiar with that literature; and if so, whether you have a view on that in the context of this broader topic.

A I only have a cursory familiarity with that literature and probably don't know it in enough detail to comment.

Q Okay. The O-linked glycans, which I think are discussed somewhere in here -- maybe it's -- page 4 is what my notes tell me. Looks like two thirds of the way down the page there's a sentence in that paragraph -- the last sentence of that paragraph two thirds of the way down says, "We note also that some preliminary investigations have found evidence for the O-linked glycans predicted by Andersen, et al."

So if I understand the situation at this time correctly, there's this thing called "O-linked glycans." They were predicted at the time to exist but had not necessarily been confirmed as to whether or not they actually existed. Andersen argued that if they were there, that had possible implications about the presence of an immune system. Our understanding is that since this time, it has been confirmed that they are present. I don't know whether you share that understanding.

A That's my understanding. Again, not -- not

based on following this literature in detail since then. At the time there was some question, but my understanding is that there has been more confirmatory evidence since then.

Q A general question, which is have any of the views expressed here by yourself or your coauthor on the discrete scientific principles or concepts changed or shifted since this was written? Is there any discrete aspect of this that you would change a little bit if you were rewriting it today, or is it all constant?

A Well, this was -- yeah, this paper was based almost entirely on scientific literature that had already been published. And so unless there were new evidence suggesting that some of that prior research is not what we had understood it to be -- and again acknowledging that I haven't followed this in detail since moving on to my current assignment. But no, I think in large -- at a high level the assessments that I made here I still would support.

Q Great. This is a similar type of question, and it may depend on the extent to which you have followed this issue since then, but whether anything related to data surrounding the Huanan Seafood Market and related issues that go to questions of various distinct lineages that may or may not have been present in that physical area, whether any of that broad topic -- A, I guess have you followed that; and B, if so, how has that informed your thinking, if at all, on

this topic?

A I have followed that from a distance and not in any great detail, but that and other evidence I've seen doesn't really change the -- the thought that I had at the time was that everything we had seen was -- suggested that a natural origin is plausible and that a laboratory origin is plausible as well.

Q Is that more or less just -- I don't want to ask you to speculate on your own personal opinion, but if I were to ask you to do that, is that more or less where you sit today, both possibilities are plausible?

A That's where I am today.

[redacted]. We can go off the record.

(Discussion off the record.)

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

BY MR. BENZINE:

Q Thank you again thus far. I want to go through a little bit more of the substance of the paper and reask what minority counsel just asked a little bit just to stage that. Understanding that you haven't followed the evidence as closely, but your views in the paper of the evidence Dr. Andersen presented has not changed significantly?

A That's correct.

Q I want to walk through a couple specific

sentences and then a couple specific ideas in the paper. Your first sentence on the first page, "The origin of SARS-CoV-2 remains uncertain," is that still your view today?

A Yes.

Q And then the second sentence, "Some of its features are unique among the most closely-related known coronaviruses, and a progenitor virus has not been identified," is that still true today?

A Yes.

Q And then the last sentence in the first paragraph, "Prominent scientists have cited their paper," meaning Dr. Andersen's paper, "as decisive support for a natural origin scenario," and then you cite, "(Calisher et al., 2020; Collins 2020)." Is the Calisher reference to the Lancet letter titled, "Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19"? Is it in the references?

A Yes, that's correct.

Q Okay. Are you familiar with that letter?

A I was more familiar with that at the time.

Q Okay. That letter stated, "We stand together to strongly condemn conspiracy theories suggesting COVID-19 does not have a natural origin." Is the possibility of a lab leak a conspiracy theory?

A Oh, in my mind are you asking?

Q Yeah.

A No. No, I don't think so.

Q And then the reference to Collins in that line, is that Francis Collins?

A Yes.

Q And referencing a blog post that he did regarding proximal origins?

A Yes.

Q I want to ask a general question. You mentioned in the paper that the closest known relative at the time -- they've found some other ones, but RaTG13 being 96.2 percent similar to COVID-19. Can you put into perspective what that means? Like, how similar is that? How dissimilar is that? What does 96 percent look like?

A Ninety-six percent sounds like -- like a lot of similarity, but -- but it's -- but it's too distant to be the direct progenitor for SARS-CoV-2 to have risen directly from that. Humans and chimpanzees are 99 percent similar, so it's still quite a ways away.

Q So that was going to be my question. That's kind of what we refer to, that it's a ways away. Humans and chimps are 99 percent similar. What is the difference in the human genome versus the SARS-CoV-2 genome? Are they -- like, how many different nucleotides, or whatever the right term

is, are they? So, like, the human genome is billions, I image. How many is COVID-19?

A I haven't seen anyone try to do that comparison.

Q Well, I'm just saying 96 percent on 10,000 different nucleotides is different than 99 percent on 3 billion.

A On a similar number -- or a different number.

Q Yeah.

A Yes, I'm not sure how one would do that comparison. It may well be that the -- there are experts who would know how to do that, but I -- I do not know.

Q No, I appreciate it.

I want to spend some time on each of the individual arguments that Dr. Andersen made and that you countered or rebutted, however you want to frame that. Starting on page 2, the part of the paper starting with 3.1 and talking about the receptor- binding domain, you list out Dr. Andersen's argument, so I won't read it back to you, but -- and you kind of get into this, but does that argument rest on an unsubstantiated assumption?

A I thought so, yes.

Q Can you go into a little bit more detail as to why? Obviously it's written here, but if you have any detail beyond what you wrote down.

A Well, they had pointed out that the receptor-binding domain would not have been predicted to be very good or optimal for infecting human cells. And for me that implied an assumption that if SARS-CoV-2, whatever was in lab, that it probably would have come about in that way where one might have a priori designed a sequence to infect human cells.

And that certainly is possible, but we showed examples of the literature of novel coronaviruses being developed in different ways, and what we -- what we found was more of an empirical approach where one might take a backbone virus, a coronavirus from one species and insert part of a coronavirus from another species to observe the effects, and all serving stated purposes of developing medical countermeasures or improving public health. But what we saw in scientific practice was much more of an empirical approach and not -- not an approach by design to achieve a specific function.

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

A Yes.

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

A That's right.

Q The authors -- and you touch on it a little bit -- rest a lot of weight on the pangolin RBDs that came out around this time that were near identical or identical to what COVID-19 had. Can you explain how that particular virus doesn't rule out a laboratory-based scenario?

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

Q So one last on the RBD. Did any of the arguments put forth by the proximal origin authors regarding the receptor-binding domain rule out the laboratory-based scenario?

A Not in my assessment.

Q Moving forward to the furin cleavage site on -- starts on page 3 and marked 3.2 on the document. Kind of -- it's going to be similar questions on all these. Does the proximal origins argument regarding a furin cleavage site rest on unsubstantiated assumptions as well?

A I thought so, yes.

Q And you discussed this a little bit, but has there been a furin site observed in any viruses in the sarbecovirus family other than COVID-19?

A Not -- not to my knowledge.

Q Do -- does that lineage of coronaviruses, the sarbecoviruses, is it common for them to recombine outside of their lineage, if you know?

A As far as I know, that occurs.

Q Okay. My colleague talked about this a little bit, but in your experience is it possible to put enough laboratory-based selection pressure on a coronavirus without a furin site to gain one?

A I don't know if that's been observed for coronaviruses. It has been reported for other viruses.

Q And is it possible to insert a furin site into a virus without leaving a trace?

A Yes.

Q Do you know, like, how people would go about doing that, what the common process is?

A Well, the tools that are available now for -- for synthesizing viruses -- and these are commonly used by labs around the world, in contrast to older tools, do not leave any -- any marks, essentially no fingerprints of where those inserted sequences -- the boundaries of them are.

So one wouldn't be able to tell from the sequence.

Q Would there be other ways to tell if it was a naturally occurring furin site or laboratory constructed? Other than, like, the lab notebooks obviously would probably have it.

A Yeah, again, this is -- so this is not a deep area of expertise for me. But as far as I know, the answer is no.

Q And Dr. Andersen's primary argument, if I can summarize it maybe too plainly, is that we saw based off your insights in related coronaviruses, so it's possible that there was a furin site in this coronavirus; is that correct?

A Yes. Yes, they did note that other coronaviruses not as closely related to SARS-CoV-2 did have these sites.

Q But they presented no scientific evidence saying to back that the furin site in COVID-19 was a natural occurrence?

A That's correct. Well, they -- the one argument they did make was that -- that in order -- and I'm paraphrasing, but in the first paragraph of Section 3.2, that one would have had to begin with a progenitor virus very similar to SARS-CoV-2, and that such a virus had not been reported. And so -- and that was another argument that we saw as not scientific because it assumed that if a virus had

been -- if a progenitor virus had been identified, it would have been reported.

Q That's the backbone argument that they make, right?

A Yes.

Q I'll ask some questions about that in a second, but finishing out the furin site ones, same question: In your estimation, did the proximal origin authors' arguments regarding the furin cleavage site rule out a laboratory-based origin scenario?

A No, not in my mind.

Q Moving on to the reverse genetics system and backbone question on page 4 marked 3.3, same original question here: Does the proximal origins authors' argument rest on unsubstantiated assumption?

A Yes.

Q You touch on this a little bit, but just for the record, are -- in your experience, is every scientific research experiment published?

A No.

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

A Yes.

Q And even simpler than that, not necessarily a

novel backbone, but is it possible that researchers just used an unsequenced or unpublished coronavirus as the backbone?

A Yes.

Q Thank you. Going into kind of the wrapping up and going into the conclusions of the proximal origin paper and just want your opinion on the conclusions they made. So the first conclusion they had -- and if you want to read it on Exhibit 1, it's the last sentence on the second paragraph in the first column, and says, "Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus." At the time or now do the facts or science support that statement?

A I don't think so.

Q The second major conclusion is on the last page kind of, like, right in the middle of the second column and reads, "However, since we observed all notable SARS-CoV-2 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." At the time or presently, do the facts or science support that statement?

A No.

Q To your knowledge -- and you touched on this a little bit in the paper -- has proximal origin been used as proof of a natural origin of COVID-19?

A It has been used to support the argument for a natural origin by many, yes.

Q Does proximal origin prove a natural origin of COVID-19?

A No, I don't think so.

Q Do you think in your expertise that proximal origin downplayed the possibility of a lab leak?

A I think it was not balanced. And in my mind, the evidence presented in the paper is -- is consistent with a natural origin, but is also consistent with a laboratory origin and doesn't weigh one way or the other. And that was really the argument that we tried to make in our work and in the document.

Q And then I'm going to ask for your own opinion. And if you don't want to give it, I will respect that you don't want to give it. What do you think is the most likely COVID-19 origin scenario?

A I am about where I was back then, which was pretty much down the middle.

Q All right. I'm going to ask a couple questions about intelligence community involvement. Hopefully it doesn't elicit anything classified. If it does, just let me know. Since early 2020, the intelligence community has been investigating the origins of COVID-19. Are you aware of those efforts?

A Yes.

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 generally aware of that announcement?

A Yes.

Q On August 27, 2021 the Office of the Director of National Intelligence released an unclassified summary of this assessment. Are you aware of and you've read that summary?

A I did read it at the time, although by then I was on to my current assignment, so I wasn't as involved.

Q Okay. Probably the same answer to this next one. On October 29, 2021, ODNI released a full declassified assessment. Were you aware and did you read that one?

A Yes.

Q While you were at DIA -- and this can just be a "yes" or "no" -- were you involved in the IC's origins investigation?

A No.

Q While at DARPA have you been involved in the IC's origins investigation?

A No.

Q Did you ever brief anyone in person or

otherwise in the outside -- I kind of already asked this -- but outside of NCMI or DIA about your working paper?

A No.

Mr. Benzine. We can go off the record.

(Recess.)

[redacted]. We can go back on the record.

BY [redacted]:

Q Commander, I have just a few more questions, mostly about things that we touched on in the previous round. First is there was a brief discussion about RaTG13, 96.-something percent genomic similarity to SARS-CoV-2, and a little discussion about proportions; in other words, if the human genome is a lot bigger than the viral genomes we're talking about here, is it really apples to apples to be comparing 96 here or 99 there. My only question is -- my understanding, but my question is is it right to say that regardless of the absolute number of nucleotides or total volume of genetic material, that 96.2 percent overlap between RaTG13 and SARS-CoV-2 tells us that RaTG13 is not the progenitor virus for SARS-CoV-2; is that fair?

A Yes, that's fair.

Q With respect to the furin cleavage site, we've talked a little bit about, okay, furin cleavage site has not previously been observed at the sarbecovirus subgenus -- I think that's the right term -- but has been observed one

level up at the genus level, which I think is betacoronaviruses. To the extent you have any views on -- sometimes it's been challenging for us to weigh the respective merits of that. How strange is it to see it for the very first time in sarbecoviruses? How not strange is that when you consider that they exist in the betacoronaviruses? My understanding is they exist in at least two of the four endemic human viruses, the common cold. So do you have any views on how unexpected it would be to see that for the first time, but it's really not the first time when you look elsewhere on the tree?

A I don't think it would be very unexpected, because we have sampled such a small portion of the virosphere.

Q Some questions about sort of the precise phrasing in the proximal origin paper. I guess first, we focused on a line on the first page of that paper in the second paragraph of the paper. It says towards the end of that paragraph, "Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus." The precise meaning of "laboratory construct or purposefully manipulated" I'll say as a reader has not always been perfectly clear to me.

We have heard elsewhere that the phrase "purposefully manipulated" was intended to mean the idea that a human,

scientist, deliberately set out to build SARS-CoV-2, constructed a genetic code that would then create SARS-CoV-2, designed it to be exactly what it is, and that there was an intent to communicate that that -- just for the phrase "purposefully manipulated." Not "laboratory construct." That apparently was supposed to mean something else. But "purposefully manipulated" was intended to mean what I just said.

And things like the pangolin receptor-binding domain with the same mutations, my understanding is that those same mutations have since been found elsewhere in a bat virus, the suboptimal computational predicted binding infinity receptor-binding domain, do seem to strongly suggest that that discrete scenario seems not to be the case. Does that seem like a fair point of view to you as well?

A It's hard for me to assess what the intentions of a scientist might have been. So this is why we stuck to the published literature and didn't try to guess what may have been in the minds of whoever may have worked on this virus.

Q And I think to an extent -- and it's difficult because it's almost divining meaning from words that don't clearly communicate them. But to the extent that that phrase would be read to indicate the method -- a theory of a method that this particular virus was or was not created by the

method of essentially original human design from scratch, from the imagination of a human scientist, it seems as if -- it seems fair to conclude that that is likely not to be the case simply because these particular mutations are seen to spontaneously exist or evolve in nature. Do you have a perspective on that discrete narrow question?

A I think my own subjective sense is that it's -- I would think it unlikely that someone dreamt up the -- every detail of the SARS-CoV-2 genome and created that. And what we attempted to show was that there were other more plausible ways of getting to SARS-CoV-2.

Q One question is what did you -- if you recall, because I know it was several years ago, but what did you take proximal origin -- you may not have spent months of your life thinking about this exact question, but what exactly did you take proximal origin to be asserting? Because there's language sprinkled in throughout this paper that could be read to not always be saying the exact same thing.

There's what we've looked at, "Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus." There's language we looked at says, "We do not believe any type of laboratory-based scenario is plausible." At the same time, on the last page of the paper they drop a sentence in that says, "It is currently impossible to prove or disprove the theories of

origin described here." They seem to have said, "We think we've proved that it's not genetically engineered."

But when we talk about serial passage in a lab versus the various zoonotic possibilities, they also say it's not possible to prove or disprove those other theories. And so we've heard occasionally an argument that, "Hey, we weren't saying it's definitely not a lab scenario. We're just saying that's just not the one that we find to be plausible." I'm just curious, you as a reader, where you felt that that paper fell on that spectrum.

A Yeah, there were some inconsistencies there, and we tried to focus on the statements that were more clear. But what exactly they intended to assert, what precisely the argument was was not always clear.

And I think what we attempted to show was that -- was that a laboratory origin, which could involve many different -- many different ways of getting to SARS-CoV-2, was plausible, and that the plausibility of that scenario is not lessened by the arguments set forth in the paper.

Q And that flows nicely, I think, into my last question, which is just that -- I think the answer to this is clear, but you would not have had any personal involvement or personal knowledge of the drafting process, whether scientific, psychological or otherwise, of the proximal origin paper; is that right?

A Correct.

[redacted]. We can go off the record.

(Whereupon, at 11:19 a.m. the interview was concluded.)