

OPEN LETTER TO THE WORLD HEALTH ORGANIZATION

March 30, 2021

To Stop the Next Pandemic,

Evidence that is Undisputed Favoring Lab Origin of COVID Needs to Be Acknowledged

By Steven Quay, MD, PhD

In reviewing the report from the World Health Organization on its search for the origin of the COVID virus, it's worth noting five significant and undisputed facts that any credible inquiry should try to explain. The WHO report fails to acknowledge the significance of these five undisputed facts.

The virus could have arisen either through a natural jump from its animal host, as happened in the preceding SARS1 and MERS epidemics, or through an unnatural jump from an infected animal in a laboratory-acquired infection, as happened four times previously when SARS1 "escaped" a laboratory when a scientist became accidentally infected. The closest lab to the epicenter of COVID is the Wuhan Institute of Virology (WIV), the center of an extensive research program on coronaviruses, the home to the genetically closest bat virus to the COVID virus, and the logical lab-acquired source.

Unfortunately, before almost any evidence was developed, the origin question became politicized, especially in the US, with one group saying the lab origin was a conspiracy theory and the other group calling natural origin a cover up.

This effectively shut down any open scientific debate. But behind the scenes scientists around the world have continued to study the question and develop new evidence. Though interpretations may differ, here are five salient facts about the virus that require acknowledgment and explanation.

COVID-19 wasn't smoldering in the community before the epidemic broke out, as was observed with previous coronavirus epidemics.

One of the frustrations in stopping natural zoonoses is that, despite the fact they begin with sporadic cases in a community months or even years before the epidemic breaks out, these sporadic cases are only identified in hindsight. After an epidemic has begun and blood tests are developed to identify those who have antibodies or virus in their blood as evidence of an infection, epidemiologists look for clues on how it began by screening archived blood samples in hospitals and clinics near the epicenter of the outbreak. For a natural zoonosis, this testing finds a small but measurable background of "silent" infections in the community that predate the epidemic.

In the WHO report they report that a retrospective examination of 9,522 specimens "stored at various hospitals in Wuhan, the rest of Hubei Province, and other provinces" found no evidence of the COVID virus. Given the results from previous coronavirus epidemics (1% to 4% positive), one would have expected over 200 positive specimens, not zero. This led the WHO to conclude: "the initial pandemic wave in Wuhan likely originated with a **single infected case** who developed symptoms sometime between October 26 and December 13, 2019."

These data on a single first patient are consistent with the previous four laboratory-acquired coronavirus infections and different from the last two natural coronavirus zoonoses, SARS1 and MERS.

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Neither the COVID virus, nor any close relative, has yet been found in nature, unlike prior natural zoonoses.

If the COVID pandemic followed the same pattern as the SARS1 outbreak of 2002 and the MERS epidemic of 2012, it should have left copious traces in nature, including in the animal species it infected en route from bats to people. Civet cats were identified as the intermediate host of SARS1 and camels of MERS, within 4 to 10 months of the two outbreaks. Yet 16 months after the pandemic began, and despite a far more intensive search, no trace of the COVID virus has yet been found in nature. According to the WHO, Chinese scientists have sampled “more than 80,000 wildlife, livestock and poultry samples were collected from 31 provinces in China and no positive result was identified for SARS-CoV-2 antibody or nucleic acid before and after the SARS-CoV-2 outbreak in China. This despite the prediction of experts favoring natural origin that the animal host would “probably have a high population density.”

Can you imagine how motivated the Chinese scientists were to have tested 80,000 specimens, trying to find the COVID virus in nature? The WHO needs to acknowledge the significance of its absence.

The COVID coronavirus had little genetic diversity at the outset, unlike prior natural zoonoses.

In their long journey from bats to intermediate hosts to humans, the SARS1 and MERS viruses accumulated a raft of genetic changes as they slowly adapted to two new host species. Diversity is the hallmark of this kind of natural process.

Laboratories work with genetically pure cultures, so the signature of a laboratory-acquired infection is a virus with little genetic diversity. Think of the vaccines we are beginning to receive; every single one of the tens of millions of them is genetically identical to every other one. That is a hallmark of a man-made virus.

The COVID virus, from the very beginning, had a remarkable lack of genetic diversity.

In the first description of the COVID virus in January 2020, Dr. Zhengli Shi of the WIV wrote, “(t)he almost identical sequences of this virus in different patients imply a probably recent introduction in humans.” Everyone agrees the virus looked genetically pure at the beginning of the pandemic.

The absence of prior exposure in the community, the missing animal host in nature, and the lack of genetic diversity point toward a laboratory origin for the COVID virus. But did the virus escape in its natural form, after collection from the wild, or was it manipulated in the lab before its escape? The following two facts bear on this issue.

The COVID virus’s powerful infectious trigger isn’t found anywhere in its related viral group in nature but has been repeatedly inserted into viruses by laboratory scientists, including at the Wuhan Institute of Virology.

Many viruses possess an infectious trigger called a “furin cleavage site.” The trigger makes them more infective, more transmissible, or more deadly. The COVID virus too carries a furin cleavage site. But of the one thousand known sarbecoviruses, the family to which COVID belongs, the COVID virus is one of only two viruses to have this trigger. And the other virus with a trigger had it inserted by scientists in a laboratory in the US decades ago. In nature, the trigger has never been seen in these viruses.

This absence of a trigger has been acknowledged by virologists as a problem and to solve it they have speculated a process called recombination might be the source. This is a process in which viruses acquire major new properties like this by swapping genetic material with other viruses in the rare event when both

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viruses invade the same cell. But COVID cannot have acquired from its cousin viruses a property they do not themselves possess. So how did it get its furin cleavage site?

Researchers, including those at the WIV, have long been adding furin cleavage sites to viruses in the lab. The purpose of these gain-of-function experiments, as they are blandly known, is to make existing pathogens more powerful, with the hope of then finding ways to stop their potential future human devastation. Moreover, the COVID furin cleavage site carries a genetic signature that is also not found in any known COVID virus cousins but is easily generated with laboratory kits to create nucleic acid sequences.

Gain-of-function experiments are so hazardous that they were banned in the US in 2014, though permitted again in 2017 after strong lobbying from US and international scientists. The WHO has acknowledged that WIV scientists were performing experiments on the closest cousin to the COVID virus in 2017 and 2018.

The presence of a furin cleavage site, probably artificial in composition, indicates strongly that COVID is not a natural virus but was manipulated in the laboratory.

The virus was highly adapted for infection of humans from the start, unlike prior natural zoonoses.

Another signal of lab manipulation lies in COVID's instant liking for human cells. The SARS1 virus of 2002-4 accumulated many genetic changes as it adapted to its new human host. But COVID was well adapted to humans from the get-go. This is just what would be expected if the virus had been cultured purposely in humanized mice – mice genetically engineered to carry the human ACE2 receptor, the target of COVID's spike protein. WIV researchers are known to have grown coronaviruses in humanized mice, often with lethal effect.

In the Terms of Reference for the WHO origin global study they write: “Current findings show that the virus has been remarkable stable since it was first reported in Wuhan, with sequences well conserved in different countries, suggesting that **the virus was well adapted to human transmission from the moment it was first detected.**”

The five facts described above point strongly to the escape of a manipulated virus, probably through an infected, initially asymptomatic lab worker, as the source of the COVID pandemic. Just possibly, by some convoluted path, a naturally emerging virus could produce the same set of facts. But the WHO needs to provide scientific evidence, facts, and observations, of that natural path with specificity and not just speculation of how it might have spread, as they have currently been doing.

The report cannot reject the simple possibility lying in plain sight, that the COVID pandemic broke out in Wuhan, on the doorstep of the WIV, because of a virus engineered in the WIV's laboratories.

Because without this recognition, and the public debate on whether gain-of-function experiments should continue, the next pandemic is right now being created somewhere in the dozens of laboratories around the world doing these dangerous experiments.

Maybe it's time for the moratorium on gain-of-function research to be restored before the next pandemic arrives.

Dr. Quay is founder of Atossa Therapeutics and author of “[Stay Safe](#),” a guide to surviving COVID. His scientific manuscript entitled, “[A Bayesian analysis concludes beyond a reasonable doubt that SARS-CoV-2 is not a natural zoonosis but instead is laboratory derived](#),” has been viewed over 115,000 times.