Anthropogenic origin of the SARS-CoV-2 pandemic

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Witch hunt or planetary danger?

An analysis by comparison with the antithesis

It was February 2020, and, like everyone, I couldn't help but wonder if the first rumors circulating about the origins of the virus that was terrorizing the world had any foundation. At first I thought it was practically certain that we had been placed "simply" in the face of the pandemic event that, at least with a centuries-old cadence, nature presents to the now not so much helpless human beings, then, after a more in-depth evaluation, I found "forced" to have to change my mind.

This article was born after an intense exchange of ideas with international colleagues that lasted more than a year, and, having reached my very personal conclusions, I finally decided to make a general picture of what I learned by acting with the perspective of analysis by comparison with the antithesis, a way of proceeding that Karl Popper explains in detail in his work "Misery of historicism":

<< If we are not critical we will always find what we want: we will seek and find confirmations, we will look away from everything that could be dangerous for our favorite theories and we will not see further. In this way it is all too easy to obtain what appears to be overwhelming evidence in favor of a theory that, if approached critically, would have been refuted. >>

The article does not aim to prove that things went in an exact way, it only has the intent to open the field of investigation to any possibility not currently discarded, as science would have a duty to do. When you read somewhere that the laboratory theory is officially disproved by mainstream science (and there are plenty of newspapers and online media that do), you are faced with a complete lie. Currently, whether one theory or another is more likely, none of the hypotheses can be canceled from the spectrum of investigation, and those who want to impose a unilateral vision are further polluting a debate already severely poisoned by politics and economic interests. The purpose of this text is, therefore, to investigate all the main criticisms leveled at the notorious (as much denigrated) hypothesis of SARS-CoV-2 leaking from one of the Wuhan laboratories using all the scientific and political knowledge at our disposal, to evaluate, therefore, if the theory should hold up or less. This document does not pretend to be a scientific study, but a more neutral journalistic investigation addressed with all the scientific and historical means at our disposal, without any ideological and / or political turbulence. Ultimately, I would like to specify that none of the elements included in this article have the will to harm in any way the Chinese community, a population with a very different nature from that of the dictatorial regime that governs it.

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We thank all the great experts in the field who, with their public and private commitment, have made possible the creation of this article, among them, I feel obliged to mention: Karl Sirotkin, Dan Sirotkin, Yuri Deigin, Rossana Segreto, Alina Chan, Roland Wiesendanger, Steven Quay, Nikolay Petrovski, Richard Ebright, and the entire team of independent Drastic researchers without whom none of this would probably have been possible.

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The key question to ask, therefore, is: is the theory of laboratory error rationally framed as a valid theory of investigation or should it be relegated to a mere conspiracy theory? Below is an analysis of all the main criticisms:

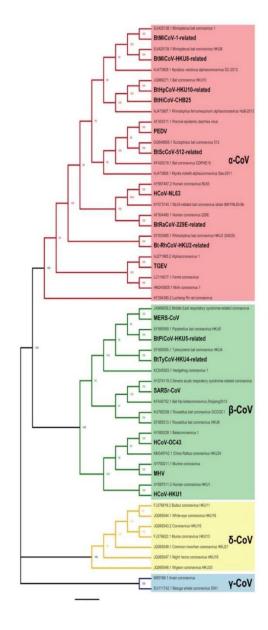
• <u>Critique # 1</u>: In history there have been several spillovers, jumps of species of a virus from animal to man. A leak from a laboratory therefore has very little chance of having occurred.

Analysis: Spillovers are common phenomena in human history, only the last century has shown several, more or less harmful, this does not mean that infections acquired from laboratory **(LAIs)** activity have not become common for a century now. There are **313** documented, and the Asia-Pacific area is the one that sees a higher frequency of this type of incident (0.8 every 15 months)¹, including the laboratory "leaks" of **SARS** that occurred in Beijing between 2002 and 2004^{2} .

Based on a few elements we can formulate an efficient statistical survey³:

- 1. Bats and other animals that harbor coronaviruses are found practically all over the world;
- 2. Wuhan's population is 11 million;
- 3. The global population is 7 billion.

From these simple elements we can evaluate the possibility that just one person from Wuhan would have been patient zero: about 1 in 630. But we can amplify the survey. We now evaluate that in 2018 the WHO announced a discussion list of priority diseases pandemics $\frac{4}{2}$, which included Ebola, Rift Valley Fever, and other viruses. In addition to these known diseases, WHO asked the experts to also name a currently unknown candidate. Drss. Shi Zheng-Li, director of the Wuhan Institute of Virology, proposed: << Disease X could be a communicable infectious disease caused by a new coronavirus originating in bats>> $\frac{5}{2}$. In other words, it did not more narrowly predict that the next pandemic would potentially be caused only by an alpha or betacoronavirus (the only ones known to infect humans were these 6: HCoV-NL63, HCoV-229E, MERS, SARS, HCoV-OC43 and HCoV-HKU1), not to mention the possibility that a possible new pandemic coronavirus would not emerge outside the preexisting branches of the phylogenetic tree (such as **MERS**, a species totally unknown before starting to infect humans), but,



Phylogenetic tree of Coronaviruses (Li et al.)

coincidentally, **SARS-CoV-2** emerges exactly among the *species related to SARS*, those that Drss. Shi Zheng-Li studied and manipulated extensively from 2005 to 2019 with **18 studies** easily found by searching her publications online.

Considering that each species of Alpha and Betacoronavirus had exactly the same chance of spreading to humans, the odds of a virus specifically of *the SARS-related coronavirus* species starting a zoonotic pandemic was **1 in 28** (and since there are certainly many others coronavirus species to be discovered, the possibilities are actually even more slim). So, if we accept the above assumptions as reasonable, the odds that **Wuhan** would have been the site of a natural outbreak for a *SARS-related coronavirus* is obtained by multiplying **1 in 630 by 1 in 28**. The result is **1 in 17,640**, quite notable for not taking it into account.

 <u>Critique 2</u>: The virus shows no obvious signs of genetic manipulation, so it cannot be artificial.

Analysis: The first study to pass the controlled review on the origins of the virus is "Proximal origins of SARS-CoV-2"⁶, it marked a milestone in the matter because it declared "unlikely" that SARS-CoV-2 has been manipulated in the laboratory only because it is not possible to notice evident signs of reverse genetic engineering, techniques that scientists know very well are not the only methods to obtain a new virus (with natural characteristics) in the laboratory. To give an example, we cite Prof. Nikolai Petrovski, an internationally renowned immunologist, who explains in an interview² how a "forced zoonosis" in vitro is extremely feasible: <<The analysis of the genomic sequences does not reveal genetic engineering interventions that artificially manipulated the virus. This, however, does not exclude human intervention on the virus. For example, one can take a noninfectious human bat Coronavirus and force its transformations by cultivating it with cells that express the human **ACE-2 receptor**, simultaneously increasing the strength of its bond with this receptor and reducing that with the ACE-2 of the bat.>> Andersen's article published in Nature later presses on the question of the lack of public knowledge of the "backbones" from which SARS-CoV-2 could have been created, assuming that the Asian laboratories have transparently communicated every virus discovered in their numerous travels, which we know has not been done. To verify this, it is enough to observe the non-sequencing of the 8 bat coronaviruses with disturbing analogies with SARS-CoV-2 found in the Mojang mine⁸ after the death of 3 miners with symptoms similar to Covid-19, the only one of these known to us is **BatCov / RaTG13** (and there are considerable doubts about its correct sequencing due to various anomalies⁹). But there are also other serious forms of extreme lack of transparency of Chinese researchers, such

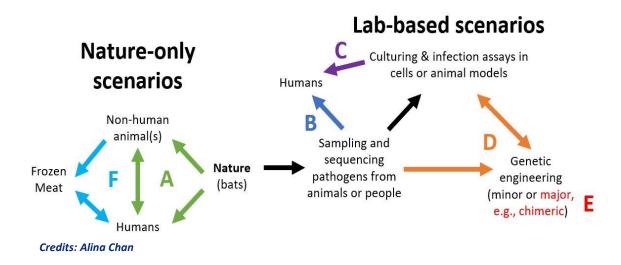
as the disappearance from the web of a **database** containing more than **22,000 virus sequences**. This database was presented in an article¹⁰ by the team of director of the Wuhan Institute Of Virology Shi Zheng-Li. The article and the correspondent database <u>batvirus.whiov.ac.cn</u> disappeared from the scientific journal's webpage in **September 2019**, but it was possible to assess that the database was modified one last time on **December 30**, the same day Chinese scientists said they had identified the new virus. The other articles published by the magazine (with the doi - digital object identifier - previous and next) are, however, still fully available.

But is **Andersen**'s article supporting the zoonosis theory the only one to have undergone **peer review** and then be published? No, absolutely not, and the others clearly open the field of investigation towards the laboratory:. 1) <u>The genetic structure of SARS - CoV - 2 does not rule out a laboratory origin</u> - by Yuri Deigin and Rossana Segreto

2) <u>Tracing the origins of SARS-CoV-2 in coronavirus phylogenies - by Erwan Sallard,</u> José Halloy, Didier Casane, Etienne Decroly and Jacques Van Helden

3) <u>Might SARS - CoV - 2 Have Arisen via Serial Passage through an Animal Host</u> or Cell Culture?

| | Natural spillover (bats or other animals to humans) A | Lab/research-related incident B,C,D,E | Cold chain trade inside China (not international trade) F |
|---|--|--|---|
| Do top experts think this is a plausible hypothesis to be investigated? | Yes. | Yes. | Yes. Mainly the WHO-convened expert team. |
| Is there a well-documented precedent of a coronavirus infection being acquired this way? | Yes, several times in different countries. Close relatives to SARS2 have been found in nature. | Yes, in different labs in different countries. Close relatives to SARS2 have been collected and studied in labs in China. | No. |
| Is there direct evidence of this being how Covid/SARS2 emerged? | No. No original animal source of SARS2 precursor or siblings reported by China or any other country. | No. No SARS2 precursor reported in the labs in China or any other country. | No. No original source of frozen foods reported to have SARS2 precursor. |
| Does the location of Wuhan make sense as the first detected site of SARS2 emergence? | Possibly, if the spillover occurred where SARS2-like viruses are found hundreds of miles away and the original virus transmitted to and resulted in an outbreak only in Wuhan. Wuhan was <u>not</u> a SARS spillover zone. | Yes, there are at least 2 labs in Wuhan collecting and studying bat coronaviruses collected across China. One hosts presumably the largest collection of SARS-like virus sequences in the world. | Possibly, if transmission of the original virus from the frozen food, leading to an outbreak, only occurred in Wuhan and not in any other city including the original source of the frozen food. |
| Do any available data rule out the hypothesis? | No. | No. | No. |
| Are all available data consistent with the hypothesis? | Yes. Furin cleavage site could have arisen naturally. | Yes. Furin cleavage site could have been engineered. | Yes. |

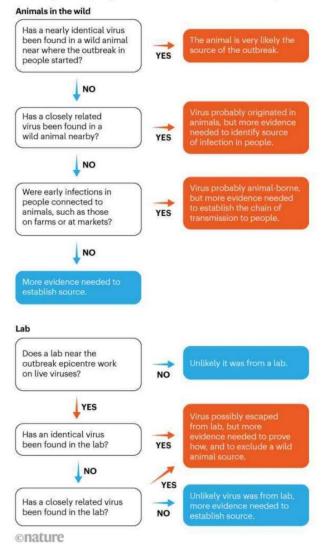


<u>**Critique 3**</u>: If the virus is natural, there is no possibility that it reached the population through humans.

Analysis: In addition to what was said above about the possibility that the virus may also be the result of human ingenuity, the virus does not necessarily have to be artificial to have brought been to the human population through human error. It should be borne in mind that the researchers of the Wuhan facilities have always been in close contact with the areas from which SARS-CoV-2 derives its phylogenetic origins. A video¹¹ published by the broadcaster CCTV-13 (and currently no longer available) shows how the us researchers of the Wuhan Institute of Virology went to the Yunnan territory to take samples and guinea pigs, in some moments it is possible to see them in action without using gloves or masks, even ending with being injured or hit on the skin by organic waste

HOW TO TRACE A VIRUS TO ITS SOURCE

Tracing the source of a virus spreading in people requires investigating a host of questions, many of which are difficult to answer definitively.



from bats. The footage was shot 2 years before the outbreak of the pandemic. Furthermore, as exposed by alarming **US cables** from 2018, the Wuhan research facilities themselves were quite dangerous due to the obvious security deficiencies¹². The same Nature magazine, months after the publication of "The proximal origin of SARS-CoV-2", Has published an article where the possibility of a laboratory leak is accepted¹³ (see image above). It should also be remembered that although the Wuhan Institute of Virology has the ability to use **BSL-4** security technology, all the SARS studies conducted in previous years were carried out in **BSL-2/3** (as can be verified by the related studies in online public archives). This allows us to understand that if someone had been infected in a completely natural way in an exploratory mission in **Yunnan** or in a laboratory, the virus would have had the opportunity to spread to the population and possibly already begin to mutate to improve its affinity to mankind. This would explain why the place of origin of the known ancestor hosted by bats *Rhinolophus Affinis*¹⁴ 2000 kms away from Wuhan was not the site of the first known outbreak after a possible spillover, but instead Wuhan was (at a very short distance from one of the main coronavirus research facilities worldwide).

 <u>Critique 4</u>: The cleavage site of furin present in the SARS-CoV-2 genome can also develop through natural selection.

<u>Analysis</u>: It is possible to develop it both naturally and artificially, but, as emerged in the <u>revised study by Rossana Segreto and Yuri Deigin</u>, there are several suspicious elements. The other known **betacoronaviruses** do not have a **furin cleavage site**, furthermore, in **SARS-CoV-2** it does not appear to be in frame with the rest of the sequence when compared with the sequences of **MP789** (pangolin coronavirus) and **RaTG13** (the virus most closely related to SARS-CoV-2 known).

Pangolin MP789 GAGICASYOTOTNS----R S V SSXA ggt gca gga ata tgt gcc agt tat cag act caa act aat tca --- --- cgt agt gtt tca agt cna gct att att (nt 23527): CASYOTOTNS-R S V RaTG13 G A GI A S (nt 23543): ggt gca gga ata tgc gcc agt tat cag act caa act aat tca --- --- --- cgt agt gtg gcc agt caa tct att att GAGICASYQTQTNS<mark>PRRA</mark>RSVA SARS-CoV-2 S O (nt 23561): ggt gca ggt ata tge get agt tat eag act eag act aat tet eet egg egg gea egt agt gta get agt eaa tee ate att Black = common for all 3 = unique to SARS-CoV-2 Red Green = unique to RaTG13 Blue = common difference of RaTG13 and SARS-CoV-2 from MP789 **Out-of-frame cleavage site (Deigin and Secret)**

Therefore, it is possible to exclude that such insertion could have originated from polymerase slippage or from releasing and repriming, since insertion mutations

generated by these mechanisms have been postulated to maintain the reading frame of the viral sequence. The possibility that the furin cleavage site may have been acquired by recombination has recently been questioned by **Seyran et al.**¹⁵ because the **SARS-CoV-2** spike protein appears to lack further recombination events in contrast to the pattern of recombination of other **coronaviruses**.

• <u>**Critique 5**</u>: WHO has investigated the matter and evaluated the laboratory hypothesis extremely unlikely, it makes no sense, therefore, to investigate further.

Analysis: The WHO has shown this year a notable lack of strength against the Chinese regime, one of its top foragers after the US government's funding cut¹⁶ After having passively facilitated the Chinese attempt to hide the epidemic (which later became a pandemic) causing important delays in evaluation resulting in enormous worldwide damage, their shortcomings were publicly highlighted and they only replied that they had done everything possible $\frac{17}{2}$. After a year, an investigation into the origins of the virus began with 17 world experts (including Peter Daszak, founder of Shi Zheng-Li's studies of bat sars-related viruses with subcontracts of \$ 200 million via the EcoHealth Alliance company) who, after two weeks of guarantine, only had the opportunity to take a two-week guided tour in which high-ranking Chinese officials (mostly politicians) wisely chose what to show them and, above all, how. The result of the investigation was, therefore, perfectly matched with the narrative desired by the regime: <<*SARS-CoV-2 probably* reaches Wuhan via the cold chain>> $\frac{18}{18}$, a possibility that the **WHO** had always rejected before and that a few days after the end of the investigation again considered unlikely, also reopening the possibility of a laboratory leak¹⁹. On March 5, the same organization, simultaneously with the release of a letter from 26 scientists for an independent investigation²⁰, communicated to the world that there will no longer be a provisional report on the investigation carried out. In light of what has been observed, it would be natural to evaluate the entire organization as totally unreliable on the SARS-CoV-2 issue for reasons of mere economic-political nature. Today, more than ever, a truly independent

• **<u>Critique 6</u>**: The Chinese regime has no reason to hide a possible laboratory error.

international investigation is needed.

Analysis: On the contrary, China has every possible reason to hide an event of this magnitude, and as a nascent superpower with roots now spreading everywhere, it has all the means to do so. As an **authoritarian dictatorial regime** that it is, China is not afraid to intimidate, threaten and strike anyone who dares to hinder it, remaining, publicly, within the limits of international diplomacy. A damage of this magnitude to all nations of the world, even if due to a trivial error, would crack all sorts of international agreements and strongly undermine the foundations of the iron communist dictatorship, not to mention the damage that would result in the imperialist process currently in full development. This event is perfectly similar to the case of **Chernobyl**, in which the communist regime of the **USSR** carried out various misdirections in order to try to hide what they had caused to themselves and to the world. The **1986** phenomenon, however, was of nuclear nature, so it was extremely difficult to cover its evident traces, unlike what happens today with an invisible pathogen whose secrets are hidden in **databases** that are no longer viewable and in sequences of genetic code unreadable for the majority of civil society. Only in **1990**, thanks to the journalist **Alla Yaroshinskaya**, did we learn of the enormous attempts at cover-up carried out by a regime aware that a similar error could have decreed its end, as indeed happened a short time later.

The possibility that China has "conspired" in order to save face (and, therefore, its hegemonic power), seems to be, for a large part of the press, an element that can only be relegated to television imagery, rather than a plausible phenomenon, such as if the dictatorships have not always implemented all forms of lies in human history in order to have the best possible propaganda results with all the authoritarian means at their disposal.

• <u>Critique 7</u>: Even if a lab were involved, taking it into consideration would do no good.

<u>Analysis</u>: Whether Chinese laboratories are involved in the SARS-CoV-2 pandemic or not, governments should use the occasion as a time for deep reflection on the safety of gain-of-function (GOF) studies. These experiments are aimed at enhancing epidemic / pandemic agents making them more aggressive, more contagious, or contagious towards living beings to which they were previously harmless. This type of research would have the noble aim of developing new prevention techniques (especially vaccines) in the event that a similar pathogen presents itself to the world. This type of applications, however, hides the enormous risk of putting into circulation the dangers from which in principle one would have wanted to safeguard, creating, instead, a real "self-fulfilling prophecy". The debate has inevitably divided the scientific community in a concrete way given the evidence that these technologies can lead to the spread of real weapons, usable both for terrorist / war purposes, but also casually spread for simple errors that are statistically always present. The issue arose in 2011, when the NSABB suppressed two studies involving modified H5N1²¹ viruses to allow for airborne transmission from ferret to ferret. Scientists warned of the danger that malicious actors could replicate the work to deliberately cause an epidemic in humans. After a long debate, the studies were published in full in **2012**²². Subsequently, in **2014**, the United States was overwhelmed by various biosecurity dangers²³: dozens of workers at the Centers for Disease Control and Prevention (CDC) were exposed to anthrax, vials of smallpox virus were found abandoned in an **NIH** warehouse, the CDC unwittingly sent samples of the influenza virus hybridized with the H5N1 virus. The accumulation of these events led to the signing of the **declaration by 200 scientists** for the cessation of these experiments²⁴ <<Until there has been a quantitative, objective and credible assessment of the risks, potential benefits and mitigation opportunities risk, as well as a comparison with experimental approaches>>. In the same year, the **Obama commission** placed a ban on federal funding for any new gain-of-function experiments²⁵. In **2016**, the NSABB published a set of recommendations for evaluating gain-of-function research²⁶, which outlines the criteria for evaluating potential benefits and risks. Michael Selgelid (Monash University, Melbourne, VIC, Australia) writes to The Lancet Infectious that the questions to ask are: << How likely is research to be beneficial? How big would these benefits be? How likely is research to cause harm? And how big would these damages be?>>. Moreover, he adds: << The evaluation of the risk-benefit ratio is not an exact science, nor is it perfectly objective: most of the time it will be very difficult to say what constitutes a situation in which the benefits outweigh the risks>>. In **2017** the **Trump commission** lifted the ban²⁷,

Conclusion

Why should a really good theory be hoaxed by people who have no specific interest in opposing it? To answer, we can use a perfectly themed analogy with the biological argument: it can be deduced that a psychological mechanism very similar to the methods of action of our immune system is involved. What i mean? In recent years we have been overwhelmed by an avalanche of fake news, social media have given prominence to the most disparate and imaginative theories, especially in the economic, political and health fields. I challenge anyone to never have come across an article on alternative medicine, from the now very common homeopathy to unlikely cures for any type of pathology (from the most banal to cancers). Such bombardment, slowly wearing out the public, sparked a visceral reaction of the masses. A real "antibody" repulsion to any form of information based on the "I'll tell you what they don't tell us" model. Impossible to blame anyone, indeed, thank God it happened. This, however, has led to the development of a sort of blindness towards those meager, more or less hidden, possibilities that rarely reveal themselves on the modern information scene. The hypothesis of the laboratory origin of SARS-CoV-2, has therefore undergone the same exact treatment of all the circulating junk information, although there are currently more scientific studies published (after having undergone the difficult process of months of peer-review) that concretely admit its possibility as a valid scientific theory. Let's add the **politicization** of the phenomenon.

To conclude, currently a fairly shared opinion in the scientific world is that there is a strong need for an international investigation carried out independently by China, the WHO, and any entity that is liable to conflict of interest. We therefore ask the states to act compactly to investigate the phenomenon, for the good of science, for the future of humanity.



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