

Analysis Proves SARS-CoV-2 Lab Origin

Analysis by [Dr. Joseph Mercola](#)

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STORY AT-A-GLANCE

- › An overly conservative Bayesian analysis shows beyond a reasonable doubt that SARS-CoV-2 is laboratory derived. There's a 99.8% probability SARS-CoV-2 came from a laboratory and only a 0.2% likelihood it came from nature
- › None of the 80,000 samples from 209 different animal species has been found to contain SARS-CoV-2
- › Of the first 259 cases in China, not one was traced back to animal contact. All were human-to-human transmissions. This is the equivalent of going to Las Vegas and flipping a coin and getting heads 259 times, which is virtually impossible
- › When one combines these two statistical anomalies, the real likelihood of the virus coming from nature is less than one in all the atoms of the universe – 10^{80} – which is a very, very large number, making it virtually impossible
- › SARS-CoV-2 has a protein signature that is similar to that found in melittin, a bee venom toxin

In this interview, Dr. Steven Quay – one of the most-cited scientists in the world¹ – discusses his Bayesian analysis,² published January 29, 2021, which concludes beyond a doubt that SARS-CoV-2 is laboratory derived. Quay is an M.D. with a Ph.D. in chemistry. You can learn more about Dr. Quay on his [website](#).

He did his medical residency at Mass General at Harvard Hospital and his postdoctoral work at MIT with a Noble laureate. He holds 87 patents in 22 fields of medicine,

including the gadolinium used with MRI imaging.

During his career, Quay published 360 papers, which have been cited over 10,000 times. His COVID origin paper, however, has already been downloaded 170,000 times. Bayesian analysis,³ or Bayesian inference, is a statistical tool used to answer questions about unknown parameters by using probability distributions for observable data.

Quay's highly conservatively-skewed analysis shows there's only a 0.2% likelihood that this virus came from nature, and a 99.8% probability that it came from a lab. His 140-page paper can be downloaded from zenodo.org⁴ for those who want to dive into the nitty gritty of this statistical analysis. He presented these data to House Representatives during a June 26, 2021, subcommittee on the coronavirus crisis meeting.⁵

Instead of using the observed statistics of the data he gathered, he radically reduced the probability to 1 in 20. When one combines all the statistical anomalies from the 26 different data points he collected, the real likelihood of the virus coming from nature is less than 1 in all the atoms of the universe – 10^{80} – which is a very, very large number, making it virtually impossible.

SARS-CoV-2 Has a Protein Sequence Found in Bee Venom Toxin

As early as January 2020, Quay knew SARS-CoV-2 could be problematic.

"Nobody was paying any attention because there was no need to at that point," he says. "I saw this virus coming out of China. I looked at the sequence of it and I remember telling my wife, 'I know what this thing is going to do in cells,' because for five years at Stanford, I was studying and was the world expert on the toxin melittin, which is a bee venom toxin, the thing that hurts when you get a bee venom ...

This melittin, this toxin in bee venom, has the same sequence that SARS-CoV-2 had ... I run a public company, so I went to the board a couple weeks later and said, 'Look, I think we can come up with some therapeutics and some ideas

around this.' We actually are in clinical trials with some products for therapeutics against SARS-CoV-2.

Then I started hearing some really crazy public health advisories around masks, social distancing and things, so I ended up writing a little book that was a No. 1 best seller for a few weeks called 'Stay Safe: [A Physician's Guide to Survive Coronavirus,]' [on Amazon](#). That took me through the summer. Then I started going back to something. I was very concerned about what I saw as properties of this virus that had never been seen before.

It's now public knowledge that the government identified one of my papers, so I was contacted by the State Department in the fall and basically was an adviser to their programs there, including a three-hour deep dive from all of the different committees or agencies there ...

I continue to push this because ... if it came from nature, there are certain things we should do differently to not have this happen again. If it came from a laboratory, there's a completely different set of things you need to do. It's not a blame game."

There Are Several Ways to Make a Virus More Dangerous

Quay recently published another paper in which he reveals that the [Wuhan Institute of Virology](#) (WIV) is also working on another virus, the Nipah virus, which has a 90% lethality rate. It doesn't take a genius to figure out what might happen if a virus with that lethality got out. Quay explains:

"[The WIV] published an early paper on samples from COVID patients in the hospital ... It's the most-read paper from the beginning of the pandemic. I did a deep dive into their raw data. The sequence is 30,000 nucleotides – the raw data's 55 million nucleotides. What you can see in there is a fingerprint of everything they've been doing for the last two years. They're doing a lot of crazy research."

As explained by Quay, the WIV has been around for about 40 years. In 2003, after SARS-Cov-1 emerged, the U.S. and France helped China refurbish the WIV into a more secure BSL 4 biolab, the only one in China. Since then, the WIV has become a primary laboratory for zoonotic viruses. It's also one of the top three **laboratories for gain-of-function** synthetic biology, which can be accomplished in several ways.

If you know what you want to alter, you can insert a new synthetic amino acid into the pathogen. If you don't have a precise idea of the change you want to achieve, but you want the pathogen to adapt from an animal to a human, you can do what is called serial passage, where the virus is passed through a series of animal and human tissues.

For example, you could start by infecting 20 humanized mice with a virus, then isolate the virus from the sickest mouse and give it to another 20. Humanized mice are genetically modified mice to have human lung tissue. After four or five passages like that, the virus will have mutated to attack and kill human hosts.

"The third way is to drop big chunks of material in there. For example, the part of the virus of SARS-CoV-2 that interacts with the cell is about 200 amino acids, so times three for nucleic acid, so that's 600. You can just drop a big piece of 600 in and instantly go from an animal to humans, or whatever direction you want.

So, those are the three [primary strategies]: Knowing what to do with single spots, randomly letting nature do it in serial passage, and then dropping big chunks in."

The Bayesian Theorem

As mentioned, Bayesian analysis is a statistical tool using probability distributions. The theorem was developed by Thomas Bayes, a 17th century Presbyterian minister and statistician-mathematician who published many papers during his lifetime. After his death, his estate discovered private notes detailing a process for understanding large complex events in a simple straightforward fashion. The Bayesian equation is A multiplied by B, divided by C. Quay explains:

"It's exactly the same thing we do when we have a favorite baseball team and we watch it during the season. Before the season, we know what they did last year. We know who the new players are, the new coaches, all those things, and we come up with what we call a prior prediction.

We rank the teams according to what we think will happen at the World Series, and that's what's called our prior, our posterior probabilities. Then the season happens and you start winning games, losing games, people get injured, new players, transfers, and you update that every week.

At the start of the World Series, you're probably quite far from where you were at the beginning of the season, because you're now down to two teams but, nonetheless, you still don't know the final analysis. One of the caveats for this 140-page work is, at the end, although I say there's a 1 in 500 chance it came from nature, but that means ... 499 times out of 500 it came from a laboratory."

Bayesian Analysis of SARS-CoV-2 Origin

With regard to SARS-CoV-2, "A" would be the prior estimate of the likelihood of it coming from a lab or from nature. "B" is the new evidence, the new probability that it came from a lab, and "C" is the probability that it came from nature. When you multiply A and B and divide it by C, you get a new A prime, a single probability. However, as new data accumulate, the answer changes.

"The first thing I did was assume the prior likelihood it came from nature or a lab, knowing nothing, basically. That has to be your starting point. Three papers informed that. One paper says that eight times a year, there's a natural jump from nature to a human.

Another paper said, once a year, there's a lab leak in Asia, so 8-to-1 [in favor of natural origin]. That's like 85% probability [that it came] from nature. I used three papers, and my starting point was a 98% probability it came from nature, knowing nothing else."

Quay did not include the three papers mainstream media and fact checkers have leaned on to debunk the **lab origin theory**, and in his paper he explains why they were excluded. In short, they relied on speculation and not science, so the clear bias and lack of scientific facts made them too unreliable.

Next, he entered 26 different pieces of evidence into the equation. The first piece of data was the fact that the virus **first emerged in Wuhan**, China, which has never happened before. Wuhan has a population of 11 million people. It's a very urban area with little man-nature contact. Wuhan also has one of only three biosafety level (BSL) 4 laboratories in the world that are conducting coronavirus research specifically. Next, he calculated probabilities.

"You know the area of China; you know the population of China. If the virus happened randomly, what is the chance it would happen in Wuhan? If there's a laboratory in Wuhan, what are the chances it would have escaped somewhere else in China and not appeared in Wuhan?"

You do the flip. If it came from nature, why did it end up in Wuhan? If it came from Wuhan, what is the probability it could have first appeared somewhere else in China? That hits your probabilities pretty hard out of the box. That was item No. 1. Then you just work through the others."

Zoonotic Transmission

One key piece that makes a big difference in this Bayesian calculation is the question of zoonosis. In order for zoonosis to apply, you must have an animal with a backbone (vertebrae) that is infected with a microbe. Malaria, for example, is not a zoonotic disease, because mosquitoes do not have vertebrae. Malaria is a vector-transmitted disease.

The key to finding the origin of a zoonotic transmission is to locate the animal. If the animal is in the community, then zoonotic transmission occurs through a natural process. If the transmission occurs in a lab, then it's a laboratory-acquired infection, not

a zoonotic transmission. Early on, we were told up to 70% of the earliest COVID patients had visited one or more markets in Wuhan, some of which have live animals for sale.

The problem is SARS-CoV-2 was not found in any of the more than 1,000 animal specimens collected from those markets. They also sampled more than 1,000 pieces of frozen food imported from outside of China, all of which came back clean. About 15% of environmental samples, however, did have the virus.

They also collected samples from all the other markets across the Hubei Province, where Wuhan is located. No virus. About 1,000 bats in Hubei were tested, and no virus was found. Over 80,000 animals representing 209 species from every province of China were eventually tested, and no SARS-CoV-2 was found.

For comparison, SARS-1 was found in 85% of animals tested. The original host was identified as the civet cat. MERS, which came from the Middle East, originated in a bat that had jumped to a camel before turning into a human virus, and it was found in 90% of animals. Yet, after the largest surveillance ever conducted in the history of the world, having tested 80,000 animal specimens, not one has been found to carry SARS-CoV-2.

"In my Bayesian analysis ... even though I should drop 80,000 into the denominator of my equation, what I did was I degraded it to the standard in clinical trials of biology to a P of .05. I said, 'Despite the fact that zero out of 80,000 had this [virus], I'm going to treat this as if it's a 1 in 20 event,' because that's the only way I could keep doing the analysis. Otherwise, I was done at the get-go," Quay explains.

To be clear, this gives a very unfair advantage to the **zoonotic origin** theory, but Quay wanted to have a complete analysis of all the parameters. Diversity is a hallmark of nature, yet there's no diversity in nature for this virus. Zoonotic proponents have argued that the virus must be found in high concentration in an intermediate species, yet not one out of 80,000 samples from 209 different animal species is a carrier of the virus.

No Animal Reservoir or Intermediate Host Has Been Found

Another key piece of the analysis is the virus itself. Bats are nature's reservoirs for coronaviruses. The bats are never sickened by them, so the virus is never rooted out. It just lives in the bats for decades, mutating and recombining with other viruses along the way. Bat-to-human contact is very rare, so most of the time, the transfer occurs between the bats, the reservoir host and an intermediate host before it enters the human population.

“Of the first 259 cases in China, not one was traced back to animal contact. All were human-to-human transmissions. This is the equivalent of going to Las Vegas and flipping a coin and getting heads 259 times, which is virtually impossible.”

That's what happened with SARS-1 and MERS. Early cases of SARS-1 and MERS were divided evenly between human to human transmission, and transmissions that occurred between different animals and humans. This means both of these viruses were most likely zoonotic in origin.

As mentioned earlier, Quay cites research showing natural jumps from nature to a human occur eight times a year, and lab escapes occur once a year. That gives us an 8-to-1 chance of zoonotic origin. However, of the first 259 cases in China, not one was traced back to animal contact. All were human-to-human transmissions.

As noted by Quay, “This is the equivalent of going to Las Vegas and flipping a coin and getting heads 259 times. When you ask your statistician to do that, it's a P value with 84 zeros and a number, so again, that's absolutely impossible.”

To understand how big this number is, the estimated number of atoms in the universe is 10 to the 80th power. Despite this showing it's more or less impossible for SARS-CoV-2 to have a zoonotic origin, Quay gave this a P value of just 0.5 (or a 1 in 20 chance) – again, just to keep the analysis going.

"It's not in the animals in nature. The virus is a pure virus ... It hit the ground with one sequence, and it makes a mistake every two weeks randomly and if it's the kind of mistake it really likes, it keeps it and then that one takes off," he says.

"Again, SARS-1, MERS, every other zoonosis, when it jumps into humans, it's a two-step process. Initially, it jumps into humans, but it doesn't have all the things it needs. It can't make very many baby viruses, et cetera, and so it burns out, and then it tries again, and it tries again. It jumps back to camels, that sort of thing.

Eventually, it gets all the mutations it needs to support human to human transfer. Then you have the foundation for an epidemic, but that's a long process. With SARS-1 it took a year and a half. With MERS, it took two and a half years in camels before it got there. What does that mean though? Every time a human gets an infection ... there is a record in their blood. They make antibodies to the virus.

Once you know that a zoonosis is going to jump into humans and leave a record in the hospital specimens and you have a test from the epidemic of the virus itself, you can go back into the hospital and find specimens. Typically, it can range from 1, to 4, to 7, to almost 20% of the specimens.

For example, people working in the market will have antibody evidence that they had the infection, whether they knew it or not.

This is a very powerful tool ... Because of the unique capability of this virus to hit human to human transmission from the get-go, [Kristian Andersen, a virologist at the Scripps Research Institute in California who published a paper⁶ supporting zoonotic origin] predicted that there would be a lot of pre-epidemic seroconversion.

These are fancy words for 'go into a hospital, take samples out of the refrigerator, test them and find a high percentage.' Of course, people took him up on that and tested over 9,900 banked specimens from December [2020] and before in Wuhan. How many do you think they found that were positive?

My statistician says they should have had 100 to 400. They got zero. You run the crank on that, and that's a 1 in a million probability.

The virus has the incredible capability of being the most aggressive human to human virus that's ever been seen in the history of virology, but it does not have the hallmark of how you would build that in nature, which is pre-epidemic human contact. You can't have both of these properties in the same virus if it came from nature.

Now, if you take a mouse that's been humanized in a laboratory to have human lungs and you serial passage there, that is an effective way to do it.

Amazingly, two months after the epidemic broke out, we're February-March 2020 now, Dr. Shi at the Wuhan Institute of Virology and Dr. Baric in America, the No. 1 synthetic biologist in the world of coronavirus research in North Carolina, published a paper saying, 'Hey, if you grow this virus in transgenic mice, it kills the mice and, by the way, they get brain infections, which is really unusual.'

I'm saying, 'Yeah, that's probably the experiment that was done in 2019 that led to the spill.'"

Again, using extremely conservative data, Quay's analysis shows there's a 99.8% probability that **SARS-CoV-2 is a laboratory creation**. If you want to read through it all, his paper can be downloaded from zenodo.org.⁷

Odd SARS-CoV-2 Proteins Suppress Your Immune Function

At the end of the interview, Quay delivers yet another bombshell. SARS-CoV-2 makes three primary kinds of proteins. The first are the structural proteins for a virus – the spike, envelope and nucleoplasm proteins. It also makes proteins that take over the cells' manufacturing process, thereby allowing the virus to replicate inside the cell. In addition to those, it also makes two very odd proteins that are excreted into your blood.

“These strange proteins, they're not the virus, they're not in the cell,” Quay explains.

When you get an infection, you get a fever, you get sweaty and you get chills, you feel like crap. That's not the virus. That's your own interferon signaling and it helps you fight the virus and probably in prehistory it told your fellow tribe members to isolate you in your own tent. So, it evolved as a social signal for survival of the tribe.

Sources and References

- ¹ [PR Newswire/Yahoo! Finance January 29, 2021, About Steven Quay](#)
- ^{2, 4, 7} [Zenodo January 29, 2021](#)
- ³ [Bayesian.org](#)
- ⁵ [Select Subcommittee on the Coronavirus Crisis, Opening Remarks by Dr. Steven Quay June 26, 2021 \(PDF\)](#)
- ⁶ [Nature Medicine March 17, 2020; 26: 450-452](#)