Cover-Up of SARS-CoV-2 Origin?

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Story at-a-glance

- The mainstream media are still protecting the narrative that SARS-CoV-2 is a zoonotically transmitted virus originating in bats. Much of the evidence for this comes from Shi Zhengli, the chief Chinese researcher studying bat coronaviruses
- While SARS-CoV-2 likely came from a bat, overwhelming evidence suggests it did not become infectious to humans through natural evolution
- A recent article by Independent Science News editor Jonathan Latham presents several different lab origin hypotheses
- Latham also exposes the fact that the Wuhan Institute of Virology failed to identify that a seven-year-old virus sample they have is the closest known precursor to SARS-CoV-2
- Many who defend the all-natural zoonotic origin story justify their stance by saying there are no signs of genetic manipulation. However, there are several ways to manipulate a virus without leaving telltale markers
- This closest-known relative was already in the genetic database under the name BtCoV/4991. However, when it was resequenced following the COVID-19 outbreak, they simply renamed that old virus, which has been on ice for seven years. Whether additional genetic manipulation was done to 4991 to create SARS-CoV-2 is unclear

Dr. Mercola Interviews the Experts

This article is part of a weekly series in which Dr. Mercola interviews various experts on a variety of health issues. To see more expert interviews, click here.

Jonathan Latham, Ph.D., is a molecular biologist and a virologist, which is a great skillset to help us understand the origins of SARS-CoV-2. Latham reviews some really intriguing evidence in this interview. He's also the editor of Independent Science News.

By and large, the mainstream media are still protecting the narrative that SARS-CoV-2 is a zoonotically transmitted virus originating in bats. Much of the evidence for this comes from Shi Zhengli, a researcher at the biosafety 4 laboratory in Wuhan, China.

As the leading Chinese bat coronavirus researcher, her career has been focused on studying bat coronaviruses for over a decade. In a recent article,[1] Latham and Allison Wilson, Ph.D., dissect research showing this theory simply doesn't hold water.

> *"Our article doesn't dispute that it came from a bat at some point, I think that is the strongest data, but what we do dispute is the mechanism by which it came from the bat,"* Latham says.

Lab Origin Theory No. 1

Latham's article lays out several different lab origin hypotheses. The simplest one is that researchers from the Wuhan Institute of Virology or another virology BSL-2 lab that's even closer to the wet market speculated to be the origin of SARS-CoV-2. In that process, one of them got infected and then passed it on to coworkers or family, either because they didn't properly quarantine or didn't realize they were infected.

This is not the most likely of hypotheses for the simple reason that few naturally occurring bat coronaviruses identified have the ability to bind to human ACE2 receptors, which is what allows them to infect human cells in the first place. In order for this theory to work, the virus would have to circulate among many people, evolving slightly with each pass.

Lab Origin Theory No. 2

Another theory is that the researchers were cloning a bat virus similar to SARS-CoV-2 in the lab in an effort to make a more infectious clone. Perhaps they placed the virus in monkey cells, humanized mice cells or human cells with an ACE-2 receptor expressed in them. A researcher may then have been accidentally infected.

> *"There have been lab escapes of viruses in which people fail to decontaminate samples and then they give the samples to someone else, or they throw them out with the trash, or some mishap arises,"* Latham says.

> *"So, the virus is either identical to the one that was collected from the wild or very little altered by the lab, but then it escapes because there's some failure in the lab. That would be a second possibility."*

Lab Origin Theory No. 3

A third possibility is that they were collecting samples and looking at genetic sequences in order to find a virus they could then alter, giving it more interesting properties. Perhaps they found some with the spike protein that had a greater affinity for the ACE2

receptor. By combining it with another virus, they may have been able to create — through genetic engineering — a more infectious virus.

The reason for mixing and matching viruses in the lab in this way is to identify potential pandemic pathogens (PPP). Meaning, two wild viruses, if they come in contact with another, might mutate into something deadly to humans.

> *"For example, we will swap spike proteins and see if the viruses that we have circulating in bats, really all they need to do is evolve better spike protein and all of a sudden, they can become pandemic pathogens,"* Latham says.

Genetic Engineering Doesn't Necessarily Leave Marks

Many who defend the all-natural zoonotic origin story justify their stance by saying there are no signs of genetic manipulation. Like several other scientists, Latham points out there are ways you can manipulate a virus without leaving telltale markers. He explains the basics of the genetic engineering process:

> *"The standard thing, historically, was you find a restriction site in two different viruses, or you may manufacture a restriction site. That gives you a cutting place in the genome … Let's say you start with virus A and you cut a bit out and you put that into virus B. Of course, you've got to remove the bit from virus B that it already has.*

> *So, you're basically swapping things and you're using restriction enzymes, which are basically enzymes that cut DNA in specific places. That's kind of the old-fashioned way.*

> *There are newer methods with PCR and so forth that are slightly more complicated. It means you're not restricted to restriction sites to do that. There are very simple cutting and pasting [methods], but it doesn't necessarily leave a scar or a mark. This is the really important point here.*

> *There are also passaging experiments. Passaging experiments are when you take a virus — say, for example, you take a virus that originally came from a bat and you put that into monkey cells, or human cells … What you normally observe with that virus is that it doesn't work too well in those cells because it's not adapted to them. It's a bat virus, so it doesn't work too well.*

> *But what virologists have learned to do is to, essentially as the viral infection is failing, take a little sample of what is inside the cell and put that into another cell. Then, when that infection builds up … you take another sample.*

> *This is called passaging. It allows the virus to evolve into a more pathogenic form against the cells that you are now putting into. So, you're always putting into the same species of cell. You can also do this with whole organisms."*

The Most Likely Scenario

As noted by Latham, until the passaged virus has been genetically sequenced, there's no telling exactly what it looks like, or how it might act. It's fairly random in that sense. Latham explains:

> *"It may have recombined, it may have mutated; there's been a genetic change, but you don't know what it is until you research it, clone it and make a new infectious clone. And so, you have the possibility that what escaped from the lab is actually not known to the people in the lab. They don't actually know what it was that they evolved.*

> *And, if they were doing those kinds of experiments, putting the live bat viruses into cells of different species — and historically we know that they were doing those kinds of experiments — then they could also develop a new virus.*

> *You can also have a combination of those experiments. So, you can have researchers who passage recombined molecules, they did the cutting and pasting part, and then they put back the cut and pasted virus into novel cells like human cells, and then they passage back, and then you evolve an infectious clone in that way."*

In this way, you can create a virus with high affinity for human cells, even though it wasn't infectious to humans in the beginning. One of the key features of SARS-CoV-2 is its spike protein has high affinity for the human ACE2 receptor. The question is, how did this affinity arise?

> *"One of the obvious answers to that question is that it was being passaged inside these human cells or that somebody cut and pasted a spike protein bound to these human receptors that they already knew worked particularly well.*

> *So, my hypothesis is that either they were cutting and pasting, or they were passaging, or they were doing some combination of both, and then that basically led to somebody in the lab becoming infected through some kind of careless event,"* Latham says.

Leaks Have Caused Other Global Pandemics

The wild H1N1 virus that caused the 1918 flu pandemic was extinct for decades. However, in 1977, there appears to have been a biosafety lab leak in China or Russia in which that virus escaped, causing a global pandemic.

> *"Essentially what happened is the virus went extinct and then a new version of the virus appeared in 1977 in China, and it was basically identical to one that had existed 20 years before … No one can explain how a virus could appear — it was basically identical — but had been somehow hidden.*

> *There was a theory that it had been in the permafrost and somebody had dug up a person from the permafrost who had died with H1N1 flu, but that was the best theory people had until they realized that it probably came from a lab that was making a vaccine."*

The H1N1 virus was temperature sensitive, and one of the things you use when you're making vaccine is a temperature-sensitive virus — a partially disabled virus.

> *"Basically, there is no other explanation than that this came from a lab and that there were labs who had stored stocks of it, but no lab has really come forward and said, 'It was us.' So, this has been kind of deduced from sequence information from the location in which it appears and so forth, but it's widely accepted by virologists,"* Latham says.

Naturally, the notion that a biosafety lab leak would be responsible for a lethal pandemic is an uncomfortable one, especially for virologists doing that kind of work. An outbreak of equine encephalitis in Venezuela has also been traced back to a laboratory leak. Then there's the H1N1 swine flu pandemic of 2009. Latham says:

> *"There's a scientific paper by a friend of mine, Adrian Gibbs ... written with two other virologists. He's a famous virologist and he says, 'This came from a vaccine. The swine flu is actually not readily accountable by the specific circulating viruses that happened to be in North American and European and South American pigs at that time.'*
>
> *Basically you can't explain it by that method, but you can explain it perfectly well by the idea that there was a manufacturer who was making bits of H1N1, one from European sequences and North American sequences, and South American sequences, and stuck them all together to make a universal vaccine, and somehow they failed to inactivate it.*
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> *So, they gave it to pigs in Mexico and that became the swine flu, the second H1N1 pandemic, and that second pandemic killed probably close to 300,000 people. We have a whole series of examples of lab escapes of viruses, so when people treat the lab escape thesis as being somehow ridiculous or outrageous or improbable, to me it just demonstrates their ignorance of the history of virology."*

Latham also addresses suspicions that HIV AIDS came from a polio vaccine, so for more details, listen to the interview. This was described in the book "The River: A Journey Back to the Source of HIV and AIDS," by Edward Hooper, and reviewed in a British Medical Journal article that you can read for free.[2]

SIV from infected monkey kidney cells that were used to create polio vaccines and used on hundreds of thousands of Africans are also suspected of being the cause of certain cancers.

Safety Breaches at Wuhan Lab

Many safety breaches have been documented at biosafety labs around the world, including the Wuhan lab. Several were documented by U.S. Embassy officials who visited the Wuhan Institute of Virology in 2018.

> *"I mean I think they're important data points but … we think it's more important that people from within China have raised questions about the bio security of this lab. Firstly, it's newly opened, so that's automatically a bit of a red flag. Secondly, there were violations cited by the internal overseeing agency in China of the kind of standards they would expect from a BSL facility.*

> *They've been trying to set up the certification systems and so forth for their labs because they're trying to set up a whole network — a whole system of animal experiments and collection stations and so forth … So, they're setting up the certification schemes and they've already been cited, according to these reports, as having violations …*

> *In the end, let me add something: One of the basics should be that you don't site these labs in the middle of a big city. So, we already have what I would say a violation to the basics. They should be in a desert or something like that, they should be in Antarctica, in remote areas."*

BSLs Promote High-Tech Solutions Rather Than Hygiene Basics

There can be no doubt that biosafety level 4 labs pose a tremendous threat to public health, seeing how they house the most dangerous pathogens in the world, and leaks are inevitable. The question is, are these risks worth it?

As noted by Latham, the existence of these laboratories drive the vaccine agenda while old-fashioned commonsense hygiene strategies such as hand-washing and protective gear fall by the wayside. The risks posed by these labs also fit right into the surveillance capitalism now getting a hard push through the roll-out of disease tracking and tracing mechanisms.

> *"An interesting thing happened the other day. Seventy-seven Nobel laureates, most of them molecular biologists, wrote a letter to the president protesting the cutting of the grants to the Wuhan lab that were emanating from the NIH. Well the man leading this effort [is] Richard Roberts. What is his scientific position?*

> *He is on the board of directors of New England Biolabs, one of the biggest suppliers of molecular biology equipment. So, they're corralling together all these Nobel Prize winners to support all this molecular biology research that costs big bucks — hundreds of millions of dollars a year to do this kind of research, money that could be going to PPE and so forth."*

That money could also go to more basic strategies such as vitamin D supplements to build up the population's immune system.

Cover-Up at Wuhan Institute of Virology Exposed

Latham and Wilson are also planning to write about what they believe is a cover-up at the Wuhan Institute of Virology. The nearest living ancestor of SARS-CoV-2 is a viral sequence currently stored in the Wuhan lab. It's said to have been kept frozen for the past seven years and nothing has been done with it.

This sequence came from bats living in a mine, and people who have worked in the mine have died of viral infections. In other words, they've had a strong reason to look into that virus sequence, and that one also happens to be the closest relative to SARS-CoV-2. Shi published one of the first viral sequences of SARS-CoV-2.

> *"Three papers came out in three days, all saying this is 'The sequence of the SARS-CoV-2 virus,'"* Latham notes. *Yet "her paper makes no reference to this longstanding sequence that they'd had in her lab. Zero reference. Instead, they say they've taken a sample from that freezer and they've sequenced it, and this is the nearest living relative.*

> *But this obscures the fact that for seven years they'd had another virus, which basically came from the same tube … But it looks like when you go searching the DNA databases, it makes it look like this virus has just been with us since December.*

> *It really hasn't, it's been sitting in that lab, supposedly unresearched. So, the question is, what were they doing with this viral sequence for seven years that may have killed three miners back in 2013?"*

In a nutshell, SARS-CoV-2 is quite possibly not a new virus. A highly conserved close ancestor was already in the database under the name BtCoV/4991. It was already in the published literature. However, when the Wuhan Lab resequenced the mineshaft sample following the COVID-19 outbreak, they simply renamed that old virus that's been on ice for seven years.

> *"Giving it a new name basically obscures the old history. They don't even acknowledge that it came from the same tube, which they now have been forced to acknowledge … It's the same virus. The sequence identity between the two samples is 100%.*

> *So, if there were one base pair different, you could maybe make a scientific argument that we should give them a different name, but there's no difference between them whatsoever. It's the same virus from the same tube, collected from the same place — the mine where the miners died … from a viral infection of pneumonia."*

Shi's genetic sequencing paper basically pretends the 4991 sequence never existed. "They've forgotten all about it; that would be the interpretation of reading their paper," Latham says. A second paper released within that three-day span identifies 4991 as the nearest living relative, and states that it comes from the Wuhan Institute of Virology.

The third sequence paper does a complicated phylogenetic analysis of the SARS-CoV-2 virus, yet it too fails to mention that the nearest living relative is 4991 and held in the Wuhan lab.

> *"What's really interesting is that everyone who sequence [SARS-CoV-2] — there was a bunch of labs that sequenced the virus around the same time — they all would have searched the database and come up with this 4991 sequence … They all would have done that.*

> *What you have to imagine is that they just get on the phone with the Wuhan Institute of Virology and say, 'Oh, the virus broke out in your town just down the road from you, walking distance, and you are the keepers of the nearest known viral sequence. Have you had a lab accident?' You can imagine dozens of labs phoning them up and say, 'How do you handle a lab accident?' …*

> *What I'm offering is evidence of a cover-up, but we don't know exactly what they were covering up. They could have been covering up something a little different, but the very obvious thing to be covering up is simply that you are researching a virus that looks uncomfortably like SARS-CoV-2 …*

> *We only have a partial sequence [of 4991]. We don't have the whole genome of this original sample. They only provided a sequence of 370 base pairs, but it is 98.7% identical to SARS-CoV-2 on nucleotides and the 370 base pairs.*

> *This is considered the most conserved part of the genome, so it doesn't necessarily extrapolate to the whole thing. What is quite possible is that, that sample comes from something that is way closer than anything we've been told about."*

Public Health Rethink Is in Order

Even if 4991 isn't a 100% match to SARS-CoV-2 (which sequencing of the whole genome would reveal), it could be close enough that you wouldn't even need a whole lot of gain-of-function experiments to end up with a highly transmissible virus. According to Latham, "That's exactly the kind of thing that could have happened."

In closing, as noted by Latham, the big picture question is, do we really want to be spending taxpayer money on all of these public health models that rely on biosafety/bioweapons research?

The justification for doing this kind of research on viruses is to prepare us for potentially devastating outbreaks, should the viruses evolve and mutate in the wild. Yet, that same research ends up being the source of our most dangerous outbreaks. As noted by Latham:

> *"These people have not managed to predict anything so far. What they've done is these incredibly dangerous experiments and then find out that the next virus comes from somewhere they didn't anticipate, or certainly didn't warn us about …*

> *This research is not really predictive, but if enough virologists get together and say that this is how we predict the next pandemic, what is the government to do? If they all say, 'That's how we should do it,' then who's going to contradict them? …*

> *I mean, you want to continue gainful employment, so why not push an agenda that's going to keep you employed, even though it doesn't serve the public good necessarily …*

> *What [should] we spend our public health money on? Do we target these individual diseases and make New England Biolabs and the Gates Foundations investors rich, or do we invest in public health in a sense that benefits everybody — prevention and nutrition?*

> *Also, the big issue too that we haven't really touched on is, why are we blaming the wildlife trade here? This is a really important question to ask because Peter Daszak, head of the EcoHealth Alliance, has been in all the media; he's been on Democracy Now!, the New York Times, Scientific American, Science Magazine, all these different outlets, basically ubiquitously blaming the wildlife trade, saying categorically it's not a lab escape.*

> *Well, he is an interested party, right? His nonprofit is funding this research. The media cannot go and ask the person who's funding it whether it came from their lab or not. It's ridiculous. But that's what they're doing and they're treating us like idiots."*

As Latham points out, the reason some wild viruses emerge is because we're destroying rainforest and building roads into remote areas. People end up catching the viruses because animals are fleeing the destruction of the forest.

So, why are we blaming the wildlife trade? If anything, we need to address the destruction of the animals' native habitats. That, however, would be very bad for Daszak's business because the EcoHealth Alliance is in partnership with the palm oil industry.

> *"We find that science — if you understand the science well enough — really helps you understand who's lying,"* Latham says. *"When you understand that part, you got a really strong anchor to base in analysis of what's really going on in the bigger picture.*

> *If you can see that a very obvious thing — the possibility here is a lab escape —and then you've got one or a few people wandering around the media saying, 'A lab escape is an impossibility, it never happened, there's no chance of it at all' — you know that they're not speaking science, that they have some kind of ax to grind. And then you see who else repeats the message, who supports them and who doesn't and so forth."*