



## **The Roots of the COVID-19 Pandemic**

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**EXECUTIVE SUMMARY:** There has been a notable shift in thinking on the genomic origin and direct source of the virus that sparked the COVID-19 pandemic. While the possibility of a natural contagion has not been ruled out, the alternative of an unnatural if primarily accidental contagion has gathered momentum, and with good reason.

The question of the genomic origin and direct source of the virus that set off the COVID-19 pandemic is being addressed in parallel by both science and intelligence agencies, with each using its own tools to compile hypotheses and draw conclusions. The genomic origin of the index virus (the strain that infected Patient Zero) has been determined to be a Chinese bat virus that underwent extensive pre-adaptation to humans, including continual transmissibility, prior to infecting Patient Zero. The open question is how, where, and when such exceptional genomic pre-adaptation took place.

On the surface, it appears that in this instance the probability of human intervention (of whatever kind) is higher than naturally occurring, spontaneous evolutionary adaptation, though it is difficult to comparatively quantify those two probabilities.

Another critical issue concerns significant mismatches and errors that occurred at the Wuhan Institute of Virology (WIV) and collateral Chinese institutions both in Wuhan and elsewhere in China during the decade preceding the onset of the pandemic, as well as thereafter. A question arising from that inquiry is whether those mismatches and errors were cases of negligence or deliberate obfuscation. The latter unfortunately appears to be predominant.

The list of anomalies is long. It includes:

- scientific papers with incoherent data/findings
- unexplained gaps, inconsistencies, and contradictions
- meaningless and twisted chronologies
- illegitimate non-transparency
- elimination and distortion of records and databases
- obscuring and possible destruction of existing viruses (including the index virus) and genomic material
- pressure put on disobedient scientists, physicians, and officials
- disappearance of key persons
- expedient interchangeability between military/defense and civilian institutions (and other entities).

All this misconduct was allegedly meant to serve one principal purpose: to hamper the tracing of the roots of the index virus. These deliberate obfuscations collectively form a powerful argument in support of the unnatural contagion concept.

In further support of this argument, deliberate and systematic obfuscations about the real epidemic impact of the virus during the first months of the outbreak were recently unveiled in detail across 117 pages of leaked documents from the Hubei Provincial Center for Disease Control and Prevention (Wuhan is the capital of Hubei Province). These documents are largely marked classified and for internal use only.

No reference is made in the documents to the roots of the virus. Curiously, however, they do mention “facilities at a bacterial and toxic species preservation center.” “Bacterial” could refer to “microbial” (including viruses) and “toxic” to “virulent.”

This debate is very complicated and contains the potential for explosive revelations on many levels, but intelligence communities around the world have stayed largely silent on the matter. This is both intriguing and unsurprising. Several Western countries, as well as Russia, India, Japan, and Australia, had formed intelligence estimates as early as January 2020 but kept their conclusions quiet.

The very persistence of intelligence agencies’ silence implies that they judge the initial contagion to have been unnatural. Had they concluded that the pandemic resulted from a natural contagion, they would probably have made that conclusion public. The US administration did indicate, several months ago, that unnatural contagion was likely, but no such statement has been formally released by US intelligence. At the levels of NATO and the “Five

Eyes,” thorough intelligence estimates have likely been produced internally but they too have not been made public.

On the scientific level, as long as time passes without identification of a non-laboratory animal—with roughly the entirety of its viral genome—as the primary host of SARS-CoV-2, the argument that the initial contagion was unnatural gains indirect credibility. (It is fairly clear that the mink, while an important non-laboratory animal host, was not the direct source of the index virus.)

Independently, many scientists from various countries around the world, including Russia, maintain that the initial contagion was unnatural. They include, for example, Prof. Joseph Tritto of Italy, who is president of the World Academy of Biomedical Sciences and Technologies (an NGO founded in 1997 under the auspices of UNESCO). He has contended that:

providing [by China] the virus [that infected Patient Zero] would have meant recognizing that SARS-CoV-2 was created in the laboratory. The presence of certain genomic inserts in a virus that developed in nature could never occur. The experiments at WIV attracted the interest of the Chinese military and medical-biological sector, which deals with biological weapons... Thus, physicians and biologists who belong to the Chinese political-military sphere joined the experiments... It is reasonable to think that Prof. Shi Zhengli (the principal investigator of WIV) acted only from the point of view of scientific prestige, without however taking into account the risks in terms of security and the political-military interests that the research would have aroused. ...[T]he virus [was] created by means of genetic engineering in a military-supervised lab of WIV, and accidentally leaked.

Within the intelligence dimension, Tritto said in August that “negotiations are underway between the intelligence agencies of five countries—the US, Canada, Australia, New Zealand, and Japan—and China. Perhaps the former, during diplomatic negotiations, would be willing to defer the Chinese responsibilities of which they have proof in exchange for the possibility of obtaining the [index] virus [in order] to develop a universal vaccine.”

In terms of vaccine development, it is of note that the most productive effort in China was conducted at the Wuhan Institute of Biological Products, a facility linked to the defense establishment that has been working with SARS-like viruses at its National Engineering Technology Research Center for Combined Vaccines, in collaboration with WIV, since 2017.

Like Prof. Tritto, senior Russian scientist Prof. Peter Chumakov (a member of the Russian Academy of Sciences) said Chinese scientists at WIV had taken extremely dangerous steps during their studies of tentative vaccines, including inserts in the genome, that gave the virus the ability to infect human cells. He added: "No one excludes [the possibility] that behind the scientists stood curators who [pointed their] actions in another direction that they needed." Various Chinese military institutes outside Wuhan also worked with important SARS-like bat viruses, often in collaboration with WIV.

The independent scientific argument posed by Italian, Russian, and many other scientists weakens the analyses that support natural contagion and strengthens the plausibility of the argument for unnatural contagion. Their reasoning and concept have been disputed but not convincingly refuted.

There is also speculation surrounding a mysterious, highly virulent, pneumonia-causing bat SARS-like virus that was in all probability isolated in 2012 in China from miners but that has strangely not been registered out in the open. The WIV was involved in that affair, too. Prof. Stuart Newman, a leading expert at New York Medical College, called it "the best-sourced explanation yet of the origins of SARS-CoV-2." It is probably not the sole possible root of the pandemic virus, but it nonetheless deserves special attention as it might have been the primordial key virus.

It would be extremely difficult to incriminate China conclusively as the developer of the index virus—whether or not it was created as a bioweapon, and whether or not it was intentionally released. Doing so could cause chaotic geopolitical polarization and prompt demands for retaliation against China. Refraining from any form of retaliation would be unreasonable if there were indeed conclusive proof, but retaliation could also wreak havoc on a massive scale. A minimized blaming of China as guilty of a preventable accidental leakage of a naturally derived virus held in an academic lab is less likely to wreak such havoc, but the likelihood that this is in fact what the intelligence agencies have determined is decreasing with time. And even if that was the extent of China's error, its devastating outcome—the spread of the virus across the rest of the world, with all the attendant consequences—remains.

Beyond the question of the mode through which the initial pandemic virus came into existence is the matter of compiling all possible vital information for developing an upgraded vaccine, anti-serum, and drug. Deciphering the roots of SARS-CoV-2 is hence highly desirable for many reasons, a main one being the need to fully comprehend the intrinsic sophistication of the virus—whether natural or man-made—so as to incapacitate it. It is also essential to trace the roots of the virus completely in order to prevent the emergence of similar pathogens. In all senses (both scientific and intelligence-based), the

roots of the virus will have to be uncovered thoroughly and objectively. This will be a global task.

One oddity is the uncanny clustering of certain peculiar properties, the common denominator of which is the exceptionally amplified and/or pathogenic affinities of the index virus toward humans. The likelihood that such a clustering took place naturally in the bio-geographic region of Wuhan is faint, but the likelihood that it took place inside WIV is high in view of the type of experiments on coronaviruses conducted there for years. This is further supported by a large variety of collateral occurrences (the above-cited examples of misconduct), which should neither be ignored nor regarded as coincidental. The complicated interplay between science and intelligence is expected to objectively account for what occurred, but geopolitical forces and geostrategic vectors might hinder progress toward that clarity.

If the only thing at issue was genomic origin or the direct source of the index virus, the whole matter would be much simpler. But the combination of the two supports the likelihood of an unnatural contagion. Close examination of the combination will prove much more meaningful than separate examinations of the two issues.

The roots of the pandemic virus are schematically analyzed in the following table.

**Possible variations of the modes underlying the generation and appearance of SARS-CoV-2 in Wuhan, 2019, and their presumed likelihood interrelations**

Direct source* Genomic origin**	Natural infection	Accidental leakage	Intentional release***
Natural evolution		→	→
Evolution via serial passages#	Irrelevant	↕	↕
Genetic engineering##	Irrelevant	↕	↕

Table created by Dany Shoham

- \* The direct source represents the course through which Patient Zero contracted the virus.
- \*\* The genomic origin represents the way in which the genome of the virus that infected Patient Zero formed.
- \*\*\* Within the context under discussion, intentional release is basically regarded as unlikely at this point in time.
- # Serial passages of capable precursor virus(es) in certain tissue cultures and/or lab animals, conducted in Wuhan.

## There could be, in principle, a combination of genetic engineering and evolution via passages, in Wuhan.

The purple arrows represent ascending likelihoods (at different rates which are not indicated, except that intentional release is considered of lowest likelihood), while the green arrows represent roughly equivalent likelihoods.

Notably, each of the three variations related to accidental leakage (reading the table vertically) has two alternative sub-variations: either that the virus was the subject of academic study or that it was explored as a potential bioweapon. This is still an open question. A definite precursor virus has not yet been found for any of the mentioned variations and sub-variations (10 in total). New scientific or intelligence findings might clarify the assessment summarized in the table. Only time will tell.

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