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:
M itch Benzine, Staff Director
ERIC OSTERHUES, Majority Chief Counsel
MADELEINE BREWER, Majority Counsel
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
WILL McAULIFFE, Majority Counsel
CONSTANCE O'CONNOR, Minority Counsel
Appearances.

For the WITNESS:

CLARK E. ERVIN, ESQ.
Squire Patton Boggs, LLP
2550 M Street, NW
Washington, DC 20037
(202) 457-5234
clark.ervin@squirepb.com

For the UNIVERSITY OF NORTH CAROLINA:

DAVID LAMBERTH, Director of Strategic Research and Compliance
University of North Carolina at Chapel Hill

KELLY MIXON DOCKHAM, Director of Federal Affairs
University of North Carolina at Chapel Hill
Office of Public Affairs
Bynum Hall, Room 300B
Campus Box 7006
222 East Cameron Avenue
Chapel Hill, North Carolina 27559
Exhibits

Minority Exhibit

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.

1 - Email cover sheet, Bates
UNC_SSCP00023674

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

3 - 1ROAI110964 Year 4 Report 188

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
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 the 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.
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.
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
c Congressions 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.

Okay.

Dr. Francis Collins.

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 --

Any conversations with Dr. Collins specific to
the origins?

No, not to my recollection.

Dr. Anthony Fauci?

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

Any manner of communication.

So -- and from this --

January 1st.

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. Auchinbue -- I've got to look at his name.

Q Auchincloss?

A Yes, Auchincloss. Alan Embry. There's a series of emails that included Maureen Beeman, 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.
377 Q Dr. Victor Zhao?
378 A Not to my recollection.
379 Q Dr. Robert Redfield?
380 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.
384 Q But more of the group calls?
385 A It was all group calls, not a person.
386 Q Dr. Michael Lauer?
387 A Not to my recollection.
388 Q Dr. David Christian Hassell?
389 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.
392 Q But it was regarding one of these three topics or COVID, kind of?
394 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.
397 Q Dr. Jeremy Farrar?
398 A Indirectly. He had someone from his group email me about a 4chan threat that had been made toward me.
400 Q Dr. Kristian Andersen?
401 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 4chan 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.
Q 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 sarsbecoviruses, 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 chow 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?
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.
A 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  
e-mails 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 Yuaen Zhou?
A  I would have to do email research to know
that. No, nothing that comes to mind.

Q    One more name. Dr. Lili Ren from the

A    Institute for Pathogen Biology in Beijing?
    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.

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, lopinavir 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
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.
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, 
ACK2 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 those 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?

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?
Before or after it emerged?

Well, in retrospect, or after it emerged.

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.

But looking back?

Just to give you an example. Let's say I took SHCoV14 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 SHCoV14 that don't exist in SARS.

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

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

Okay.

Okay.

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

Never.

Okay.

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?

A 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 UNC, 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?

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. 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.

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.
1252 Q Good morning, Dr. Baric.
1253 A Good morning.
1254 Q We would just like to ask you a few questions
1255 about the 2015 paper testing the SHC014 spike protein you
1256 coauthored in Nature Medicine. We discussed this paper some
1257 in the previous round.
1258 A Correct.
1259 Q I will introduce the paper now as Minority
1260 Exhibit A.
1261 (Minority Exhibit A was
1262 identified for the record.)
1263 BY MR. ROMERO.
1264 Q So in this paper, among other findings, you
1265 found that the SHC014 spike on a mouse-adapted backbone
1266 showed reduced pathogenicity compared to the full length
1267 mouse-adapted SARS backbone. Does that sound right?
1268 A That's correct.
1269 Q So the full length mouse-adapted SARS backbone
1270 has a name, MA15. And as you understand things, you helped
1271 to create that virus?
1272 A Yes, the virus was originally created in
1273 collaboration with Kanta Subbarao at the National Institutes
1274 of Health. She did the serial passage of the original SARS
1275 strain, which could replicate, but not cause disease in mice.
1276 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
gineered 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.
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 passed in subculture many times. The live polio virus was passed 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-à-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 SfCo14 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 20 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 SHC014 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.

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 SHC014 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 SARS014 spike compared to the SARS 2003 spike, the SARS 2003 spike binds the human ACE2 better than SARS014. But in the mouse, the SARS014 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.
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?
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 immunosuppressed, 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 1B 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.
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.

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,
A 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. AI 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.)
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?
1977 Q Yes, correct.
1978 A Yes.
1979 Q Is that your comment?
1980 A Yes.
1981 Q So I'm just going to read it.
1982 "In the US, these recombinant SARS CoV are studied under
1983 BSL3, not BSL2, especially important for those that are able
1984 to bind and replicate in primary human cells.
1985 "In China, might be growing these viruses under BSL-2. US
1986 researchers will likely freak out."
1987 Now, when I read that comment, I take it as advice against
1988 doing this work in a BSL-2, when it should be done in a BSL-3
1989 lab. Is that what you meant by the comment?
1990 A I think I'm responding to the comment above
1991 from Peter Daszak in two ways. First, I'm informing him,
1992 just in case he doesn't know, that a lot of the virus
1993 discovery work and culturing work that the Chinese do with
1994 zoonotic coronaviruses is done at BSL-2. The animal work
1995 they do is actually at their BSL-3, but the culturing is at
1997 And that while there aren't any actual U.S. regulations, but
1998 the Baric lab does this all under BSL-3. So anyone who had
1999 collaborated with us or had obtained the viruses from us
2000 always did it at BSL-3. And all of our paperwork said we're
2001 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 MIV1 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 Google 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. On to 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.
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 essentially, 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 DRC 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.

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

It's a fair concern.

Thank you.

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

Mr. Wenstrup. Thank you.

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.

That's correct.

How do you know that?
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 SADS 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.)

BY MR. BENZINE.

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
cloning is a virus called WIV1, which I don't think they
gineered 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 SADS molecular clone from
2452 2016 on, and they failed. It’s not easy technology. So we
2453 started three years later and beat them to press, just to
2454 show you. And I had no interest in teaching them how to do
2455 it faster, either.
2456 Q That was going to be my next question. Did
2457 you have any -- did you teach them any of the intentional or
2458 hard-to-track change techniques?
2459 A The only person that I ever really worked with
2460 on a molecular clone was George Gao, and this was prior to
2461 the 2020 SARS2 pandemic virus.
2462 If you remember, MERS coronavirus transmitted from the Middle
2463 East to Korea and infected a lot of Korean
2464 scientists -- sorry, citizens. One of those was a Chinese
2465 citizen who moved back to China and traveled back to Beijing
2466 and infected -- that they sequenced the virus from. And they
2467 couldn't culture it. So he asked me if I would be willing to
2468 help make a molecular clone for that virus.
2469 So we designed -- we worked with him -- actually, we reviewed
2470 their design, and so they tried to make a molecular clone.
2471 They failed. Ultimately, they never got it to work. They
2472 sent the clone to us. This was around 2016. We actually
2473 recovered the virus, it's still sitting in my lab. When I
2474 told them we have the virus, he never answered me, and so
2475 it's still sitting in my lab, and I've never used it.
2476 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.
A 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?
Remember that 90 percent of those cases are
asymptomatic.
Right.
85, 90 percent. So imagine trying to chase a
transmission cycle.
Yeah.
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.
Who just walked around with it.
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?
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.

A lot of people.

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.

Not that we've seen.

BY MR. BENZINE.

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?

They had to have done a blast search.

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

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. STRONG.
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.

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?

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

Just that it's hard --

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.

It certainly seems plausible, based on certain --

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

BY MR. BENZINE.

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 lock 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
correspondence?

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. OONI 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 SCoV4 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.
A 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.
A The Witness. But publicly, the group that released it --
Mr. Benzine. 2021.
A 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 BamBI sites in the SARS
2878 coronavirus 2 genome. Now, one of the first things you
2879 notice is that those same sites are present in many of the
2880 bat strains that exist. So if they are engineered, if you
2881 use them to engineer SARS2, they wouldn't normally be in the
2882 same location in the bat strains.
2883 The second thing is, they do count six pieces, but one of the
2884 pieces is about 8 KB and the other is about 300 base pairs.
2885 If you look at any of the molecular clones that I've
2886 engineered, with SARS, they're usually 5 KB apart, so that
2887 you have five or six KB pieces that you can work.
2888 Having a tiny little piece like that, if I looked at it, that
2889 would irritate me, like, to no end, and we would silence it,
2890 one of those sites. And then separate this, so that the
2891 fragments are of equal size. The first size piece is also
2892 too small, and so it leaves larger pieces, and the larger
2893 clones are unstable with passage.
2894 Q       Okay.
2895 A       So you would want it more equally distributed,
2896 unless there was a region that was super toxic. If there was
2897 a toxic region, then you would have a little piece. There's
2898 no toxic site there.
2899 Q       Thank you.
2900 A       So this is biostatistical BS, in my opinion.
2901 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 1B 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.)
BY MR. BENZINE.
Q So this is the agenda for a National Academies
of Sciences, Engineering, and Medicine meeting on Data Needs
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.

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 --

Hopefully, he didn't say anything negative.

This is a quote from Dr. Andersen's Slack messages. "I should mention that Ralph Baric pretty much attacked me on the call with NASM, 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.

Can you read that again?

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

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 NAScEM, 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.
3002 A What do you mean, it's redacted?
3003 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.
3005 A So he's talking to somebody else, then.
3007 Q Yes.
3008 A Okay. No, I would just say that's inconsistent with what I've said publicly and privately that can be verified.
3011 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?
3016 A I looked at it before this meeting. I figured you guys might ask.
3018 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.
3023 But the first conclusion was, "our analysis clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus."
3026 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 --
3052 BY MR. BENZINE.

3053 Q A de novo, built virus.

3054 A What they would have had is no true actionable 
3055 intelligence, and said it was engineered. Because if you 
3056 don't have a backbone sequence that's close enough, you don't 
3057 have any substrate on which to build anything that could have 
3058 been close enough to SARS that people would have said it was 
3059 novel. So we still don't have a backbone sequence that's 
3060 close enough.

3061 Q The second conclusion was, "we do not believe 
3062 that any type of laboratory-based scenario is plausible."

3063 Do you agree with that?

3064 A I signed a paper that said that that 
3065 was -- that a laboratory scenario needed to be carefully 
3066 evaluated. I think that says it all as well.

3067 Q And then after the fact --

3068 A Which is also inconsistent with the statement 
3069 he just made.

3070 Q It is. I'm not a scientist, but even reading 
3071 that confuses me beyond just the science.

3072 A It's the first I've ever heard it, so I'm very 
3073 confused about it myself, yes.

3074 Q After the fact -- and then there's a reporter 
3075 at Science Magazine named John Cohen.

3076 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
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
But Dr. Daszak did end up signing it?
He did end up signing it.
Did you have any conversations regarding his change of heart?
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.
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.
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.

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.

They said there was no chance, what?

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.)


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?

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.

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

Yeah.

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

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.

Sure.

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?

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?

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 ACE2, 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.
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?

It says it wasn't created in a lab.

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

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.

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?

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.

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?
Absolutely.

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?

Yes. So this goes back to the review of the chimeric viruses with SHC014 and WIV1.

Despite all the data that argued that it was attenuated, one of the things that NIH 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 what 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-19, there were no
transmission levels for any coronavirus, so we had no
information on that. And it wasn't until -- because SARS-
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

A

Sure.

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 MA10, which
was called MA10 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 SARS 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 broadth 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 OC43, 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.

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.

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
going 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
times over all across the globe.
And looking for new niches to colonize, yes.
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.
That's correct.
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?

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.

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.

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.

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. 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
DIRECT 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.
Okay.
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 GOP, 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
day deal with it.
Q Another question we've had is obviously	
there's biosafety and security regulations that govern how
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	
tem 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
e-mail. 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.

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?

No.

Do they publish every sequence that they collect?

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 PIs 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.
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.
That's correct.
He didn't after year 4.
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.)
BY MR. SLOBODIN.
So we have a two-page excerpt from the year 4
RPFR, 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.
The year 4 report is on the MERS coronavirus.
I don't know what you're looking at, on the --
The first page.
You have page 25?
This is --
So at the bottom, In Vivo Infection of Human
ACK2 Expressing Mice with SARS-related CoV S Protein.

Okay.

And then if you could, look at the next page at the top of the two charts.

Okay. 35B. That's here, okay. Looking at genome equivalents.

Okay, what's the question?

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.

Which?

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.

Mm-hmm.

So if you go to the last page.

I need to read this whole paragraph, I'm sorry.

Take your time.

Okay, what's the next thing?

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 --

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?

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.
I'm going to answer it honestly.

I'm just trying to figure out what this means.

I guess I'm trying to ask the question, for you to, in essence, say they were noncompliant, 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.

Right.

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.

We're trying to get back to the oversight --

Yeah.

-- 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 SFC014 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 SNC014 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 SNC014 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
eperiment 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 RPDRs 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 NIH.
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.

A 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 RFPR 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.
Okay.

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.

I just want your opinion.

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.

But the experiment is already done. That's my point.

I am going to talk about that, because what you just said alarmed me a lot.

Yeah.

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.)
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.
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.
So that's --
I think, if you did the statistics on those
numbers.
That's my question, is that this wouldn't have
triggered F3 because it's not a human virus.
It doesn't matter whether it triggered F3 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.
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 -- PFPs. 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 PFPs, 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.

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.

Q    Do you think it's two experiments, the year 4 and the year 5?
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.

To prove that they're replicable?

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. BERNZINE.

Should the year 4 have triggered?

I'm sorry, I keep forgetting.

That one.

I think it should have. There's no statistics here, but I think it should have triggered a review.

Thank you.

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.

So going back to DEFUSE, which I believe is Minority Exhibit B, the proposal.

Yeah.

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
20 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.
Okay. And then do you have a moment where
your memory was sort of jogged about DEFUSE?
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 know 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.

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.

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, 
obody's ever measured cathepsin L, and nobody measured the 
other proteases that chew at that S1 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

As I understand, to see what you've got?

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?

That was published after, I guess, SARS2 emerged.

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 --

It didn't have a full furin cleavage site, just two or three of the residues. It was close, right?

Right.

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 --

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?

Sure. So SARS 2003 is the backend, 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 or 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's 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 backends and a couple intermediate ones because that's what's best for countermeasure development.
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.)

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. STRON.

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 R01 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 know 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 coming 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.

Okay.

Some others may disagree.

(Majority Exhibit No. 6 was identified for the record.)

BY MR. SLOBODIN.

So this is a letter from the NIAID vice chancellor to you. I'm only interested actually in one sentence on the second page.

All right.

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 CDF 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. AI predictions mediate effect. 
All of the products that are being developed in 
organisms 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.

So my question to you --
Mr. Ervin. Can we make this the last one?
Mr. Slobodin. Yeah.

-- is in trying to figure out the sweet spot
on this policy.
It's very difficult.
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?
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. 

Sure.

It shouldn't be the standard.

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.

It should have been statistically powered.

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?

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 AI program that could look at the common cold, look at all the common cold viruses, like 170 of them, and you run AI 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 AI 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.]