Uncovering the Origins of COVID-19: A Scientific Discussion

TRANSCRIPT

Discussion

- David Asher, Senior Fellow and former Department of State COVID-19 lead investigator
- Dr. Steven Quay, CEO of Atossa Therapeutics
- Professor Richard Muller, professor of physics at the University of California, Berkeley

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David Asher:
Welcome everyone. I'm David Asher, a senior fellow here at the Hudson Institute. I had the honor over the last six months or so at the US Department of State to run a investigation into the origins of COVID-19. Our event today will feature two of our more prominent thinkers and researchers in this area of the COVID-19 origins issue, the lab leak hypothesis being one hypothesis that's been in the news of late. And of course the continued possibility, however faint it has become of late, that this came out of zoonosis or a natural environment. And of course there's an in-between, which is a combination of the two. So our speakers are Dr. Steve Quay and Dr. Rich Muller, Dr. Quay is the CEO of a company called Atossa Therapeutics listed on the NASDAQ. It's a biopharmaceutical company, developing therapeutics for breast cancer and other conditions of the breast.

Dr. Quay has written literally hundreds of peer reviewed medical articles. He has an incredible track record as an inventor, too. You can look at his patents in Google and you'll be amazed by how many he has and how important they are in the history of recent medicine. And he also has applied his incredible background in biology, both as a biologist, chemist, virologist, and many other offshoots.

To understand the scientific evidence behind COVID-19, Dr. Richard Muller is one of the greatest astrophysicists in the world. He has applied himself in many other domains, including earth, climate warming, and all sorts of planetary and extraterrestrial phenomenon, the skies that surround us in the heavens above, and he has spent decades advising the US Department of Defense and other government agencies on weapons of mass destruction, and the hard science related to them.

We are today going to in part highlight an article that they wrote in the Wall Street Journal, as an opinion piece recently called, The Science Suggests the Wuhan Lab Leak Theory, COVID-19 Pathogen has a Genetic Footprint That Has Never Been Observed in Natural Coronavirus. I will turn it over to Dr. Quay and he will begin to give a presentation for about 25 minutes or so followed by a presentation from Dr. Muller and then a discussion which I will moderate. Thank you. Dr. Quay?

Dr. Steven Quay:
Thank you, David. It’s a pleasure to be speaking today on uncovering the origins of COVID-19, a scientific discussion. I’ve titled my presentation, Six Undisputed Facts. This is a shorter version of a longer paper I have published entitled, the Bayesian Analysis concludes beyond a reasonable doubt that SARS-CoV-2 is not natural zoonosis, but instead is laboratory derived. It's been downloaded about 161,000 times. I sent it in draft form to all of the members of the WHO team and other prominent virologists. I've received no substantive criticism at this point in time. As a reminder of what we're going to talk about today, what is a Zoonosis, it's important to remember it has three elements. There's always an animal and then a microbe that's infecting that animal, and then the microbe jumps to humans. So those three elements of a host animal, a microbe and human are common to all Zoonosis.

Now, SARS-CoV-1 is an interesting example of the discussion we're going to have today because it began as a community acquired zoonosis, first appearing in workers in wet markets and restaurants in southern China. But after the WHO declared the epidemic over, the next cases after that point in time, were all laboratory staff members working with SARS in the laboratory, and then getting sick. In fact, I did a small analysis of the hospitals that they went to and they were all very close to their laboratories, about 15 kilometers. And as a parallel analysis, all of the first patients in Wuhan were much closer to the WIV, the Wuhan Institute of Virology.

So today we're going to talk about six facts, four that relate to whether the zoonosis began in the community or was laboratory acquired. And to that address the question of, was this an unmodified natural virus that escaped from the laboratory or had it been genetically manipulated? Now, with
respect to the community acquired infection, we all believe that the bat is what's called the reservoir host. So this is a host that doesn't really get sick, but forms a place where the virus can live for decades and decades, gaining mutations. There is no intermediate host, the host to jump to humans that we are aware of. And the laboratories that I’m talking about for this exercise are really three, although the Wuhan Institute of Virology is the dominant one. But the Wuhan CDC, which is very close to a market is in contention and a place called the Wuhan Institute of Biologic Products, a vaccine manufacturer is also in the mix.

So the first challenge for a natural origin is what I call the location problem. The first patient is 1500 kilometers from the closest ancestral host in nature, but only 3.4 kilometers from the closest ancestral host in a refrigerator of the Wuhan Institute of Virology. To put this into US term, it's like somebody walking down the street in Manhattan and getting infected with a virus from the Everglades in Florida.

So what do community-acquired Zoonosis and laboratory-acquired zoonosis have in common? Well, remember they both begin with an animal or tissues from an animal. So in the laboratory, you might have animal cells growing in a Petri dish and they get infected with a virus, and then a staff member gets infected. So, that's what they have in common. What they have in distinction and will be the focus of today's presentation is really these three things that can be summarized nicely for the community-acquired zoonosis as diversity and for the laboratory-acquired zoonosis, a singularity. So when you think of those three elements we spoke of before that the animals with a community-acquired infection, there are many animals, high levels of population infection. The virus is very genetically variant because it's been in the animals for weeks, months, years, there's a lot of genetic variability and there are many pre-epidemic infections in the human community, which we'll talk about in just a minute.

The laboratory-acquired zoonosis, on the other hand is a singularity. It is one animal or one test tube with animal cells. It's one genetically pure virus, because in the lab, we always work with pure viruses, otherwise it's too complicated. And there's no pre-epidemic infection in the community, of course, it's one lab worker walking out one day, asymptomatically infected and then starting the process.

So let's talk about this term, what's called Seroconversion Evidence. So one of the hallmarks of a community-acquired infection is this practice, abortive infection where it jumps from animals to humans, but it doesn’t have all the mutations it needs to support human to human spread. So what you get is multiple humans that have this infection, it burns up, they may not even know they have it. But the way to identify it is once an epidemic has occurred, you go back into the geographic region of the starting point. You go into the refrigerators of hospitals and blood banks. You pull samples out and you test them for the virus, from the epidemic because you now have an assay for that.

The beauty is that you do not need to know where the host is because you’re relying on the antibodies. You're relying on evidence of infection in the community before it comes about. Again with SARS-1 the civet cat was the intermediate host and it was jumping to humans repeatedly, but burning out because it didn't have all the mutations it needed. On November 16th, 2002, it got that last mutation it needed, to not only jump into humans, but to support human to human transfer.

In a lab escape model, of course you have a pure culture of a virus exiting the laboratory with a single human, maybe asymptomatically, walking into a subway and spreading the virus, and so you won't find it in the community at all. So the first fact I want to speak about that everyone agrees on is that there is no pre-epidemic infections. COVID-19 wasn't smoldering in the community before the pandemic began as was observed with previous coronavirus epidemics. So the WHO report in March states, a total of 9,522 stored samples from patients with influenza-like disease in Wuhan or the surrounding area in late 2019, were tested for SARS-CoV-2 with an established assay. They were all negative.
So based on similar testing for the two previous coronavirus epidemic, SARS and MERS, a middle Eastern virus in camel's to humans, you would have expected 1 to 4%. So just remembering the numbers here, that's 100 to 400 patients with stored samples, where you should find the virus, and there were zero. So running the math on this, the probability that a community-acquired zoonosis like the previous, would have this resolved, is literally less than one in a million.

In fact, Dr. Shi and Dr. Daszak, these are key play players in this whole process, Dr. Shi is the Head of the Wuhan Institute of Virology. She's worked for over a decade with Dr. Daszak, the President of EcoHealth Alliance. In 2018, they published a very interesting paper on serologic evidence of bat to human viruses in Yunnan, Southern China, where we think SARS-CoV-2 came from, and for this study, they actually used a control group from Wuhan. They wrote in their paper, "As a control, we collected 240 specimens from blood donors in Wuhan, 1,000 kilometers away, where inhabitants have a much lower likelihood of being infected." And of course in their study, zero of those patients were infected. About 2.7% in the southern province actually had evidence of coronavirus infections.

So with respect to no pre-epidemic infections, it's a singularity. Fact two, is that there are no animal hosts exists. Neither the COVID virus or any close relative has yet been found in nature, unlike prior natural zoonoses. So this is quite incredible because this surveillance exercise that China did over the last year is unprecedented in biology, largest effort ever done to find something in nature. More than 80,000 wildlife, livestock and poultry samples from Wuhan, from Hubei, the province it's in, from all of China, all 31 provinces were tested, and there were no positive results for either SARS-CoV-2 antibodies, meaning an animal that had an infection or the virus itself, which is an extremely sensitive test.

In May 2020, Dr. Anderson and other virologists published a seminal paper, it's been downloaded over a million times, in which they predicted based on the properties of the virus, that, "The animal hosts would probably have to have a high population density in order to achieve the outcome that happened." And of course, we know running the math again on this, that the prevalence in the population has to be less than 0.004% to get these results. And again, a reminder the Wuhan Institute of Virology testing SARS-1 or MERS, the other two coronavirus infections, over 90% of the animals in the markets were positive.

So again, the probability that SARS-CoV-2 is a wild origin with this result, is again, less than one in a million. In fact, just a reminder, SARS-CoV-1 in 2003, it took us four months to identify the civet cat shown here on the left, as the intermediate host. With MERS, it took a little bit longer, nine months to find the camel as the intermediate host, and we're now at 18 months, and we do not have an intermediate host. So it's one animal and probably because they didn't look at any animals in the laboratory is one of the foundational reasons it was missed.

Fact three is that SARS-CoV-2 started genetically pure like the synthetic vaccine. So we've all had experience, we've now given tens of millions of vaccines in the United States. And every vaccine is genetically identical with every other one. That's a man-made genetic product, that's the hallmark. And in fact, COVID coronavirus had little genetic diversity at the outset, again, unlike prior natural zoonoses. So some of the most prominent virologists and names in the world here have all commented on this unusual property. Dr. Baric probably the preeminent synthetic biologist in coronaviruses in the world wrote, "That early strains showed limited genetic diversity, suggesting that it may have been introduced as a single source." Dr. Shi herself, this is very interesting, she put a draft of a paper on January 23rd up on the internet, and she wrote, "The almost identical sequences of this virus in different patients imply a probable recent introduction in humans."

Sometime after that, and before it finally got finalized February 3rd, she realized the implication of that, because that sentence is no longer in her paper. Way back in April 2020 before the investigation and everything, the WHO said, "All published at genetic sequences isolated, suggest a single point
introduction in the human population around the time the virus was first reported in humans, in Wuhan in December 2019." And Dr. Rambaut and Holmes, the two virologists who came up with the classification system for the SARS-CoV-2 coronaviruses wrote, "That because of early sampling and genome sequencing, we know that we have the root sequence is identified and because many of the genomes from the earlier sample cases are genetically identical, and it's also probably identical to the most recent common ancestor, we have a lot of information and they said, "This occurrence is different to previous viruses and epidemics, where there is a great deal of genetic diversity in the virus."

Here's a little example of how this kind of work is done. So because the mutations are two relative. So every mutation in a virus and infection, when it gets passed on, is on top of the previous ones. What you have on the left is an experiment where 10 patients are sequenced and there's 10 mutations. And you look at a pattern to see who gave the infection to whom. And what you see is that mutation one is in all of the 10 patients, but mutation two is not in patient A. And then you see oh, my gosh, mutation three is not in patient B. You run this through a computer algorithm and you get this pattern here, which is genetic evidence that patient A gave the virus to patient B, C, D, et cetera.

We see there's over 1.9 million sequences here, and everyone can be traced back to a first genetic index patient. The first patient with the most ancestral genome. So let's see who that patient is. Well, it turns out it's a 39 year old man with a bronchial lavage specimen. That's a deep specimen from the lungs that was collected on January 5th. He was not part of any market. He was not exposed. He stayed at a hospital near the market. But it's quite telling that he was in the hospital. He was in the General Hospital of the Central Theater Command of the People's Liberation Army of China, about three kilometers from the Wuhan Institute of Virology.

This information was available to the public, to the world, to me on January 30th 2020, but I'm quite sure that you're hearing about this first genetic patient at a PLA hospital for perhaps the very first time now. Let me be very clear, I think I and everyone else believed this began sometime late September to perhaps early November. So the virus actually began then, this is only the first sequence patient that we can say is the ancestor of all human infections in the world.

So once you know this process, where... So you have clade A, which is that index patient. Once you know how this got from bats to intermediate host in the laboratory or the world, to clade A. And then two mutations here is shown, gets you to the next clade and the next clade. You can rank order all 176 million cases.

Why is this important? Because if you find a source or if you identify, hypothesize maybe this began in a market, then the simple thing is to test, "Well, is it clade A in that market or did the virus come into the market?" So fact four is a very important fact. Again, there's no disagreement. This is from the WHO report, all the markets, where there is genetic information about this virus are all downstream from that first patient at the PLA hospital. So they're all either clade B or what we call clade A.1, where it's in clade A, but it has an additional mutation from that PLA. So the WHO report itself documents that this could not have begun in the markets with the data that we currently have.

It also allows you to test other hypotheses. So here's one, testing the environmental specimens. If it began in a market, then the simple thing is to test positive. And finally, if it began in a market, then the patients in the market should be clade A. They should not be clade B. So busy slide, I get it. But these four patients over here, that I'm circling next to the PLA hospital, those are the four clade A patients. Zero of those four, have any relationship to the markets. These orange boxes are the 11 early patients with an association to the market. 11 out of 11 of those are clade B.
So really the Chinese CDC had in May of 2020, said it as succinctly as anyone can, that the virus went into the market, it did not come out of the market. So it's a little frustrating that we continue to talk about, "Maybe this began in the market." It could have before we had this data, but I think we now have to reflect on that hypothesis in light of this data.

An additional frustration is that the WHO report actually censored early non-market related cases. On the left is a Lancet paper in January, February 2020, where you see color coded that three of the first four patients had no relationship to a market. So the blue is not market-related, whatever that brown color is market related. And we knew early on that three of the four cases were not related to a market. This same data in the WHO report on the right, actually censors those early non-market cases. So their chart of the same data now begins later than the beginning of the Lancet paper and their first three patients all begin from the market. This is not science. This is obfuscation. So with respect to the three predictions we had on laboratory-acquired zoonosis, they are all met.

Let's now turn to the two undisputed facts about whether the virus was a natural virus, or whether it was gain-of-function research. Fact five is the fact that we all agree on. That COVID's powerful infectious trigger isn't found anywhere in the related viral group in nature, but it's been repeatedly inserted into viruses by laboratories in the past, including the Wuhan Institute of Virology.

So this is a chart showing 58 viruses that are closely related to SARS-CoV-2. And what I mean closely-related, is this is a sampling of all of the virus that had a common ancestor, most recent common ancestor, MRCA about a thousand years ago. So this is basically the last millennials diversity in this class of coronaviruses that SARS-CoV-2 resides in. And this sequence of amino acids S-P-R-R-A, shown here, is not found in any of these viruses. So for the last 1,000 years, these viruses in nature have been existing and doing all their things, recombining, but without ever generating a furin cleavage site.

I call this the immaculate insertion, because it has two aspects of uniqueness. One is that what I've just described, it is the only spike protein in this class of coronaviruses that has a furin insertion site. There's no other sites. And the one way that these things can be acquired is by recombining with a virus from the same class that has something different. So one poor bat gets two viruses. The viruses start exchanging genetic material, and you come out with this hybrid virus. But you can't acquire something that doesn't exist in the population. And at the protein level, it doesn't exist. There's lots of codes, genetic codes for furin sites. So now we look at the code and we come up with what we talked about in our Wall Street Journal op-ed, which is the CGG-CGG double codon.

This is a language. If genetic material is a language for telling protein factories how to make proteins from genetic material, these are two words that these coronaviruses never use. They've never put CGG-CGG together in codons, anywhere in the world. So it's a double uniqueness. The first has probability of one in greater than 100,000. The second, one in 500,000. And yet, we know that laboratories have been inserting furin cleavage sites since 1992. Every case that they do it, it's always a gain-of-function. It's the surest way to guarantee you're going to gain a function. And I show here a map of the labs, locations of the labs, because this is a worldwide activity. It's not just China and it's not been recent. Again, it started in 1992.

So one of the things that a furin cleavage site does, is it permits immediate cell surface fusion. So again, a very complicated slide, but this little picture on the left here is SARS-CoV-1, which has to go through this complicated process to get into a cell. It takes time and it's also inefficient. On the right side, you see that the SARS 2 interacts with the membrane and bingo, the genetic materials inside. This allows not only expanded species tropism, but more importantly, and probably more lethally, it expands the cellular tropism, the different cells in the body that this virus can infect. So with a furin cleavage site, you can get into the lungs, but you can't get into the heart, the brain and the endothelium. And this is really
telling, because these are the areas where the most severe infections and where the lethal infections are coming from.

So with this information, why did Dr. Shi, the head of the Wuhan Institute of Virology, not feature this furin site in her seminal paper? If the site came from nature, an innocent virologist would have been highly motivated to describe the first example of a furin cleavage site in this class of coronaviruses in a thousand years of evolution. This busy slide, I apologize, but this is from her paper, on the left. She stops at position 675. Now, if she'd gone just six positions further, she would have disclosed the furin cleavage site, she did not.

A little while later, a French Canadian team highlighted this when they were the first to describe the furin cleavage site. And remarkably in that paper, they called it a gain-of-function to this virus for efficient spreading in humor populations. And in their title, they say, "This cleavage site is absent in any coronaviruses from this same clade."

Now, if I had wanted to describe to you what experiments were probably going on when someone got infected, I could have done it, I could have come up with a hypothetical description, but in fact, this published paper from Dr. Baric in North Carolina and Dr. Shi and her colleagues at the Wuhan Institute of Virology, published in early 2020 is exactly the experiments I would describe being the foundation for a lab-leak hypothesis. So this paper is entitled The Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2, the ACE2 enzyme. So I've been doing laboratory research for 30 years, I've kind of gone through this paper and they had to hit everything right on the nail and had to have begin no later than January 28th to get this study done in time to publish it. But this is exactly the kind of work that probably was going on in earlier 2019.

Fact six is that the virus is highly adapted for infection of humans from the start, unlike prior natural zoonoses. And growth in humanized mice would allow this lab adaption, like in that previous paper. I call this the pre-adaption trifecta, because whether you look at the entire genome, just the spike protein or the factory equipment that the virus uses in the body, it's all pre-adapted. At the whole genome level, this paper by Dr. Alina Chan and colleagues from the Broad Institute shows that in SARS 1, there were two phases. There was an early phase, where it hadn't perfected human-to-human transfer. And then a later phase, a consolidation phase, where human transfer was going on. And SARS 2, of course shows only this later phase.

If you look at just the spike protein, you get this incredible set of experiments from a group in San Francisco. They basically said, "Okay, there's 200 sequences in the spike protein that are important for binding. There's 20 different amino acids. There are already 20 there, but let's create all 3,800 other possible spike proteins and test every single one of them in the laboratory for affinity, for binding to ACE2." So these are two charts that have all 3,800 experiments. So the brown is where it made it worse. The white is where it was indifferent, and only these little blue squares is where it improved it. And only 0.5% of changes in these 3,800 amino acids made an improvement. Remarkably, nature did this experiment itself because the UK strain, which is this mutation right here in blue, it's N501Y. In the fall of 2020, it was a rapidly expanding case. It proves this research, and it also establishes the validity of this process.

One of the last pieces of evidence, the State Department has said that they have evidence that three cases of SARS-like infections occurred in the fall of 2019. China, the Wuhan Institute of Virology and WHO have all said, "This did not occur." Myself and DRASIC, our colleague, Gilles Demaneuf did a statistical analysis of whether this was possible based on the incidents of COVID in Wuhan in the first half of 2020. And our analysis shows that there's a one in trillion chance that no one at this institution had SARS-CoV-2.
So the prediction with respect to lab versus community was met in all three cases. Two findings that are associated with gain-of-function, the furin site and serial passage pre-adaption are our met. And so, in my opinion, without a public debate on whether gain-of-function experiments should continue without a change in current regulations, the next pandemic is right now being created somewhere in the world, where this dangerous work is being done.

I'll stop there. Thank you, [David 00:29:58].

David Asher:
Thank you, Dr. Quay. That was an unbelievable presentation in its comprehensiveness and it's relative understandability for people who are not biopathology, biovirology experts. It's a incredible dissection of a very complex series of questions surrounding what happened in China with the outbreak of this disastrous disease. Dr. Muller, please give us some thoughts from your end.

Dr. Muller:
Thank you. Thank you very much. David. I've been working in national security issues for many decades as a high level advisor to the US government on everything from counter-terrorism to the nuclear issues to biological warfare. And so when this broke out, at first, I was happy. Well, happy it wasn't biological warfare, but was just a natural outbreak and China had said that they had studied it very quickly. Everybody was saying they were transparent. They had looked at... It came from the Wuhan market. They had identified the bat, but then as time went on, other papers started coming out. There was a paper from China that said, no, there are no bats at the Wuhan market. And 900 feet away is the CDC level biosafety level three laboratory that works with coronavirus. And it began to sound kind of funny. Now the outbreak had taken in Wuhan, which was the only place in all of China that has a biosafety level four laboratory. It's the center of the world for research on bat coronaviruses. But is that just a funny coincidence? Well, I have a saying, I call unlikely events can happen. In abbreviation, UECH, pronounced UECH. So every time there's an UECH, it doesn't mean that there's something that really is cause for concern. But I had learned in my decades of work in science that whenever there's an UECH, pay attention. We'll look at it a little bit closer. One out of 10 of those things may turn out to be a really important.

So I started reading these papers and I could in fact read the papers. The biology isn't that advanced, but I had difficulty evaluating the quality of the paper. So I decided to solicit some friends of mine who were in the virology and get some help. So I called up one person whose name many of you would probably recognize, a very important person, done outstanding work in this field. I won't say whether he won the Nobel prize or came close. He was in that category. And I said, look, I'm reading these papers. I need some help. Could you read these for me? He said, "Well, actually no, it's not the sort of thing I have the time to do." I said, "Well, what about someone in your laboratory? Please." He said, "Look Rich, let me tell you the truth. Nobody in my laboratory is going to work on the possibility that this was a laboratory leak." Why not?

Because if it gets out that they are even looking at that, they will be blacklisted by China. There'll be labeled an enemy of China, and we're all collaborating with China. China's does some of the best work in the world. We all have co-authors. That will all stop. The Chinese communist party will put an end to it. That's one of the most chilling conversations I have had in my entire life. What that meant was that China was exercising control over United States, freedom of expression, freedom of speech. US scientists didn't want to even discuss this issue for fear of what China would do. As I said, that is a very frightening conversation I had.
I called other people too. One person who was working in a large laboratory, an old friend of mine, I called him up and said, "Can you get someone in your lab to help me with this?" And he said, "Rich, you going to vote for Trump? I'm not going to do anything that will help Trump get reelected." I'm not a political person, but I was not doing this to support Trump. But this was the impression that Trump, because he had come out and said it wasn't laboratory leak that therefore doing this work would lead credence to Trump, which might throw the election.

I called up another friend of mine who was also at the Nobel level category. And he was very interested, but he's not a virologist. So he called up his virology friends. He couldn't get anybody in. So this is I think something that is really chilling, is really, really scary. Well, let me talk a little bit about what I saw as I looked into this. And we all have this famous scientific method.

And one of the things that I became aware of in reading some of these scientific papers was what I call misdirection. Now, one of the things that is still being used almost everywhere in this field is what lawyers call conclusionary argument. Conclusionary argument is where you start with a conclusion. And then you look for evidence that supports that. And you attack anybody who has evidence supporting another theory. So this is pervasive in this field. People assume it is a zoonotic origin. They don't give it defense of that. They just say, I'm not going to believe anything else unless you give me a smoking gun. If you don't give me a smoking gun, then it came from a natural source. But whoa, wait a minute. What's the evidence for the natural source? In this kind of misdirection, they try to hide the fact that they're not trying to... They're not depending on evidence for zoonotic.

The other thing they do is they take a hypothesis as if it's evidence. So for example, when it's shown that there is no animal source at the Wuhan market, then they say, oh, well, maybe it was frozen meat. Ah, the theory has been revived, as if they had presented evidence. No, what had happened was the evidence had proven their previous hypothesis was wrong. Now they're trying to bring it back. And it's a hypothesis. It's not an evidence. You'll see this over and over again.

Let's go back in time to early 2020, when the Lancet had an article in February, Nature Medicine had an argument in April. 77 Nobel laureates came out with a statement shortly afterwards that if you look back at these articles and I can go through these in detail, but I don't have the time. If you look back at these articles in detail, you find they don't hold up very well with time.

I just to give an example, the Nature Medicine article made two arguments. It said we can rule out that it was a laboratory leak. And here's the reason. One is our analysis shows clearly that the fearing cleavage site, that the spike protein was not optimized. Now, they didn't give the analysis. They just say, it's not optimized. And anybody doing this in the laboratory would have done a better job at this. That was their biggest point. The second point was that they didn't know how to make it, that there was no backbone on which to do it. Those were the two sites, the two arguments. The first argument, as Dr. McWaine shown, there's now positive, conclusive evidence that this was 99.5% optimized.

So as we look back on these old articles, it's worth reading them again and seeing what their logic was. And there really wasn't much there. So let's look at the original argument back a year and a half ago was that this just looked like everything. And China had... Indeed, it looked like it had just been another one of these releases from a wet market that had happened many times before. That's our starting assumption. That that's what it is. But if you look back on history, you find there are many, many cases in which illness leaked from a laboratory.

You go back to 1977, the world flu epidemic that was eventually tracked to a leakage of a laboratory sample. In 1978, smallpox killed a UK lab worker, anthrax in 1978. There's a long history of this, even SARS. There were six cases. The last six deaths from SARS in 2003 came from laboratory leaks.
So laboratory leaks do happen. The idea that you should assume... Why do people assume that it is not a lab leak? I think part of the reason is one, they're afraid of insulting China. Two, they're afraid of the consequences if it is a lab leak. What does that mean? That is somewhat scary. Okay. Other people say to me, I want a smoking gun. And I say, do you want a smoking gun for the zoonotic release? Oh, well, they want a smoking gun. Well, Dr. McWaine went through a series of discoveries. Each one of those should qualify as a prediction made by a scientist a year and a half ago. When this came out, scientists could have said, well, there should have been prior infections in hospitals. We will look for them and find them. And then, unexpected events can happen.

Well, there aren't any, but oh, we can explain that away. Okay. They should have predicted that the animal hosts would be identified. The other for previous infections, they had been identified relatively quickly. And now there was an unprecedented effort to do this with enormous work. And so, they will find this animal and okay, maybe it's not a bat. Maybe it's a pangolin and so on. They searched 80,000 animals. If they made this prediction, we would have said, this was a prediction denied. This was a prediction that says the hypothesis was incorrect.

Another UECH, multiple source evidence. The fact that in natural cases, you don't just have one jump to humans, but have multiple choices. No, it didn't happen. The fear and cleavage site. If you had made a prediction about the fear and cleavage site, you would have said, well, when we look at this thing, if there's a fear and cleavage site there, there are 36 different fear and cleavage sites there that are possible, 36 different combinations. How likely is it to be the same one that Zhang Li had inserted in her one experiment in which she inserted fear and cleavage sites, one in 36. Oh, the one that cannot naturally turn out to be the exact same one, the same double CGG that she had used in her laboratory. That's another embarrassing UECH.

The rapid evolution before... The fact that it was optimized, that it came out perfect for humans that... No, these things evolve. Another UECH, how many UECH's can you take? And I haven't even mentioned the one that had just happened to be in the one city of the world that had a biosafety four laboratory, and there are many, many other things here about the hospitalizations that I didn't mention. So I would say this. Let's look at the case today in an objective, non-conclusory way. Let's get rid of our fear of being accused, of being anti-China. Or even worse they call us pro-Trump or racist even. Well, get that out of the way. That's not part of science. Let's look at this objectively. What is the evidence for a zoonotic? Well, back a year and a half ago, we had the Chinese evidence, but they have withdrawn that. There is no evidence that is zoonotic.

For the lab leak, we have Dr. Quay's five points, six points, but there are more than that, too. This is the point at which we have a scientific inclusion. Based on the science, this was a lab leak. All the other evidence about illnesses, about what hospitals people were in, about why was the Wuhan laboratory closed for two weeks in October? All of these things are things that now we explore in order to learn more about the lab leak, but the fact that it was a lab leak, the scientific evidence is overwhelming. And it's time to really now do the forensic investigation, not to find the guilt, but to find out what really happened.

Well, thank you, Dr. Muller, very much for those comments and observations. However, obvious some of these facts may seem at this stage what's amazing to me in reflection of the experience of having conducted an investigation for the US government into the origins issue with assistance from the two of you and dozens of other scientists, I want to add it's a large collective effort involving our national laboratories, who are a huge repositories of knowledge and insight into the world of biology and biological warfare.

One of the contentions that's been made including by myself is that there was a tie into biological warfare related research development. Not necessarily building a weapon, I've never said that, but
capability development, we'll call it, that seemed to be occurring at the Wuhan Institute of Virology in the synthetic biology arena where it is at the top of the field in most aspects in China or certainly one of the top institutes related to viriological gain of function.

And the question I have is, what do you both, maybe we'll start with Dr. Quay, think about this issue of safeguards regarding US government funding and collaboration? And do you believe, in your estimation, that gain of function research being conducted there, at the time unidentified, classified military funding... But into a very high stage of evolutionary advancement of a coronavirus variant called RaTG13 that had been harvested in Yunnan in 2012 in the south of China. And the State Department, our declassified fact sheet, had been put out that that had been used since at least 2016 in scientific manipulative experiments as a backbone by one of perhaps other progenitors as well that they had harvested from the case.

Do you think that the US government should continue to be funding work in mainland China related to bat born corona viruses or any other viruses given what's happened here? And you think that there has been any gain of function in terms of our understanding of viruses as a result of the funds and personnel and scientific knowledge transfer from the US to Wuhan. Sorry for a very long question there. But maybe Dr. Quay real quick, if you could? And that Dr. Muller.

**Dr. Steven Quay:**

Yeah. David, thanks. I mean, I'm going to stick it in the science lane if I can, if that's okay? I've studied pretty carefully gain of function research that's been going on for about 20 years. The hope is that you can identify what nature will do and then come up with therapeutics or vaccines. And that's the Twitter version of what the work is about.

The challenge is that, in a good afternoon in a gain of function laboratory, you can put 500, 600, 700 years of what would be natural evolution into a virus in an afternoon. So, I don't think what they're doing in the lab has much relationship to what's what's going on in nature. And I want to point out another aspect that not only is there an issue around gain of function, where you're in the laboratory and you're doing these manipulations and making viruses that never existed in nature, but there's something I would call gain of opportunity. Where you take a virus from a bat cave in a place where the population density is a couple of people per square mile, and you bring them to the middle of Wuhan next to the subway that handles a million people a day. I call that a gain of opportunity. And I think these are the kinds of things we should rethink in terms of safety and also the kind of research we do.

**David Asher:**

Professor Muller, do you think that we were unintentionally aiding and abetting an act of proliferation in effect by collaborating on advanced gain of function work with the Chinese government?

**Dr. Muller:**

Well, I think the fact that the lack of transparency is what bothers me the most. We should not be funding a laboratory where we can't go into the laboratory and talk to the scientists, where we can't look at what they're doing, look at their logs. This is open scientific research. The goal here is not like in a private company where you're trying to patent something and you have to keep something proprietary. The goal here is open information for everybody. And without making any decision on whether gain of function makes sense or not, we should certainly never fund any laboratory that does not allow transparency. Now, ironically back a year and a half ago, the signers of the Lancet letter complimented China on its transparency. And in retrospect, they were so wrong, so wrong. With them closing their files...
and their closing access, and with key whistle blowers over there vanishing so we can't contact them. Never, never again should we fund any research, particularly in this area, where the whole purpose is to help humanity and they are closing down and not letting us in.

David Asher:
Yeah, that makes a great deal of sense to me. Dr. Quay, a point that we've discussed just before this discussion online began, do you think the Century of Biology could turn into a Century of Bio-warfare. Even if this wasn't the result of a military funded program? There was one going on. Let's imagine that COVID-19 was harvested in a bat cave itself, and just somehow got out of a lab through a leak... Which seems possible, but perhaps improbable given the sequence combination of bat backbone and pangolin receptor binder, and a human cleavage site. Putting that aside, what are your fears? I would like to hear first from Dr. Quay and then Dr. Muller about what non-state and state actors might learn from this epidemic/pandemic regardless of origin.

Dr. Steven Quay:
Two ideas I'd like to speak to, briefly. I think there might've been a self-governing aspect of any sort of bio weapon work, because you'll always need a vaccine for your own side, right? I mean, if you're going to make a bio weapon, you have to not kill yourself. And I think what happened here in retrospect, if you think about it is we probably provided, I want to say a half a billion maybe more, dollars worth of research that had been done primarily in the US many times by private companies on just how good and how quick you can make these RNA vaccines.

I think we suddenly opened the flood gates where you can say, "I can have a bioweapon in the morning and I can have a vaccine in the afternoon." Other aspect is the terror, non-state folks. Paper in Switzerland, in February, where about 30 guys spend $5,000 bragging about the fact that they could get Sars-CoV-2 to grow in bakers yeast and they can get it to express. I did an op-ed basically saying, "Would you like some coronavirus with your sourdough?" That paper has been downloaded 80,000 times. And I have to wonder how many people are on somebody's watch list somewhere who downloaded that paper? So those are my two cents on that aspect.

David Asher:
Dr. Muller.

Dr. Muller:
Yeah. I think World War III is going to be biologic, not nuclear. I think that it may even be a hidden war. Previous wars you know who you're fighting. But, I don't believe China did this one purpose. Yes, they developed this weapon, but I don't think they released it on purpose. If they wanted to release it on purpose, they would have had an infected person travel to Fort Dietrich and release it around there. They would have done something clever like that, so it would be blamed on the United States. This was an accident.

But what it illustrates more than anything else is that you can attack another country without killing people. Well, you kill people, but you can attack another country without dropping weapons that blow things up. Economic warfare, I believe, is going to be the next war. And what this has illustrated better than anything else is if you have a bio weapon and you have a vaccine for your own people, that you can wreak devastation on the economies of other countries, of competing countries with very little loss yourself. So yeah, this is a genuine threat. No, it's not going to be nuclear war in the future, it will be economic bio war.
David Asher:
Dr. Muller, when you look at this issue of vaccination... And by the way, the reason I'm concerned about it and I was concerned at the State Department, is that the WIV across the street was developing advanced vaccine capabilities. They weren't mRNA as far as I understand it, there is even some allegation among some scientists that I have interviewed who worked with both the WIV and the Wuhan Institute for Virological or Biological production across the street, that the vaccine development was for a pan beta coronavirus vaccine. And if it did include COVID-19, could this be actually a antidote to a perspective, not realized weapon development lay capability? And is that the type of thing that we need to be investigating further as we have this 90 day surge underway by the US intelligence community?

Dr. Muller:
Yeah, this is exactly the sort of thing you do. I want to separate, that's kind of speculation though and those clues from the solid science that we've presented today. There's a lot of things that can be disputed and everything you've said is among them, that's why it requires more investigation. I just want to emphasize that with Dr. Quay said and what I said, we stuck to the indisputable evidence that this was a laboratory leak.

Given the fact that it's a laboratory leak, there are so many questions that are raised. Why were there no infections, virtually no infections, outside of Wuhan? I can speculate that they had started spreading the vaccine earlier. But today, we want to just make a point of the fact that there is solid science that really has no dispute. And that is that this came, possibly inadvertently, I believe it was inadvertent, from a laboratory in Wuhan. That the virus itself... There are people who want a whistleblower, they want an eye witness. They want someone to say, "Oh, guilty, guilty. I'm the one who developed this thing."

Well, we have that whistleblower, it's the virus itself. And what Dr. Quay and the other virologists have shown, is that there's enormous information within the virus itself. China could prevent people from talking, they could prevent whistle blowers from coming, they could lock up their own scientists so that we can't talk to them, they can make them disappear. But the virus got out and the virus came to the rest of the world and it is carrying with it this detailed message that is full of great information. And analyzing that, I think, was the first great stage in this investigation. It will go down in history as a remarkable scientific achievement. Now let's follow up and figure out what we have to do? What are the clues? What did they really do, in detail?

David Asher:
Yeah. And thank you so much to both of you for your intellectual and empirical effort to try to actually provide evidence to a debate that has been remarkably devoid of hard evidence among some of the world's most leading scientists. This is one of the things I found most distressing at the State Department when I called NIH and others and I said, "Send me over your file on the origins issue so we can just check the box and say this didn't come out of a lab." And there was no file provided to us. Maybe they have a very extensive one, but why they kept it secret from the State Department remains a mystery.

We'll continue this examination at the Hudson Institute, in collaboration with scientists around the country, and indeed around the world. We're always looking for an alternative hypothesis to be demonstrated with evidence. I always want to emphasize if someone in the scientific community can come forward with specific evidence that is a provable and plausible, at the very least, to people like us we'd certainly like to hear it and provide an audience for that.
Thank you to you both. Have a wonderful day. Thank you, Hudson viewers and we appreciate your support and participation in our events, which we hope to bring back online live sometime in the not-too-distant future. All the best.