

## Expert Scientists Testify on Virus Origin

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### STORY AT-A-GLANCE

- › Expert testimony from two scientists adds to evidence that clarifies the origin of COVID-19, which they believe leaked from a laboratory in Wuhan, China, as a result of controversial gain-of-function (GOF) research
- › There is no evidence to support the theory that SARS-CoV-2 emerged from a wet market in China, and no animal host or widespread animal-to-human transmission has been found
- › SARS-CoV-2 has a unique trigger on the surface called a furin cleavage site and a unique code in the genes for that site called a CGG-CGG dimer; these markers do not exist in natural coronaviruses, but are known to have been used in GOF research
- › SARS-CoV-2 was preadapted for optimal human-to-human transmission, another sign of GOF research

Two scientists were called as witnesses at the House Oversight and Reform Subcommittee on Select Coronavirus Crisis hearing, held June 29, 2021.<sup>1</sup> Their testimony adds evidence that clarifies the origin of COVID-19, which they believe leaked from a laboratory in Wuhan, China, as a result of controversial gain-of-function (GOF) research.

Many have stated that we'll never truly know the origin, short of China confessing or a [whistleblower](#) coming forward. But as Richard Muller, Professor Emeritus of physics at

the University of California, Berkeley, stated during his testimony, “We have a whistleblower, the virus itself.”<sup>2</sup>

Muller, who has worked on scientific efforts that have won Nobel Prizes, states that the virus, which came out of China, carried with it genetic information about its origins.

“In my mind, there are five compelling sets of scientific evidence that allow us to reach this very strong conclusion that, yes, it was a laboratory leak,” Muller said. Dr. Steven Quay, the first scientist to testify, came to the same conclusion that COVID-19 has a laboratory origin, based on “six undisputed facts that support this hypothesis.”

A summary of the evidence, which they review in detail in the video above, follows, in the hope that, by revealing the true origin of COVID-19, we can help to prevent future pandemics and related loss of life.

## **‘Could They Have Come From Our Lab?’**

Quay is a physician and scientist with an impressive background, including hundreds of published articles that have been cited over 10,000 times. Quay holds 87 patents across 22 different fields of medicine, has invented seven FDA-approved medicines – and believes that [SARS-CoV-2 came from a laboratory](#) in China.

I recently interviewed Dr. Quay and we will post it soon. But in his research paper of 140 pages, which is more like a book, he makes a strong argument that there is virtually no chance that the SARS-CoV-2 virus is from nature. How unlikely? Imagine all the atoms in the universe and then imagine trying to find the same atom twice. That would be far more likely than the virus coming from nature.

As early as December 30, 2019, there were signs. This was the day Shi Zhengli, Ph.D., the director of the Wuhan Institute of Virology’s (WIV) Center for Emerging Infectious Diseases, also known as “bat woman,” was told about a novel coronavirus that had caused an outbreak of pneumonia cases close to WIV.

“Could they have come from our lab?” Shi, who had been studying bat-borne viruses since 2004, including SARS-like coronaviruses, wondered.<sup>3</sup> Since then, evidence has continued to accumulate that COVID-19 likely emerged from a laboratory in China after having undergone some sort of manipulation to encourage infectiousness and pathology in humans, known as **gain-of-function (GOF) research**. According to Quay:<sup>4</sup>

*“In the last 18 months, we’ve learned an intense amount about the origin of the pandemic, but one of my frustrations is that virologists and science writers around the world seem to want to ignore what has been learned and the inevitable conclusion it reveals.*

*As inconvenient as it is, I believe the evidence conclusively establishes that the COVID pandemic was not a natural process, but instead came from a laboratory in Wuhan, China, and that it has the fingerprints of genetic manipulation for a process called gain of function research.”*

## **Quay: Six Undisputed Facts Suggest COVID Leaked From Lab**

Quay stated that six undisputed facts support the hypothesis that SARS-CoV-2 leaked from a lab.<sup>5</sup>

- 1. COVID Didn’t Begin in a Seafood Market** – In the early days of the outbreak, China told the world that the COVID-19 pandemic began at the Hunan Seafood Market, a wet market in Wuhan, because half the initial cases were associated with that location. This is reminiscent of other coronavirus outbreaks, including SARS-Cov-1 (SARS) and Middle East respiratory syndrome (MERS), both of which began in animal markets.

However, “after 18 months, we know it [COVID-19] did not begin in a market in Wuhan for three reasons,” Quay said. First, none of the early COVID patients from the Hunan market were infected with the earliest version of the virus, meaning that when they came to the market, they were already infected.

“Four patients with the earliest version of virus had one thing in common,” Quay said. “None had exposure to the market.” Second, none of the environmental specimens taken from the market had the earliest virus either, which means they also came into the market already infected.

In addition, 457 animals from the Hunan market were tested, and all were negative for COVID. Another 616 animals from suppliers to the Hunan market were also tested, and all were negative. Wild animals from southern China – 1,864 of them, of the type found in the Hunan market – were also tested and found to be negative for the virus.

- 2. The Virus Has Not Been Found in an Animal Host** – Scientists have tested 80,000 samples from 209 different species, but the SARS-CoV-2 virus has not been found in a single specimen. “The probability of this for a community-acquired infection is about 1 in a million,” Quay said. “This is what you’d expect for a lab-acquired infection.”
- 3. No Cases of COVID Were Detected in Blood Samples Prior to December 29** – If the virus had emerged naturally from a wild animal, a small number of cases would likely have already been in circulation. But, “after testing 9,952 stored human blood specimens from Wuhan hospitals from before December 29, there was not a single case of COVID in any specimen,” Quay said.

“It was expected that between 100 and 400 would be positive. The probability of this for a community-acquired infection is also about 1 in a million, but this is what you’d expect for a lab-acquired infection.”<sup>6</sup>

- 4. No Evidence of Multiple Animal-to-Human Transmissions** – With prior coronavirus outbreaks like SARS and MERS, 50% to 90% of the early cases were clearly linked back to various animal-to-human infections. For SARS-Cov-2, 249 early cases of COVID-19 were examined genetically and they were all human-to-human transmission.

For a community-acquired infection, Quay said, “This is the probability of tossing a coin 249 times and getting heads every single time. This is, however, what you’d

expect for a lab-acquired infection.”

**5. SARS-CoV-2 Has Two Unique Factors That Point to GOF** — SARS-CoV-2 has a unique trigger on the surface called a furin cleavage site and a unique code in the genes for that site called a CGG-CGG dimer. “These are two independent levels of uniqueness,” Quay noted. Furin is a protein coding gene that activates certain proteins by snipping off specific sections.

To gain entry into your cells, the virus must first bind to an ACE2 or CD147 receptor on the cell. Next, the S2 spike protein subunit must be proteolytically cleaved (cut). Without this protein cleavage, the virus would simply attach to the receptor and not get any further. “The furin site is why the virus is so transmissible, and why it invades the heart, the brain and the blood vessels,” Quay explained.<sup>7</sup>

While furin cleavage sites do exist in other viruses like Ebola, HIV, zika and yellow fever, they’re not naturally found in coronaviruses, which is one reason why researchers have called the **furin cleavage site the “smoking gun”** that proves SARS-CoV-2 was created in a lab. The entire group of coronaviruses to which SARS-CoV-2 belongs does not contain a single example of a furin cleavage site or CGG-CGG code, Quay said.

Quay’s Bayesian analysis of **SARS-CoV-2 origins** revealed that finding a CGG-CGG codon pair in the furin site of SARS-CoV-2 is “a highly improbable event,” and this can be used to adjust the likelihood that SARS-CoV-2 is of zoonotic origin to only 0.5%, while the likelihood of laboratory origin is 99.5%.<sup>8</sup>

Further, since 1992, WIV and other laboratories around the world have inserted furin sites into viruses repeatedly as part of **GOF experiments**. “It is the only sure method that always works and always makes them more infectious,” Quay said. WIV was also known for their broad use of CGG-CGG codon pairs.

Quay wrote in his analysis, “Scientists from the Wuhan Institute of Virology provided the scientific community with a technical bulletin on how to make genetic inserts in coronaviruses and proposed using the very tool that would insert this CGGCGG codon.”<sup>9</sup>

**6. SARS-CoV-2 Optimized for Human Transmission** — Quay's last point focused on SARS-CoV-2 being preadapted for human-to-human transmission. "Specifically," he said, "the part of the virus that interacts with human cells was 99.5% optimized. When Sars-1 first jumped into humans, it had only 17% of the changes needed to cause an epidemic." How was SARS-CoV-2 "taught" to infect humans so efficiently in a laboratory?

A commonly used GOF method to optimize SARS-CoV-2, Quay explained, would have been serial passage in a lab on a humanized mouse to develop human-like pneumonia. In short, researchers infect the humanized mouse with the virus, wait a week, then recover the virus from the sickest mouse. That virus is then used to infect more mice, and the process is repeated until you get a virus that can kill all of the mice.

The challenge is to create the humanized mice to begin the process in the first place, but it's known that part of WIV's GOF research involved using humanized mice for experiments to determine which coronaviruses could infect humans, as well as research to make viruses that weren't able to infect humans do just that.<sup>10</sup>

Other reports also claimed that WIV was carrying out research infecting humanized mice with novel bat SARS coronaviruses in 2019, and years earlier video was released showing WIV scientists working with little or no protective gear while working with live viruses.<sup>11</sup>

What's more, according to Quay, WIV acknowledged they've been working with [humanized mice, developed by Ralph Baric](#), Ph.D., at the University of North Carolina at Chapel Hill, at U.S. taxpayers' expense.<sup>12</sup>

## **Five More Signs That Point to a Lab Origin**

Muller largely agreed with Quay's testimony and added five points of his own, which further solidify the high likelihood that COVID-19 came from a lab.<sup>13</sup>

- 1. Absence of prepandemic infections** – Like Quay, Muller found the absence of prepandemic infections in more than 9,000 samples taken in Wuhan to be highly suspect. “It’s unprecedented,” he said. “It didn’t happen with MERS or SARS.”
- 2. Absence of a host animal** – Muller brought up the [February 2020 Lancet letter](#),<sup>14</sup> in which a group of 27 scientists, including Peter Daszak, who has close ties to WIV, condemned “conspiracy theories suggesting that COVID-19 does not have a natural origin.”

If you look at The Lancet letter, Muller said, they say you can dismiss a lab origin because China identified the host animal and even went so far as to praise China for its openness. “This paper, The Lancet, does not read well when we look at it 16 months later,” Muller said, noting that a host animal hasn’t been found.

- 3. Unprecedented genetic purity** – Echoing Quay, Muller also said that SARS-CoV-2’s unique genetic footprint is unlike that of other coronaviruses like MERS and SARS, as well as that of other types of natural viruses. But, he said, “It is exactly what you would expect if you’d gone through gain of function.”
- 4. Spike mutation** – Muller also highlighted the unique mutations in the SARS-CoV-2 spike protein. “The fact that there’s no known way for that spike mutation to get there other than a gene insertion in a laboratory is a very powerful argument,” Muller said.
- 5. Virus was optimized to attack humans** – This is something that has never happened in natural virus releases, Muller said, “but it does happen if you run it through gain of function.”

While there is no evidence in favor of a zoonotic origin for SARS-CoV-2, “each one of these things is compelling by itself,” Muller said. “If we had any one of the five things, we should conclude that the evidence strongly favors the lab origin.” And we have not one of the five, but all of them. Muller also shared an anecdote that occurred with a colleague of his – a story he says is “as horrifying and more frightening than almost anything else in my life.”

In the early days of the pandemic, he called on an expert virologist friend to help him review literature suggesting there may have been a lab leak. The friend said no, so he asked if someone in his laboratory could do it. But the answer was no again. Muller pressed him on the refusal, to which he responded:

*“If anyone in my laboratory is discovered to be working on a laboratory leak hypothesis, China will label us enemies of China and the laboratory will be blacklisted and we will no longer be able to collaborate. We collaborate all the time with China. Nobody will take that risk.”*

“The idea that China has managed to interfere, to break United States’ freedom of expression, freedom of investigation, freedom of thought through this collaboration is really scary,” Muller said, calling it “one of the most chilling conversations I’ve had in my life.” Ultimately, however, the truth will prevail as long as the long-censored lab-leak theory and evidence in support of it continue to go mainstream.

## Sources and References

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