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I have added links to some of the exhibits. Details are at the end of this file.
("PI" means "principal investigator".)

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Robin Whittle 2024-05-23 https://vitamindstopscovid.info/07-origins/

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COMMITTEE ON OVERSIGHT AND ACCOUNTABILITY,
SELECT SUBCOMMITTEE ON THE CORONAVIRUS PANDEMIC

U.S. HOUSE OF REPRESENTATIVES,

WASHINGTON, D.C.

- INTERVIEW OF : RALPH S. BARIC, Ph.D.

MONDAY, JANUARY 22, 2024

The Interview Commenced at 10:07 a.m.

Appearances

MEMBERS OF CONGRESS:

Brad Wenstrup, Ohio,

For the SELECT SUBCOMMITTEE ON THE CORONAVIRUS PANDEMIC:

MITCH BENZINE, Staff Director

ERIC OSTERHUES, Majority Chief Counsel

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PETER SPECTRE, Majority Professional Staff Member

JOSEPH ROMERO, Minority Counsel

ALICIA YASS, Minority Senior Counsel

MILES LICHTMAN, Minority Staff Director

For the COMMITTEE ON ENERGY AND COMMERCE:

JOHN STROM, Majority Counsel

ALAN SLOBODIN, Majority Chief Investigative Counsel

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Exhibits [Links inline, below. "Bates" is a legal indexing system. RW]

Minority Exhibit Page No.

A - Nature Medicine December 2015 article.

A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence.

B - Document, DARPA-PREEMPT-HR001118S0017.

Majority Exhibit No. Page No.

1 - Email cover sheet, Bates

UNC_SSCP00023674.

2 - The National Academies of Sciences, Engineering, Medicine, Expert Meeting Agenda, Bates REV0000809.

3 - 1R0AI110964 Year 4 Report.

[This is really 1R01AI110964. RW]

4 - Letter dated May 28, 2016, with attachment.

5 - Document, PREEMPT call (EHA, Ralph & Time of UNC) - 2 March 2018.

6 - Letter dated May 15, 2015, from Chernay Mason to Ms. Barbara Entwisle and Ralph Baric, Ph.D., Bates commencing UNC_SSCP00002629 229

PROCEEDINGS

Mr. Benzine. We can go on the record.

This is the transcribed interview of Dr. Ralph Steven Baric conducted by the House Select Subcommittee on the Coronavirus Pandemic, the Committee on Oversight and Accountability, and the Committee on Energy and Commerce under the authority granted to them by House Resolution 5, House Rule 10, and the Rules of the Committee on Oversight and Accountability and Committee on Energy and Commerce.

This interview was requested by Chairman Brad Wenstrup, Chairman James Comer, Chair Cathy McMorris Rodgers, Chairman Morgan Griffith, and Chairman Brett Guthrie as part of the Committee's oversight of the federal government's response to the coronavirus pandemic.

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.

Pursuant to House Rule 10, the Committee on Oversight and Accountability has jurisdiction to investigate any matter at any time. And pursuant to House Rule 10 and 11, the Committee on Energy and Commerce has jurisdiction for public health service agencies, including the National Institutes of Health and the entities it funds, as well as federal biomedical research and development.

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

The Witness. Ralph Steven Baric, B-A-R-I-C.

Mr. Benzine. Thank you. Dr. Baric, 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. We recognize that you are here voluntarily and appreciate that.

Under the Select Subcommittee and Committee on Oversight and Accountabilities 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 present with you today?

The Witness. Yes.

Mr. Benzine. Will counsel identify themselves?

Mr. Ervin. I'm Clark Ervin at Squire Patton Boggs.

Mr. Benzine. For the record, beginning to my left, will the rest of the Majority staff and the additional staff members, please introduce themselves with their name, title, and affiliation?

Mr. Strom. John Strom, senior counsel, House Energy and Commerce Subcommittee on Oversight Investigations, Majority.

Mr. Osterhues. Eric Osterhues, chief counsel, Select Subcommittee, Majority.

Mr. Slobodin. Alan Slobodin, chief investigative counsel, Majority staff, House Energy and Commerce Committee.

Ms. Brewer. Madeline Brewer, counsel for the Majority, Select Subcommittee.

Mr. Spectre. Peter Spectre, professional staff member. Select Subcommittee, Majority.

Ms Yass. Alicia Yass, senior counsel, Select Subcommittee, Democratic staff.

Mr. Romero. Joseph Romero, Democratic counsel, Select Subcommittee .

Mr. Lichtman. Miles Lichtman, Democratic staff director of the Select Subcommittee.

Ms. O'Connor. Constance O'Connor, senior counsel, Committee on Energy and Commerce Subcommittee on Oversight and Investigations.

Mr. McAuliffe. Will McAuliffe, chief counsel for the Minority, Energy and Commerce Committee, Subcommittee on Oversight and Investigations.

Ms. Dockham. Kelly Dockham, director of federal affairs at UNC Chapel Hill.

Mr. Lambeth. David Lambeth, counsel for UNC Chapel Hill.

Mr. Benzine. Thank you.

Mr. Chairman?

Mr. Wenstrup. Brad Wenstrup, Chairman.

BY **MR. BENZINE.**

Q Dr. Baric, before we begin, I would like to go over the ground rules for this interview. The way the 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 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 an hour to ensure completion of that specific line of questioning, including any pertinent follow-ups.

In this interview, while one member of the staff for 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.

To ensure the court reporter can properly record this interview, please speak clearly, concisely, and slowly. The court reporter cannot record non-verbal 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?

A I do.

Q 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 and we will attempt to clarify, add context to, or rephrase our questions. Do you understand?

A I do.

Q 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?

A I do.

Q 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?

A I do.

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

A I do.

Q Is there any reason you are unable to provide truthful testimony today?

A No.

Q The Select Subcommittee 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?

A I haven't read the regulations, but I understand what you're telling me.

Q All right, thank you. Ordinarily, we take a five-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 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?

A I do.

Q Do you have any questions before we begin?

A No.

Q Thank you. I want to start really briefly and run through your education and experience.

Where did you attend undergraduate school and what degree did you graduate with?

A I attended North Carolina State University, actually on a swimming scholarship. I studied zoology and received a bachelor of science degree there. I stayed on at North Carolina State University in the Department of Microbiology, where I received a Ph.D., studying emerging alphaviruses.

From there, I went to University of Southern California, working with a researcher who focused on coronaviruses, specifically a virus called mouse hepatitis virus. And then from there, I went to my faculty positions, which I assume you're going to ask next.

Q Yes. More, I guess, who is your current employer and current position?

A Currently, I am a William R. Kenan, Jr. Distinguished Professor of Epidemiology and Microbiology and Immunology in the Gillings School of Global Public Health at the University of North Carolina, Chapel Hill.

Q And did you hold any academic positions prior to joining UNC?

A I was hired at University of North Carolina as an assistant professor in the department of parasitology in laboratory practice. Ultimately, that department was merged into the Department of Epidemiology in the School of Public Health. And so I continued on as an assistant professor in the Department of Epidemiology. Moved on to associate professor, and then eventually full professor. And then a few years later, distinguished professor.

Q And you currently run a lab at UNC?

A I do.

Q How many people report to you in the lab?

A Somewhere between 40 and 50. It depends on how you count. There's undergraduates that come through and do work, actually, more training to help move them forward, either in graduate school or medical school. But they're not really doing detailed scientific investigation.

Q And then what are kind of your normal duties or roles and responsibilities?

A Review research, come up with ideas, try to be innovative, problem solve. So if people are having experiment problems with getting experiments to produce results, I usually am a big help. I perform a lot of help with problem solving. I write grants, I teach, perform service for the university. I think basically all faculty do research, service, and teaching, if that -- you're asking more globally. I didn't know if you were asking more specifically or not.

Q No, that answers the question.

A Okay.

Q Do you currently hold or have you previously held any positions on boards of companies or nonprofits?

A Yes, I am on the scientific advisory board of Vaxart, the scientific advisory board of a company called Adagio, which changed their name to ILiAD. I have been on the scientific advisory board for Takeda Vaccines, and on the scientific advisory board for Sanofi Pasteur with their vaccines as well.

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

A No.

Q Thank you. I am going to go through a list of names, and just to the best of your recollection if you had conversations with these folks, email, over the phone, in person, regarding the origins of COVID-19, the Wuhan Institute of Virology, or EcoHealth Alliance, beginning January 1, 2020, until now.

A Okay.

Q Dr. Francis Collins.

A Yes, Dr. Collins, and Kizzmekia Corbett, and I were honored by the governor of the State of North Carolina for making contributions to humanity. That was the Governor's Award. And Dr. Collins sent me an email in 2021 saying congratulations. I congratulated him back, so —

Q Any conversations with Dr. Collins specific to the origins?

A No, not to my recollection.

Q Dr. Anthony Fauci?

A This is emails, or calls, or all of the above?

Q Any manner of communication.

A So — and from this —

Q January 1st.

A I mention that, because the first time I actually met him was at basically a conference on developing strategies to move forward with MERS coronavirus, research objectives, back in 2014. So that was the first time I met him.

But after January 1st, 2020, I was on a phone conference with him on February 1st of 2020 that had to do with the origins. I met with him in his office with several staff, high level staff, both including himself and other representatives from both the extramural and intramural program for NIH on, I think, February 12, 2020. And I believe that's it.

Oh, yes, I was also part of — we were both part of an email exchange that was associated with the Red Dawn group, which was basically trying to help prepare the United States to respond to — to track and respond to the emerging COVID-19 pandemic.

Q Thank you.

BY **MR. STROM.**

Q On the Fauci meeting, you mentioned you said — I may have just misheard you — intramural and extramural NIAID staff?

A I believe so, yes.

Q Do you recall any names?

A Yeah. Auchinhue — I've got to look at his name.

Q Auchincloss?

A Yes, Auchincloss. Alan Embry. There's a series of emails that included Maureen Beenan, and someone else that I believe were also there. A few other names that I can't recall.

Q David Morens?

A I can't recall whether he was there or not.

BY **MR. BENZINE.**

Q Emily Erbelding?

A We had email exchanges, and I actually talked to her beforehand to try to find out what people wanted to talk to me about. So I believe she was there, but I had never met her personally, just talked to her on the phone.

So it wouldn't surprise me if she was there.

Q The same topics and timeframe. Dr. Lawrence Tabak?

A No, I don't think so. Not to my recollection.

Q We touched on Dr. Auchincloss, but any conversations with Dr. Auchincloss outside of the mid- February meeting?

A I think there were some group emails, not one-on-one emails like in May, but I can't recall the exact nature of those emails. I'm sure you have my emails, so you probably can figure it out.

Q Dr. Cliff Lane?

A I don't believe so, no.

Q Dr. David Morens?

A I don't believe so.

Q Dr. Ping Chen?

A Not to my recollection, no.

Q Dr. Victor Zhao?

A Not to my recollection.

Q Dr. Robert Redfield?

A He was part of the Red Dawn group emails as well. So all of us — none of us, I think ever, including Fauci, ever made every single call, so we would have been on some calls together.

Q But more of the group calls?

A It was all group calls, not a person.

Q Dr. Michael Lauer?

A Not to my recollection.

Q Dr. David Christian Hassell?

A Yes. He emailed me, I think on the 2nd of February, sometime in February, but I can't recall actually what the substance of that was.

Q But it was regarding one of these three topics or COVID, kind of?

A It occurred after the origins call with Fauci, so I imagine it was something along those lines, but I can't recall the detail. I would have to see the email.

Q Dr. Jeremy Farrar?

A Indirectly. He had someone from his group email me about a 4chan threat that had been made toward me.

Q Dr. Kristian Andersen?

A I met Kristian at a couple of meetings. He emailed — I think we were on the National Academy Origins sort of committee together, so we would have interacted there. He was on the call, on the February 1st call, so he was there. I believe he emailed me the next day, and we were going to have a call. But for the life of me, I can't remember any details of that call, or whether it even happened.

Q Dr. Michael Farzan?

A I've known Mike Farzan for a long time, all the way back from the 2003 SARS epidemic, and so we have communicated over the years. I believe he was on the May 1st call, now that you mention his name, but I don't believe we had any other direct emails with him.

Q May 1st or February 1st?

A Sorry, February 1st.

Q Dr. Eddie Holmes?

A I've known Eddie Holmes for a while as well. He also emailed to pass on a 4 chan threat. But otherwise, no.

Q Dr. Ian Lipkin?

A I've known Ian Lipkin for a long time. We were funded together on a grant that he was PI on for about five years. Any time I go to New York, I visit him and talk to him, sometimes stay at his house. We talk about science off and on all the time, potential collaborative research that we want to do, interesting results. He's a friend and a colleague.

Q Any conversations regarding the origins of EcoHealth?

A I think several months after, I don't exactly remember when I was in New York City, but we did talk about origins at that time. He told me about his trip in person, in detail. We may have had a call on it as well, but he talked about his trip to China early in the pandemic, when he went to offer his assistance.

We talked about the diagnostic tests that were being run and the lack of standardization among those tests, which was probably his promoting, you know, resulting in some inaccuracy in the reporting numbers, and offered to help with that. He did mention George Gao's call to him, I think at the end of December, so we've talked about that.

But I guess at some later date, after the Science paper that I signed with others to say that the lab leak theory needed to be looked at in more detail, he called me up to ask me why. And I sent him a couple of papers that the Chinese had published, where they were doing virus discovery work under BSL-2 conditions, which is one of the main reasons why I felt that the potential laboratory escape hypothesis shouldn't be, in essence, put under the rug.

Q Do you recall what those papers were?

A I could provide them for you —

Q Okay.

A — if you wanted.

Q That's fine.

A But they were basically Zhengli Shi's papers.

I can tell you her original paper on this, which was in Nature around 2012, they were very vague about safety conditions. They said they followed Chinese regulations. But in a Journal of Virology paper, and I believe a PLOS Pathogens paper are the two, I think, they actually stated that they were doing the culturing work under BSL-2. And then they continued that even into September of 2020, which I thought was irresponsible.

Q Not the biosafety level that you would conduct that work at?

A Well, I think you have to put it in perspective. So biosafety regulations in the United States are very clear, but they're heavily focused on known human pathogens.

So when you move into animal pathogens, pathogens that are in animals, where you don't really know the threat level, to some extent, that becomes a decision between the investigator and the local IBC, which may or may not talk to federal authorities about whether this is appropriate or not.

So, for example, when we started working with zoonotic coronaviruses, our underlying hypothesis was that there are strains that exist in nature. They may be rare, but they could — they could potentially infect human cells. And if that's your hypothesis, then you do it under BSL-3.

Q Yeah.

A The Chinese came to a different — their biosafety regulations are different. But, again, when you ask me about specific regulations, as the Chinese would say to me, Ralph Baric doesn't determine the biosafety levels in this country, in China, right?

Q Yeah.

A So it's just different. So we were at a higher level containment in the United States. And then anyone who would ask me for these viruses, I would insist that it be done at a higher level containment. So I kind of set the standard in the United States.

Q Moving on with the communications questions. Dr. Andrew Rambaut?

A Not to my recollection. Yeah, I don't even know who he is, sorry.

Q Dr. Christian Drosten?

A I know Christian Drosten. We were members of the Nidovirus Taxonomy Committee. So there was a large number of emails between us and other members of the committee about naming the novel coronavirus. Originally, it was called — what was it called, 2019 novel coronavirus, or something like that, right?

And so that committee determined that we should name it SARS Coronavirus 2, based on its viologenase, how closely related it was to other sarbecoviruses, although it represented completely different branches of the tree.

So the branch of the tree before SARS Coronavirus 2, there were two branches. One were called clade 2 strains that couldn't use human receptors or grow in human cells. And the second was the SARS coronavirus 2003 related strains, like WIV1 and SHC014 and a bunch of other viruses. So it's on this branch of the tree. These have 6,000 nucleotide differences than SARS2. So it was a new discovery.

So the taxonomy group basically says that it was closely enough related to SARS1 and caused similar disease features, that it should be named SARS2.

Q Do you recall receiving any pushback from the Chinese?

A The Chinese were very unhappy about that. I think several members of the committee received a lot of pushback. I believe they ultimately wrote a paper that they published saying that — giving their reasons why they didn't like that name.

Q Do you recall any of the reasons?

A I actually didn't read the paper, because I didn't want to put up with the nonsense. But so you would be asking me to speculate. I would guess that the SARS coronavirus 2003 impact on Chinese society, and their view of their nation was very — was very extreme.

And so they're very sensitive. They're probably very sensitive to any suggestion that they failed to put in appropriate policies that would prevent another SARS-related virus. That would be my guess, but I was not in the room, right?

Q Thank you. Dr. Ron Fouchier?

A I've known Ron Fouchier for 15 years as well.

I'm part of a scientific advisory board for a CEIRR grant, which is a center of excellence in virus research that is run out of Mount Sinai. And Ron Fouchier is a member of that group.

And so I'm familiar with his research. We talk about his research when we had those meetings, I think they were by Zoom, after COVID-19 occurred. He was one of the few researchers that didn't shift his influenza virus program into the COVID-19 at the time. So we didn't talk too much about origins. He was on the February 1st call.

Q Do you recall any conversations with him regarding kind of, like, genetic manipulation or being able to manipulate viruses without leaving a trace?

A By — from 2020 on?

Q Mm-hmm.

A Okay. So from 2020 on, there are a variety of ways that you can make recombinant DNAs that are identical to the sequence of a virus. One of the first ones was an approach we developed using class IIS restriction enzymes that you can orient either within the sequence of the virus or on the outside of it.

So when they're on the outside, the way the enzyme is cut, it cuts in the virus sequence, and it leaves actually the virus sequence is the overhang. And they're different sequences, so you end up with directional cloning.

So typically, with a restriction enzyme, if you cut and you add an enzyme to make them come together, there's no directionality to it, because the ends are all compatible. So you get these large concatemers in a random fashion.

But some enzymes, especially the ones that were associated with the approach that we developed, leave variable ends that are unique, and can only link up with a complementary three or four nucleotide. So that, then, allows you to assemble a genome without leaving restriction sites that you engineered into the genome.

Now, you might ask why. I mean, the reason you do this is the primary sequence of the virus is virulence determinative. So if you manipulate the primary sequence, you can attenuate and get a different phenotype than you get from wild type.

So the way that we would deal with that is that we would then engineer in signature sequences or mutations that would say this was made in the Baric lab. So I guess to answer your question more thoroughly, you don't have to do that, okay? The other approach is now the synthetic DNA approaches allow you to get much larger clones within the range of direct synthesis.

And then there's another approach. There's a company that does gateway cloning that allows you to assemble genomes commercially that I believe that you can, or may or may not decide you want to leave a trace. And then there's other bacterial enzymes that they've used to make full length genomes of bacteria species that the enzymes chew on one part of the DNA. And so they leave an overhang that's specific for the other fragments.

So, yeah, a variety of approaches that are available.

Q Any conversations with Marion Koopmans?

A I've known Marion Koopmans for years. She and I both worked on noroviruses for years. And so if you look historically through my emails, we talked off and on. I don't believe when she took — recently took the job to run the sort of emerging infectious disease group in the Netherlands in the beginning of the COVID-19 pandemic, I can't recall any emails between us.

Q Dr. Michael Worobey?

A Let's see, I don't believe so, but I think he was at the nidovirus meeting in Switzerland this year, and I talked to him there. He may have been at — either him or Dr. Garry were also at the emerging infectious disease meeting at the NIH, and I talked to him there as well.

Q Garry was my next one. Dr. Robert Garry.

A Okay. I don't think any direct emails. But the nidovirus conference, I think so.

Q All right.

A But the nidovirus conference, I think so.

Q Dr. Jonathan Pekar?

A I don't believe so.

Q Dr. Florence Debarre?

A Oh, she emailed me, I don't remember when. She's an evolutionary biologist in France, so she emailed me.

Q Dr. James LeDuc?

A I've known Jim LeDuc also for a long time. I think he sent me — I'd have to look at some notes. Yeah, he invited me to be part of an origins group in, like, March 2020, but I couldn't — I couldn't do it, because I was swamped with other responsibilities, so I didn't participate.

Q Any conversations with him regarding biosafety at the WIV?

A He was a member of the National Academy group. This is prior to 2020, so National Academy of Sciences in the United States and the National Academy of Sciences in China held three joint meetings, one in Beijing, one in Harbin, and one in Galveston Island, about biosafety and biosecurity. So in the context of that, there were discussions about biosafety and trying to harmonize — in essence, trying to harmonize and to teach each other's group about standard practices and that kind of thing. But it wasn't more like there was a small group sessions, where we talked about biosafety. It was more of the science that we were doing and the levels that it was done at.

Q Dr. Shi Zhengli?

A I've known her mostly by email. I think we have met at a couple of meetings from about 2010 on. I have emailed her, she has emailed me, and I have emailed her back since January 2020.

Q Anything specific to origins or what was happening at the Wuhan Institute?

A Most of our email exchanges, I think they began — they started initially with the naming of the virus. She was one of the scientists that sent me an email complaining about the name at some point. We had a couple of email exchanges about some transgenic mice that I had sent her under MTA that she was supposed to use at the Wuhan Institute of Virology that somehow ended up at a commercial group in China that they were trying to sell. There's emails about a Cell paper that we were coauthors on.

I seem to recall there may have been an email after the paper in Science saying about the potential for — to open up the

investigation, almost — if it did occur, almost assuredly would be negative. But, again, you guys have my email, so you may know better than I do.

Q The transgenic mice that you sent to the Wuhan Institute under an MTA, you just said they ended up at a Chinese commercial group. How did you learn that?

A I had a friend, a former post-doc from my lab who works at the University of Maryland, Matt Freeman, sent me an email or a phone text, I don't exactly remember which, which had a product development plan on it saying how much the mice were, which infuriated me because, to some extent, NIH guidelines, should you receive a grant, and journals, should you publish in journals, have a requirement that you share reagents with other collaborative groups, and it's done under MTA. And you don't try to make a profit off of somebody else 's discoveries.

And so the mice, again, I think it was around 2015, the paperwork started. It probably took a couple years to get through China, because it's really hard to get anything in or out of China, but I think by 2017 or so, they might have the mice. We would have it in our shipping records. So I don't know the exact date, but I just remember it took a long time.

I'm sorry, what else is your question?

Q I guess, like, what is your presumption there, that you provided the Wuhan Institute with these mice, they had extra mice, and then sold them off, or do you think you were kind of taken?

A I think in an expanding epidemic, there was a desperate need for research groups to have access to mouse models, so they could test countermeasures. It was a very good reason to share reagents across nations, because wherever an outbreak occurs, that's where countermeasure development starts.

So it makes a lot of sense, just from a global health perspective. What doesn't make sense is that it ends up at a company, and the company is now trying to sell it back to the United States with our emerging pandemic occurring here to make a profit off. So that was infuriating.

Q Any conversations regarding the origins with Dr. George Gao?

A I've met George off and on, a famous influenza virus researcher, who ultimately became the head of their CDC during the pandemic. George emailed me to share a paper that he had published on one of the earliest variants of concern called D614G. We had published on that, so he sent that. More recently, he sent me an email inviting me to China to do this kind of post-COVID thing that I decided not to go to.

Q And we're going to talk about this more, so just briefly, conversations with Dr. Peter Daszak about the origins?

A Just briefly about origins. So I think he, as well as — I don't know, several other people, as well as seeing it on ProMED myself, sent me an email telling me that there's an unknown respiratory disease in China, I think around the 30th of December. So whenever that came out on ProMED. And then on the 5th, he also emailed me to mention that it was probably a coronavirus.

Q On January 5th?

A Around January 5th. I also had received emails from other people that it was a coronavirus on January 5th. And by the 6th or so, I also knew it was a coronavirus, because I was asked to review a paper.

Q Any conversations with Dr. Ben Hu?

A Not to my recollection.

Q What about Dr. Lanying Du?

A My capacity to link Chinese names to the researchers is not good.

Q She was at the Blood Center of New York, and is now at Georgia State.

A I don't think so, not to my recollection.

Q And Dr. Zhou Yusen or Yusen Zhou?

A I would have to do email research to know that. No, nothing that comes to mind.

BY **MR. SLOBODIN.**

Q One more name. Dr. Lili Ren from the Institute for Pathogen Biology in Beijing?

A If she did, it would not have been a person-to-person email, I don't believe. It would have been a group email.

So one of the things that was occurring in the early days of the pandemic was that the National Academy set up some phone conference calls between Chinese scientists and American scientists. And they usually lasted an hour. And basically, the goal of those calls was to discuss patient care, diagnostics, public health control measures, those types of issues, and basic science questions.

So it was very likely that there were several members from China that would have been on that call. You had two pages, two to three pages of pictures with names under them, and I didn't take screenshots, or anything. So I couldn't tell you. The one person I know was on it was George Gao, and Zhengli Shi was also on. Those are two people definitely I recall.

BY **MR. STROM.**

Q For the January 6th paper that you reviewed, do you recall if that had the sequence of the virus?

A It did. When it was first sent, it did not.

All three reviewers immediately asked for the sequence.

BY **MR. BENZINE.**

Q Do you recall what the paper was?

A So review processes are normally confidential, so if I tell you what journal it is and this comes out, then I — can we go off the record, so I can tell you that?

Q We can go off the record and talk, about it, and determine what to do. And I can talk to Clark about redacting if we need to.

A Just the review process is supposed to be confidential. So I would prefer that it remain confidential, although I guess, to some extent, the paper got accepted, so

Mr. Benzine. We can go off the record.

(Discussion held.)

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

BY **MR. STROM.**

Q Dr. Baric, you referenced receiving a January 6th paper that was subsequently published?

A 6th or 7th.

Q It was subsequently published in Nature, showing that the virus — the unknown outbreak was caused by a coronavirus.

A Yes.

Q And then you mentioned earlier that the sequence of the virus was not initially provided. Do you recall when you got access to the sequence?

A Within about 12 hours from requesting it from the journal. And just for point of clarity, I knew it was a coronavirus before I received the paper.

Q Do you recall if that version of the sequence had the furin cleavage site in it?

A Are you asking me in the context of January 6th or 7th, or are you asking me in the context of —

Q You don't recall seeing a sequence that omitted —

A No.

Q — the furin cleavage site?

A No, it was not omitted.

BY **MR. BENZINE.**

Q Was this the first time that you saw the sequence?

A Yes.

Q You also said, and ProMED did a notification on December 30th, and you said that was around the same time you were made aware. Were you made aware by the ProMED notification or through other means?

A Well, the ProMED announcement came about the same time I heard from other people that it was — that there was an unknown respiratory disease in Wuhan.

Q Who did you hear from?

A Peter Daszak, I believe Mark Denison sent me an email. It wouldn't surprise me if Matt Freeman sent me an email. Corona virologists, it's a small community, so friends email all the time. And if there's an unknown respiratory disease in China and you're a corona virologist, you're thinking it could easily be a coronavirus.

Q And then you said January 5th was when you knew it was a coronavirus. Am I remembering that right?

A Yes.

Q How did you know that?

A So I'm blanking on his name. Fred — so Fred Hayden is a clinician at the University of Virginia, who does clinical trials for either vaccines or immunotherapeutics or drugs against respiratory viruses, severe respiratory viruses.

And he had — Chinese scientists had contacted him around the 2nd or 3rd. And Fred was a member of the scientific advisory board for our center for excellence in translational research that was run by Rich Whitley out of the University of Alabama.

So he knew we had a paper that was in press in Nature Communication that compared remdesivir to what the Chinese considered was the gold standard for the treatment of the SARS-related infection, which was an HIV protease inhibitor cocktail, lipinavir and ritonavir. So working with Gilead in that paper, we had done a careful comparison of the efficacy of those drugs compared to remdesivir in mouse models, both MERS and SARS coronavirus in 2003.

So Fred called me to ask me if I would be willing to share that paper with the Chinese, so that they could take a look at it. So I said, yes, and two days later, he informed me that — by email, confidentially, as well as a couple other people. So again, it's probably in my email. So if you look for his name, you'll find him. But he told me that it was a coronavirus and a SARS-related virus and was about 70, 80 percent identical to the original SARS strain. The sequence confirmed that.

Q Thank you. My last kind of question in this bucket, have you ever had any contracts, agreements, or other binding paperwork with the Chinese Academy of Sciences or the People ' s Liberation Army?

A I don't believe so. I've never had any funding from China.

Q When we interviewed Dr. Daszak, he testified that — and there's emails to this effect of him putting your gmail on emails, and dropping your UNC email, so it wouldn't go through the state FOIA law. And I think a lot of it was probably what you were referencing, the threats on 4chan and various things, and trying to quell those a little bit while the emails were getting FOIAed.

A He didn't do that email on my request.

Q Do you recall having any conversations with him regarding putting your gmail on things?

A I told him it was irresponsible to do that, and I was very unhappy with him, so, yeah.

Q I appreciate that. Do you recall, just for our own kind of, like, document retention, do you recall putting your UNC email back on or —

A What do you mean back on?

Q So Dr. Daszak would drop your UNC email, trade it out with your gmail. Do you recall saying, no, I need to -- this needs to go under my UNC email?

A At some point. I don 't know how quickly I did, but at some point, I did. I can't tell you exactly when. I know that I would oftentimes answer, if he sent me something by gmail, I would oftentimes send it back regular mail. But I can't say that I did it every time.

Q I'm just trying to understand. Not a substantial amount of communications over your gmail, most of it over your UNC account?

A I don't think there's a substantial amount of communication, but there would have been some because of that, yes.

Q Prior to this interview, did you have communications with anyone on that list regarding the interview?

A No.

Q Have you had any conversations with Dr. Daszak since his interview in November?

A Well, we're part of an emerging infectious center disease grant that's run out of Southeast Asia that includes a bunch of Southeast Asian countries except China.

So it's along the border. So if you want to know — if you really want to get to the questions of origins and whether or not there are zoonotic strains very similar to SARS coronavirus, you need to be along the Chinese border. You need to be as close to China as you can.

So that's where he set up his emerging infectious disease center. So we have quarterly reports and we have calls that we share information and data. There is year-end progress

reports that we have to write up that we submit to the grants.

And then, occasionally, I think there's a meeting each year that the NIH puts on to have the different centers come together, and share kind of what they're doing and be reviewed by an outside review committee.
So, yeah, there's going to be emails back and forth about that.

Q Nothing about his interview, though?

A No, I did not talk to him about that.

Q In the spirit of saving paper, I'm not going to introduce Dr. Fauci's calendar from February 11th. But that's when his calendar at least says that you met with him.

A Was it the 11th?

Q I'll introduce it.

A No, it's okay, I believe you.

Q Yeah, February 11, 2020.

A Okay. I was there for a reverse site visit, so it sort of got blended in, so I don't exactly remember which date it was.

Q And you already said it took place — and I just want to ask, Dr. Fauci was there at the meeting?

A He was there for a short period of time. I already mentioned some of the names that were there. So he was there for somewhere between five and ten minutes, at most. And he got — a secretary came in and said that he had a call in the SCIF that he apparently had to go to, so he apologized. So he wasn't there for the whole time.

Q Do you recall, specifically while he was there, what you discussed?

A Well, these meetings, they always start off with kind of pleasantries. But ultimately, the goal of the meeting, to my recollection, was primarily focused on the 2015 paper that we published in Nature Medicine that basically, in my opinion, warned the world that there were viruses that existed in nature that could threaten human health.

And so the first thing they wanted to do was talk about that paper, and then they wanted to talk about the regulatory — the P3CO regulatory compliance that was associated with that.

Q Do you recall the specific conversations regarding the science of the paper?

A Yeah, sure. So I said that we had access to the spike of proteins of this virus called SHC014 that was provided by Zhengli Shi before she published it, which was generous. Most scientists would not do that.

Later, she sent the plasmid on filter paper and coding the spike sequence of that virus as well. But that's what we had. And so — and it's also cheaper, synthetic DNA costs at the time, like the spike gene may cost $3,000, a full length genome may cost 17, 18,000. So we weren't a wealthy lab. So

it's a high-risk event to build a full-length virus, especially if you don't have the sequence. So we synthesized the spike gene and decided to place it into the context of the SARS coronavirus 2003 mouse adapted strain.

So we talked about that. And then we talked about the specific experiments that were done, the first of which we compared the growth of this isolate to the parental virus that we introduced the spike gene into. And it replicated the same. So from our perspective, in terms of P3CO, that's not called gain of function, that's called retention of function, right?

We also looked at its ability to use different receptors, ACE2 receptors from different animals, like the mouse, the bat, the civet, and the human. And the chimera used those receptors as well as the original SARS coronavirus strains. So, again, no gain of function, it was retention of function. So we looked at the growth in primary human cells and they were the same. Ultimately, at some point — and I should probably put this in the perspective of a timeline.

So we were approved to do these experiments in early 2014 before the pause occurred from the Obama administration. So by the time the pause occurred, we had already isolated the chimeras and were in the process of isolating, if we hadn't already isolated, the full length viruses as well.

So once we knew the spikes, could program infection, then you could take a chance and spend $17,000 and see if it works, because there's a chance. There's a high error in sequencing.

So that's the background. So then we — ultimately, we compared the chimeras to the full length SHC014 virus, in which they grew about the same again as well, no real change in any of those growth phenotypes. And then we went into animals. The parental virus, in this case, it was the SARS mouse who had the strains 100 percent lethal, the chimera was not. It caused weight loss and the animals recovered. Now, when you went into the older, vulnerable animals, again, the wild type parent was 100 percent lethal. And the chimera caused about 10 percent mortality, but most animals recovered. So that is, again, a loss of function, it's not a gain of function.

That information was all provided. So when the pause occurred — and then I explained this in the meeting. When the pause occurred, we had that data. And so if you were already doing experiments when the pause came out, you had a choice, you could either pause or you could continue your studies. The pause affected anything new that was funded.

So two things happened. In terms of new research that we were doing, we were given a waiver to go forward with making a MERS model, and you have that paperwork. In the case of the 2015 paper, we paused and put in all the paperwork saying these are the phenotypes that we see in the virus. As far as we were concerned, the data is not consistent with a gain of function phenotype. And ultimately, the NIH reviewed that and came back and said that they didn't think it was gain of function, either, and I could proceed. So then we proceeded and eventually published the paper.

So that kind of whole context, that's kind of — and Fauci left in the early stages of that discussion, right, because that took about 25, 30 minutes. I don't know how long it took, probably too damn long probably.

Q Less than 25 or 30 minutes. So was that the primary purpose of this meeting, was to review —

A Yes.

Q Like NIAID employees wanted to review that paper, and see if it had gone through the proper channels?

A Yeah, I think I was also asked how closely related were these viruses to the SARS2 strain, which I already mentioned to the committee that they're on different branches of the phylogenetic tree, they differ by 6,000 times. So one is not regenerative of the other, and that's been published by six or seven groups so far.

Q In that meeting, did they ask you any questions about the Wuhan Institute, what research they were doing?

A I don't recall that. I don't believe so, but I think you have to Look at it from my perspective, which is I'm being called to talk about a paper I published on the gain of function regulation. And I'm freaked out that perhaps I didn't do the paperwork right. So I was focused on that.

Q Okay.

A And by the way, I did all the paperwork right.

Q We appreciate good paperwork around here. At that meeting, and we're going to talk, about this proposal in more detail, so we don't need to talk, about the science. But at that meeting, did you bring up the DEFUSE proposal to DARPA?

A No.

Q Why not?

A Mostly because I had forgotten about the DEFUSE proposal in DARPA, quite frankly. I read a lot of grants. And so the grant was not funded, so I moved on.

Q I appreciate that.

BY **MR. WENSTRUP.**

Q When COVID hit, we were all in lockdown and started doing research. And I was looking for how do we treat people, what do we do? We don't have a test, we don't have a definitive treatment for this. It's called novel for a reason.

And one of the things that I came across was your 2015 article. And the first thing that occurred to me was gain of function, loss of function, regardless, to me, it was, like, wow, this can be done? And so for me, I was kind of like, this is kind of concerning here.

And I'll talk about that again in just a minute, but in all of your research over the years, how close have you ever come to creating a virus similar to SARS-CoV-2, as far as structure, pathogenicity?

A Before or after it emerged?

Q Well, in retrospect, or after it emerged.

A So before, I think what you need to think about is that no one had the sequence. So if you don't have the sequence of the pathogen, you don't have any guide to how to synthesize it or make it.

Q But looking back?

A Just to give you an example. Let's say I took SHC014 and I wanted to convert it to SARS-CoV-2. The first thing I have to know is the sequence of SARS-CoV~2, because if I don't know that, what I do know is that there are 6,000 mutations -- let's say if I do it, there are 6,000 mutations that exist in SHC014 that don't exist in SARS.

Q Let me clarify, because I'm not trying to get into that.

A Well, statistically, you have to make four to the 6,000 mutants which can't be done.

Q Okay.

A Okay.

Q My question really is maybe unrelated, maybe it's from a MERS virus, whatever. Anything close to the pathogenicity?

A Never.

Q Okay.

A The only time that statement would be true would be with variants of concern that emerged after SARS emerged.

So the first mutant that we made was a virus called D614G, which emerged in February, and then displaced the original Wuhan strain. So in that case, you have the sequence to guide your mutagenesis. The epidemiology indicated a new mutant had emerged in the population that was displacing everything else, and so it was a simple insertion of that nucleotide into the genome.

Q When you were doing this type of work, what BSL level were you?

A Always worked at BSL-3.

Q What safety guards do you employ against that? You, personally, in your work?

A So in our laboratory, we have a negative containment facility that is powered by backup fans, so there's two fans. So if one fan fails, there's a backup system that keeps the negative pressure. All of those backup fans are on the redundant power. And so emergency power. So if there's a failure in the system, it maintains. If everything fails, then the facility is designed to go neutral. So in other words, there's no air flow in or out. Within the facility, there are biological safety cabinets that are the primary containments for working with a pathogen. Those are also on emergency backup and also battery pack powered. The battery pack power gives you about 30 minutes. So if there's a complete failure of all power

and the facility goes negative, the hoods stay on, which gives the researcher and the facility about 30 minutes to decontaminate everything, clean it up, and put everything away.

Now, our staff, the minimal regulations I think is lab jackets and goggles and an N95 mask. We take personal protective equipment at a much higher level. So we Wear full Tyvek body suits with double gloves. People have an apron on top of the Tyvek suit, which is normally — if there was any kind of aerosol or accidental spill, it would go on the apron.

And then you have a hood and a shield that comes down to about here with a portable air breathing apparatus that pumps the air through Hepa filters and other chemical filters to pull out other toxins in the air.

So if you think about protective barriers, it's basically a layered redundant system, where you have the negative containment facility, the hood. You have personal protective gear, and then you have SOPs that are in place, standard operating procedures, that are also designed to be redundant, so that if one thing fails, you have a backup.

When I was setting up my BSL-3 lab, I was impressed by this television show called Seconds to Disaster. And in Seconds to Disaster, the common thread was always that there were redundant systems that had to fail before it occurred. So we put as many redundant systems as we could think of.

Q So in that vein, what level lab was used when you were working with Dr. Shi Zhengli in 2015, the work that was maybe done in Wuhan, do you know?

A There wasn't any work done in Wuhan. All the work was done at ÜNC, except for one experiment that was involving — they had taken the SHC014 spike and placed it in a lentivirus, a pseudovirus.

So, in other words, just the spike of SHC014 was placed into a virus particle. That's a single hit virus that can infect one cell, and then it can't spread. And it's used as a sort of bio-containment approach to ask questions about the functions of viral genes.

And in this case, they did an experiment to ask whether the pseudotype virus they had could infect and use human ACE2 cells. And it couldn't, and the reason for that is that a lot of the fundamental approaches that had been developed to make pseudotypes with coronaviruses weren't very efficient in 2015.

We subsequently did a lot of work with Barney Graham as we moved in to evaluating Moderna mRNA vaccines against MERS, to work out the technology, so that those pseudotype systems became much more efficient; So that you could do neutralization assays. Subsequently, they've been used all the over the United States and the world. So they didn't do any live virus work associated with that paper.

Q Have you ever had a sense that research you did or some others in the field were doing could lead to a change of direction, where the outcome is different than expected?

You talked about when you have a hypothesis, and so you think this will be okay to do, you don't expect it to be a pandemic pathogen. But have you ever had that concern, like, were you ever worried that the — and also were you ever worried that the capabilities that you develop the expertise for could be used in some nefarious way or lead to a pandemic pathogen, not necessarily your work, but somebody else's?

Like I always refer to when the Wright brothers invented the plane, they weren't thinking of flying into the buildings and killing 3,000 people, right, but somebody did.

So when you have this type of technology, were you ever concerned that, hey, we've got to be careful who's doing this type of work because it's pretty dangerous, or can be?

A Yeah, so we did — I think a responsible scientist has to think about that. And I always call it the sort of unintended consequences, right? You're doing a series of experiments. But evolution follows its own path, not the path that you might necessarily think it 's going to.

So there's always a chance, some risk, for unintended consequences in any kind of virus evolution experiment.

Q Evolution, I understand that. You can't really control that, except try and monitor it through surveillance, things like that. But I guess what I'm driving at is, one of the roles of this Committee is to have plans for the future. And so how do we protect ourselves?

Because the technology exists, and so we have to come up — or try to come up with ways as a country to make sure we have all the checks and balances in place, so an adverse reaction doesn't occur, either accidentally or intentionally by someone else.

A So I can tell you what things we put in place in the 2015 paper. So for example, although we published the approaches for how to build molecular clones of coronaviruses, we never had anyone from Dr. Shi'S lab or any of the Wuhan Institute of Virology come to our lab and train. We never taught them.

In fact, if you look at their cloning technology, they use baculoviruses. They may assemble some of the full length molecule using some of the enzymes that we have, but they implant it directly into an insect virus to maintain it as a baculovirus, which was a technology developed in Europe, not my technology.

We think our approach is safer because we've divided the genome into six pieces, so there’s no way any of those can initiate an infection. And we don't assemble until we're in the BSL-3. So it's fundamentally safer than what was done by others.

In terms of how we built the chimera, we didn't publish the sequence of the virus that we built, and we didn't share the sequence of that chimera with anyone at the Wuhan Institute of Virology. So we didn't give them the template on how to build the recombinant virus.

Q Is that your own precaution?

A Actually, that last precaution was done in collaboration with discussions with NIH, with our program officer, and the journal. And to some extent, it was a natural extension for — in response to the transmissible flu

studies, and whether or not the virus sequences should be made available.

Ultimately, after the pandemic, we received a bunch of requests for the full-on sequence, and then we made it available just because there were conspiracy theories that were beginning to bounce around, that that virus was the cause of the pandemic in China. And people wanted to see the sequence. So for transparency, we really had no choice but to make it available.

Mr. Wenstrup. Thank you.

BY **MR. STROM.**

Q One quick follow-up on the Chairman's question. But there isn't any sort of formal export review procedure for these kind of dual use technologies?

A Yeah, export control regulations do — they're complex.

Q Yes.

A And so the University of North Carolina has an export control group that regulates that. And so if we were going to have to — if we were going to send anything to China directly, that at least it would be looked at in that context of export control, yeah. But those rules are kind of vague.

Mr. Benzine. I think we're at time. We can go off the record.

(Recess.)

Ms. Yass. We can go back on the record.

BY **MS. YASS.**

Q Good morning, Dr. Baric. My name is Alicia Yass. I am senior counsel for the Democrats on the Select Subcommittee, and we want to express our thanks for you making the trip to come up here and for voluntarily agreeing to speak with us. We do have some questions for you today as well, and I will start by turning things over to my colleague, Joseph, for our first section.

BY **MR. ROMERO.**

Q Good morning, Dr. Baric.

A Good morning.

Q We would just like to ask you a few questions about the 2015 paper testing the SHC014 spike protein you coauthored in Nature Medicine. We discussed this paper some in the previous round.

A Correct.

Q I will introduce -The paper now as Minority Exhibit A.

(Minority Exhibit A was identified for the record.)

Nature Medicine December 2015 article.

A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence

https://www.nature.com/articles/nm.3985---

BY **MR. ROMERO.**

Q So in this paper, among other findings, you found that the SHC014 spike on a mouse-adapted backbone showed reduced pathogenicity compared to the full length mouse-adapted SARS backbone. Does that sound right?

A That's correct.

Q So the full length mouse-adapted SARS backbone has a name, MA15. And as you understand things, you helped to create that virus?

A Yes, the virus was originally created in collaboration with Kanta Subbarao at the National Institutes of Health. She did the serial passage of the original SARS strain, which could replicate, but not cause disease in mice. And after about 15 passages, the virus became more pathogenic. There were six amino acid changes associated with the increase in- virulence in the mouse, which we then engineered into the molecular clone that we had built to make a mouse-adapted strain that's been widely used in select agent labs across the U.S.

Q Could you help us understand the scientific need to create this mouse pathogen virus, and what its uses ended up being?

A Sure. One of the fundamental problems in the development of small molecule inhibitors and immunotherapeutics in drugs, as well as understanding the basic mechanism by which a virus causes disease, is that as viruses traffic from one species to the next, they oftentimes lose virulence.

So the original SARS coronavirus virus strain, for example, caused 10 percent mortality rates in humans. But if you infected a mouse, it barely would grow to 10 to the 5th in the mouse. They didn't lose any weight, but the virus replicated primarily in a few cells in the mouse. So if you're developing drugs or antivirals or vaccines, it's actually very easy to make something work against a virus that's crippled in a model. It's not crippled in humans, right, so — and standard practice is that you want to develop a model that closely phenocopies the human disease outcome.

So this particular mouse-adapted strain, MA15, targeted epithelial cells in the airway, club cells at the transitions between the airways into the gas exchange, in essence, the little balloons that puff up and down, the alveoli. And targets AT2 cells in there, just like it does in the human. It results in an acute respiratory distress syndrome disease outcome, where there's a tremendous amount of fluid and a fibrin deposition in the lung. There's a breakdown of the alveoli/epithelial barrier that allows flooding. So, in

essence, the mouse or the human patient infected with the original SARS strand is basically drowning in their own fluids.

It also strips — kills AT2 cells, which makes surfactant, which — you know, when you get a balloon the first time out of a bag and you try to blow it up, it's really hard to cause it to inflate. Without surfactant, that's what your alveoli are like, it's hard to breathe.

So the mouse model that we created mimicked the human disease phenotype as closely as we could, and it was lethal, especially in the older animals. So now you have a model that grows to higher titer, close to 10 to the 8th, it targets the right cells, the right organ, causes the right kind of disease. So now you have a rigorous model to develop small molecule inhibitors. And this was really important for us.

One of the things that drove the 2015 paper was that SARS coronavirus emerged in 2003. It was controlled by public health intervention strategies because it didn't transmit until you got clinical disease. People thought it was a fluke, one-off, it's not going to happen again. Then MERS coronavirus emerged in 2012, again, highly pathogenic, 35 percent mortality rate, but it didn't transmit very well. So that data made us ask the fundamental question: What is the risk level that exists in nature? This paper, in essence, said the risk in nature — that risk existed in nature. And then the mouse models were then used to develop countermeasures.

So almost immediately in parallel with this paper, we started working with Gilead Scientific to evaluate nucleoside inhibitors that might work against the coronavirus family. After testing a bunch of things, we eventually got down to remdesivir, demonstrating that it worked against the MERS coronavirus and the SARS coronavirus. That led to a companion paper that included these viruses in 2017 that said these are broad spectrum antivirals that work in robust animal models of disease. And the preclinical data was now available to move into the clinical trials. So that's why animal models are so important.

Ultimately, remdesivir, molnupiravir, the Moderna vaccine, I don't know if we ever did the Janssen vaccine. But several therapeutic antibodies had all made it through the FDA and into the clinic, went through our lab, and many of them touched these viruses that were developed in the 2015 paper. These same viruses are being used for universal vaccine design for all sarbecoviruses and all betacoronaviruses. So if you want to really protect the public, you have to have the appropriate virologic reagents that challenge the effectiveness of either your drug or your antibody or your vaccine and prove performance.

So ultimately, the goal of what resulted from this paper was the idea that we had to develop drugs, we had to develop immunotherapeutics that were broadly active. And we had to develop vaccines that were broadly active. And that paper, including the viruses, the human viruses that occurred, were included in studies that were used with the Moderna vaccine as well.

So, again, animal model development is key to this. It's, again, very, very easy to make drugs that work against

something that barely replicates, but then when they get into the humans, they fail. So that's the basis for it. That's probably a little longwinded. I apologize. Anyway, that's the thought process.

Q So it sounds like this mouse-adapted virus was created to parallel the level of pathogenicity that I guess humans would experience?

A Yes, with an important caveat. So a long history in virology is that serial passage of a pathogen that's adapted to one species, as it moves to another species, it rarely becomes a generalist. It usually loses its ability to cause severe disease in the original species. So serial passage has been used in virology for decades to make live virus vaccines, like the measles vaccine was passaged in subculture many times. The live polio virus was passaged in subculture to basically adapt it to the new environment where it loses its capacity to interact with host proteins that are specific to the natural host, and so it becomes attenuated.

Q Is there a sense that because MA15 has enhanced replication and lethality, that it has been preadapted to be pathogenic in mice, that it is unsurprising that by removing its spike and replacing it with the spike from another virus, say SHC014, the resulting chimera would be less pathogenic than the full length original MA15?

A That's a really good question. So it depends on the biochemistry and the receptor binding capabilities of the virus that you drop into the backbone of the strain that you chose.

So in this case, the mouse-adapted strain, without question, had been selected for its ability to replicate and cause disease sufficiently in the mouse. It may be more difficult to make a virus more virulent than that. So if you dropped the SHC014 spike in there, the most likely phenotype is the mouse phenotype.

Q You also coauthored another 2016 paper,

"SARS-like WIV1-CoV poised for human emergence." Does what you just said also hold true for, like, creating a WIV1 MA15 chimera and comparing that to full-length MA15?

A Yes. So in the 2015 paper, we only compared pathogenesis in wild-type mice. In the PNAS paper in 2016, we compared pathogenesis in wild-type mice and also humanized mice that express the human ACE2 receptor. And if I remember correctly, the WIV1 virus was more attenuated than the wild- type virus. I would have to look at the paper to be 100 percent sure.

Q So back to the 2015 Nature Medicine paper, it also had two other things to say about the SHC014 spike protein vis-a-vis wild-type SARS Urbani.

I would like to first just lay out those two things, and then ask you, at the time you wrote this paper, how you viewed those things together, and if there was any significance when juxtaposing them.

The first was that full length SHC014 was less pathogenic in mice than full length SARS Urbani. Does that sound correct?

A Both of them caused little, if any, weight loss, so I think they're pretty comparable. Comparable is the better word. Sorry, not "compare-able." I grew up in

south Jersey, it happens, sorry.

Q And the second was that the SHCØ14 spike on an MA15 backbone was more pathogenic in mice than the SARS Urbani spike on an MA15 backbone, correct?

A Yeah, that was — yeah. So in the discussion of this paper, we put in a statement saying that depending on how you compare gain of function and loss of function values in the system, the selection system that you're using, you can get different values. And that review panels need to be aware that when they review these things in the future, that they need to carefully consider the context of what kind of experiment is being done.

So in this paper, we never did a head-to-head comparison of the mouse-adapted strain that was missing the single amino acid change in the spike that helped it to be mouse-adapted. So if you took the five mutations set where you had five of the six mutations without the spike-like protein, it was more — it lost some of its virulence potential.

Now, both of them are attenuated. And so you're asking me the question, in an attenuated backbone, which one is more attenuated. We never did a head-to-head comparison, right? So the experimental conditions like the age of the mouse, that's a little bit different. The mouse models and emerging coronaviruses all have this striking age-related phenotype. So after about 2Ø weeks, again, depending on the virus, the virus becomes more virulent as a function of age, just like in humans. So it recapitulates that phenotype.

So to do this experiment properly, you actually need to set up the conditions where you have all three viruses with the same age mice that were housed under the same conditions, and then infected in the same dose.

What we quoted on in this paper was that in the experiment where we removed — in a different paper, where we removed the spike and you compare the clinical outcomes, the weight loss outcomes, there's a little more weight loss with the SHCØ14 as compared to the mouse-adapted virus, without the mouse-adapted spike mutation.

So that's the problem with gain of function or loss of function. Depending on how you can compare it, you can end up with different phenotypes, and that's what we've tried to say at the end of the paper to future people doing this kind of work, that they needed to be aware that the conditions that you do these kind of experiments, and how you compare outcomes can have an effect on loss and gain of function phenotypes.

Q So to the extent this question of- comparing the different outcomes was on your mind, what were you thinking about whether this spike protein from SHCØ14 could be used to create something more pathogenic than SARS Urbani?

A Well, there's no data. So the only data you have is that you can do a minimal tweak of pathogenesis in a mouse, not a human. We don't have any data on humans. Is that what you're asking, in the context of humans? Or are you asking me whether I can make a more virulent mouse virus?

Q Well, in mice, and then also, I guess, transgenic mice later.

A Yeah, ultimately, the — so I believe the biochemistry on the SHC014 spike compared to the SARS 2003 spike, the SARS 2003 spike binds the human ACE2 better than SHC014. But in the mouse, the SHC014 spike binds the mouse a little better than the human. So little tweaks in ortholog receptor usage that exists within the bat population can tweak it a little bit in directions, yes.

Is that answering your question? I'm hoping I'm answering your question.

Mr. Romero. I think so. I will turn it to Alicia.

BY **MS. YASS.**

Q I will say, we have a cursory understanding of all the science you are talking about, so we've done our best to get up to speed on it to have this conversation with you today. I want to talk to you about something a little more 10,000-foot view, not in the weeds of the science, but about, in general, zoonotic origin of a human virus, and what that would look like.

We've spent a lot of time in this Committee talking about lab leak versus zoonotic origin, and I think it's good to get a sense from somebody who is doing this work day-to-day on what that would be.

So for a little bit of historical context, for zoonotic jumps with coronaviruses or even other viruses in general, could you just talk a little bit about how zoonotic jumps would happen or have happened?

A In the context of coronaviruses?

Q Or any other viruses, if that makes it easier for you to talk about.

A Well, the first thing that has to happen is that human populations have to come into close contact with animals that encode these viruses. So that's obviously the first thing.

So there are, like, people in the extractive industry who may be loggers or hunters or, you know, gathers or collects bushmeat, those kind of people are the most likely to come in contact with zoonotic viruses and become infected.

Now, the vast majority of contacts where zoonotic viruses actually are introduced into a human being, most of those don't progress. The recent data with coronaviruses, for example, that was published in Southeast Asia argues that there's somewhere between 50 to 60,000 exposures where people working with bats come in contact with bat coronaviruses, and actually seroconvert. That means they get infected, probably had very mild disease and recovered 50,000. So if you think about how many — well, let's put it in the context of coronaviruses.

So 2002, SARS emerged; 2019, SARS2 emerged. That's 17 years times 50,000 exposures a year, it's actually a little higher. So about a million exposures between human disease outbreaks. So the vast majority of exposures are self-contained and do not transmit to another person, and then do not establish or colonize the new population. But this is occurring all the time.

And so when you get to origins, for example, and you ask the question, what's more likely, is it a lab leak or is it natural processes? You're looking at one in a million, a million exposures occurring over 17 years versus what happens in a laboratory setting. No chance it's even close. And the diversity in nature, hundreds of millions of times more diverse than what was in the Wuhan Institute of Virology.

So that gradient is huge. And if you consider that, it's more likely to be a natural event than it is to come out of the laboratory. The data — that's what the data screams.

So that's the first event, is that most of those events don't actually spread and cause severe disease or transmit. So why is that? And I can tell you better for coronaviruses. I can tell you for other viruses. But for coronaviruses, for COVID-19, there are 49 what are called susceptibility loci in humans that regulate how bad the disease is going to be. There are 25 host proteins that interact with the virus to let it replicate well. So when an animal virus is coming from a bat into a human, there's a lot of variation in those 25 genes that the virus has to be able to walk through and adapt to, and it takes time and it takes mutation.

Now, the starting virus can make a difference. If it has a lot of intrinsic capability to use — and these host proteins are all kind of conserved, if many of them are conserved, it's easier for them to make it through, but most of them can't.

And then there's other barriers for pathogenesis. There's a whole set of genes for pathogenesis, which is important for producing symptoms and bringing the virus up to the right part of the upper respiratory tract, so it's sneezed and transmitted. And then there's other barriers for transmission to occur. So for a sarbecovirus to make that transit, it's hard, and the data in nature support that. So other viruses face the same fate.

Now, some viruses use the same receptor across species, for example, like flu. But some of those receptors in an animal are expressed in the upper respiratory tract or the gut, and in the human, it's only in the lower respiratory tract. So when H5 infects an individual, it's a horrible lower tract respiratory infection, but it doesn't replicate in the upper respiratory tract. So that's why I don't think it can transmit, so the virus has to figure that out.

And so that's why most zoonotic transmission events in nature fail. And it's the same thing in the research laboratory.

When you start, like, resurrecting bat viruses, and it sounds scary, but there are huge barriers. Even if you consider that, let's say that there was no protective barriers at all, humans have a huge number of protective barriers in terms of susceptibility loci that are in place to prevent that from occurring.

In addition, humans have been exposed to four contemporary coronaviruses which provide some level of cross-immunity for new viruses to come in.

So it's not a simple thing like there's a virus out there, you know, that looks like Pac-Man, it's got a big smile on its face and saying, give me a human, because I'm going to

eat them, and then I'm going to keep eating. It's a difficult process for most of them.

But, again, the important thing to consider when you think about biosafety is that some of them may have an easier route than others, and it's the ones with the easier route that you have to be concerned about.

Q We've spoken about China. You've mentioned Southeast Asia is where currently a lot of research is being done on emerging viruses. What general characteristics or traits do China and Southeast Asia have that might be ripe for these zoonotic spillovers? We know several viruses have come out of that area in the past 20, 30 years.

A Well, the scientific community has stated to the Chinese government several times that open markets are conduits for virus emergence. And that's because they stack animals on top of each other, including all kinds of wild animals.

And also, there's an illegal trade. I don't know, what do you call people — I guess they're smugglers, right? People who bring — there's smuggling of animals into China as well that are brought into these markets as well that are sold. And so you have, in essence, mixing vesicles where- a large number of different viruses in different mammals are brought in close proximity. And when you think about these susceptibility loci, they're going to vary for each animal.

And so some animals are going to be — if you take a bat virus, some bat viruses, sarbecoviruses can use a rabbit and a camel and bat receptors for entry. Others use 30 different mammalian receptors for entry.

So some of those viruses may be able to slip -- they get through this, they go to another species, they're replicating, they're adapting. Some of those mutations allow more cross-jumping, and these mixing vesicles provide really efficient ways for viral disease emergence. And Chinese scientists, European scientists, and American scientists said that if you don't close these open markets down, you're going to have another sarbecovirus.

So if you ask me — one question could be, what was the cause of the pandemic? It's policy failure. There's plenty of science that said, close your markets, shut down the illegal trade and smuggling of animals. Otherwise, you're going to get another sarbecovirus. And they didn't do that.

It's not only China that has open markets and traffic in bushmeat. It happens in Africa and South America, many different countries. And so also in the context of huge metropolitan areas. And so in essence, human beings are creating the appropriate environment for virus emergence. And so if you look at the 21st century, we've had somewhere between eight and 12 emerging pathogens that have occurred in 20 years. This is not going to slow down.

Q Thinking about some of the past zoonotic spillover viruses that we've had, SARS1 and MERS specifically, from our understanding, researchers didn't immediately know the path and what animal the virus had come from. Is that your understanding as well?

A Well, the research in the flu field had always argued that open markets were a good conduit for virus emergence, for mixing of influenza virus strains. So the

research community that's interested in emerging viruses know that anywhere where there's going to be the interaction between large number of animals and human populations is a potential way for virus emergence to occur.

So you look as a civilization moves into and deforests areas, these are boundaries where emergence occurs. Open markets are boundaries where emergence events occur. Farming practices, anything that sort of changes the ecology or causes ecologic mixing is a way for this -- what was your question again?

Q When we look at a virus and are trying to figure out the zoonotic point of origin, we don't always know right away which animal it came from. It may have passed through a couple animals before it got to humans, and that path is not always immediately clear.

A Yeah, so in the case of SARS coronavirus, for example, because of what I just told you, one of the first places people start looking are animals in the area where the outbreak occurred. And so in the case of the SARS coronavirus 2003 outbreak, they found that people working in the open markets had a higher seropositive rate to these viruses, as compared to people outside of that work area.

And they looked in the animals in those markets, and they found virus strains that were 99.8 percent identical to the SARS coronavirus 2003 that were transmitting in civets and raccoon dogs, and it was mostly happening in the metropolitan areas.

I think Zhengli Shi went back to look at the farms that were producing the animals, and very, few of those farms had virus. So it was somewhere in the transportation and the bringing large numbers of animals together that they become infected and they can potentially spread it to humans.

Humans also in this case, in the case of 2003, could also reinfect the civets, setting up a transmission cycle. In the case of MERS, it was a change in practice associated with camels, where large numbers of camels were moving up from eastern Africa into the Middle East and being maintained as large herds.

And they became seropositive and were transmitting MERS viruses probably as early as 1990 or so, unrecognized as causing -- either they didn't cause serious disease or they were causing some level of clinical disease that was going unrecognized.

Now, that doesn't mean that you need an animal reservoir, right? I think that's really important. Because I just talked to you about viruses in nature that have different intrinsic levels, you know, of being positioned to emerge, like SARS coronavirus 2019 can use 30 to 40 mammalian receptors. One of the viruses that's close to it called pangolin GD can use all those same receptors and the mouse receptor.

So there are strains in nature that have that intrinsic capacity as a generalist to bind ACE2 molecules of many species. Now, they don't necessarily need to set up a reservoir. We published a paper in 2023 on this, where a virus like that could infect a pangolin. And most people — I could hold a pangolin and get it close to my face and not freak out. I would have trouble with a bat. I don't

know about the rest of you, but I would have trouble holding a bat close.

So a pass-through species is where a bat may infect another species, because the receptors in many of these barriers have been naturally circumvented. Then that virus is brought in close contact to a human. And if it's the right human, who has the right combination of susceptibility loci that make them more likely to be infected, or if they're elderly, or if they're partially immunosuppressed, all of these functions could allow the virus to infect that person and begin to replicate and adapt.

And especially if they're immuno suppressed, because it doesn't clear, and that gives the virus plenty of time to make mutations and then transmit to another person. So in the case of SARS-CoV-2, large herds of pangolins don't exist. It's an endangered species. But the concept of one species acting, in essence, as a pass-through species is certainly possible. And I think it was one individual that infected some of the mink colonies in Europe, and exactly how the virus jumped from humans to deer is also open. And then deer back to humans is open.

So again, this clade, which is called IB that's SARS2-related, at least the viruses within the first 13 or 14 of them that had ever been identified that are the closest thing to the SARS2, all from Southeast Asia. So if you hear, like, the virus came from somewhere else. No, it came from Southeast Asia. But all — many of them have this feature of more of a generalist capacity. So the second possibility is pass-through.

Q Sure. And just to be clear that I understand some of what you just said, it sounds like even though, for some of the example viruses, there's very clear evidence on pieces of the transmission of the virus, the entirety of the path is not always 100 percent settled?

A That's correct.

Q And when we're looking at the SARS-CoV-2 or COVID-19 pandemic, it sounds like you feel strongly that it was a zoonotic or natural origin. But would you say that it's not settled yet what the origin of the COVID-19 pandemic was?

A Again, I have at different times speculated on three possibilities. The first is natural origin. The second is accidental escape from the laboratory setting, which can also include collection, which you can ask about if you'd like more details on that. And then the third would be the possibility of engineering.

There is no hard evidence to support engineering. Initially, for example, the receptor binding domain was argued to be completely unique and perfectly positioned, perfectly designed to bind the human ACE2 receptor. Well, no, there are virtually identical strains in bat strains that are found in nature. So it's not been engineered.

[The following paragraph contains what I regard as two typos: "infinity" should be "affinity" and "origin" should be "original". RW]

In addition, that spike gene has undergone successive sets of — the RBD has gone successive adaptive changes that increases bind infinity for the ACE2 over a thousand fold. It is not perfectly designed. It's just like the origin SARS1, which underwent specific changes that enhanced its transmissibility as it was spreading. The exact same process. So the RBD is out.

The second idea that it was engineered, there was a very bad bioinformatic paper, for example, that said — it came from the HIV — which was total nonsense.

The better argument was that there might be a super antigen site, but there was a paper that was just published that said, no, there's no super antigen site. So, in essence, the scientific process says, okay, if this is the hypothesis, let's do experiments to see if we can disprove it. If we can't disprove it, then it's likely.

So far there's no backbone genome that's close enough to have been engineered in the SARS2. Most of the components that were originally argued as being engineered failed. The only one that's left is the furin cleavage site, which has multiple explanations.

So that leaves two possibilities. The first is escape from the laboratory. And you can't rule that out, because they do work at BSL-2. You just can't. But for the reasons I talked about earlier, just on the frequency and the exposure level in nature versus lab, it's massively -- what's that called, massive -- the scales are massively weighted to natural origins, yes, sorry.

Q Sure. And taking out bioengineered, I think there's much consensus that that is not what we're looking at here. But with the lab leak and zoonotic, there would be possibilities for it to be somewhat more of a combination of the two. I'm thinking about, specifically, you said researchers go out and collect samples, they bring them back to the lab. Maybe they do no manipulation on it, so it's just whatever they collected out in nature. Something happens, there's a lab accident, and somebody is exposed to a virus and gets infected.

While I understand this would be very rare, that would sort of be a combo of a lab accident with a natural virus, correct?

A Yes, and still be a natural virus that inadvertently escaped the laboratory, because biosafety practices weren't sufficiently robust.

Now, when you think about collection, at least the group at EcoHealth and the groups that they collaborate with, again, I haven't been in the cave with them, but the pictures that I have seen is they're fully dressed in Tyvek suits and with all the protective gear. So, in essence, they are collecting — in essence, in laboratory appropriate conditions, and then bringing the samples back. Their weakness is trying to culture the viruses at BSL-2. It's just the chance of an accident is increased under BSL-2 conditions, as compared to BSL-3.

Q And I wasn't suggesting that this is what happened, just more that it's a possibility. One of the things that our Select Subcommittee is focused on

is preventing the next pandemic, because, as you've said and as we're all aware, another pandemic does seem like a distinct possibility in the future. So we want to be learning lessons from this most recent pandemic to bring forward.

You've talked about some policy ideas that were brought to China on ways to limit exposure to viruses, but are there other policy solutions that you think we should be considering to better prepare us for the next pandemic?

A BSL-4 laboratory practices are well harmonized across the globe. BSL-3 practices are not well harmonized across the globe. And so there's quite an amount of variation that exists within BSL-3 laboratories from — I don't know, from like conditions that I just described in our laboratory compared to the minimal conditions, which, depending on the pathogen, can actually be a lab coat and goggles, some sort of eye protective gear and gloves. And so that would be for a non-respiratory transmitted virus that may require bloodborne transmission or something like that. But different countries have different standards for how they work with pathogens. And it's not just China, for example. And so it would be good if, globally, there was a standardized set. There are other nations that also say they have BSL-3 facilities that do this work, where I would look at it and go, I don't want to do BSL-3 work in that facility, just because the standards aren't sufficiently high. I had another thought, too, that has now escaped me. Doggone it.

Q Well, if I could just summarize that. I think we all know the virus doesn't know nations' borders, and can easily go across borders. And research is being done in these different countries, so it sounds like international cooperation and collaboration is key to preventing the next pandemic.

A Yes, I would also, I guess, like to make the statement that regulation — I actually have no problem with the current GOF or DURC regulations. I think they're appropriate, they're focused on pathogens of potential high consequence that we have a risk, that we know about risk.

I have concerns about regulations that cover all of microbiology, for example. And my concerns are related to leadership. Leadership in terms of the scientific capabilities, leadership in terms of economic leadership.

The bio-ag community, for example, is a multi-trillion dollar community, which may be the major economic driver of the end of the 21st century. And if we overregulate and put too much regulatory restrictions on that community, we will lose that economic battle.

In addition, doing high containment research actually spurs the development of safer practices and safer facilities and safer equipment for biosafety work at a higher containment.

So if you restrict it so much that very few people do it, those kind of advancements won't occur and will stagnate the system. And then I think there's biosecurity in terms of preparedness. What are the capabilities, what do you look for?

So over-excessive regulatory restrictions on emerging pathogens or high containment research can be equally disastrous to the U.S. in the future. So there's a

risk-benefit ratio. And if that risk-benefit ratio is wrong, the risk to the competitiveness of the United States could be impacted more than the benefit that would ever occur from the restrictions. And, unfortunately, you guys have to figure that out. I don't have to figure that out, but you guys have to figure it out.

Q We appreciate your view on that. And one point of clarification. Early in that answer, you referenced the current GOF regulations. I assume you're referring to the current gain of function regulations, which are the P3C0 framework; is that correct?

A The P3C0 framework is designed around — is specifically gain-of-function research related to viruses that are considered PPP. Those are viruses that either have the potential for high transmissibility in humans or high pathogenic outcomes in humans. And so it's a limited number of viruses that fall within that sphere. So for example, natural pathogens like zoonotic pathogens, at least my reading of the regulation, they don't fall within that category.

If you're looking for -- if you're looking at — if you're designing like mouse-adapted viruses, as was asked earlier, so that you can make better universal vaccines or test the breadth of drugs, those are exempt. If you're doing it to identify strains that are high risk, those are exempt under the current regulations.

I'm talking about the harmonized regulations that are being discussed now, or the DURC regulations are mixed with the gain-of-function regulations, and currently, it's being considered that any animal, human, or plant pathogen or agent be under review.

Now, the definition of agent is not defined, so the agent is someone or something that has an effect. AT has an effect, right? Biochemistry studies to identify what escape mutations can occur in a virus provides information that could be used as dual use. It has an effect. mRNA vaccines elicit an immune response, it has an effect. It can be used to deliver things to human hosts in a positive or negative manner. It has an effect.

So you have these huge economic engines, CRISPR technology, and fixing genetic disorders that is coming head-on with these regulations. And the economic impact of that could be huge. Again, that's not my areas of expertise, it's your guys' area of expertise.

I just hope you're aware that this is not insignificant, and in the harmonized regulations, they don't discuss the long-term impact of the regulatory structure. Like I said, I have abided by the regulatory structure to the best of my ability. I think the regulations are appropriate, especially early on with the coronaviruses. There were no drugs, there were no vaccines, there were no therapeutics. I mean, the human population was completely vulnerable, so we needed to have that in place.

But remember how difficult it is for a zoonotic virus to move into a human. Most of the cases of laboratory escape that have led to transmission, these are human pathogens that were in the lab that already knew how to transmit. I don't know of any cases where a zoonotic virus immediately — you know, they could infect somebody. But they're subclinical

infections, they don't spread. At least to date.

Again, it's not — it's a balance. If you ask me whether that could never happen, well, of course it could happen. There's a risk there. And, again, governments around the world have to deal with that risk capability, and try to balance it as carefully as they can. And it could easily go in either direction in a disastrous way.

Q Thank you for that context. I am going to change topics here, and I want to draw your attention to something that was briefly mentioned in the first hour, but the DEFUSE DARPA application.

So on that grant proposal, you were not the leader of that team, correct, you were listed under other team members?

A I was a coinvestigator, I was not the lead.

Q Thank you. So there was a draft proposal that was submitted amongst the team members, and you received that draft, correct?

A Yes, I probably got a couple of drafts at various times.

Q There is one draft that has been made public, so I'm just going to introduce that as Minority Exhibit B.

(Minority Exhibit B was identified for the record.)

Document, DARPA-PREEMPT-HR001118S0017

[Here is the unredacted PREEMPT proposal from Drastic. RW]

https://drasticresearch.org/wp-content/uploads/2021/09/main-document-preempt-volume-1-no-ess-hr00118s0017-ecohealth-alliance.pdf

https://www.darpa.mil/program/preventing-emerging-pathogenic-threats

https://web.archive.org/web/20201101063951/https://www.preemptproject.org/

BY **MS. YASS.**

Q Does this look familiar to you?

A Unfortunately, yes.

Q Now, a lot of hay has been made out of this draft proposal. And specifically, there is a comment that you made, which, unfortunately, there are not page numbers. But if you count through one, two, three — the fourth front page that is double-sided, there's a comment from you — or that's been attributed to you. So I will make sure that is actually you. But on the very bottom, there's a comment that is identified as BRS17. Was that your comment?

Mr. Ervin. You mean 7?

The Witness. This comment 7 or 8?

BY **MS. YASS.**

Q It's identified "Commented," and then in brackets, "[BRS17]."

A In the U.S.; is that correct?

Q Yes, correct.

A Yes.

Q Is that your comment?

A Yes.

Q So I'm just going to read it.

"In the US, these recombinant SARS CoV are studied under BSL3, not BSL2, especially important for those that are able to bind and replicate in primary human cells.

"In China, might be growing these viruses under BSL-2. US researchers will likely freak out."

Now, when I read that comment, I take it as advice against doing this work in a BSL-2, when it should be done in a BSL-3 lab. Is that what you meant by the comment?

A I think I'm responding to the comment above from Peter Daszak in two ways. First, I'm informing him, just in case he doesn't know, that a lot of the virus discovery work and culturing work that the Chinese do with zoonotic coronaviruses is done at BSL-2. The animal work they do is actually at their BSL-3, but the culturing is at BSL-2.

And that while there aren't any actual U.S. regulations, but the Baric lab does this all under BSL-3. So anyone who had collaborated with us or had obtained the viruses from us always did it at BSL-3. And all of our paperwork said we're going to do it at BSL-3.

So I'm letting him know there's a difference, and I say, "US researchers will likely freak out" to make sure he pays attention.

Q Great. And this was not the final proposal that was submitted, correct?

A I don't believe so, no.

Q And that final proposal was finalized by EcoHealth Alliance, not you, correct?

A I did not see the final proposal that went in, I made comments on it, but the final proposal, I didn't receive until after it had been submitted.

Q And to be clear, that final proposal was not accepted by DARPA, correct, it was not funded?

A That's correct.

Q Dr. Daszak made a comment on the draft proposal as well, and suggests the one you mentioned, beginning with, "If we win this contract, I do not proposes that all of this work will necessarily be conducted by Ralph." That was your point of concern?

A Yes.

Q But he was saying, "If we win this contract," correct?

A "If," yes.

Q And the contract was not awarded?

A That's correct.

Q And as far as you know, the research that was outlined in this proposal has not been conducted through funding of other means?

A Certainly not by my group. I don't know what China did, and I don't know what their grant funding was subsequent to this grant.

So there was no evidence that they were doing this kind of work. Well, there was evidence that they were building chimeras using WIV1 as a backbone, so they were doing some discovery work about the functions of spike genes of zoonotic strains that they discovered later on, but I don't know if they did any of the engineering or anything.

Q Because you had not been involved in any of that work?

A I had not been involved, no.

Q We've had heard others say that SARS-CoV-2 is the only virus in its subgenus with a furin cleavage site, although if you go one level above, there are other viruses with the furin cleavage in the genus. The DEFUSE proposal included inserting a furin cleavage site at the S1/S2 juncture. So just a discrete question about that. Are S1/S2 furin cleavage sites found in other coronaviruses in nature?

A They're found in many betacoronaviruses and some alphacoronaviruses, yes.

Ms. Yass. Thank you. Dr. Baric. We can go off the record.

(Recess.)

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

BY **MR. WENSTRUP.**

Q Dr. Baric, is it possible that SARS-CoV-2 spent some of its life in the lab before the pandemic took off, even if it was brought into the lab from nature? Let me ask you this. Is there a way to find out? In other words, I'm thinking of, like, lab notebooks and documented sequences. Should, that be possible?

A If you had access to the laboratory notebooks, if you had access to the safety records of the Wuhan Institute of Virology, if you had access to the sequence databases, the level of assurance that you would have would be greater. No question.

Q Which we didn't really have?

A Which we don't really have, that's very true.

Q And again, this is like going through a process, but — so the sequences, they come from the lab, that's where the sequence is read, if you will, and maybe that's not be the right word.

A Well, so many of them are collected in nature. They may collect it in inactivating chemicals so they maintain it as RNA, So I don't know how they actually break it down. So what they might do is half the samples may be nucleic acid, the other half may be a guano that would have live viruses.

Q But there are data banks?

A They would probably have —

Q Whether it's found in nature, developed in a lab, they should be in the data bank, right?

A It depends. Sorry to be -- but the problem is you have a certain level of depth that you can get at with sequencing that typically isn't going to capture everything. If they have 100 bats, it's not going to get everything in it.

The second problem is, the way they normally culture viruses is they will pull samples, guano samples from 10 or 20 bats which they haven't gotten a full sequence on. And in the cell culture system, you could have what's — a process called recombination, or it's kind of like the way viruses have sex with part of the genome, where one virus would joined to the other. And those wouldn't have been in the database, but you would have seen sequence signatures that something came — was a recombinant that had information —

Q Here's where I'm going. SARS-CoV-2, that was sequenced from human clinical samples in December of 2019, January of 2020. But if you later found in a previous data bank of sequences where there's maybe thousands, if you found that same sequence, it would imply that it was in the lab at some point?

A That's correct. If it was in their sequence database and they sequenced it, it would have been in one of their samples. Now, whether they would have recognized it as being a thing of concern or not is a whole other question, because you're looking at potentially millions of sequences.

Q I'm thinking you've got the sequence from the human. Can you do a Goggle search and see what's in the databank?

A As soon as they had the sequence in humans, the Chinese had to have done a blast search to ask in the repository of sequences that the Wuhan Institute of Virology had, was it there or not.

Q But we don't know that answer?

A That's true, we do not..

Q But normally, here, for example, you can track that, and when was it put in, who put it in?

A That's correct.

Q That answers my question. Onto another topic. Do you now or did you have a security clearance at any time?

A Let me ask a question. Is security clearances, is that kind of stuff — is that --

Q Top secret?

A — under security rules or not? If I have a security clearance, am I allowed to say that?

Mr. Ervin. It's okay to say whether you do.

The Witness. Yes, I have a security clearance.

[Over two pages of material was blanked out. RW]

BY **MR. WENSTRUP.**

Q So I look at the advisory board — and I'm not sure if that's the right name — at NIH that reviews grants.

And as Dr. Fauci said, once they're done reviewing it and they're okay, I just sign them. That's what he said. So I'm concerned, and if we're doing something in a foreign lab, are the people on the advisory board aware of the risks?

A This is the NIH advisory board?

Q Yes. And maybe you don't know, but I'm curious.

A I've never been on those. They have — basically, there's a review panel that will review them, and it will be scientists made up from across the country. Now, they may raise the issue that the expertise may or may not be available, especially if they feel that there's gain of function or DIRC related concerns. They may raise the issue, and then that would immediately go to the program officer.

If they don't and the program officer, who is supposed to read the grant, reads the grant and sees an issue, they will flag it. And through either of those processes, I guess there's some kind of discussion that probably occurs in between.

Q Yeah.

A They will then notify the PI of the grant that there's some concerns related to — and there's some concerns related to this grant that need to be addressed. So, for example, like on the grants where they may have looked at my — they were concerned about gain-of-function research, they would then list what experimental protocols they were concerned about and may ask you to address it.

Q My concern is, if they're the ones doing that, what they don't know, they don't know, the advisory board people. So they can't express concerns if they're not aware of what the concerns are about that lab. And I'm not just talking about China. It could be anywhere.

A Yeah.

Q So my concern — I think my feeling is — if we're going to do something in a foreign lab, there should be somebody on there that has that background.

A To support what you just said, the transmissible flu work that was done by the Dutch, there was some concern about whether NIH should fund that lab. And they put in — they then requested that they do all kinds of additional biosafety and stuff for the facility before they funded it. We're buddies with Europe.

Q Yeah.

A It's a fair question to ask whether, you know, if a nation state says it's going to accept U.S. money, there should probably be some kind of upfront agreement about being able to — especially if it touches on any kind of sensitive subject.

Q From the intelligence side, too. If you're getting a grant in an adversarial nation, does that grant come with some warnings before you go there? That's where I'm going.

A But again, just to clarify, in this case, in the case of the EcoHealth grant, they were proposing to do work with zoonotic viruses that were not subject to the gain-of-function regulations. In other words, they weren't increasing — they weren't working with PPPs. Those are strains that they knew were highly pathogenic or transmissible.

They were working with zoonotic viruses that were not well characterized. So there's some inherent risk there, but it may not have triggered everything going up from the NIH, because it didn't make those regulations.

Personally, I think it would have been in everyone's interest to look at that more carefully. But there are gray areas in regulatory science that things slip through, so, yeah.

Q And that's my concern. That's where I'm going.

A It's a fair concern.

Q Thank you.

A I don't disagree with it. I think it's a fair concern,

Mr. Wenstrup. Thank you.

BY **MR. BENZINE.**

Q I want to talk about the Wuhan Institute, and any knowledge that you may have had. You made a comment, I think it was in the hour before lunch, that a lot of the work happens at BSL-2, but the animal work happens at BSL-3.

A That's correct.

Q How do you know that?

A Their regulations state pretty clearly that they don't consider culturing bat viruses at BSL-2 as a biosafety concern. I also had that verbally confirmed by Zhengli Shi at a meeting in Harbin, when I was telling her she should move it all to BSL-3, and the reasons why. So I know that. And she also in that meeting said that all animal work is done at BSL-3.

So I think the news reports also talk about — and I don't know this, don't know the details again, but I thought the news reports said that there was big biosafety discussions sometime in October and November about whether they should change their regulations.

I will note, you probably don't know this, we worked with a swine pathogen called severe acute diarrhea syndrome

coronavirus, which was causing 99 percent lethal outbreaks in China. So we synthetically resurrected that virus and studied its biology, showed that it could grow in human cells, not very well, but it could grow in human cells, especially human enteric cells. And we wrote in that paper that all work on this should be done at BSL-3.

The Chinese have been working on it at BSL-2 labs. And in 2012, we had a virus called porcine epidemic diarrhea virus sweep through the country and kill millions of pigs. Ultimately, because of that paper, I have heard that they've moved all their SARS research to BSL-3.

So in that particular instance, I think it's an example of where science done in one country can sometimes have a really positive impact on another country.

Q I want to introduce what will be Majority Exhibit 1.

(Majority Exhibit No. 1 was identified for the record.)

Email cover sheet, Bates UNC_SSCP00023674.

BY **MR. BENZINE.**

[12 lines blanked out. RW]

-- pursuant to a statute passed by the House, the Office of Director of National Intelligence had to release a report on specific intelligence they had on what the Wuhan Institute was doing, and what their capabilities were. I just want to read some passage from it, and ask if you have any personal knowledge of it.

And for now, yes or no is good. And we can figure out, if yes, if we need to go any further.

The ODNI assessed that WIV personnel have worked with scientists associated with the PLA. Do you have any knowledge of that?

A I wouldn't know whether a Chinese scientist was a member of the PLA or whether they were -- unless they cleared — unless they said it directly, and then, for whatever reason, I remembered.

Most of the time, the times I've gone to China and seen a lot of Chinese scientists were a couple years apart, so there's no memory. Except for Zhengli Shi and George Gao, and more visible ones that traveled a lot. I can't remember them from one meeting to the next.

Q ODNI also said — and this kind of tracks what we've been talking about — that the WIV first possessed SARS-CoV-2 in late December 2019. Is that kind of consistent with your understanding, that they at least had the sequence in late December?

A It would be shocking to me if they did not have the sequence before January 1st. And I have seen — I think it was Jerry Farrar's book, Jump, where I think there's a note between him and the evolutionary biologist out of Australia --

Q Dr. Holmes?

A Dr. Holmes, thank you. I have a problem with names — noting that the Beijing — I didn't see this until that thing came out, that the Beijing sequencing company had sequenced it on the 27th.

But it makes sense to me. And it would also make sense to me that 23 days before that, they must have had PCR confirmation that it was a sarbecovirus. So I would say they had probably had enough sequence information to know it was a new coronavirus, maybe a sarbecovirus, before Christmas.

Q So that goes to my next question. I was going to read that passage, so I'm glad that you've already seen Dr. Farrar's book.

But you've told us, Dr. Daszak has told us, Dr. Farrar accounted in the book, ODNI said that China knew that this was a coronavirus by late December.

A Yes.

Q The dates can fluctuate, but they reported it as an undiagnosed pneumonia. Does that concern you, that they knew what it was, and didn't report it as such?

A You just asked a political question. And so the political question is where countries around the world and the leadership in countries around the world, how transparent do they want to be and how quickly do they want to be transparent? And there are some scientific questions. The first question is, if they had one sequence, they might want to get a second one to confirm it before they announce it. That would be a logical thing to do.

Number two, you have to think about it, you can't — it's not appropriate to think about it in the scale of the pandemic that eventually happened. You have to think about it as where things were in December, late December. In which case, they — well, at least they claimed they had no evidence that it was highly transmissible.

And if you follow their literature, the first real case that they tracked for transmissibility, the exposure occurred on the 31st in one hospital, relatives flew in to see them, I think on the 1st, and then flew home on the 2nd. And then two or three of them became infected. And that ended up being the first report of transmissibility, which I think was published, I don't know, late January or somewhere in January.

So in the interim of finding out the sequence, it would make sense for a government to want to confirm it at least within a second patient, because it could be that a second patient gives you a totally different sequence than which one's causing the pandemic. A fair question to ask.

So I would expect some hesitation. I would also expect the Chinese government to be very sensitive about wanting to report that it was a SARS-related virus, especially if they didn't think it was transmissible.

So it's unfortunate it was delayed. I'm not sure that — it's harder for me to say what would happen in other governments around the world. In fact, you guys would probably know better than I would how quickly the CDC, if they found a new virus that looked like it was highly

transmissible, would they report it immediately or would they call the State Department and warn and talk to Congress and the President first.

You would think there would be almost some kind of -- you don't want the President or the leadership of the House or Senate to come out and say, what? You don't want to have them ask "what" to a reporter, I hadn't heard about it. So there's going to be some time there, but certainly by the beginning of January, they probably would have had the information.

BY **MR. WENSTRUP.**

Q So I was in Vietnam. Our CDC there did really, I think, good work in Vietnam to help Vietnam. We have a CDC representative in China. Any thoughts on whether that person was engaged or not early on?

A I don't know whether the U.S. CDC representative — are they in Beijing or Wuhan? Where are they?

Q I think Beijing.

A One of the problems with that sort of autocracy is the regional areas, if I understand correctly, the regional areas in China don't want to report they have got a problem to the higher levels. So I would guess that they were hesitant to pass it up the chain just because of the structure of their government.

Q Or involve the U.S.?

A Or definitely involve any other countries, Not just the U.S., but any other countries.

BY **MR. BENZINE.**

Q ODNI also reported that the WIV has created chimeras and SARS-like coronaviruses, and had the capability to use techniques that could make it difficult to detect.

Intentional changes. We kind of talked about that.

In your work with them, did you understand that they had that capability?

A They use baculoviruses, and their molecular clone is a virus called WIV1, which I don't think they engineered with class IIS restriction enzymes that don't leave any sequence. So I think there's a sequence signature in that virus. I would have to go back and reread the paper.

Q Okay.

A But in general, yes, they had the technology to do it, but it would have — they had — they really struggled with trying to develop other molecular clones, like they were working on developing the SARS molecular clone from 2016 on, and they failed. It's not easy technology. So we started three years later and beat them to press, just to show you. And I had no interest in teaching them how to do it faster, either.

Q That was going to be my next question. Did you have any — did you teach them any of the intentional or hard-to-track change techniques?

A The only person that I ever really worked with on a molecular clone was George Gao, and this was prior to the 2020 SARS2 pandemic virus.

If you remember, MERS coronavirus transmitted from the Middle East to Korea and infected a lot of Korean scientists — sorry, citizens. One of those was a Chinese citizen who moved back to China and traveled back to Beijing and infected — that they sequenced the virus from. And they couldn't culture it. So he asked me if I would be willing to help make a molecular clone for that virus.

So we designed — we worked with him — actually, we reviewed their design, and so they tried to make a molecular clone. They failed. Ultimately, they never got it to work. They sent the clone to us. This was around 2016. We actually recovered the virus, it's still sitting in my lab. When I told them we have the virus, he never answered me, and so it's still sitting in my lab, and I've never used it.

Q The last major point that ODNI states is that there were Wuhan Institute researchers that were ill in the fall of 2019. The illness doesn't necessarily support or refute either hypothesis or prove that it came from a lab. Did you have any awareness of any Wuhan Institute researchers being sick in the fall of 2019?

A I've heard this report, but I'm not — and I've heard that they've been named, but I haven't actually seen any of the data that supports that. So I don't know how authentic it is. I mean, there's, what, 5, 600 people who work in the Wuhan Institute of Virology. I don't know the full number, but — and there was flu going on at the time, so it wouldn't surprise me if they got sick. And I believe they — if they're just getting physicals, they go to the hospital. So that's their medical care system. So looking at it from that point of view, that doesn't tell me anything.

Q Okay.

A I will also note one other thing. If you look at the molecular clock of the virus, it emerged in the middle of October, late October, not the middle or end of November. So people who say that those were the first cases, no chance.. There were five or six transmission cycles at least before they would have been infected.

BY **MR. STROM.**

Q Is there -- and I think everyone who has sat through one of these things is going to roll their eyes, because I ask this in about every single one of them.

A I haven't sat through one of these, so I get to roll my eyes.

Q You're welcome to do it. It won't be reflected in the transcript.

A That's right.

Q The 177 official WHO China corona reported cases, if you put the molecular clock to mid-October, then all of the activities around that — the market in Wuhan is actually two months or so?

A It's a major problem with that Wuhan study — that market study, yes.

Q Can you just elaborate on that a little bit? I don't have the expertise.

A Okay, so keep it in context. The context is, what do you have data for?

Q Sure.

A And the only thing we have really solid data is that the market was the site of amplification in late December, January. That's still two months from the origin date, based on a molecular clock, which means it was circulating somewhere before it got there. And the question is, where was it?

Q To that point, I guess without getting too far away from our next set of questions, how hard -- you're talking about several hundred, if not several thousand human cases by the time you're getting into January -- early January, late December?

A Remember that 90 percent of those cases are asymptomatic.

Q Right.

A 85, 90 percent. So imagine trying to chase a transmission cycle.

Q Yeah.

A Early cases are almost impossible, because most — many asymptomatics are in the middle of it. So now you have a case here and a case here, but they're actually truly linked by someone in the middle.

Q Who just walked around with it.

A Yeah. And you can't unravel that transmission cycle until you do deep sequencing on both of them. And then you look for SNPs, and you can say, this patient is linked to this patient. It had to go through somebody else because there's another marker.

So all that — so it's a fundamental problem with the papers that are reported to prove -- they write it too strong, I think, but they're very passionate about their data. And to be fair to them, it is the best data that's out there, that they can't — they don't have the early cases. What they have, they have the cluster in the market and they have two SNPs, which they argue are indicative of two different zoonotic introductions, which other people argue with. It's one nucleotide that's making that call, so it's — it actually claimed there were two independent introductions.

Q And they had some —

A It's a stretch. It's a stretch. There are a lot of virologists that look at that data and go, mmm.

Q Because it looks like, as I understand those two differences between the two lineages, it's one looks marginally more like an ancestral bat virus?

A Yes.

Q And one looks a little more humanized?

A At one nucleotide level. And they don't know what the ancestral bat virus really was.

Q Sure.

A So from my perspective, clearly, the open market was a conduit for expansion of the disease. Is that where it started? I don't think so.

Q Keeping in mind the Chinese government's ability to cover things up, is it at all worrisome to you or notable to you that we don't have a second market or a third market or additional lineages coming out of nearby cities, like we saw with SARS1, where you had sort of a wave of spillover into the human population?

A Remember that the Chinese Health Minister, I think on like the 24th of January, said community spread was rampant and asymptomatic spread was rampant. And they quarantined.

Q A lot of people.

A Within a few days of that, they quarantined 65 million. They came in and cleaned the market in Wuhan on, like, the 30th of December. What I don't know is whether they went to every other market in Wuhan and other surrounding large metropolitan areas, or when they found them, they just wiped out — they cleaned those out. I don't think — I don't have any information on it. I don't know' if you have any information on it.

Q Not that we've seen.

BY **MR. BENZINE.**

Q The last kind WIV-specific question. The Chairman brought up about the importance of databases, and you concurred that if you did a blast search, that it would be kind of common practice for someone to do a blast search of the sequence to see if it was in there?

A They had to have done a blast search.

Q It was reported that the WIV database went offline in September of 2019, and was no longer public, at least publicly accessible?

A That's what I've heard, yes.

Q Do you have any other knowledge of that, or just based off the public report?

A I think the rumors that I heard was that they were — they shut it down because they were getting hacked.

Q You just put the --

BY **MR. STROM.**

Q But you didn't talk to Zhengli Shi about it?

A No, I didn't know until it was reported.

Q You mentioned WIV1. Do you know if the WIV had access to additional backbones or unpublished full-length virus?

A I'm sure they were working on other full-length molecular clones. But the ones that they published — they were having trouble with it, because the ones that they published, they were taking the spike gene and dropping it into the backbone.

One of the problems with sarbecoviruses, especially the full-length construct, is there are toxic regions. And in bacteria, when you try to maintain them, the toxic regions either kill the bacteria or the bacteria kicks them out. And so you end up with deletions in your construct.

So we get around that by keeping the genome fragmented. It's another reason we would keep it fragmented. Besides biosafety issues, it's stable that way. Full-length constructs suffer from that.

The group that actually developed the bat technology in Europe solved that problem in another coronavirus by carefully measuring where the region of toxicity was, and then inserting in a splice site. So they destroyed it and then allowed the splice site to rejoin the live virus. The Chinese bat clone doesn't have any of that kind of higher level.

Q But I guess when you're saying that they only have WIV1, that is based on what they published. You don't have any insight?

A That's based on what they published. I don't have any insights.

Q Just that it's hard --

A I guess I'm speculating, but I personally think I'm speculating near 100 percent certainty that they worked on that with a full-length clone. They would want to do that.

Q It certainly seems plausible, based on certain --

A That's the trajectory, so why wouldn't they have to be trying? They have to be trying.

BY **MR. BENZINE.**

Q I want to jump ahead and talk about the February 1st, 2020 conference call you referenced when I went through the names. In the email back-and-forths, and the notes and the invites, you're not listed anywhere, but you were on that conference call?

A I wasn't listed on any of the invites?

Q No.

A I didn't know that. I'm kind of surprised. They clearly reached out to me. I don't know why they didn't reach out — this must have been within the NIH staff?

Q No, there was a conference call with Dr. Fauci and Dr. Andersen?

A Wait, you're talking about the February 1st call.

Q Yes, sir.

A Not the February 11th call.

Q Correct.

A I'm sorry, I was confused. Can you restate the question?

Q The February 1st call with Dr. Fauci, Dr. Andersen, and Dr. Farrar, and ten or so others, we have gotten emails from almost every American participant on the call, and haven't seen your name come up anywhere. So I was surprised to hear that you were on it. But I want to confirm that you were on the call?

A I think I was. My recollection is this meeting was heavily dominated by the evolutionary biologists, who were split on the origin of the virus. Is that the meeting you're talking about?

Q That sounds right.

A So I must have been there.

Q Do you recall how you got invited?

A No, I thought I was on the email chain, to tell you the truth.

Q I want to read a little bit from Dr. Andersen's interview.

A Okay.

Q We asked him these questions and asked him about the call.

He said, "Ralph Baric, for example, is a name that came up. We all know Ralph, Ralph is a very important coronavirus biologist, but we also know that Ralph had very close associations and collaborations with the Wuhan Institute of Virology, for example. So if this did, in fact, originate from a lab, then, of course, he would not be a person to have on a call like this."

A I must have been on that call. He may not have known it. It was — again, right now, I have huge uncertainty about what call I was on, but he was there.

Q I think we're talking about the same call.

A I think we're talking about the same call. But I was on a phone, so it wasn't like a Zoom link for me. I didn't have anyone else 's picture. So I was hearing mostly names, or I knew who they were, who was speaking.

Q And you don't recall how you got on to the call?

A I don't recall how I got invited.

Q Okay.

A No, I would have to look it up. I thought I knew, but apparently not.

Q And you've discussed a little bit about the kind of back-and-forth of the people split on the origins question.

A Yeah.

Q Do you recall anything else from that conversation?

A There was a fairly strong consensus, I think that was building toward the end of the call, that there wasn't data to support engineering, that there were other alternatives for the furin cleavage site.

The receptor binding domain was still a little uncertain at that time, but if I remember correctly, one of the first pangolin strains had been sequenced and the sequence was available, which was very close to the SARS2 sequence, which argued that the RBD itself was natural origin.

So that actually — you know, in scientific method, you're trying to disprove a hypothesis. That actually was more against the current hypothesis, which was somebody tinkered with the residues in the RBD and made something totally unique. That couldn't have been the case, since it was already in nature.

The furin cleavage site, the discussion was mostly around how furin cleavage sites can get in by natural replication-related processes. And so polymerase — coronavirus polymerases can recombine. And there are group 1 coronaviruses that have snippets of group 2 coronaviruses in the spike. The spike is like super plastic. It can tolerate all kinds of genetic change. And so it's possible it could have been inserted from another one. When polymerases are moving down template strands, they can slip back and then start again. You can duplicate sites.

And then they evolve independently. They can stutter, where they're put in additional residues. And in the case of flu, the design of the sequence, right around that polyclonal cleavage site in flu is designed to confuse the polymerase and make it slip. And that's how it gets introduced in flu to make it pathogenic in birds.

So those kind of things were possible. So there's other alternatives for the furin cleavage site, and so — and there was no backbone, nothing.

The other problem that they faced is that they only had a few genomes to look at. I think at that time, there were

probably around 30, 40 genomes, maybe, max. Some of them. they couldn't use because the sequence quality was low read. And they needed more naturalized.

So there was a lot of uncertainty from the evolutionary biologists, in terms of whether it could be lab escape or whether it could be natural processes, because both of them, it can pass between virus and culture, you'll get mutations. If you come from nature, it's got mutations.

So it's hard to distinguish that, but what you could say is that it's normal evolutionary processes. It's not something unique.

BY **MR. WENSTRUP.**

Q One thing you might find interesting, which they didn't know at the time, but it's since been declassified or unclassified. ODNI has come out and said, well, they did have pangolin coronaviruses in the lab.

A Hmm, okay. Actually, didn't they publish a paper like in September on the pangolin virus?

Q I'm not sure the date.

A It was very confusing, because different groups sequenced the same samples. And the first group had this low impact paper, nobody noticed. And then the next group was in Nature, and they came from the same place. It was all very confusing.

BY **MR. BENZINE.**

Q I want to ask about the furin site a little bit.

Dr. Garry, after the call, in the notes, expressed, concern over -- he called it a 13 nucleotide insertion that was created at the site, and said I just can't figure out how this gets accomplished in nature, but in a lab, it would be easy.

How would you kind of refute Dr. Garry's points there?

A The sequence, you only need to insert three amino acids to make a furin cleavage site. Four is a nucleotide. Four amino acids went in asymmetrically. Why would anybody engineer that and do it that way, putting in an extra residue which is a proline, which puts kinks in proteins, it usually screws things up. And ultimately, that proline changed within a few — within one or two variants.

So that didn't make a lot of sense to me. But if you were going to engineer it, I guess the question would be, you don't need to put four amino acids in, it's easier to put three amino acids in, in the frame. And also, you'd probably want to put one in that was efficient. The sequence in SARS2 is not a very efficient cleavage site.

Q So Dr. Garry was just kind of wrong?

A You can make — no, I'm not saying he's wrong.

I'm just saying that means if it went in that way, then it was nefarious purposes to begin with, right? Because you're basically trying to cover up what you did.

I don't think — I mean, when I looked at it, when it went in asymmetrically, that was more akin to recombination for me. Because recombination is not always perfect. Sometimes you have perfect recombination, but oftentimes, you have its offset and it introduces additional residue. One nucleotide or two nucleotides, depending on how it goes in, it's sort of the random process of recombination.

BY **MR. WENSTRUP.**

Q Since we're on that sort of vein, referring to that DEFUSE proposal. And then this article of January 22nd, "Scientists say EcoHealth Alliance's DEFUSE proposal was a blueprint for SARS-CoV-2." And then from April of '23, "Endonuclease fingerprint indicates a synthetic origin of SARS-CoV-2." And that's by Bruttel.

So I'm just reading from this, and I'm really seeking your Opinion on some of the things. Have you read those, by any chance?

A I have.

Q So —

A I have read this proposal.

Q I know you've read that. So as they say in there, "and the EHA plan was to use six segments to assemble synthetic viruses to use unique endonuclease sites that do not disturb the coding sequence and to buy BsmBI" —

A Can I answer those three questions? That's the standard way we've been doing genetics since 2003.

Q Okay.

A So none of that is novel.

Q Okay. And the EHA proposal would create chimeric spikes, insert new receptor binding domains, and human furin cleavage sites.

A Can we stop before the furin again?

Q Sure.

A Absolutely, the proposal talked about making chimeric spikes with WIV1 and SCH014 as the backbone. The sequence would come from the Chinese, depending on — it would be some work with pseudotypes beforehand to make some kind of down selection about which ones you might want to work with.

And then, primarily, because of cost, the first thing you do is you drop them into those backbones to see if they could program infection. So that's nothing new either in that proposal — the DARPA proposal came out, what, 2020?

Mr. Strom. Proposed in 2018.

The Witness. But publicly, the group that released it —

Mr. Benzine. 2021.

The Witness. Okay.

BY **MR. WENSTRUP.**

Q After the FOIA?

A No, it was done before the FOIA.

Q And looking at the proposal, it appears there may have been a willingness, not necessarily by you, to do some of this work in the BSL-2 in China.

A There was no willingness on my part to do any of this work.

Q That's what I wanted to clarify.

A Let me make that clear.

Q That's fine. So in Bruttel, it says, "the restriction map of SARS-CoV-2 is consistent with many previously forwarded synthetic coronavirus genomes and meets all the criteria required for an efficient reverse genetic system." And then they discuss the rather improbable odds of a coronavirus having the patterns seen in SARS-CoV-2 without engineering. That's an opinion.

A That is an opinion.

Q And then they report a high likelihood that SARS-CoV-2 may have originated as an infectious clone in vitro.

So what they're reporting is what EHA proposed to do is what is actually seen in the SARS-CoV-2 genome. I want to know if you agree. And if I give you this from the article, because at first blush, I have no idea, you may know, the top line.

A Yeah.

Q Does that makes sense to you? Do you see that?

A So the first thing, what these are — these lines describe naturally occurring BsmBI sites in the SARS coronavirus 2 genome. Now, one of the first things you notice is that those same sites are present in many of the bat strains that exist. So if they are engineered, if you use them to engineer SARS2, they wouldn't normally be in the same location in the bat strains.

The second thing is, they do count six pieces, but one of the pieces is about 8 KB and the other is about 300 base pairs. If you look at any of the molecular clones that I've engineered, with SARS, they're usually 5 KB apart, so that you have five or six KB pieces that you can work.

Having a tiny little piece like that, if I looked at it, that would irritate me, like, to no end, and we would silence it, one of those sites. And then separate this, so that the fragments are of equal size. The first size piece is also too small, and so it leaves larger pieces, and the larger clones are unstable with passage.

Q Okay.

A So you would want it more equally distributed, unless there was a region that was super toxic. If there was a toxic region, then you would have a little piece. There's no toxic site there.

Q Thank you.

A So this is biostatistical BS, in my opinion. And they come up and say that the pattern here is unique, and they do that by comparing most of the pattern to clade 2 and clade IB coronaviruses.

So the statistical number that they have for the ones that are far away is much more, and it gives them statistical power to make the claim that it was engineered.

Q Thank you.

A And it's a pathetic piece of work. By the way, you can see how I engineered the SARS-CoV-2 genome since it's published, and you will see that it's completely different than this.

Mr. Benzine. I want to introduce Majority Exhibit 2. It's more to refresh your recollection on dates and people and stuff.

(Majority Exhibit No. 2 was identified for the record.)

The National Academies of Sciences, Engineering, Medicine, Expert Meeting Agenda, Bates REV0000809

BY **MR. BENZINE.**

Q So this is the agenda for a National Academies of Sciences, Engineering, and Medicine meeting on Data Needs for COVID-19 from February 3rd, 2020.

A He did send me an email. Did I say he sent me an email?

Q This is a different meeting.

A Okay. I always worry about names, about saying I didn't get an email.

Q Absolutely. Do you recall attending this meeting?

A This would have been by Zoom.

Q Yes.

A So I can't say with 100 percent certainty, but I can say that, most likely, yes. I would have to check my calendar, but I think I did. I was certainly part of that committee.

Q Understanding you're not 100 percent sure, but do you have any recollection of what was said during this?

A Well, I think the purpose of this meeting -- I think the purpose of this particular meeting was to outline an agenda for the group to write a report on origins. And so part of the meeting was to review the statement of work that had been given to the National Academies to try to come up with this plan.

And then I don't recall what Fauci said at the meeting. Yeah, I don't recall what Fauci said at the meeting. And then there was discussion about writing objectives and things like that. That would have occurred. And what different groups need to get together to try to start formulating a

response.

Also, I think we had -- we may have had outside speakers come in and things like that, to try to inform the committee, but I would have to look. I would have to review the agenda. Part of the problem here is there's all kinds of things going on simultaneously, and so I could easily get things confused.

Q Under a subpoena issued by this Committee, Dr. Andersen produced some Slack messages to us between him, Dr. Holmes, Dr. Garry, Dr. Rambaut, and then some were redacted, and we reviewed them in camera.

Regarding this meeting, he said something about you, and I would like to get your side of the story on what he said. So this is —

A Hopefully, he didn't say anything negative.

Q This is a quote from Dr. Andersen's Slack messages. "I should mention that Ralph Baric pretty much attacked me on the call with NASEM, essentially calling anything related to potential lab escape ludicrous, crackpot theories. I wonder if he, himself, is worried about this, too."

I'm just trying to get your side of this.

A Can you read that again?

Q "I should mention that Ralph Baric pretty much attacked me on the call with NASEM, " National Academies, "essentially calling anything related to potential lab escape ludicrous, crackpot theories. I wonder if he, himself, is worried about this, too."

A I don't recall this. So because of this, I'm going to at least say one thing that I gave in the BSEC meeting on January 25th or 26th. My summary of the origin of the pandemic was the following.

There are three potential causes for, that pandemic. First is natural origin, second was laboratory escape, and the third was genetically engineered.

Q And what was the date of that again?

A January 25th or 26th of 2020. So I don't know where he's coming from. That may have been his interpretation, but I'm surprised. I'm really surprised.

Q When we saw it, I wanted to make sure we got your perspective on the record.

A Can you read it one more time?

Q Yes. "I should mention that Ralph Baric pretty much attacked me on the call with NASEM, essentially calling anything related to potential lab escape ludicrous, crackpot theories. I wonder if he, himself, is worried about this, too."

A I'm really surprised about this, because I wrote a piece on his origin paper in Immunology, and said that laboratory escape was possible because of safety procedures in their laboratories. So it's not consistent with what I also reported to other groups publicly on when interviewed. So I don’t believe he's attributing that to the right person.

Q That's fair. And I wish I could show you the

message, but like I said, it's redacted, so I don't have it.

A What do you mean, it's redacted?

Q When Dr, Andersen's counsel produced the Slack messages to us, they redacted some. So there's a big black box over them, and we requested to review them in camera.

A So he's talking to somebody else, then.

Q Yes.

A Okay. No, I would just say that's inconsistent with what I've said publicly and privately that can be verified.

Q Dr. Andersen was then the lead drafter of "The proximal origin of SARS-CoV-2" that came out in Virological in February, and then Nature Medicine in March. I know you're aware of the paper. Have you had an opportunity to review the paper in the last four years?

A I looked at it before this meeting. I figured you guys might ask.

Q So it came to two kind of conclusions. The first in the summary, and we've heard different stories from different authors, of the reviewers kind of ramped up the language to, we — when we said laboratory construct, we meant like bioweapon, all kinds of things.

But the first conclusion was, "our analysis clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus."

Do you agree?

A I would agree with that statement, in terms of the data that was available at the time. That's absolutely true. It's still true today.

Q Laboratory construct, how do you define laboratory construct?

A It doesn't matter how I define it. What matters is how they define it. I would -- laboratory construction, to me, personally, would be an engineered virus.

Mr. Strom. One that does not have —

The Witness. You have a molecular clone, and you reconstruct it somehow in the laboratory.

BY **MR. BENZINE.**

Q Like serial passage wouldn't fall under laboratory construct?

A No, I don't think so.

Q Okay.

A But they may have interpreted it that way. You would have to ask him.

Q We did.

A Did he answer?

Q I would have to go back and look. I think — what I recall from that, both from their hearing and the interviews, is that they meant bioweapon or --

Mr. Strom. A de novo

BY **MR. BENZINE.**

Q A de novo, built virus.

A What they would have had is no true actionable intelligence, and said it was engineered. Because if you don't have a backbone sequence that's close enough, you don't have any substrate on which to build anything that could have been close enough to SARS that people would have said it was novel. So we still don't have a backbone sequence that's close enough.

Q The second conclusion was, "we do not believe that any type of laboratory-based scenario is plausible." Do you agree with that?

A I signed a paper that said that that was — that a laboratory scenario needed to be carefully evaluated. I think that says it all as well.

Q And then after the fact —

A Which is also inconsistent with the statement he just made.

Q It is. I'm not a scientist, but even reading that confuses me beyond just the science.

A It's the first I've ever heard it, so I'm very confused about it myself, yes.

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

A I know him.

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

A John contacted me.

Q Were you the --

A No, I was not. I was not. I was building suspense.

Q So Dr. —

A And it worked.

Q It did. Part of it is because Dr. Holmes thinks you were the one that contacted John Cohen.

A Well, that's why he may say it. He and — I'm forgetting his name, sorry — Andersen. If that's what they thought, he may have been really irritated with me if he felt that it was me, but it was not.

Q What did Mr. Cohen contact you about?

A He was asking me the same question you asked me, was I the author of that statement? And I said, no, I

was not.

Q Do you know who is?

A No, I don't.

Q Shifting to another publication, going a little bit back in time, but the Lancet correspondence from February 19th, 2020.

A This is the Daszak request for support of Chinese science?

Q Yes.

A Okay.

Q You're obviously aware of it. Dr. Daszak testified, and I'm quoting, that you didn't want to be on the letter, and that you were very hesitant. Do you recall Dr. Daszak asking you to join the letter?

A Yeah, there is an email chain, but I can tell you what preceded the email chain was a phone call, where he asked me to be on that correspondence. And I said, no, that I felt that we both had a conflict of interest because we work with Wuhan Institute of Virology. That if we were on it, and that could be construed as, in essence — what's — sorry, I must be getting tired, because I'm forgetting the terminology.

Mr. Strom. Competing interest or a conflict.

The Witness. Like we were doing it for our own benefit, right? So I didn't think it was appropriate to sign it. The next day, he emailed me and said that he talked to Linfa Wang, and he agreed that we shouldn't be authors.

And I did something I normally don't do, which is say more words' than "great," which is what I usually said. But I said, great, it's better this way, or something along — the summation was it's better this way. So that's the genesis of that.

Q But Dr. Daszak did end up signing it?

A He did end up signing it.

Q Did you have any conversations regarding his change of heart?

A No. I think it was a mistake on his part, and later, I think when he went — when he was part of the WHO committee that went to China to review it, he also had a conflict of interest. And that it would have been better for the scientific community if he hadn't attended.

Q You've kind of already answered this, but I'm going to ask it very directly. In the letter, it said, "we stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin," that was widely construed as any kind of lab leak hypothesis is a conspiracy theory.

A I think you might want to put that in context, because the context of that letter came out shortly after a report went up on a reprint server saying that the SARS2 genome had pieces of HIV. And what that researcher had done is he had done sequence comparisons under the most relaxed

conditions possible, and so he allowed big deletions and things to occur.

So you could allow those deletions to occur and say, okay, is there a sequence of HIV in SARS2, and, boom, it occurred.

What he didn't tell you is if you did the search on all the biota in nature, you would have found it like in a pine tree, and all kinds of other stuff.

So the scientific community was really upset about that paper, because it was — my wife told me not to describe it that way, so I'm not going to describe it that way, but it was really poor quality science, and ultimately, the group retracted the paper.

There were several groups that immediately showed what they did, and why it was inappropriate. That letter came out shortly -- I believe came out shortly after that report. And so that was the first big conspiracy report, which would have dominated that letter. So keep that in context.

Q That makes sense. And like John said about rolling eyes, everyone in here is going to roll their eyes when I say this, but we have kind of had this recurring theme of people getting out in front of their skis and maybe writing a little bit more than they know or mean, to combat things. So, completely understand the HIV sequence was a conspiracy theory. They could have written that, understanding that you didn't sign it, but they could have said that was a conspiracy theory, not any theory suggesting COVID-19 does not have a natural origin.

A They said there was no chance, what?

Q We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin.

A Yeah, I would say, that date, I would probably have been more comfortable not signing it, in any event, even if I didn't have a conflict of interest.

Mr. Benzine. Thank you. We are at our time, so we will take a break and go off the record.

(Recess.)

Ms. Yass. Back on the record.

BY **MR. ROMERO.**

Q So, Dr. Baric, in the previous round of questioning, you were asked about your attendance on a February 1st conference call, and you mentioned that on that call, there was some talk about the pangolin virus, its receptor binding domain, and its similarity to the RBD of SARS-CoV-2. Does that sound correct?

A That's correct.

Q So as far as the highly scrutinized February 1 call that we've come to understand was organized by Dr. Jeremy Farrar, we have talked to other scientists, other virologists who attended that call, and we were told that, at that time, they didn't actually know about the pangolin virus.

So hearing that, and knowing that you were on a lot of calls around this time in early February 2020, is it possible that you weren't on the February 1 conference call organized by Jeremy Farrar?

A Since I apparently wasn't on the email invite, there's uncertainty in what call I was on. But certainly Dr. Fauci was there, certainly there were four evolutionary biologists there, certainly there were people like Ron Fouchier, who I think was also on the call, and several other corona virologists, so I'm pretty sure I was on that call.

And I believe that the statement was from one of the evolutionary biologists that the sequence of the pangolin virus either was out, or it might have been coming out. I may have misspoke and said it was out, but it was out very shortly thereafter. If it wasn't out at the time of the meeting, it was within a couple of days, and I may have pooled them together. But within a few days, those sequences became available.

So that might be a memory lapse. There's already a potential memory lapse about whether I was even on the call, so — but I'm pretty sure I was on the call.

Q Okay. So last hour, I think around that time — it ended with a discussion about the "proximal origin" paper.

A Yeah.

Q So we would like to ask a few more questions about that paper, and some of the conclusions reached.

A Sure.

Q Again, related to its conclusion that SARS-CoV-2 is not a "purposefully manipulated virus."

So again, we have interviewed the authors, and our understanding through those conversations is that "purposefully manipulated virus" refers specifically to the idea of deliberate engineering. So that would mean combining bits and pieces of genetic material in order to create a virus. And there are other techniques that are encompassed here, but constructing a chimera, I believe, would fall under this concept.

A Sure.

Q So the paper rules out purposeful manipulation on two grounds. Premise 1 is that the virus, SARS-CoV-2's receptor binding domain, which is housed on the spike protein, is imperfect. And you have kind of gone into this discussion in our first hour of questioning, that no scientist would intentionally construct a virus whose receptor binding domain would not perfectly bind to human ACE2?

A No, I don't think I — you need to say that again. I'm not sure I would have said it the way you said it. Can you say it again?

Q Okay. So our understanding is that the receptor binding domain of SARS-CoV-2 is an imperfect receptor binding domain that does not bind perfectly to SARS-CoV-2. Does that sound correct?

A It binds well to human ACE, but it is not perfectly designed to bind to human ACE.

Q So. I guess the question is, what does that say about the possibility that this receptor binding domain was constructed by a scientist?

A I think the more telling information that's also in that paper is that there's a pangolin sequence that I think has four amino acid changes in it over several hundred amino acids in the RBD, which indicates that it's more likely a natural origin derivative.

I think this was then later substantiated by sequences from Thailand isolates, like BANAL-52 that only had one amino acid change in that region and not in a receptor binder, which argued again that it was natural, it's related to natural isolates.

So what's your question again? I'm trying to understand the context of it.

Q So I guess, on the one hand, we have a receptor binding domain that can bind to a human ACE2, but does not perfectly bind to human ACE2. And on the other, we have a pangolin virus found in nature that has a very similar, if not identical, receptor binding domain.

A Except it binds much better to human ACE2.

Q Okay. So taking those two things together, what does that say about the likelihood that this receptor binding domain in SARS-CoV-2 is not natural and was created in a lab?

A It says it wasn't created in a lab.

Q Okay. So that's kind of the conclusion that the "proximal origins" authors possibly reached in their paper?

A I think I said that I was in agreement with their interpretation of the data as it sat at the time, that there wasn't any evidence, scientific evidence that it was engineered. It doesn't mean that that kind of data won't emerge in the future. It just means that, at that moment in time, there was no data to support it.

Q I guess that kind of flows into a criticism of that conclusion of the "proximal origin" paper that, in the abstract -- and correct me if you disagree. But is it possible that SARS-CoV-2 is a chimera that was constructed by taking a receptor binding domain from a virus similar to the pangolin virus and attaching it to the backbone of a virus that is similar to RaTG13?

A If you took the separate binding domain of SARS2 and put it into RaTG13, every evolutionary biologist in the world would say, hey, somebody took the SARS2 or some other RBD and stuck it into RaTG13, which has about 1100 or 1200 nucleotide changes, a fingerprint all across that genome that says, I'm RaTG13. And if you put a SARS RBD in it, it still says, I'm RaTG13 and somebody stuck an RBD in me. So the footprint would have been there.

There's no genome close enough that is engineerable using current standards that could have resulted in SARS2.

Q Okay.

A Now, that may happen in the future, but at this time — and at this time, it was not going to be possible. And it was even worse because, let's say if you're going to engineer it, if you're going to engineer it, that means you don't know what the sequence is.

So with RaTG13 -- and I tried to point this out before, there's like — I'm going to do it 1200, it's actually 1100 and, I don't know, 47, or something like that, but the math is too hard. So there's about 1200 changes, so it's four to the 1200th power of combinations of mutations that you have to try to get SARS2. That's a huge number.

Now, I'm going to tell you why it can't be done. The transfection efficiency of a molecular clone for coronaviruses was, at best, 5,000 cells. So that means you can quarry 5,000 genomes at a time. Four to the 1200th power is a whole lot of zeroes. I calculated it out. One researcher would require something like 500,000 years. So if you've got 100 researchers doing it, you could get it down to 54 years. Then you have the problem of figuring out which one was going to be pathogenic in humans. So that's just the start. So it's not possible to actually do that with the current technology.

Now, people will say, well, you can do shotgun mutagenesis across the genome, but you still have all those genomes that you have to filter through to the one that would be pathogenic in humans.

How would you select them? I know how I would select them. I'm not going to tell you how I'm going to select them, but I would, because you don't want me to answer the question on the table unless you press me.

Mr. Romero. I think that's good for the "proximal origin" questions, so I am going to turn it over to Alicia.

Ms. Yass. Great.

BY **MS. YASS.**

["One log" means a factor of 10, AKA 10 to the power of 1. Log(10) == 1. Dr Baric's explaination of some of the history behind this on page 98 below - page 204 in the original PDF. RW]

Q So I am going to ask you. Dr. Baric, some questions about what's been termed the one log growth rule. This Committee previously spoke to Dr. Daszak, and during his interview, he said that the idea for his one log growth rule that EcoHealth Alliance worked on and used in its grants with NIAID in their year 3 award conditions for their study of bat coronavirus, and he said that he got the idea for this rule from you, and work that you had previously done. Are you aware of this?

A Absolutely.

Q So Dr. Daszak said, as he was responding to questions that he got from NIAID about his work and the gain of function pause in effect at the time, and he said, "I got advice on what a good proper response to this should be from Ralph Baric, who responded to other requests for that." Did you speak to Dr. Daszak about your use of the one log growth rule?

A Yes. So this goes back to the review of the chimeric viruses with SHCØ14 and WIV1.

Despite all the data that argued that it was attenuated, one of the things that NTH wanted us to do or think about was to come up with some criteria that you would use as a benchmark that if it happened in your lab, let's say we put those viruses in some other system and suddenly they're growing like bandits, or they grew tenfold higher in a humanized mouse for some reason. We needed a benchmark. They wanted a benchmark.

They didn't want to give you approval to move forward without some other regulatory -- not a restriction, but a regulatory benchmark that if you saw this benchmark, you would immediately pause, you would immediately tell your local environmental health and science committee to say, listen, I found this growth phenotype that's tenfold above what we would have normally seen with this virus in this system.

They would have looked at it, and communicated with NIH. And then we would have had a call about what to do. And the outcomes could be destroy the virus, which is fine. Alter the containment conditions, maybe move it up to BSL-4, which would mean we wouldn't work on it anymore, or — I can't think of a reason, like right now, I would be alarmed if we continue with it, so I would probably destroy it. But I can't think of a reason why they would say, don't worry about it, and go forward, right?

But from their perspective, they're developing new regulations for things that had never been regulated before, and our application was one of the first ones that went through. And so in the discussions, the back and forth discussions, we decided that there needed to be some kind of additional benchmark that you could use as a way that would tell the research community and the university and the NIH that you've got an unexpected result and you need to stop. And you need to then debate and discuss and make an informed decision on how to move forward.

Q Thank you.

A So he called me and asked me what we did, and I told him that's what we did.

Q In your use of this one log growth rule, in your research, we would just like to hear a little bit about that. But specifically thinking about the measurement for the one log growth, we have heard some witnesses talk to us about using a PCR measurement, others talk about using viral titers. So can you please explain the difference between those measurements and how you utilize them in your experiments.

A Sure. So viruses, RNA viruses when they replicate, they have an error rate. They also make mistakes when they package viral genomes into the virions which are released from the cells. So sometimes they're not infectious.

In addition, some of the errors that occur during replication can be lethal, so those viruses are not infectious. So in virology, for RNA viruses, there's a function called

particle to PFE ratio, where you count the number of virus particles and you ask, can they form plaques in monolayers, or what's the titer, what's the — it's usually plaques and monolayers.

You can also do it in animals, too, and you have to titer down to — it depends on how well a virus — if a virus is lethal, one PFE, you can use a mouse. So you could put the virus in a mouse and figure out exactly what the lethal dose is or the number of plaques.

So if you have a monolayer of cells, so you've got holes in them, so you count those plaques and those are viable viruses that can infect cells. So we use viable viruses to infect cells, because that tells us exactly what number of cells in that tube can infect a cell.

PCR will detect anywhere from 100 to 1,000 fold higher titer than is seen with plaque assays for RNA viruses because of this particle to PFE ratio, and the numbers of particles that are noninfectious. So we always focus on particle PFE. I wouldn't do it with — I wouldn't use the Standard with PCR genome equivalents, because the particle to PFU — there's a genetic term called epistasis, and that's where mutations at one location affect the viability and the function of sequences in another location. So when you make a chimera, you break apart epistatic interaction, so the particle to PFE ratio can shift.

So you could think you had a high titer by PCR, but by plaques, there wouldn't be a tenfold increase.

Q So ——

A So I would prefer — I mean, we preferentially do plaques. I don't know whät NIH regulations are, what other people may ask.

Q But just in the most simple terms, you're using that because it's more accurate and more reliable?

A Yes. In simple terms, I think it's a more reliable metric of the potential hazards to the experiment.

Q Does it also give you realtime results as the experiment is happening?

A Within a week or two, yeah, sure.

Q And we would just be interested in hearing your perspective on how virus growth relates to a virus's pathogenicity or transmissibility, particularly in the context of this rule.

Is it as simple as if a virus's growth is enhanced by more than one log, then that virus has been made more pathogenic or transmissible, or are they not necessarily correlated?

A It's complex.

Q Okay,

A In humans, there is a general correlation between titer and disease severity. In individuals, that relationship may not hold. And I can describe it best in the context of mouse experiments with a genetic — what's called a genetic reference population called a collaborative cross. You can infect collaborative cross mice with the same dose of virus, and the virus grows to identical titers at day 2 and

4. And it clears at the same rate. One animal doesn't lose a drop of weight, the lungs are clean, completely subclinical infection. The next animal, lose 25 to 30 percent of its weight loss, it can die, the lungs look like a liver, and that's because of all those host susceptible loci that occur after the virus gets in and replicates. So it's complex.

Q Sure.

A So when we do a correlation analysis in outbred rodent populations, there is no correlation between titer and disease severity, but there are individuals where it correlates, okay? So it's a function of genetics and individual variation.

Now, the second part Of your question had to do with transmissibility. Prior to COVID-1 9, there were no transmission levels for any coronavirus, so we had no information on that. And it wasn't until — because SARS1 doesn't grow very well in the hamster and nobody tried transmission studies.

So in general, with COVID-19, there seems to be a correlation between titer and transmission. But transmission is contrived. There's about two inches apart in two cages for airborne transmission and air blows from one to the other. It doesn't happen in nature, like in humans.

Q Sure.

A So in that scenario, it's kind of a contrived model. In real life, it's probably multigenic, it's stability of the virus, it's where it grows and how easily it aerosols. Different people clearly make different size particles when they breathe and talk, some make very small particles, they're more likely to aerosol; others don't, make large droplets. So it's very complex in terms of transmissibility.

So I don't think that's been studied sufficiently to give you a clear answer except, in general, it's thought that higher titer in the right compartment correlates with more efficient transmission.

Q And just from your use of this one log growth rule, what has your experience been in it being a good guardrail or benchmark, as you said?

A Well, we haven't done anything that's triggered it yet, so we're happy with that. Again, generally -- well, we haven't made chimeras in quite a while. But in general, when you make a chimera, you're breaking apart some epistatic interactions, so in general, it's a little more debilitated, so the virus has to pass it a few times to figure out how to fix itself.

Q I appreciate that science lesson. I'm going to change topics a bit. We have heard from multiple witnesses that the creation of a vaccine for COVID-19 happened almost miraculously fast, and they credit this speed to the fact that coronavirus research and mRNA research had been going on for years prior to the COVID-19 pandemic. You were a part of this process, both with ongoing research and active involvement in the COVID-19 vaccine testing, correct?

A That's correct.

Q In terms of the development and testing of a COVID-19 vaccine, in 2020, your involvement was running safety and efficacy trials for Moderna's vaccine using your lab's chimeric coronavirus strains, human respiratory cell cultures, and lab mice. Is that accurate?

A For the COVID-19 vaccine, I don't think we tried any — we used any chimeras. The only thing we really used was the mouse-adapted SARS2 coronavirus, the MAIO, which was called MAIO in this case. It was ten passages in mice that produced a lethal infection.

But I can tell you that our involvement with mRNA technology started in 2016 in collaboration -- 2016, early 2017, in collaboration with Barney Graham and Kizzmekia Corbett at the NIH VRC, where they had just worked. Well, Jason McLellan and Barney had really worked out the technology to freeze the coronavirus spike glycoprotein in what was called the prefusion state, which had all the big, juicy neutralization epitopes in the right context.

So they wanted to evaluate mRNA vaccine performance, and so they contacted us and we worked with them on mRNA vaccines for MERS coronavirus mostly, but also BARS coronavirus in 2003, and were actually writing the paper in December 2019 when COVID hit. And so we stopped writing the paper.

When they received the sequence, they ordered the constructs. I was told that I had to have a mouse model available by the end of April, so my job was to make a robust mouse model in sufficient time to test that vaccine in April and May, so that the final reports could be compiled, including some studies that were designed to look for what are called variant phenotype vaccine associated — oh, crap, I forget the name. Do you have to type everything that I say? Great.

Q We're all allowed to have those moments.

A I'm having a moment. But they're probably going to become more frequent over the next hour, I have to admit. But it's vaccine associated deleterious outcome. In this case, there's something, either the vaccine enhances the availability of the virus to grow or it causes some kind of pathology. And it needed to be tested for that, because, earlier,- it had been shown with earlier vaccines with the SARS strain that you've got those phenotypes. My job was to make the mouse model and design those experiments and have them all done by April.

Q And we've heard from multiple people that this was all on a timeline that was way faster than any other vaccine.

A It was very stressful.

Q I'm sure.

A It was very stressful.

Q You mentioned that you had been working on this, on vaccines, prior to 2016. I know, reading articles and research that you've done, it seems like you've been working on a pan-coronavirus vaccine for many years, and that's been one of your research focuses; is that right?

A Well, again, the discovery work we did said that there was a zoonotic virus. There are animal viruses out there that are high risk. You don't know which one will evolve. So the only kind of countermeasure you can make is

broad spectrum. It either has to be a broad spectrum drug, or you have to have a vaccine that provides like an umbrella of breadth to many strains.

And so what you try to do with your discovery work is to find the strains that are the most different, and then some in the middle. So then you can say, well, it works on the bookends, it works in the middle, I hope it works against the new thing, right?

Q Sure.

A That's the only way to do it.

Q You mentioned a little bit throughout today some therapeutics that you were testing before and other research that was sort of useful for the pandemic. Can you elaborate on what pieces or findings from research prior to the pandemic were- useful in determining and finding vaccines and therapeutics once the pandemic was widespread?

A Well, certainly having isolates and robust mouse models of human disease, using the human strain of MERS and the SARS strain that caused human disease were really important. But that captured this much of the variation. like a paper thin sliver of the variation that exists in the family.

So you need, to have natural, other zoonotic isolates with robust mouse models, so you'll be able to really evaluate the performance of the vaccine when it's not a perfect match, because when the vaccine's not a perfect match is when all these adverse reactions can occur, or you have this because you have a breakthrough.

So we did discovery work. That discovery work is important because it gave us breadth both with MERS and with SARS. In addition, at the same time, we were part of a grant that was funded to try to develop drugs against coronaviruses, with Mark Denison at Vanderbilt and Gilead were collaborators. And so Gilead was gracious enough to provide a fairly robust panel of nucleoside inhibitors that we screened working down to remdesivir, that we then moved from — the classic approach 'was, you know, cells, continuous cells and culture, to primary human cells, to- the animal models, and demonstrated that it not only worked against SARS and MERS, but it worked against all these other bat coronaviruses, other human coronaviruses, other animal coronaviruses, 12 different viruses.

So we knew it had broad spectrum. So now the hypothesis is, you have a broad spectrum drug. Any new virus comes along, you immediately test the hypothesis and evaluate remdesivir, molnupiravir, Paxlovid, therapeutic antibodies, vaccines, to see if they provide breadth. And simultaneously, you use that information in a reiterative fashion now to develop broader-based vaccine platforms.

So one of the innovations that we did was to take spike glycoproteins across the phylogenetic tree, blend them together as a chimera, delivered on mRNA vaccine that would provide neutralizing breadth against a greater percentage of the strains.

Q So would it be accurate to say that research on a pathogen that's not yet infecting people gives scientists a basis to make their hypotheses for how a pathogen that is infecting people may react to therapeutics or a vaccine?

A It's more than that. It's absolutely essential. You have no idea of the breadth of performance of your product if you don't have natural isolates available in the virus family.

So, for example, calls to shut down discovery work in the natural world will basically mean that the U.S. is at greater risk for future emerging diseases because we don't know what's there, and we can't test products against it.

Q Agreed.

Ms. Yass. And I think that leads into some questions my colleague will have for you.

BY **MR. MCAULIFFE.**

Q Good afternoon. Will McAuliffe from the Energy and Commerce Committee.

You mentioned a lot about, I think, things that are sort of fairly out of our control, both the American scientific enterprise and then certainly the U.S. government, in terms of what other countries do, wildlife trade, markets in urban centers that may be engaging in things that are risky from a natural spillover and viral evolution context, right? I mean, as you said earlier, some of that is like a political question, it's not really somebody in the government here can push a button and change what everybody else is doing.

A That's absolutely correct.

Q Despite what we would like to do sometimes, often, maybe. So thinking of the things that are in our control, and following up on some of the things that Alicia was talking about, it seems like leading up to the COVID-19 pandemic, there was already an anticipation, as a result of SARS and MERS, that this is a type of virus that is going to continue to present a threat to people that we need to be looking closely at. Is that fair?

A Yes, with the caveat that many scientists and many public health officials felt that the risk was very low, and that's because the original SARS strain was controlled by public health intervention strategies, completely because you didn't transmit that various until you got really sick, and asymptomatic spread was zilch.

With MERS, it didn't transmit efficiently except for a few super spreaders, like, transmitted it really efficiently, which actually tells you a little bit about the potential, right?

Asymptomatic infections occurred and they could transmit, which is a little bit different, but it wasn't very efficient. It could be controlled by public health interventions.

So the — I'm forgetting the word. Standard is not the word that I want, but the standard in the field was that if a coronavirus emerged, it would be subject to control by

classic public health intervention strategies. And that was lunacy to me, because human coronavirus 0043, HKU1, 229E, and NL63 transmitted efficiently and have been transmitting efficiently for anywhere from 100 to 800 years in human populations. And in the animal world, efficient transmission and pandemics were occurring. That means they have the rudimentary intrinsic capacity to do that.

We just got warned. That's how I viewed it. We were warned that nature had some things in store for us and we weren't paying attention to it.

Now, in NIH's defense, they funded research specifically to do work on developing drugs against coronaviruses. They funded work with Barney Graham and our group to develop mRNA vaccine technology. We were eventually going to get to nanoparticle-based technology, but the pandemic hit before it was there.

So NIH had it on their threat list and were supporting fundamental research, which in the end, saved millions of lives across the globe, but there was resistance to that idea, and many health officials thought that it wasn't going to be an issue.

Q Is it fair to say that that kind of resistance can result less from a desire to potentially downplay a threat altogether versus choosing among competing priorities of threats to people with limited resources?

A Absolutely. I think — I can only speak for -- I can't even speak for NIH. I can speak for what my opinion is, right?

Q Yes.

A So my understanding is NIH uses data to determine policy. The experiments with transmissible flu — I need something to drink, excuse me.

The experiments with transmissible flu were to address a question about policy. And the virus had emerged in '99, it was still around in 2009, half the scientific community was saying there's some risk or some fraction. Some fraction of the community was saying it couldn't get through fitness trials to be able to cause -- to be transmissible. Never was going to happen.

The other part of the community said, yes, that it could. And NIH is spending a lot of money on surveillance, vaccines, developing drugs, spending a lot of time and resources on this. They wanted to know the answer. So they had meetings with the WHO, and the FDA, and the USDA, and the CDC to determine priorities. And the priority was, we need to ask the question, is transmissibility possible.

The answer was yes. And that continued to result in drugs, surveillance. You can go to the CDC site and get a whole list of mutations that are associated with pathogenesis or transmission.

So these types of questions provide information for policy. Policy then implements it in terms of some kind of strategy to try for preparedness.

Did I answer your question? I get off on a tangent. I'm losing focus.

Q This is all very interesting. Don't worry about it. I think one of the questions I have, then, is investments like the ones that NIH made prior to the COVID-19 pandemic, there were folks during the time of those investments who thought maybe those weren't as wise as other investments that could be made.

A Absolutely.

Q Now, we're sitting here with the benefit of hindsight.

A Yes.

Q And again, I'm sure those people had other very good, pressing concerns. But is one of the lessons, as we sit here trying to figure out what should we bring back, what does Congress do, is one of the lessons to make sure that there are adequate resources for NIH and other research institutions, such that even within prioritizing, you're not having to wholesale exclude a category of threats because you think it is less at a time. And there can still be background work that is happening at all times that may suddenly, over the course of weeks, become incredibly relevant to the entire world?

A That's correct. And a potentially risky experiment may be in the pipeline in making that decision.

Q So that's what I want to talk about as well.

I think you gave a very helpful background on how we should sort of think about risk, and that it seems like some of the folks who are thinking about risk the most are those who are physically entering into a lab and interacting with different things that pose different kinds of risks under different kinds of circumstances.

But I think, with all the understandable discussion that we've had about risk at top of mind, the potential or actual reward, I think, can sometimes get pushed to the side, or the reason for why it is being done.

And folks who aren't familiar, who haven't sat in a room and listened to this and been educated numerous times by scientists about why this work is done, could sort of walk away from reading an article or seeing a headline and thinking, why would we touch viruses? Why would we think about it? This seems dangerous, these are dangerous things. Why can't we just sort of, like, leave it alone and just treat whatever we have that we know exists and people, are getting sick with.

But it seems like one of the reasons for this work, and I'm curious — correct me on this. One of the reasons for this work is, as you said, viruses are constantly evolving on their own. It's not like they only evolve in a lab. Frankly, that is a tiny sliver of where anything with a virus is changed. It is evolving and changing many, many, many times over all across the globe.

A And looking for new niches to colonize, yes.

Q And some of them may pose a very distant threat, and then there may be some currently in animals that are on the cusp of becoming an actual threat to the human population.

A That's correct.

Q So one of the things I've come to understand from all these conversations is some of the work that is happening in a lab where' you are examining and altering a virus to something that at least we don't know yet has happened in nature, we haven't collected it from nature, but it may well exist, is to be able to sort of see around the corner and say, this is where nature may be heading next. And what would that mean for the human population and what defenses do we currently potentially have against it? Do they work? Do we need something new?

Is that a fair assessment of why you do viral alteration in a lab?

A Well, that's the fundamental reason that we built the chimeras in the 2015 and 2016 paper, was to assess the threat level that existed in nature. And it was either going to be a very rare event, or it was going to be more frequent. And our data said that there was a large reservoir of viruses that could potentially be threats, and that we needed to develop countermeasures of some kind.

That was not done through policy of the NIH. Those particular experiments were done at the individual level.

Q So again, thinking of folks who hear about the term gain of function or hear about viral work in labs, it can sound scary. I mean, it is scary if you're not doing it right.

A Yes, it could be. It could be very scary, yes.

Q But the goal is not to come up with something that nature wouldn't, just out of curiosity and your fascination and to just spend grant money and see what happens. The purpose is more to anticipate where nature may be heading next on its own, and be a step or two steps ahead in terms of being able to either develop new practices, whether it's public health policy, whether it's therapeutics, vaccines, other countermeasures. The point is to be ahead of nature, not to do something that nature otherwise may not, and create some new kind of risk?

A Well, again, just to make sure we're all on the same page, in the '90s, I participated in a large number of studies that actually demonstrated that coronaviruses could undergo RNA recombination at high frequency.

So that means if you took two coronaviruses that were somewhat closely related and put them in cells at the same time, 30 percent of the progeny are recombinants. That's the highest among any of the RNA viruses. So this is a normal mechanism that coronaviruses use to cause diversity.

So I think there was a question earlier, could you take parts of different viral genomes and sort of build the SARS-CoV-2.

Actually, the recombination analysis using natural isolates says SARS2 is a creation from three or four recombination events with animal strains.

Now, keep in mind that that kind of analysis is only as good as the sequence of the number of genomes you have, right? So if you get double the number of genomes, you may find, well, this region wasn't really a recombinant, it was evolving by natural -- by genetic descent from an ancestor.

But in general, recombination processes are fundamental to how coronaviruses replicate. So for a corona virologist, building a chimeric spike in the laboratory isn't doing anything different than nature does all the time.

Q That's very helpful. In terms of being able to monitor viruses in wildlife, understanding that we will never have perfect information as much as we wish we could, there's simply too many animals, too many things going on. Is it fair to say that one of the lessons from the pandemic is that wildlife monitoring is an essential part of our pandemic preparedness and potential response? Should we be doing as much or more of it, I guess, as we were prior to the pandemic?

A I think so, because there's pretty clear networks in terms of how natural products flow from the wild into small cities to large cities. It's like airline networks, you know, they can say these three cities in the world are the most likely cities to experience a pandemic first, just because of flights.

We can do the same thing with how products travel from very rural areas to urban areas. And that's one of the goals of the Southeastern — the center grant that we are on emerging infectious diseases, is to try to track those conduits, so that you know where to place a surveillance network that would capture these emerging coronavirus or pathogen events that occur from nature and animals.

Q And having advanced notice of viruses that are either prime to jump into humans or maybe prime to jump into an intermediate host, and then into humans, that's the ideal, right, if we could actually spot it before it made the jump into the humans, and say, this will infect humans inevitably, and we can take steps now in terms of medicinal countermeasures, but also maybe isolating populations, changing animal populations, changing practices, being able to take steps before it jumps, or maybe just immediately after. It may happen in a more rural area.

A I can build a really nice example of this, is public health intervention strategies. So SARS 2003 emerges as an R0 and transmits to about three people. SARS2 emerges, transmits to about 2.8 people. They have the same transmission rate.

When you apply public health intervention on that, the original 2003 strain now went below 1 to 0.7. SARS2 went to 1.4. What that means is the doubling time went from three days to 15 days. What happens in that interval? You have more time to develop countermeasures. It's not perfect, masking and social distancing was not perfect, but it was slowing the spread.

And one of the things you do not want to be in the beginning of the pandemic is one of the first patients in the hospital with a new disease, because physicians don't know how to treat it, and they are using historic references of this organ disease to try to figure out how to treat the clinical symptoms. That means they're, to some extent, making intelligent guesses, and they don't always work out. So people die. And the physicians communicate and they say, this didn't work or that didn't work, but this is working. And the clinical medicine gets better within about a month or two.

["Sheer" surely should be "shear". RW]

At that point, they stop -- you know, two or three months in, they stopped using respirators. Why? Because the respirators were causing all kind of sheer stress in the alveolar region of the lung that were killing people who had COVID because there was so much damage in that region anyway.

A And they rolled them over and they gave them different breathing apparatuses and the survival rate went up.

Those kind of things occur in the beginning of a pandemic. So it doesn't matter — if you don't like social distancing, after six months or after eight months, the importance of those actually falls, but in the beginning, it's so dramatically important. And any kind of early surveillance has this big impact on the survivability of the population and individuals' health.

And so rapid diagnosis, rapid intervention with public health, doing whatever you can to slow that spread to give physicians time to learn with less patients than having the hospital filled with them, and the clinical medicine gets better and more people survive. So all of that is intricately linked.

Q Thank you.

A Later on, it's probably of less value, but in the beginning, absolutely critical.

Mr. McAuliffe. Understood. We can go off the record.

(Recess.)

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

BY **MR. BENZINE.**

Q I want to discuss the NIAID grant processes a little bit.

A Sure.

Q And you can sense some of the confusion from the Chairman on how steps in the process, especially for foreign labs and foreign collaborators including biosafety. But I want to talk about the scoring process really quick. If a grant receives a fundable score, the lower the better, does it guarantee that it will be funded?

A Usually if it's within, the pay line, it will be funded, unless there's some flag that comes up during the post review process.

So in essence, the review committee will rank order the grants based on scientific merit. That information then goes to council, where typically program officers do short presentations on each of the programs, each of the projects that are sort of in the fundable category, and there will be discussion there.

If there are concerns, there will be another round of review. I don't know whether it occurs before it or after, quite frankly, but there will be another -- like, if there's GOF or DIRC considerations, those will have to be satisfied before the money is released.

I don't know if there's instances where grants that receive really fundable scores were then not funded at council. What typically happens at council is that the National Institutes, all the different institutes, have priority areas. And so grants that come close to those, close to fundable scores that would make the percentiles, but are in high priority

areas, they're usually pulled into council and then presented for special consideration for funding.

Q Okay.

A And that usually — it usually, as I said, requires that it meets one of these criteria of special emphasis areas within one of the institutes.

Q And then during the course of the grant, is it the principal investigator's responsibility to monitor sub-grantee compliance with the terms and conditions?

A The PI of the grant is responsible for all of those issues, yes. Typically, those are all set up before the grant of money is released to any of the subs. So you have to show your animals, you know, your animal use forms are in compliance. If you are doing DIRC or GOF, that has to have been reviewed, and there has to be some resolution to whatever was presented. Biosafety of the facility has to be validated by the university, and the university will then review and sign off on all that stuff.

Q So that touches on one of the questions. From all the people we talked to at NIH and NIAID, it's been unclear how the U.S. government vets foreign labs' biosafety.

A I think the best answer you can get to that is to talk to them about what they did with Fouchier's laboratory with the transmissible flu, because I think there was some vetting of that facility before he was allowed to proceed.

I'm also 99 percent sure that was not done in China, for example, right? They receive some certification and accreditation for their BSL-3/BSL-4 facility based on Chinese regulatory, but I don't — I have not run PI foreign grants, so I don't know exactly how NIH deals with that, or whether they do deal with it.

Q Another question we've had is obviously there's biosafety and security regulations that govern how you do things. You've taken it a little bit of a step further of erring on the side of caution.

A We try to.

Q And if you don't know, you don't know. But for U.S. money going abroad, do the foreign labs have to follow U.S. standards or is it the standard in the country that they reside?

A I don't know the answer to that. For BSL-4, it would be straightforward. Yes, the standards are pretty much uniform across countries just because of the cost of building those facilities.

BSL-3 is much more difficult. BSL-2, probably more similar across countries except for certain pathogens. And I told you one gray area. Animal zoonotic viruses is a gray area because nobody really knows the threat level associated with them if there hasn't been a human infection.

So you would have to ask NIH administrators how they deal with that. My guess is they or no one else probably deals with it all that well.

Q So we have heard the CDC does it, the State Department does it, DOJ does it, NIH does it, the principal

investigator does it. And to us in Congress, when you hear five people are doing it, it means nobody is doing it.

A Well, and basically it's a sign that the regulatory framework around that particular set of pathogens is gray, And so people are — there's individual initiative that's occurring.

Q I want to shift gears and talk about EcoHealth and Dr. Daszak a little more, in specific, the grant work with the WIV.

When I asked about your gmail earlier, you expressed some frustration or upsetness that that happened, that Dr. Daszak would put your gmail on things. What's your current relationship with Dr. Daszak?

A I generally don't harbor a lot of ill will toward people. Peter is a good man who is trying to make a difference in the world, and he firmly believes that there are questions that need to be answered. Sometimes he's overexuberant in how he does things, and he doesn't think it through very clearly.

In the case of my gmail, sending that out to everyone and saying use his gmail, don't use his regular email because he gets FOIAed all the time, ensures that I get FOIAed in all my email. And he apologized for that.

Q I want to talk about — you touched on the one log growth and there might be a couple follow-up questions. But talk about more 2020 to present, and just if you had conversations with him regarding some of the enforcement actions that NIH was taking.

So in April 24, 2020, NIH sent a letter to EcoHealth terminating that grant. Did you have any conversations with Dr. Daszak regarding the termination?

A I hadn't received any of the money to do anything on that grant yet when the termination notice hit. So he called me and told me that the grant had been terminated and that the EcoHealth lawyers were looking into it. So I knew about it. But in terms of how that would impact my program, that was a very small component on that grant.

Q When did you get added to the grant?

A After the first round. So it would have been the second round, I don't know exactly. I can't remember.

Q So going into year 6?

A It would have been going in — if year 6 was around 2019 or 2020, that's when I would have been a part of it. And my role was to study a couple of the viruses that the Wuhan Institute of Virology found that they were willing to share with me. So I always viewed that as not number one or number two on the list, maybe number five or number six on the list.

Q I understand.

BY **MR. STROM.**

Q I think I understand what you're saying. But when you say not one or two on the list, but number five on

the list, is that as far as they are giving you the fifth most interesting virus that they had found?

A Well, to be fair to them, they did the discovery work and they're going to choose the priority of what they want to work on first. And so I'm not going to get the dregs, that would be an unfair characterization, but I'm not going to get number one. I'm going to get somewhere down the list, which is okay, and I understand that process.

Hopefully, it would be something that they felt would be interesting as well.

BY **MR. BENZINE.**

Q In July of 2021, Dr. Lauer informed EcoHealth that at this point — at that point, they were 22 months late on their year 5 progress report. Did you have any conversations with Dr. Daszak regarding that?

A No, that was the first set of — that was the first grant that I was not part of.

Q We've asked almost everybody this, and our understanding now is that it's common to be a little late on progress reports, but maybe not 22 months late. Is that fair?

A NIH really tightened down on that timing. They used to be pretty lax, actually more lax than you might imagine, but not 22 months. You know, some people might delay — well, there's a couple reasons to delay. One reason you can delay is, you don't have to write a final report. If you have unspent funds and you roll it over to a one-year extension, that means by definition the final report goes in at the end of that extension.

So I don't know if they rolled money over and they did a one-year extension, in which case, it wouldn't be 22 months late, it would be eight or nine months late.

So I would look into that and see what the scenario was. I don't know the scenario. So if they didn't — if they didn't do a one-year extension, then 22 months is — it's not in the middle of the bell shaped curve, it's on that side.

Q Absolutely. We've also been going through this, and you touched on it a little bit, but the difference between — we have to operate with what we know, what's been published versus what we don't know, the always kind of known unknowns.

Do researchers in your field publish every experiment that they conduct?

A No.

Q Do they publish every sequence that they collect?

A I don't believe so. Sometimes you get distracted. You can be working on an area — we were doing several research questions on a SARS-related virus when MERS came along, and we immediately pivoted to MERS-related research, as you might expect. And then post-docs may leave and take jobs, and then you end up with a dataset which the PI has to write the paper, which is almost like death for the paper.

Q That makes sense.

A There are other PI that are better than me, but I can tell you that if I have to write the paper and it's — I'm constantly getting pulled away to do other things, and so it's just — time passes.

Q In the year 5 report, obviously before your time on the grant, EcoHealth reported an experiment that exhibited a greater than one log growth, and that experiment, or at least that data was not reported in year 4. Dr. Daszak says the year 4 experiment and the year 5 experiment are the same ones.

A Can you — was the data presented in year 4, or was it presented in year 5, or was it presented in both?

Q Both, but different.

A Oh. What does different mean?

Q Year 5 had the actual greater than one log growth data.

A Okay.

Q Year 4 didn't have that. Under Daszak's grant, which we talked about, he had to immediately stop and report anything that showed a greater than one log growth.

A That's correct.

Q He didn't after year 4.

A Or if there was an increase in pathogenesis.

So did he show an increase in pathogenesis with those studies?

Mr. Slobodin. It might be helpful — I have an exhibit here. I think this would be helpful to you, Doctor.

Mr. Benzine. This will be Majority Exhibit 3.

(Majority Exhibit No. 3 was identified for the record.)

1ROAI110964 Year 4 Report

[I think this is the following. RW]

https://www.nih.gov/sites/default/files/institutes/foia/20211020-risk-of-bat-emergence.pdf

BY **MR. SLOBODIN.**

Q So we have a two-page excerpt from the year 4 RPPR, and then a two-page excerpt this is all on the humanized mice experiments or experiment and the results that were reported, you know, what parts of it. If I could have you take a moment to review.

A The year 4 report is on the MERS coronavirus.

Q I don't know what you're looking at, on the --

A The first page.

Q You have page 25?

A This is --

Q So at the bottom, In Vivo Infection of Human ACE2 Expressing Mice with SARS-related CoV S Protein.

A Okay.

Q And then if you could, look at the next page at the top of the two charts.

A Okay. 35B. That's here, okay. Looking at genome equivalents.

Okay, what's the question?

Q I will give you a little more prep here to give you the full picture.

If you go to the third page of this, the excerpt for year 5, and you'll see Specific Aim 3: Testing Predictions of CoV Inter-Species Transmission.

[This is PDF page 15. RW]

A Which?

Q It's the narrative section, again at the bottom of the page. It starts off, "In Year 5, we continued with in vivo infection experiments," and then there are charts on the following page.

A Mm-hmm.

Q So if you go to the last page.

A I need to read this whole paragraph, I'm sorry.

Q Take your time.

A Okay, what's the next thing?

Q If you could take a moment there just to see those two charts — I'm sorry, three.

Mr. Ervin. On the last page?

BY **MR. SLOBODIN.**

Q So you have got a survival chart, you have got one with the brain tissue, and then two slides —

[PDF page 16. RW]

A Pathology.

Q — with the lung tissue.

A Yeah.

Q So now, if you look to both excerpts, so if we can go back to year 4.

A Yeah.

Q There is a statement in there, and it's supported by the figure 35 on the left-hand chart about mice challenged with the WIV1 SHC014 spike have experienced about a 20 percent body weight loss by sixth day post infection, while two other chimeras produced less body weight loss.

Does that body weight loss have any significance?

[PDF page 59, which has "25" and "Page 28" on the lower right. RW]

A So for example, on figure 34 on the first page, you can see those error bars with significant markers.

Q Right.

A So they did statistics, right? So on the weight loss, the percentage of stark body weight on figure 35, they go through day 6 and there's no statistics, right? There's no error bars. So I don't know how many — to know — how do you want me to answer this question?

Q Well, just honestly.

A I'm going to answer it honestly.

Q I'm just trying to figure out what this means.

A I guess I'm trying to ask the question, for you to, in essence, say they were non compliant, you need statistical values here that show that the weight loss of the chimera was greater than the weight loss of WIV1. And they don't tell you the number of animals and they don't have error bars.

Q Right.

A So the data looks like they lost more weight.

I would personally believe they lost more weight. But if you were thinking about it as regulatory or some sort of action against the grant, you probably need to know statistics here, because the argument you may get back, let's say people were arguing as — if I were a lawyer, I would say, well, they had insufficient animals for statistics, so there's no statistical difference between the two, so there is no difference.

That's why I was trying to answer. I wasn't trying to be circumventive. I am just trying to tell you that that's where you're going to end up with this argument.

Q We're trying to get back to the oversight —

A Yeah.

Q — which you were raising the opinion about cautioning policymakers about not overregulating —

A Sure.

Q — important virus research. So one of the things we're trying to look at is to see, how are things being overseen? And there are obviously current discussions going on, on how that oversight process can be tweaked.

A Yeah.

Q And NIH took compliance actions and took certain positions on this, but we would like to get your professional judgment on a couple of questions about what's in these reports.

A Okay. To add on to this.

Q Yes, please.

A The titer that's next in 35 has error bars.

So they — if they had sufficient animals numbers, there would be a statistical difference between — all of their data is arguing that the WIV1 backbone that they have, especially with SHCØ14 spike, is more pathogenic than WIV1, which would be a gain of function in which they would then be required to have paused the experiment and told NIH that here's the data, we need to discuss it.

At this point, they don't mention statistics anywhere here, and they don't talk about animal numbers, so there's uncertainty in what I just told you.

Q Right. Now —

A However, the biology would argue — the biology would argue, since SHCØ14 likes the mouse receptor better than WIV1, WIV1 is — we talked about it one time. The gradient of phenotypes that you're measuring, WIV1 is down here at the bottom and SHCØ14 is down here, you've really set your experiment up for a gain.

Q Okay.

A So it's probably a gain, but sort of the more compliant thing that you're thinking about is there are no statistics.

Q There are no numbers. You don't know the samples.

A You don't know numbers.

Q Right.

A So that kind of information would be really important.

BY **MR. STROM.**

Q Is there a reason that they would run an experiment like this, where they're not trying to make it statistically —

A They have the statistics. They just didn't put it in.

Q We were wondering if it's a pilot program?

A It probably wasn't nefarious. It probably was just they were writing a report at the last minute and somebody gave them figures without error bars, and they just stuck it in. But at the same time, it leaves some uncertainty about the gain of function.

BY **MR. SLOBODIN.**

Q What about the NIH program officers? Do they just not really critically review this stuff? I mean, you're looking at this. I mean, there's some pretty basic issues as far as error bars and basic numbers, like a sample size.

A Yeah.

Q You tell me, because I don't live in this world. Are they that lax that they wouldn't even raise the question? I'll take that they rushed this to meet a deadline and they included this in the report, but is there no quality

control at all on what's in these RPPRs on the NIH side?

A There is quality control, because I've had program officers —

Q Okay.

A look at reports that we put in and ask questions.

Q Okay.

A The broader question is, I think what NIH should probably do is there should be some sort of specific flag on any grant that has DIRC or GOF — that touches on DIRC or GOF with a list of things that have to be in the grant. And that's not there.

So then the program officer is not just dealing with one grant, they're dealing with probably a pile of — they may get two grants funded, two to three grants funded a year, they last five years. They may have 15, 20 grants because they also usually have several different virus families that they're studying. So they may just get lost in the workload.

That's not an excuse. There's a way to deal with that probably from a regulatory standpoint that would be more efficient, and it would specifically say you need to know the answer to these questions on this particular application, and it's flagged at a higher level, it's ranked higher in terms of oversight.

Q Okay.

A I don't believe they do that, but they might. You should ask NTH.

Q Sure. And then just on this right-hand chart, this is on the viral load in the lung tissues.

A Yes.

Q If you look at the bar graph, two days post infection. If I'm reading it right, and you tell me, I'm looking at the bar for WIV1, and it looks like it's 4.7 or maybe, I don't know, something like that, and the bar right next to it SHC014 is close to —

A I think the bar graph on day 2 is SHC014.

Q Yeah, I'm saying there's more than one line.

A Oh, yeah, there's no titer in the other one. So basically, that's saying that SHC014 is going to the brain faster than WIV1.

Q This is one, year 5?

A This is brain.

Q Oh, I'm still on year 4.

A Sorry.

Q So on year 4, the bar graph shows two days post infection.

A Yeah, there's two logs difference in genome copy number.

Q So my question is —

A Almost certainly is statistically significant if they had more than three animals in each group.

Q So my question is, when are these measurements taken? When would the WIV/EcoHealth have known about this result? Because I'm hearing two different things. One is --

A From me?

Q No, from the virology community.

A Okay.

Q From your colleagues. So one way, a two-week experiment with these humanized mice, testing these chimeras. They would take these whatever specimens at these intervals and then do all the testing on them or measurements all at the same time, so there's no variation on the — in other words, you wouldn't know until the end of the experiment, until you did all the measurements. Or do you do them pretty close to realtime while -- during these intervals? When do you do the measurements?

A If you're doing realtime measurements, in this case, you probably would wait until the end of the experiment. At least I would. Then you have a single standard curve, and everything is done at the same time, so you can put it on that standard curve.

Q But here's the problem.

A I probably wouldn't do it at day 2 and day 4, day 6. It's just the workload to set up the experiment and the time it takes to do it means you're doing it four times, versus if you did it all at once, it would be one-and-a-half to two times.

Q So let's go back to this one log viral growth.

A Yeah, two logs.

Q Well, this is two logs here.

A Yeah.

Q But in terms of there was language, I think you know at this point, because it has been pretty publicly reported. But EcoHealth Alliance required it.

A Tenfold.

Q So my question, though, is this. The language says if you see it, you're supposed to stop the experiment and then notify the IBC and the NIH.

A In their case, the WIV should have notified the PI.

Q Right.

A And the PI should have immediately notified the NIH.

Q But when?

A As soon as the PI found out within some short period of time of doing the experiment.

Q So say, hypothetically — we don't know the date of this experiment.

A I do not.

Q No, we don't, either. Nobody knows because we didn't get the lab notes. But it would appear maybe it was the early part of 2018, because they submitted this RPPR in April of 2018.

So let's say it was conducted in January 2018, just for the sake of the hypothetical. So this experiment, first, I don't understand, if the experiment's already done by the time you're taking your measurements, then what's the point of even having that policy? It's already done. There's nothing to be stopped. It's all done. The stoppage requirement doesn't make any sense.

A How would you stop something before you didn't know it occurred?

Q Well, that's what I'm trying to get at.

A Okay.

Q You don't know when one log virus growth occurred — in excess of one log virus growth occurred until the end of the experiment. And yet NIH is saying, well, stop the experiment if you see it. But Dr. Daszak says there's a single experiment, this was it, they split up the reporting of the results.

And so — and NIH is saying, well, there's no violation here because, yeah, there was a difference of day 2, but we only count it at the end of the experiment and then they converged again.

Do you agree with that?

Mr. Strom. The transient nature of the viral growth doesn't cause it to trigger the policy?

The Witness. Yeah, I can't comment on what NIH or Daszak said about this. I can only give you my opinion.

BY **MR. SLOBODIN.**

Q I just want your opinion.

A So there was a tenfold difference in titer early on, so that would alarm me. It was still present in day 4, and eventually by day 6 or 8 in the brain, it would — I'm not sure — lung tissue. At some point, those titers merged. But the other phenotype that's going on is that the chimera is causing much more weight loss, so it's more virulent. So what I would have done is stopped the experiment at that time and notified NIH.

Q But the experiment is already done. That's my point.

A I am going to talk about that, because what you just said alarmed me a lot.

Q Yeah.

A And you're suggesting that you do one experiment, you're done, you're never going to do any work with that virus again. That's not the case. There are all kinds of things you can do here, evaluating vaccines, they may want to look at host expression patterns in the animal, they may want to do all kinds of systems biology analysis. So this basic experiment here, the whole beginning to ask the fundamental question, why is the chimera more virulent? So if that regulation was in place, you're talking about another dozen set of experiments that occurred that could potentially occur along this research pipeline. And you don't want to do that.

The risk of one experiment versus a dozen experiments or 20

experiments is very different, okay? But the way that you just said, what's the use of it, because the experiment's over, what you've really said is you should never do any experiments at all on the potential of enhanced disease. On the potential of enhanced disease.

And so if the U.S. government wants to do that regulation they certainly have every right to put it in place and the U.S. scientific community needs to follow it, but we're going to be behind.

Q I'm not implying that. What I'm implying is whether this system of oversight is adequate.

A That's a very fair question.

Q For public confidence.

A That's fair.

Q To go forward with the virus research. That's what I'm trying to explore with you, because it looks to me like there's some serious questions about this. I mean, as an outsider, it doesn't make sense. They don't talk about that this is — like you providing a fuller context, but if you want, I can go to the letters, and maybe we'll do that so you can see the exact —

A Are these comments from the PI to the NIH?

Q I am going to try to shorten these up.

Mr. Strom. This will be Exhibit 4.

(Majority Exhibit No. 4 was identified for the record.)

Letter dated May 28, 2016, with attachment.

Mr. Benzine. One question.

BY **MR. BENZINE.**

Q Dr. Baric, you've read the year 5 paragraph now, the in vivo infection where five of the seven mice infected with just the WIV1 backbone survived, but only two of the eight mice infected with the WIV1 SHC014.

A You should be able to do the statistics on that, and it should show that there's a statistical difference, which means there was an increase in virulence and the entire review process would have been triggered.

Q So that's —

A I think, if you did the statistics on those numbers.

Q That's my question, is that this wouldn't have triggered P3 because it's not a human virus.

A It doesn't matter whether it triggered P3 or not. It triggered the regulation that they agreed to in the document to follow. So if that statistics — your problem right now is you have no statistical significance on here. So I'm just saying from kind of a legal position, you're in a gray area if you want to be successful.

Mr. Slobodin. But what he just read to you had numbers, the year 5 had numbers.

The Witness. That's right. But they weren't put into the figure, but they are in the text. So the data is there for you to determine statistics if you want to, if you can link it. Well, you have mortality statistics, so you can probably do that.

BY **MR. BENZINE.**

Q So my question is, and we've gotten different answers on everything, and it depends on if you're using the P3 definition or whatever definition. This reads like a gain of function to me.

A Okay. So what year was this? I just want to make sure I'm in the right gain of function regulation.

Q 2019.

A So it's the NSABB regulation. So the NSABB regulations say a potential pathogen, a potential pandemic pathogen is a pathogen that shows increased replication — I'm sorry, increased pathogenesis or transmissibility in humans. Humans. This gets to the DARPA grant, by the way.

Natural isolates that exist in nature are not considered. PPEs — PPPs. So the backbone virus that they're working with is a natural isolate. The virus that they're moving the spike from is a natural isolate. Neither of those are potential PPPs, because they've never been documented to infect a human and they've never been documented to transmit. It's a gray area because we do know they can use human receptors.

So your alarm level should go up a little bit, but it doesn't trigger the regulation because of that. Now, the chimera is a gray area because you're putting one from the other, and so — but the regulation, I don't believe, is specific on that.

The second part, the next part is that if they're doing these experiments for surveillance purposes or for vaccine purposes, even if they've engineered them and they're not PPPs, they're exempt.

So the regulatory framework from 2017 actually argues that these are exempt. Now, the gray area is that — and you have to go back to the Obama administration. They said they were concerned about SARS and MERS coronavirus. The NSABB and the National Academy of Science, I believe, said that was SARS and MERS coronavirus that were in the definition. Bat sarbecoviruses or bat merbecoviruses were not included in the definition.

["funnel" surely should be "panel". RW]

Other people outside of that review funnel that were not part of Obama's administration or part of the NSABB review say that that was a bureaucratic switch of the regulations that were supposed to cover all merbecoviruses and all sarbecoviruses. It never says that in the regulation. It says SARS and MERS coronavirus.

So based on those regulations, yes, this is — as my interpretation, is that, yes, these would be exempt. But is it a gain of function phenotype? Absolutely. You can't argue with that.

BY **MR. STROM.**

Q Do you think it's two experiments, the year 4 and the year 5?

A Almost certainly. The second one — let's see. The first one stopped at day 6 and the second one stops at day 14. So they probably set up a repeat. Normally, you want to repeat experiments.

Q To prove that they're replicable?

A To make sure that they're correct. So again, that's — the reason why one experiment triggers, because you would want to review that before you proceeded.

BY **MR. BENZINE.**

Q Should the year 4 have triggered?

A I'm sorry, I keep forgetting.

Q That one.

A I think it should have. There's no statistics here, but I think it should have triggered a review.

Q Thank you.

A If you're going to put in a metric that you're supposed to respond to, you don't want it to be sloppy, right? You don't want it to be variable. You want to say if it crosses the line, you call NIH and you let them know. That's my feeling.

BY **MR. STROM.**

Q So going back to DEFUSE, which I believe is Minority Exhibit B, the proposal.

A Yeah.

Q That same page, and again, unfortunately, it's not numbered, but I believe it is page 4. It’s got comments 16 and 17 on it.

A Right.

Q So I would like to focus on comment 16. I realize it's coming from Dr. Daszak and not from yourself, but what is your recollection of what he's trying to convey there?

A I think — I mean, it's pretty straightforward, right? He's saying that he's going to revisit this topic if, after potential review, the grant — and that he's going to focus it more in terms of U.S. research for work at BSL-3 than in China. And my response to that is this is a bad idea.

Q So the part is — so that DARPA is comfortable with our team. So is that to minimize the appearance of the WIV portion in the grant?

A You're going to have to ask him exactly what he was thinking. I think there's a variety of ways you can interpret it, but I think my response indicated that I was concerned about his statement.

Q And then but you don't recall the time, and it looks like you guys had either standing fairly periodic calls as drafts were going through iterations. I'm not sure how involved you were with those, but you don't recall that coming up in any conversations?

A I recall this being a very last minute production to put the grant together. And so I don't recall many calls beyond the first one, which was to establish, the team that was going to go after the question and what the question was going to be.

Q Sure?

A And then different groups were writing different parts that were being assembled and sent around. So some parts of the grant, I may not have seen until the last time I read it, and I never saw the final copy until after it was submitted.

BY **MR. BENZINE.**

Q Is there sort of post-award wiggle room on who does what? The way I read it, and in fairness, you're not Dr. Daszak, so we can't get into his mind, and we got these documents after we interviewed Dr. Daszak, so we're in a tough spot, too. But, once we get the funds, we can then allocate who does what exact work. Is that kind of standard that you can shift the grant after it's been awarded?

A The PI has control of the budget, so they can move money any way they want. They can take people off the grants. I have removed people from grants before who weren't being productive.

In essence, the PI is responsible to be a steward of the federal money and the public's money. And if people aren't doing their job, it's their responsibility to remove them from the grant. If they don't, sadly enough, they're not doing their job. I hope I've done my best over the years.

Q This just seems like intentionally hiding the ball.

A Yeah, the optics don't look great. I agree.

Q I want to —

Mr. Benzine. I'm sorry for cutting you off.

Mr. Strom. You're fine.

BY **MR. BENZINE.**

Q I wish there were page numbers, but it has comment 24 on the page.

Mr. Strom. Third to last.

BY **MR. BENZINE.**

Q It 's in the resume section, and the comment from Dr. Daszak on this one. "I'm planning to use my resume and Ralph's. Linfa, Zhengli, I realize your resumes are also very impressive, but I'm trying to downplay the non-U.S. focus, of the proposal, so that DARPA doesn't see this as a negative."

This comment, taken in conjunction with the last one, seems like an intentional effort to hide the Chinese portion of the grant in order to get funding.

A That's a fair question to ask him.

Q Did you have, any conversations with him about this while this was being written?

A You saw my comment, which was again designed to stimulate, let him know that there's sort of a fundamental difference, and that this is a concern.

Q All right.

BY **MR. STROM.**

Q You mentioned that in the first hour, but essentially, that you kind of forgot about the DEFUSE proposal?

A Yes, I did. People probably say no chance.

Q And I'm trying to battle hindsight here.

A Yeah.

Q But it would be helpful for context, I think, if you could share just how many SARS-related coronavirus proposals you were sort of working on in a given year, because there's about an 18-month gap between this proposal being put forward and then the pandemic.

A I believe I have the record at University of North Carolina for submitting grants and getting grants rejected.

Q Okay. A rough approximation in sort of a year-and-a-half period?

A In one year, I know that I submitted at least 2Ø grants.

Q Okay,

A Some years, it may actually be higher, because of the few times I -- so you can write grants a couple of different ways. One way is where you're a PI, where you're responsible for really putting it together.

The second is co-investigator, where you're writing like a section, but you're not responsible for completely doing the entire grant. You read it and make comments but you usually don't — you're not refining it, refining it to the very end, but you build a section.

And then a third level is where you're kind of an investigator, where you're not actually leading a lot of the work, you're providing some support and you're providing a CV that says, I can do this set of experiments that they need, and I will be there to do it. But you're not actually working.

So if you use that strategy appropriately, you can write a lot of grants.

Q Okay. And then do you have a moment where your memory was sort of jogged about DEFUSE?

A After it was released by — I forgot the name of that group that — the computer sleuths that found it and released it, and it popped up on the news. And I was thinking, what's this? And I read it. Yeah, I wrote the grant, part of it, yeah.

I can also tell you one of the drivers that sort of stopped me thinking about that line of research was we were interested in protease cleavage sites, for example, because it was a second barrier for virus emergence. And we were having — there were several MERS-related strains and SARS strains that we couldn't culture. We knew the clone was infectious and the virus could replicate, but it couldn't spread.

So what we realized is that if we add exogenous trypsin, another protease, if you put it in the media, some of those viruses will grow. It's a simple solution to the problem. So you didn't exactly have to engineer anything to make it grow. So we published a paper on that, and we used that on a variety of viruses. It's kind of a simple solution to a more technologically different approach.

Q So within this DEFUSE team, whose idea was it to sort of target the cleavage site for that S1/S2 junction? As I understand it, they occur randomly in a series of different viruses, but the location itself, the location within the genome is important for it to work.

A Yeah, so it's — there's a lot of redundancy in proteases that cleave the coronavirus spike. So to start off, the idea of manipulating the protease was clearly mine.

No question.

I want to take you back to what the — I have to look at my notes here. But I want to take you back to what the proposal requested. This was in response to the National Biodefense Strategy. They wanted to improve U.S. biosecurity by detecting and containing bio threats adopted for active posture, stem ID outbreaks at the source.

They wanted to understand both pathogen interactions, and they wanted to develop models that you could look at how those viruses jumped between species. And they wanted to know down to the nucleotide level, down to the nucleotide level how the viruses jumped.

Now, there's two ways to do that. You can do loss of function which tells you a potential mechanism, it 's not causal. And the reason it doesn't tell you that is if you knock out one of those protease sites, and the best example is with furin and SARS2 that' was done later, you knock out that furin site, you knock out cleavage by two or three, at least one other restriction enzyme, which is TMPRSS2, nobody's ever measured cathepsin L, and nobody measured the other proteases that chew at that SI boundary. But that deletion wasn't furin specific, it was a generalized processing defect, because it was a loss of function mutation.

So the true interpretation of the furin cleavage site in SARS2 is that if you disrupt cleavage of spike, it's going to be attenuated because none of those proteases can chew. All right? So it's not specific. Gain of function experiments allow you to say this site —

Q This is it?

A — is it, right? Now, the way the furin cleavage site was built in that grant, at least in the earlier versions, some of that may have been lost as they tried to condense it to get it to fit, was that the first part was that we were fundamentally interested in why didn't sarbecoviruses have a furin cleavage site.

There had been studies done in 2010, 2011, 2012 using pseudotypes. Catherine Holmes published one in JB, there was a Chinese group that published it, where they dropped the furin cleavage site into the SARS1 from 2003. There was no increased infectivity, there was just a little, bit more fusion between the cells. So no really big phenotype.

Another example of furin cleavage sites with coronaviruses, a researcher at University of Pennsylvania knocks out the furin cleavage sites in mouse hepatitis. No change in pathogenesis for the ability of the virus to replicate.

Feline infectious peritonitis virus, it's an enteric form, it's got a furin cleavage site, it replicates, and it got very mild infection. When the furin cleavage site is lost, it kills the cat. So it's, a flip, right? Furin cleavage site is the loss of — it's protecting from virulent disease. So the data going into that proposal, the exact role of furin cleavage site was not clear. We were interested in it because most other coronaviruses in family had those sites. Why didn't sarbecovirus?

So the way the grant was designed was that the discovery group would look, as they did discovery, if they found one with the furin cleavage site, we would first study the pseudotypes.

The second thing we would do is move it into the chimeras to see what the effect on applicants was. The third thing was we would probably build virulent viruses and study pathogenesis, and then we would knock out the furin cleavage site.

Q As I understand, to see what you've got?

A To see what would happen. If you knocked it out and you lost all the virulence, then you're going to think twice before you start dropping it into things, right? So it's a step-wise process. It's not like it's portrayed in the news where researchers were going to take furin cleavage sites and just shotgun them into every coronavirus they could find until they found something happened. It was a systematic process that was initially designed.

And it wasn't just the furin site. It was also TMPRSS2 sites, it was also HAT, and the cathepsin L protease. So there were four proteases we were interested in.

Q Was there also an effort to identify, and it's maybe RMYN02, if that's the one I'm thinking of that has a partial?

A That was published after, I guess, SARS2 emerged.

Q Would that have been one that if this project had been done, that you — the team would have been interested in to see what additional -- I guess I'm wondering, you talked about —

A It didn't have a full furin cleavage site, just two or three of the residues. It was close, right?

Q Right.

A And so some people argue it was on the way to get a furin cleavage site, but I personally don't believe that. It just had additional residues in there, so —

Q And then on the other aspect of looking -- and this may relate to sort of the search for a broad spectrum coronavirus vaccine. What was the rationale between looking for a SARS-related coronavirus that sort of a 10 to 20 percent divergent in the spike from SARS1?

A Sure. So SARS 2003 is the bookend, right? You know how much variation. WIV1 and SHC014 have about 8 to 12 percent variation in the spike or the RBD. The clade 2 strains like HKU3 have 30 to 35 percent variation in the spike, they've got deletions in the RBD, they can't use human ACE2 receptors.

If you take those two numbers, subtract 10 of 12 from 35, divided by 2, added to 12, you get a number between 20 and 25. And that was our prediction, that there would be strains with that much variation that could still use human ACE2 receptors.

It turns out SARS2 had 22 percent variation, so we were within the range, but we were really not completely right. In MERS, there are strains with 35 percent variation in the RBD that could still use the human. So in reality, it is probably much greater than 20, 25 percent.

Q Really?

A That was our estimate. And the reason we're interested in that, the strains with the most variation become important for developing countermeasures in vaccines. So if you have a strain that's really different than therapeutic antibodies, you can look for broadly neutralizing antibodies. They may not work. Your vaccine, if you have an animal model, you can ask, does it cover this much variation? And if it doesn't, it gives you the starting material to develop a second generation vaccine that can capture it. So again, that variation -- I have no interest in simply resurrecting every single coronavirus.

Q Sure.

A I'm interested in the bookends and a couple intermediate ones because that's what's best for countermeasure development.

Q And this came out in the recent FOIA release.

I can make it an exhibit if it's helpful. But there was a call about PREEMPT EcoHealth and Ralph is the title, March 2, 2018.

There's a bullet here that says, "another idea is... if. you build chimera that broadly reduces heterogeneous population of SARS-related coronaviruses in bat caves, this might be something you'd want to develop for humans.

"RB has already generated SARS-like chimeras with RBD from group of bat viruses called 293, which is 20 percent different" — sorry, "(for S1), which is 20% different than the epidemic strains."

Mr. Ervin. Could we look at that?

(Majority Exhibit No. 5 was identified for the record.)

Document, PREEMPT call (EHA, Ralph & Time of UNC) - 2 March 2018.

The Witness. So in 2008 or 2009, we had a PNAS paper where a clade 2 SARS-related virus called HK3, which is about 30, 35 percent different than SARS, we made a molecular clone for that, and it could infect cells and it could replicate but it couldn't spread to the next cell.

So we did an experiment with Vanderbilt University where we took the receptor binding domain of the 2003 SARS strain and swapped it into the HK3 backbone. So we built a chimera. That virus could grow, but it was highly attenuated in mice. I can't remember the growth curve comparisons.

BY **MR. STROM.**

Q HKU3 is one of the standard cold causing viruses?

A No, HKU3 is a bat coronavirus that is very different. So the coronavirus tree with three branch — I can't use these. No, I can't do that.

Q Anyway.

A So the three branches —

Q It's not videotaped, so you're all right.

A That's good.

Q But so the same three group of viruses.

A It's called — there's a clade 1A, which is SARS 2003; a clade 1B, which is SARS2; and a clade 2, which is bat strains that don't grow on human cells, don't use human ACE2 receptors. They have deletions in their receptor binding domains, so they don't even engage human receptors.. Those could replicate, but they couldn't cause disease. So we wanted — we were asking a fundamental question about recombination. Are the RBDs interchangeable between coronaviruses by recombinatory practices. And so we inserted the SARS RBD into the HKU3 backbone and it replicated. It was attenuated in mice. We ultimately passed it in mice and made a more mouse-adapted strain.

Why would we want to do that? Well, variation in the polymerase is important for testing drugs without breadth.

Was it 293, is that what it says?

Q The group of bat viruses, generates SARS-like chimeras with RBD from a group of bat viruses called 293.

A So the experiment I just told you about was 2008 or 2009. We took that backbone around 2012 and introduced a triple chimera. In essence, it had, if I remember correctly, the HKU3 NTD, the SARS1 RBD, and the S2 domain from this other bat virus. I actually don't think it's 293, I think 3 is a typo. It might be 96, but I would have to look at the recombinant DNA thing that I submitted to UNC, which I have, by the way.

So in 2012, in the fall of 2012, we made that virus and had recovered it. And then MERS kind of hit and then we didn 't do very much on it besides showing that it was replication competent.

Q Okay.

A So this is a clade 2, clade 1A chimera. It's got mostly the HKU3 backbone, but what it showed is that all three major components of the spike glycoprotein are interchangeable.

Q And then my last question relating back to something that Dr. Wenstrup asked, I guess —

A And that was before any GOF regulations were in place, so it was IBC approved at UNC.

Q As of like December 2019, what was, I guess, the SARS-related coronavirus you had at UNC that would be most similar — we'll start with sort of the whole genome level to SARS-CoV-2. Even if it's just a percentage, if you can't remember the specifics or in-house designation for it.

A All the clade 1A strains, like SARS, SCH014, WIV1, are anywhere from 22 to 25 percent different than COVID-19. The HKU3 virus, I don't remember how similar it is to — I would have to go back and look at the data. I would be surprised if it was less than 1A, because it has so much more variation to begin with.

Q I guess my question is, Shi Zhengli went back to her holdings and found RaTG13. I don't know if you did a similar one just to see if you had something similar from a previous —

A I don't do surveillance.

Q Well, that would be —

A So I don't go out and collect bat samples. I had a research assistant professor that did some bat discovery work in Maryland, and he found mostly group 1 coronaviruses at the time. So we didn't — I don't do bat discovery, so I don’t have large repositories of bat samples to look for coronaviruses.

Q Okay.

A I usually look for sequences, and if I find something interesting, then I'll go after it.

Mr. Benzine. I have one final question.

BY **MR. BENZINE.**

Q Notwithstanding what we talked about earlier and discussed, at any point during the intelligence community's review of the origins, were you contacted by any agencies?

A FBI, CIA, and many other three-letter agencies.

Q Okay, to help with their review?

A Yes.

Q And did you tell them substantially what you told us today?

A I did. I said there were three potentialities for the origin.

Mr. Benzine. Thank you. We can go off the record.

(Discussion held.)

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

BY **MR. SLOBODIN.**

Q So why did — when we're reading the grant documents — we're going back to the humanized mice experiments.

A This is the EcoHealth RØ1 in the first five years of the grant.

Q Right.

A Okay.

Q And the mice — as I understand, the mice for that experiment were obtained from your lab?

A I don't believe so, but I don't know for sure.

Q Well, you were telling us before that you had the mice, that you were curious about them commercializing —

A That's correct.

Q — the mice you shared through an MTA?

A Yes. And the discussions to send those mice to them started in 2015, and I think I told you I was unsure of whether they got them in '16 or '17, and when they had sufficient numbers to do it.

Q Why would they want your mice? There's plenty of mice in China. In the grant documents here, they said they got them from Wuhan University. So what, was it that's special about your lab's mice that they wanted them?

A I knew that researchers in China developed humanized mice in 2004 at Peking University. And actually, I tried to get those mice and they tried to send them to me, and the Chinese government sort of shut it down. That researcher got out of coronavirus research, so I assume he left the colony. And I didn't know that they had access to

humanized mice. I got a request and I responded to it. So I don't know if these were my mice that came from our lab or not. It's a good question to ask. I don't know.

Q But you didn't get any details from them in the request about why they were coining to you?

A No, I think the MTA agreed that the first paper they published with it, they would include me as an author, and that was the 2020 paper..

Q Did —

A On SARS2.

Q Did they include any specifications, like age, gender, type of mice?

A In the Cell paper?

Q No. When they wanted to — when they were trying to get —-

A No, they just request mice. So you send the breeding pairs, and then they breed them.

Q Okay. What is the scientific basis for the one log difference in virus growth being used as sort of a marker, a benchmark as you called it? Where does that come from?

A Plaque assays have some level of variability in the ability to distinguish between differences. So there's about 15 to 20 percent variation in plaque assays. So if you take a virus ten to the sixth, and you do a series of plates with the same stock and titers, you'll see titers ranging from like — I have to do the math — eight times ten to the fifth. That's not the right number, I'm getting tired.

But you're going to get a range between like eight times ten to the fifth, and two times ten to the sixth, so you get some variability in the response just because of the distribution of viruses in the 200 microliters that you take out of the sample and place on the plate.

Q Is there a study on that? How did it become a standard? Is that something you've always done through your career as a virologist?

A For virus titer? Yeah, I started in graduate school.

Q So it had nothing to do with a gain of function regulation?

A It had nothing to do. The tenfold value was — I think was — well, we were asked to come up with a metric. A tenfold value, you can be pretty sure is statistically significant.

In general, in humans, there's a correlation between increased titer and disease, so that means there's some level of potential risk even though we know that host genetics can make a big difference in that, so -- but that's not really what the purpose is.

The purpose is to have some kind of metric that provides a meaningful bar that you use to initiate additional review processes. There are other ones that you could use. You can

use the degree of fusion, but that's really hard to measure especially in 2014, 2015, 2016. You know, how big the fused areas are, how many nuclei are in the fusion area. There are other metrics you can use. But this was a very straightforward, very definable, quantifiable measure that is meaningful. And we felt that was — that if you saw that difference, then you should at least pause and discuss it.

Q Okay.

A Some others may disagree.

(Majority Exhibit No. 6 was identified for the record.)

Letter dated May 15, 2015, from Chernay Mason to Ms. Barbara Entwisle and Ralph Baric, Ph.D., Bates commencing UNC_SSCP00002629 229

BY **MR. SLOBODIN.**

Q So this is a letter from the NIAID vice chancellor to you. I'm only interested actually in one sentence on the second page.

A All right.

Q And it's at the bottom. And it's the last paragraph, the first sentence that says, "NIAID acknowledges that if any unanticipated outcomes are observed, including enhanced virus growth greater than one Log in any mammalian cells, enhanced virus titers by greater than one log in any mammalian cells, or enhanced clinical disease or death in mice as defined by significantly increased weight loss, percent mortality, or decreased mean day to death, you will immediately stop all experiments and notify NIAID and the UNC-Chapel Hill IBC of the results."

So where did that formulation come from? Because that's not just on virus. This seems to be a little more — how would you describe it?

A It's absolutely to the letter of the State Department's gain of function pause in 2014. So the way the pause of 2014 read was any increase in pathogenesis or transmissibility in any mammal, okay, any mammal. All 6400 Of them that exist on Planet Earth, there's only one BSL-3 facility that handles aquatic species, and the whales can't fit in them. There's no whale cell lines that I know of. So this was an impossible metric for any scientist to follow. NIH recognized that after they — this came down from the State Department, it didn't come from the NIH.

In the NSABB, the revived regulations of 2017, they dropped the mammal requirement because it was experimentally not doable.

So the way that regulation really should have meant is anyone doing a gain of function experiment needs to stop now because you cannot measure it in every single mammal, either as a cell line or whatever, because they don't exist.

Also, who wants to do it? You know, you have to test it in 6400 cell lines. Really? I'm not going to do that experiment. I'm not going to do the experiment at all, because it's crazy.

And so in the revised revision, they dropped any mammal and focused on humans, which was reasonable, at least in my

opinion. But you see the dichotomy, how can you do it? And if you want to see animal in vivo studies, there's one BSL-3 facility with water in it in the United States, and it's for little things, not for whales.

Q So the question to take away on this lesson, on overseeing these types of research proposals where there are risk issues, should there be one consistent standard that every researcher has to meet? And two, should it specify certain data elements that should be included with a certain level of detail?

A Statistics should be there.

Q Okay.

A Statistics definitely should be there. I like the 2017 regulations, quite frankly. I've lived by them, I think they're appropriate. They're focused on pathogens that are risky. The DIRC regulations don't include any coronaviruses, but they cover 15 pathogens and six or seven experiments of concern which are well articulated. So it's very well articulated. Things get added to that list as the scientific community says, hey, there's a pathogen here that needs to be included on this list.

The harmonized regulations that recently the federal government asked for public comment on had- three pieces in it. One piece was to use -- apply the regulations, the DIRC regulations and the GOF regulations pulled together on any human animal or plant pathogen and agent. And agent was not defined. So you look it up in the dictionary and it says it's something or someone that mediates an effect. mRNA vaccines mediate effect. Al predictions mediate effect. All of the products that are being developed in microorganisms where you're dropping — you're basically farming the genetic information on Planet Earth to build synthetic biosynthetic pathways to make two carbon molecules, which is the basis of the petrochemical industry and perfumes and drugs, that is all now subject to those regulations as written.

I personally think we're going to crush the bio-economy with that regulation. So I wrote that and said this regulation is too extreme, because it doesn't distinguish between any pathogen, and it closes down potential commercial — economically commercial and viable research pathways that are going to drive the U.S. economy in the future.

And so I'm concerned about that because overregulation is going to be — it's sort of the risk-benefit. The risk-benefit of a flu experiment is if it gets out and it's truly transmissible, it can kill a million to a billion people. That's pretty quantifiable, right? That's high risk. But working with a virus that's mildly pathogenic, that most of us get exposed to when we're two years of age and get repeated exposures the rest of our life, that's not a big risk. Even if you engineered it, it would have a huge problem getting past the immunity that's in the population. So you can't do these regulations with a sledge hammer. You have to use a scalpel. And that means there has to be some refinement and consideration for the long-term impact of those regulations on scientific leadership, our economy, the biosecurity field, the biosafety fields, and entrepreneurship, innovation, discovery. And if you close all that down, microbiology is gone to China, and they have a

ten-year plan to be number one, and we're helping them.

That's my interpretation.

Q So my question to you —

Mr. **Ervin**. Can we make this the last one?

Mr. **Slobodin**. Yeah.

BY **MR. SLOBODIN**.

Q — is in trying to. figure out the sweet spot on this policy.

A It's very difficult.

Q As part of the implementation to address public confidence in the safety of this research, we have this policy, sort of this backup system talking about the one virus log growth. Maybe there are other things, but right now you said that's the best?

A To be frank on that, if you get a bunch of virologists and bacteriologists together, they may come up with a better metric. This is what I came up with.

Q Sure.

A It shouldn't be the standard.

Q So my question is, whatever it is, if you implement a policy to make sure the research is being done safely and to be prepared in case of an unexpected outcome, shouldn't that policy be consistent with every grant research proposal that's being reviewed, the same rule for everybody?

Or is there such a thing as different versions of this? Should there be certain standards or certain template and pieces of information, like how it's to be measured, when it's to be measured, certain statistics, you've got to include certain information? Because Daszak is saying, oh, well, there was nothing here anyway, we weren't statistically powered. This doesn't make any sense. Why were you even doing research if it wasn't statistically powered.

A It should have been statistically powered.

Q So my point is, what should that regime look like? Shouldn't there be — to me as an outsider, I do not understand. I think we're going to see as we're doing this oversight, variations in how this virus log growth is articulated and how it is applied by the NIH. And that raises concerns about whether that's really a good way to go to address this public confidence issue.

So what should that look like? To what extent should there be some standardization for that kind of rule?

A Let me address your first comment, which was more focused across all of virology or microbiology.

There are things in this world that you're not too concerned about if you get infected with. The common cold is certainly one. But I bet your concern level would go way up if it was Ebola. And so there are pathogens that are at much higher threat level than others.

So because of that, and because of their biology and how they transmit and where they cause disease and how severe the

disease is, there is a gradient. It is not one standard fits all. There has to be some level of flexibility in interpreting those regulations that you develop that make intelligent and informed predictions about what should be regulated and what should the standards be.

And there's going to be some variation in that. And there's some things that probably shouldn't be regulated, unless the technology or the capabilities in the scientific community occur that would allow for DIRC related research to occur.

So if you figured out — let's say if you had an Al program that could look at the common cold, look at all the common cold viruses, like 170 of them, and you run Al programs and say, okay, I want to make a new rhinovirus that escapes all the immunity that could have been made if you got infected with all of them, let's say if Al ever got there.

Number one, as a nation, if this was — you might want to know if that capability existed. You would want to know when that technology emerged. You might want to think about how you would apply those standards to things that are low risk or high risk.

So depending on the technology and the capabilities, those are just things that, you know, you might find smarter people than me that can come up with a better standard for regulatory control. But I just think there's a lot of variation in pathogenesis and pathogens, and how they cause disease and how they transmit.

And we should stay focused on those pathogens that are the highest risk level that we need to develop countermeasures for, so that we have things in our box that we can rapidly implement in the population to protect them, should either one emerge from nature or by some sort of nefarious purpose.

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

[Whereupon, at 4:32 p.m., the taking of the instant interview ceased.]

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Document history

Robin Whittle rw@firstpr.com.au

2024-05-05 This is the first stage of several versions of this
text which I am preparing for:

https://vitamindstopscovid.info/07-origins/

I got the original PDF from:

https://oversight.house.gov/wp-content/uploads/2024/04/Baric-TI-Transcript.pdf

This was apparently released just before the public
testimony of Petar Daszak on 2024-05-01:

https://oversight.house.gov/hearing/a-hearing-with-the-president-of-ecohealth-alliance-dr-peter-daszak/

The PDF is of page images of a scan of a printed document.

There is no searchable or copy-and-pasteable text layer.

I added on using the OCR (Optical Character Recognition)
facility of PDF-XChange Editor Plus. Then I selected all
and copied this text to Notepad++.

There I edited it to:

1 - Remove line numbers.

2 - Space out paragraphs with blank lines.

3 - Fix the typos I found.

I retained the page numbers.

This is that file:

2024-05-01-Baric-testimony--plain-text.txt

I removed the page numbers and created a double space after
sentences, as in the original, which is easier to read.

I added in the names of the exhibits inline where they are
cited, and in some cases links to PDFs and notes on PDF page numbers.

This is: 2024-05-01-Baric-testimony--plain-text-refs.txt.

I brought this into MS Word and made a PDF, with clickable links.
This has a text layer, and so can be searched and the text selected,
and copied to the clipboard.

I used an indented style with a larger typeface for all text attributed to Dr Baric.

This is available from:

https://vitamindstopscovid.info/07-origins/#baric

2024-05-23 Fixed typos, including OCR glitches. Fixed some formatting problems. Changed two instances of “SADS” to “SARS”. Added notes about the meaing of “one log” and “PI”.