

**Led by Science: The COVID-19 Origin Story**  
**SELECT SUBCOMMITTEE ON THE CORONAVIRUS CRISIS**  
**Opening Remarks of Dr. Steven C. Quay, MD, PhD**

Congressmen Scalise and Comer, Members of the Subcommittee on the Coronavirus Crisis, Ladies and Gentlemen.

My name is Steven Quay and I am honored to speak at this forum. I am a physician-scientist with over 360 publications on a wide range of topics in science and medicine. I have 87 issued patents in 22 different fields of medicine, including the chemistry of RNA drugs like the Pfizer and Moderna vaccines. I have invented seven FDA-approved medicines that have been used by millions of people worldwide.

I appreciate the non-partisan approach the Subcommittee is taking today. Clearly, science in the last few years, but especially on topics related to the COVID pandemic, has been coopted by geopolitics. Thus, I am here, not as a mouthpiece for any political party, but as an American scientist.

I dedicate my testimony today to the more than 600,000 Americans that this pandemic has killed so far with the hope that by clarifying the origin of COVID we can help to prevent future pandemics and the loss of innocent lives.

Given this backdrop, I will be keeping my remarks today to matters of science. I will state facts and evidence about the pandemic that I have collected. I will explain why those facts lead to certain conclusions, allow a particular inference, or rule out a hypothesis about the origin.

Today's testimony is an effort to answer the question posed on December 30, 2019, by Dr. Zheng-li Shi, the head of coronavirus research at the Wuhan Institute of Virology. She had just been told that a novel coronavirus had caused an outbreak of pneumonia at hospitals close to her laboratory in Wuhan. In what I believe was her last unscripted public utterance, she has been quoted as saying,

“Could they have come from our lab?”<sup>1</sup>

In the last 18 months, we have learned an immense 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 we have 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 through a process called ‘gain-of-function’ research.

There are six undisputed facts that support this hypothesis.

As a reminder, all zoonoses are diseases that involve a virus infecting an animal, the animal coming in contact with a human, and then the human being infected.

**The question of the origin of a zoonosis is the question of the location of the animal.**

In natural zoonoses the animal is in nature, a cave, a farm, or a market. The infected human comes in contact with that animal.

For lab-acquired zoonoses the animal is in a laboratory, or in cells from an animal in a petri dish and the human works in the lab.

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<sup>1</sup> <https://www.scientificamerican.com/article/how-chinas-bat-woman-hunted-down-viruses-from-sars-to-the-new-coronavirus1/>

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In deciding between a natural origin or a laboratory origin, there are six facts no one disagrees with:

1. The Chinese first told the world that the COVID pandemic began in the Huanan Seafood Market because approximately one-half of early cases had been associated with that location. This would have been reminiscent of the two previous coronavirus epidemics as both SARS1 and MERS began in live animal markets. However, after 18 months of investigation, we now know it did not begin in a market in Wuhan for the following three reasons.

First, none of the 11 patients from the Huanan market or another market were infected with the earliest virus, meaning they came into the market already infected. The four patients with the earliest version of the virus all had one thing in common: none had any exposure to the Huanan Market.

We knew in January 2020 from public scientific databases that the patient with the earliest first complete virus sequence was a 39-year-old man treated at the General Hospital of Central Theater Command of the People's Liberation Army of China, located on Wuluo Road in the Wuchang District of Wuhan, about 3 km from the Wuhan Institute of Virology. After 18 months and almost 3 million viruses sequenced worldwide his virus remains the earliest.

Second, none of the environmental specimens from the market had the earliest virus meaning they came into the market. This included 1055 samples of frozen food in the market, all of which tested negative for COVID.

Third, 457 animals from Huanan market were tested; all were negative for COVID. 616 animals from suppliers to the market were tested; all were negative. 1864 wild animals from Southern China of the type found in the market were tested for COVID and were all negative.

These data, from the publicly available WHO Report establish that it did not begin in the Huanan Market or any other market in Wuhan.

2. Failing to find it in any market in Wuhan, the search was expanded to all of China. But after testing 80,000 samples from 209 different species from other markets, farms, and nature, the virus has not been found in a single specimen. The probability of this for a community-acquired infection is about one in a million.

This **is** what you expect for a lab-acquired infection.

3. After testing 9952 stored human blood specimens from hospitals in Wuhan from before December 2019, there was not a single case of COVID in any specimen. It was expected that between 100 and 400 would be positive. The probability of this for a community-acquired infection is also about one in a million.

This **is** what you expect for a lab-acquired infection.

4. There is no evidence of multiple animal-to-human transmissions. With two prior coronavirus outbreaks, SARS1 and MERS, 50-90% of early cases were from various animal-to-human

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infections. For SARS-CoV-2, 249 early cases of COVID-19 were examined genetically, and they were all human-to-human transmissions. For a community-acquired zoonosis, the probability of this occurring is the same as flipping a coin 249 times and getting heads every single time.

This **is** however what you expect for a lab-acquired infection.

5. SARS-CoV-2 has a unique trigger on its surface called a furin cleavage site and a unique code in its genes for that site, called a CGG-CGG dimer. So two independent levels of uniqueness. The furin site is why the virus is so transmissible, why it invades the heart, the brain, and the blood vessels. Viruses like Ebola, HIV, Zika, Yellow Fever, all use furin sites, and this is part of the reason for their deadliness. But the entire group of coronaviruses to which SARS-CoV-2 belongs does not contain one single example of a furin site or one CGG-CGG dimer code. A comprehensive study by an MIT group shows that there has never been a furin site or the CGG-CGG letter code in this group of coronaviruses for at least 1000 years –since William won the Battle of Hastings in 1066 to become monarch of England.

But since 1992, in Gain-of-Function experiments, the WIV and other laboratories around the world have inserted furin sites into viruses repeatedly. It is the only sure method that always works and makes viruses more infectious. And the CGG-CGG code found in the COVID virus is commonly used in laboratories around the world, including the WIV. You can literally order it from a supply company on the internet.

By the way, some virologists have said, “But Dr. Quay, furin sites and codon dimers occur in one or more of the other four groups of coronaviruses and with a process called recombination a COVID-like virus could easily pick one up.”

This is wrong for three reasons based on well-known, fundamental biology.

Because coronaviruses **do** exchange genetic material so easily the very existence and stability of the five distinct groups is evidence from nature that there must be barriers to the exchange of genetic material. I have spoken previously about the one-thousand-year stability of the group COVID belongs to. If recombination was easy this group would have been merged with the other four into a single group over the last millennium. Two things stop recombination between groups.

First, recombination happens when one poor bat is infected with two different viruses and during that co-infection genetic material is exchanged. Here, the groups of viruses that have furin sites or CGG dimers don’t infect the same bat species as the COVID-like viruses that don’t have these features. The COVID virus can only exchange genetic material within its own group; a group that has not had a furin site or a CGG-CGG dimer for a thousand years.<sup>2</sup>

Second, even if you force two different viruses into a cell in the laboratory, unique gene sequences are required for genetic exchange or recombination to occur. The “hot spots,” where exchange can occur are different for each group and incompatible between different groups.

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<sup>2</sup> Dr. Shi and Daszak, of the EcoHealth Alliance are responsible for some of this research proving the COVID virus has no natural method to pick up a furin site.

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In a clever use of this concept, Dr. Ralph Baric, a leading coronavirus scientist from North Carolina, once made a vaccine candidate that was resistant to recombination by using synthetic biology to change the Hot Spot gene codes.

6. Finally, SARS-CoV-2 was pre-adapted for human-to-human transmission from the first patient. Specifically, the part of the virus that interacts with human cells was 99.5% optimized. When SARS1 first jumped to humans it had only 17% of the changes needed to cause an epidemic. As evidence of the relevance of this work, the UK strain that emerged in the fall of 2020 that was more infective was a change in one of the few spots that was not optimized at the beginning.

Some virologists may claim the COVID virus was not pre-adapted and point to evidence it has been mutating a lot since it first emerged. Making new variants like the Delta Strain currently in the news. But the details tell another story. COVID does randomly make, on average, about one genetic mistake every two weeks. So, after a year of circling the globe, it will naturally have on average about 26 changes somewhere in its gene code compared to when it started. But the vast majority of those mistakes are either neutral, having no effect on the deadliness of the virus, or actually detrimental, making the virus weaker. Less than 1% actually improve the virus.

So how do I believe the COVID virus was taught to infect humans in a laboratory?

A commonly used Gain-of-Function method to optimize the COVID virus would have been by serial passage in a laboratory on a humanized, genetically modified mouse that can develop a human-like pneumonia. You infect the mice, wait a week or so, and then recover the virus from the sickest mice. Then you repeat. In a matter of weeks this Directed Evolution will produce a virus that can kill every humanized mouse.

However, it is a challenge to create these humanized mice for the serial passage in the first place. Here, the WIV has acknowledged that for several years they've worked with humanized mice developed in Dr. Ralph Baric's laboratory in North Carolina and funded at US taxpayer's expense.

In closing, let me say to the families of those who have died from COVID, I am dedicated to applying my scientific and medical expertise to understanding how this pandemic happened and, importantly, helping put safeguards in place at our research institutions to be sure this never happens again.

Thank you.