

Possible release of the coronavirus from a Chinese laboratory

By Javier

A crude translation from the original in Spanish [here](#).

April 20, 2020

This content is almost 2 years old

I am not one of those who subscribe to conspiracy theories for free, but it is a fact that conspiracies occur when the interests are large enough. Is it impossible that the SARS-CoV-2 causing the COVID-19 pandemic is a virus out of a Chinese laboratory? The answer is clearly no.

There is a real, unproven possibility **that what is happening to us is self-inflicted**. In this article I will present the evidence and opinions in favor that the SARS-CoV-2 virus causing the COVID-19 pandemic accidentally escaped from a Chinese microbiology laboratory due to poor safety measures. There is strong pressure for such evidence not to be presented, but it is not for me to determine whether such evidence is sufficient or not. What I do believe is that **the evidence needs to be investigated openly to determine the origin of the virus**. The problem is that when the consequences of something are tremendous, a conspiracy of converging interests is self-organized to hide it. If China were responsible for the release of the virus from one of its laboratories, even if by mistake, the economic claims would be impossible to assume even by the world's second largest economy and the consequences would be impossible to foresee. The maintenance of the "status quo" and the pressures then become unbearable to silence and discredit those who question the official truth.

But in this blog under anonymous name and free of any pressure only the scientific truth is worshipped, and I give a damn about the qualifiers that apply to me. If I have to say that the climate crisis does not exist because science has not proven it, it is all based on computer models, and its forecasts have been failing for 40 years, I have no problem saying it, and if I have to say that there are enough indications to merit an international investigation to determine if SARS-CoV-2 was accidentally released from a Chinese laboratory, I have no problem saying it either.

1. The background to 2015

As I mentioned in paragraph 5 of the February 25 article "[Coronavirus Scenario 2: Enemy at the Gates](#)" (too bad the government and its experts didn't read it), **the hypothesis that the virus may have escaped from a lab is not far-fetched**.

In November 2015, an article was published in Nature Medicine describing the creation of a chimera virus in China in which they put the SARS receptor on a coronavirus adapted to infect mice and showed that the chimera virus efficiently infected human cells. [A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence](#)

A week later, a commentary in the journal *Nature* highlighted the risks of this type of research. [Engineered Bat Virus Opens Debate on Risky Research](#)

*... other virologists question whether the information obtained from the experiment justifies the potential risk. Although the extent of any risk is difficult to assess, Simon Wain-Hobson, a virologist at the Pasteur Institute in Paris, notes that researchers have created a new virus that "grows remarkably well" in human cells. "If **the virus escapes, no one could predict the trajectory,**" he says.*

Although the article in question does not indicate where the experiments were conducted, only that they were done under P3 biosecurity, among the signatories of the study were **two researchers from the Wuhan Institute of Virology**. This shows that in 2015 there were researchers in Wuhan working on altering coronaviruses to make them more infectious in humans for research purposes.

Interestingly, the editor of *Nature* added a month after some of us began to air this precedent the following note to the article:

*Editor's note, March 30, 2020: We are aware that this article is being used as a basis for **unverified theories** that the novel coronavirus that causes COVID-19 was designed. There is no evidence that this is true; Scientists believe an animal is the most likely source of the coronavirus.*

Why do the editors of *Nature* take sides with the animal hypothesis? It is a hypothesis that has not been verified either. And they talk about scientists as if they were a group in agreement, but the truth is that there is disagreement among scientists, as we will see. But *Nature* also took sides on anthropogenic versus natural climate change, and it's a serious problem when editors of major journals take sides in scientific disputes, for their power to make and break careers and politically direct scientific research while distorting scientific debate by presenting fallacious science by consensus.

2. Proximity to the focus

On February 6, two Chinese researchers associated with two Wuhan universities uploaded a paper to the ResearchGate scientific repository titled "**The Possible Origins of the 2019-nCoV Coronavirus**". The article, which had not been reviewed, received a digital object identifier (DOI: 10.13140/RG.2.2.21799.29601) and was assigned the article number 339070128. In that very short article, **the researchers discussed the possibility that the virus had been accidentally released** from a laboratory, based on the fact that according to municipal reports and the testimonies of many residents and visitors of the Huanan market, bats had never been a food source in the city and were not sold in that market. Since it was late in the fall and the market is in a densely populated area the likelihood that the source of the virus was a bat that had flown to the spotlight is negligible. According to the article, either the virus was in another animal unknown on the market, or it had been released from a nearby laboratory.

The Chinese scientists highlighted the presence of **two nearby laboratories where bat coronaviruses were worked**, the Center for Disease Control and Prevention of Wuhan, which is less than 300 meters from the Huanan market and what they provided a Google map (see figure 1), in one of whose laboratories work with bat viruses captured hundreds throughout China, and the other the Institute of Virology that is 12 km from the market, where as we have seen there were researchers working on the design of chimeric coronaviruses endowed with the capacity to infect humans.

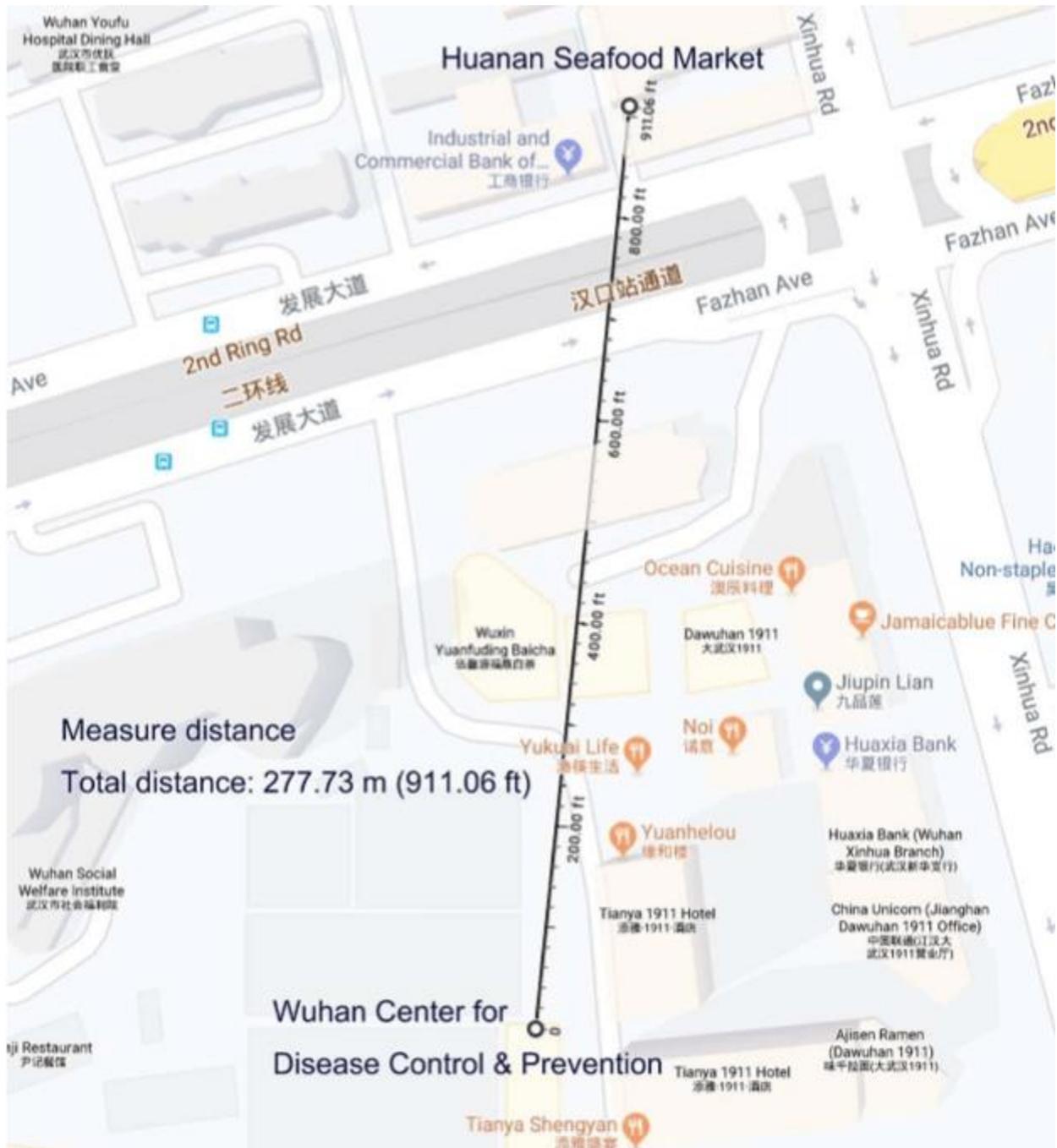


Fig. 1 Map of the vicinity of Huanan Market, important focus of the epidemic, where the Wuhan Center for Disease Control and Prevention is also located at a distance of less than 300 meters. Source: [The possible origins of the coronavirus 2019-nCoV.](#)

The work concluded that in addition to a possible natural origin by recombination and intermediate animal guest, it is most likely that **the killer virus** (as is, killer coronavirus) had **originated in a Wuhan laboratory**. After having a strong impact on the network, the work was picked up by some media that do not fear the Chinese government, such as the Daily Mail, which published the following article on February 13: [Did the coronavirus originate in a Chinese government laboratory? Scientists believe the deadly disease may have started at a research facility 300 yards from Wuhan Fish Market](#)

The work was removed from ResearchGate by one of the authors, as can be seen by searching for the article through its doi identifier: <https://doi.org/10.13140/RG.2.2.21799.29601>

If the authors are not chopping stone in a Chinese re-education field, they will be looking for a way to apologize for daring to suggest something similar. However the internet does not forget and the article can be found on alternative sites like [this one](#).

3. Neither the Huanan market nor the pangolins

One of the problems is that the "official" explanations have serious holes. **There were no bats in the Huanan market**, and yet SARS-CoV-2 is 96% identical to the CoV RaTG13 of bats and clearly belongs to a cluster (group) of bat coronaviruses (see Figure 3 in my article "[Everything you ever wanted to know about the coronavirus...](#)").so an intermediate animal is needed for a natural origin that for the moment remains unknown.

On March 30, an article was published in Nature by Chinese researchers proposing that the origin of SARS-CoV-2 was in [pangolins: Identifying SARS-CoV-2 related coronaviruses in Malayan pangolins](#). The problem is that the sequence identity is only 85.5 to 92.4%, too low to be convincing when it is already 96% to that of bats.



Fig. 2 Why would anyone eat this charming and endangered little animal?

And a major paper published in *The Lancet* on February 15 analyzing the 41 patients admitted to Wuhan's Jin Yin-tan hospital before January 2, 2020, who were subsequently confirmed to be positive for SARS-CoV-2 showed that not only **the first of the cases**, which had developed symptoms on December 1, **it had no relation to the market** or to those subsequently infected, but 33% of early patients had no relationship with the market. [Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China.](#)

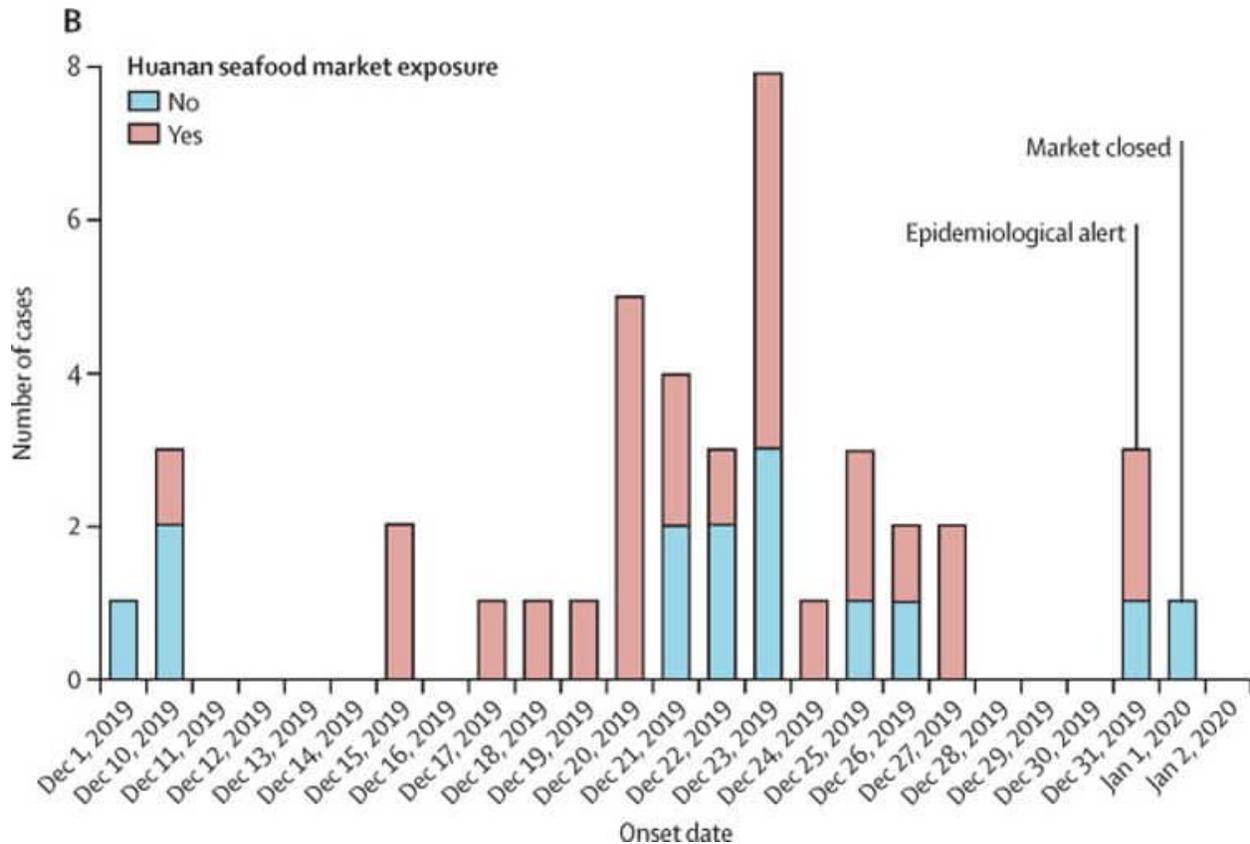


Fig. 3. Relationship with the Huanan market of early patients. The first case of the hospital and two of the next three were unrelated to the Huanan market. Source: [The Lancet](#).

The inevitable conclusion is that **the virus had been on the loose in Wuhan since November** and someone infected took it to the market where it was a focus of **secondary infection** in mid-December.

Specialists in virus evolution agree with this interpretation. **Andrew Rambaut**, from the University of Edinburgh, analyzing multiple sequences from different patients has traced the probable origin of [the virus in humans in](#) mid-November, and his [opinion](#) is that the virus infected its first human no earlier than October 30 and no later than November 29. For all these **reasons, the Huanan market hypothesis has been discarded** by experts.

4. Three possible origins

Kristian Andersen of the Scripps Research Institute in La Jolla, California, and colleagues discuss in a March 17 [paper](#) the three possible origins of the virus. With respect to its closest relatives, SARS-CoV-2 **presents an insertion of four amino acids** between the two subunits of the protein that forms the spines of the virus that constitutes a [poly-basic] cutting site for various proteases such as furin. This cut-off site, which is not present in the most similar viruses, does exist in other human coronaviruses such as HKU1 and in several influenza viruses where its presence has been shown to be **associated with high pathogenesis** in birds. This sequence has also

been shown to be acquired by viruses after repeated passes in culture or between animals.

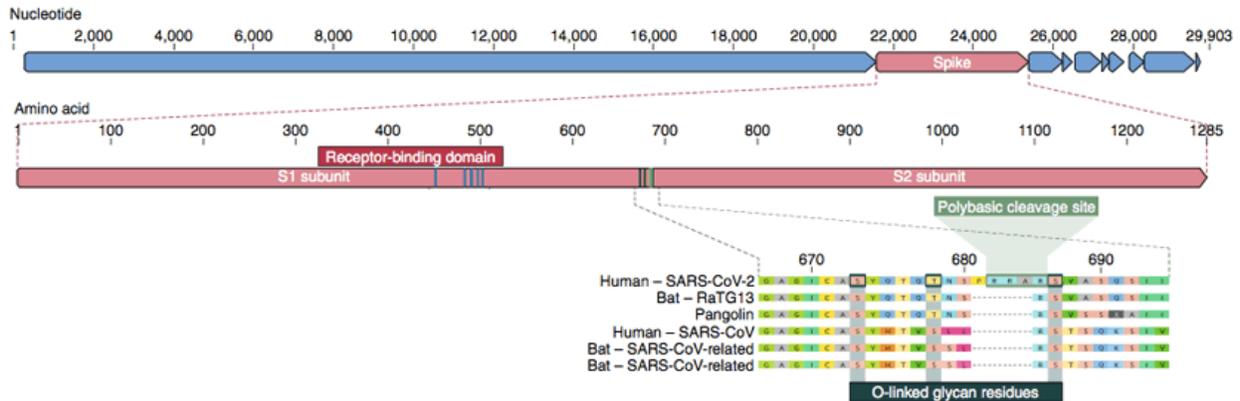


Fig. 4. Features of the spine protein of the human coronavirus SARS-CoV-2 and other related coronaviruses. The insertion of the poly-basic cutting site for proteases is highlighted. Source: [Andersen et al., 2020](#).

Andersen and colleagues support that to acquire that cut sequence that its relatives do not have, the virus has had to have one of the following origins:

4.1 Natural selection in an animal host before jumping to humans. We return to the unknown animal that cannot be from the market where the secondary focus began in December. It is possible and it is the explanation that has the most support.

4.2 Natural selection in humans after jumping from an animal. This requires that the virus has replicated and infected numerous humans without causing severe symptoms (cryptically) before acquiring pathogenicity with the recombination cut-off sequence with another virus. I consider this explanation much less likely since it requires assuming that high pathogenicity comes from that sequence of which there is no evidence. In fact, the SARS-CoV-1 responsible for the 2003 epidemic does not have that sequence and is much more lethal than the SARS-CoV-2 responsible for the current pandemic. But if so, there would be traces of it, since the virus before mutating would have spread and would be detectable a posteriori in stored samples as it happens with coronaviruses that cause colds. It could also be determined whether by losing that sequence the virus loses its high pathogenicity in laboratory experiments.

4.3 Artificial selection by multiple passes in culture and accidental release from a laboratory. Andersen et al., consider this explanation unlikely because it would require several changes to occur from a SARS-like virus to produce the modifications found in SARS-CoV-2, or that the original virus already had some of them, however it says that an original virus more similar to SARS-CoV-2 has not been described in the literature, nor has a study been published that required prolonged passes in human cells expressing the ACE2 receptor.

This explanation, however, is unconvincing, because **we know that the Chinese have been intensively researching bat viruses** in the Wuhan centers and we have no idea of the sequence of all those viruses or their resemblance to SARS-CoV-2. What we can be absolutely sure of is that if one of those viruses was SARS-CoV-2 or a first cousin the

Chinese now are not only not going to say it, but they are going to bury the evidence and who knows if the scientists responsible for it. In China, the authorities shoot you in the back of the head for trafficking drugs.

5. It is highly unlikely that this is a design virus. The retracted Indian article

On January 31, a group of researchers from the Indian Institute of Technology in New Delhi uploaded an unreviewed paper to bioRxiv titled: [Mysterious similarity of unique inserts in the spine protein of 2019-nCoV to gp120 and HIV-1 Gag](#). In the article they compared the sequence of this protein (figure 4) between SARS-CoV-1 and 2, and found 4 insertions, the fourth being the cutting site that we have talked about in the previous section (see figure 4). They then put a table **comparing these insertions with sequences chosen from two different HIV-1 proteins** belonging to certain subtypes of the AIDS virus from patients in Thailand, Kenya, and India.

And of course, they rolled it brown. Since these two viruses infect different types of cells, everyone interpreted that the mystery was only solved if someone had put those sequences there, that is, **their thesis implies that the virus responsible for COVID-19 was of design**, and they rained criticism. They were soon made to know that those short sequences are found everywhere among viruses and that there are over a million HIV-1 sequences, so choosing certain subtypes is malpractice. At the same time, all the conspiracy websites gave them absolute credit and pointed out that Indian researchers had shown that the virus had been released after sequences of the AIDS virus were inserted into it. **The authors retracted the paper within a few days**, which for an unpublished paper (bioRxiv is a repository, not a journal) is extremely rare, saying it was a preliminary study and they would do a revised version. Frankly, I doubt they will republish anything about it.

In what must be a world record five days after the Indian paper appeared, the **Chinese had a paper debunking it** submitted and accepted by the journal Emerging Microbes & Infections: [HIV-1 did not contribute to the 2019-nCoV genome](#). Apart from doing a better search, which identifies those four sequences in all kinds of organisms and viruses, the article of the Chinese destroyed the main argument of the Indians, because the coronavirus that most resembles SARS-CoV-2 is the CoV RaTG13, as we have already said, which was obtained from a bat in Yunnan (China) in 2013, and **in it are present three of the four insertions**. Of the **four, only the protease cutting site (fourth insertion) is actually new** and is very common in other sequences of various origins. It is the most widespread opinion among experts and I share it, that **SARS-CoV-2 is the product of selection (or an accident), not human engineering**, because if it had been designed based on the knowledge we have of coronaviruses it would not have been designed that way. One can only design what one already has in one's head. We didn't know what SARS-CoV-2 was capable of until we've seen it in action and studied it, so we couldn't have designed it. Which is not to say that the virus didn't come out of a lab, just that **it's highly unlikely that it was manufactured on purpose**, neither by the Chinese nor by anyone. The changes it presents in its sequence are consistent with a natural

evolution. At least I don't think anyone manufactured it on purpose (they wouldn't know how to do it as it is) let alone that it was released on purpose. What a coz has hit us all the bug, Chinese included.

6. Luc Montagnier's hypothesis of accidental design

Luc Montagnier is the French scientist who led the team that **isolated the HIV virus from an AIDS patient for the first time in 1983**. The discovery was embroiled in a prominent three-year dispute with Robert Gallo's American laboratory, which also claimed responsibility for the discovery. The dispute, behind which was the patent money, was resolved in a personal meeting between François Mitterrand and Ronald Reagan in 1986 in which they agreed to share merits and rewards. At that time I followed the subject with great interest because of my concern about pandemics and for me it was clear that reason accompanied Montagnier's group. In 1993 it was proved without a doubt that the Gallo virus came from Montagnier's laboratory and when in 2008 the Nobel Prize for the discovery was awarded **it was given to Montagnier** and a researcher on his team, ignoring Gallo's contributions.

But Luc Montagnier's immense scientific credit has been squandered over time, which is a real shame. As Le Figaro recounted in his article ["The Slow Scientific Collapse of Professor Luc Montagnier"](#) began to damage his reputation after his participation in the 2009 anti-scientific documentary "House of Numbers: Anatomy of an Epidemic", where he exposed that AIDS infection could be avoided with a good immune system, and that poor diet and oxidative stress were responsible for Africa's problem with AIDS. The problem is that, beyond the fact that a good immune system never harms, there is no data that confirms such a pilgrim hypothesis. The HIV virus is a specialist in bypassing the immune system. In 2010 Montagnier took aim at Jacques Benveniste's discredited theory of [water memory](#), one of the biggest scientific fiascos in the journal Nature. The previous year he had published an article defending that **DNA emits electromagnetic waves capable** of inducing the appearance of new DNA at a distance where there was no DNA [teleportation](#).

It seemed that Montagnier had hit rock bottom in 2017 when **he partnered with anti-vaccines** in a Paris theater and declared that we are responsible for slowly poisoning the entire future population with mandatory vaccinations, prompting more than 100 of his French colleagues to denounce his statements, certifying his scientific death. However, the father of the AIDS virus still has the ability to surprise negatively by his **radical scientific opinions** and on April 16 he appeared in an interview broadcast on a podcast by the French medical dissemination portal **Pourquoi Docteur** with explosive statements.

[EXCLUSIVE: By Prof. Montagnier, SARS-CoV-2 is a virus manipulated by the Chinese with HIV DNA!](#) (podcast in French).

In this interview Montagnier not only subscribes to the erroneous hypothesis of the retracted Indian article of **the four insertions from HIV but** claims to have analyzed the sequence to the smallest detail with a mathematical colleague, Jean-Claude Perez, **having reached the same conclusion**, which is obviously false, at least in terms

of detail, or I would have seen that those sequences are very common because they are so short. Not only that, but he says he knows that in Wuhan they were working on an AIDS vaccine using coronavirus, which makes very little sense (coronaviruses do not induce long-term immunity and are mucosal viruses, not blood), and Montagnier claims that this led to the accidental creation of SARS-CoV-2 whose release was due to poor biosecurity. He has also claimed to believe that foreign elements in the coronavirus sequence could be removed with electromagnetic waves.

Anyway, **why keep making firewood**. The problem is the damn principle of authority (*argumentum ad verecundiam*) which is one of the most insidious fallacies there is for its abuse by Tyrians and Trojans. In 1660 the Royal Society of London chose its motto "**Nullius in verba**", take the word of no one, which we should always welcome. In science one should never trust anyone's word, only the evidence he presents. The same conspiratorial sites that rightly question the authority of official scientists gladly and unchallengedly accept the authority of alternative scientists like Montagnier who present no evidence. The evidence is the only thing that should guide us, and the evidence shows that **Montagnier is wrong and a dangerous bastard**. As I said, too bad.

7. The accidental release hypothesis

Infodemic is the term chosen by WHO in its 15 April [COVID-19 situation report No. 86](#) to improve information about the pandemic and combat misinformation. Some media have decided on their own that the word exclusively **defines the epidemic of false information about the virus and the disease**. The problem is that both WHO and **governments contribute to spreading misinformation** and have proven not to be completely reliable sources when it comes to the pandemic. There is no doubt that they are not so in terms of their origin. The current WHO director, the first non-doctor in its history, was defined by the editor-in-chief of The Lancet as a "dictator general" after appointing Robert Mugabe, famous for his human rights violations, as a WHO goodwill ambassador. On January 14, the WHO was saying that there was **no evidence that the coronavirus was transmitted between humans** when the situation had clearly already gotten out of control in Wuhan. The attitude of the WHO towards China that hid data, delayed the alarm and fabricated false explanations like that of the market has been shameful and unjustifiable justification. I have long signed [the petition for him to resign as director of the WHO](#), which is already in its fold of one million signatures.

From this blog I strive so that the information provided is truthful and adjusted to the highest scientific standards available, and today **the hypothesis that the virus could be released accidentally from a Chinese laboratory cannot be described as false information**, because it is certainly possible.

Let's review some facts. The virus most similar to SARS-CoV-2, CoV RaTG13 was found in a bat captured in china's Yunnan province, 1500 km away from Wuhan and in a species of bat not found in Hubei (province where Wuhan is). This is the medium horseshoe bat *Rhinolophus affinis*.

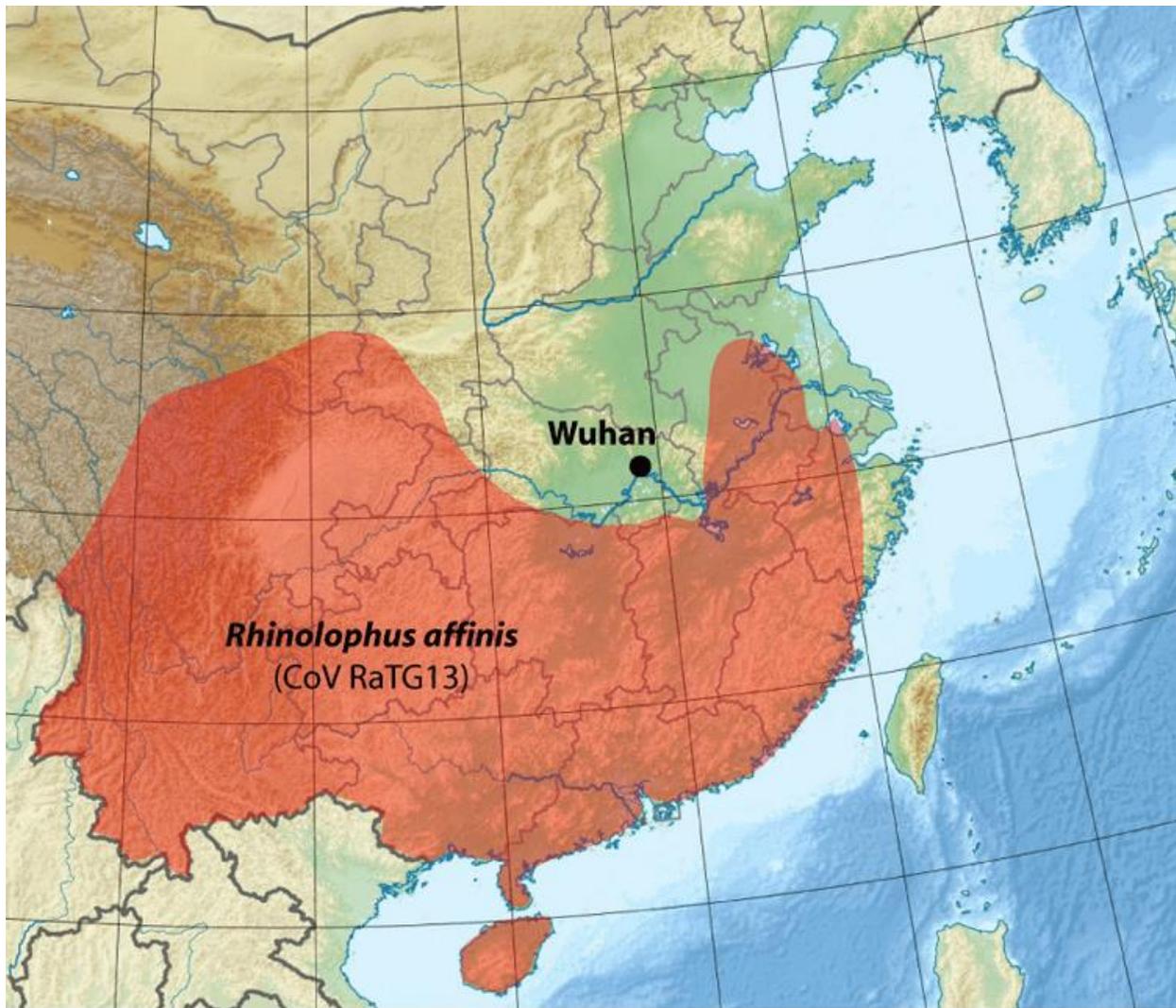


Fig. 5. Distribution in China of the medium horseshoe bat *Rhinolophus affinis* in which a specimen from Yunnan presented the CoV RaTG13 virus, and location of the city of Wuhan. Source: Wikipedia.

But while CoV RaTG13 and SARS CoV-2 are very similar, Trevor Bedford of the University of Washington [places them at least 20 years away from development](#), although that's only true if they've evolved in bats, the rate of evolution could be much higher in other species or in crops. A recent work deposited in BioRxiv shows however that the pattern of mutations that differentiate CoV RaTG13 and SARS CoV-2 is different from that of other coronaviruses, favoring silent mutations (no effect on the protein sequence), and synonymous substitutions, indicating a co-evolution under strong selective pressure not to change. [Comparative genomic analysis revealed specific mutation pattern between human coronavirus SARS-CoV-2 and Bat-SARSr-CoV RaTG13.](#) In my opinion that makes it unlikely that they have evolved in different organisms for a long time or that SARS-CoV-2 is a recent modification from CoV RaTG13. This would support a recent origin of human SARS-CoV-2 from bats. It also makes it virtually impossible for the virus to be designed from already known viruses.

And there is another problem. Although the Coronavirus CoV RaTG13 was collected on July 24, 2013 from the feces of the bat *Rhinolophus affinis* the sequence was made public in the Genbank on **March 24, 2020** (access number [MN996532](#)), following [an article](#) published in Nature on the origin of COVID-19 dated February 3, 2020. This study was done, you would never suspect, at **the Wuhan Institute of Virology**. What a surprise. **They have characterized and grow dozens of coronaviruses other than bats from all over China of which no one knows anything.** Andersen savvy, you have no idea about the coronaviruses that the Chinese keep. If the SARS-CoV-2 pandemic had not occurred, we would not have known anything about CoV RaTAG13.

So on the one hand we have the possibility that a coronavirus closely related to that of **a type of bat that does not occur in Wuhan** was going to infect an animal that we do not **know** in which it spread and possibly mutated until a specimen of that unknown animal was taken to Wuhan and in November 2019 infected a person we do not know where (not in the Hunnan market), that infected others until in early December someone took it to Wuhan's Hunnan market.

On the other hand, we know that the Wuhan Institute of Virology and the Wuhan Center for Disease Control and Prevention have dozens, if not hundreds, of stored coronaviruses that they have not released any information about, one of which **could have been SARS-CoV-2 that would have escaped them.**

Since William of Occam [is my barber](#), I would say **the second explanation is simpler** when it comes to explaining why SARS-CoV-2 was in Wuhan in November 2019. It is true that there is no evidence of it, but that does not mean that you should not try to get it.

Accidental releases of pathogenic organisms are not something hypothetical but unfortunately our bread and butter every year in biomedical research, which has already caused multiple deaths. **The influenza A H1N1 virus** reappeared in 1977 in China and the Soviet Union, producing a global pandemic after decades of absence. Experts were able to prove in [a paper in 2010](#) that it was a laboratory strain from 1949-50 that had eluded someone, although they could not determine in which of the two countries. Between 1966 and 1978 two British laboratories **escaped smallpox three times**, causing at least 80 cases and three deaths. **In Venezuela in 1995 the equine encephalitis virus escaped causing** tens of thousands of cases in Venezuela and Colombia, with more than 300 people dead. [The virus was shown to be identical to one isolated in 1963](#) that was being used to produce a vaccine in a laboratory located at the epicenter of the pandemic. **Since the 2003 SARS epidemic, the virus has escaped six times from laboratories**, once in Singapore, once in Taiwan, and four times in the same laboratory in Beijing! **In 2007 there was an outbreak of foot-and-mouth disease in the United Kingdom**, a contagious disease in artiodactyl ungulate animals (pig, cow, sheep), 4 km from a P4 biosecurity laboratory where a vaccine was being carried out with a strain from 1967 and which [escaped them transported by trucks in mud contaminated by a defective drain](#) . It had an estimated cost of £200 million. Every year there are hundreds of biosecurity incidents involving pathogenic organisms. Fortunately, the vast majority do not result in epidemics.

Fig. 6. The location of the Wuhan Institute of Virology (red marker) with laboratories of biosecurity level P4, in which it works with very dangerous viruses, in the urban area of a population of 9 million inhabitants is crazy. Are these people still smoking opium? Google maps.

8. Conclusion?

The Chinese are the only ones who know what has happened and their behavior is very revealing. After resting on their laurels while the epidemic broke out, they behaved very differently from the outside than from the inside. On the outside, they tore the WHO with the unproven human contagion when they knew that people were infecting them everywhere and tried by all means to downplay it by using the WHO to delay the declaration of a pandemic and criticizing that other countries took restrictive measures with travelers from China or that it was called **the Chinese virus**. They acted as if they had released the virus from doomsday by strictly quarantining 60 million people and applying severe control measures on those who tried to disseminate unauthorized information. As a result, many Western governments like ours thought that the epidemic was not serious (look what they do, not what they say), and that the virus was under control in China, when it was loose around the world.

It is possible that an unknown animal infected patient zero in early to mid-November in Wuhan. As I mentioned on the blog, [Connor Reed](#), a Briton in Wuhan, developed the first symptoms on November 25 and is not patient zero. **Patient zero was infected in an unknown place**, and unless he dedicated himself to visiting caves where medium horseshoe bats hibernate hundreds or thousands of kilometers away, he could not be infected from a bat that does not exist in Wuhan at a time of year when bats do not fly. But it is also possible and much simpler that SARS-CoV-2 was accidentally released from **one of the two laboratories located in the city of Wuhan that we know harbor bat coronaviruses**. And it is simpler because it **explains the presence of the virus at that time and place**, precisely a few kilometers from the most expert group in all of China in bat coronaviruses, that of [Shi Zhengli](#), which is known as **the Chinese "bat woman"**. It is simpler because it **does not require unknown animals** to shelter coronavirus. And it is simpler because it **does not require explaining the zoonotic contact** that made the virus jump from an unknown animal to a human. If the virus had been grown in human cells, which Shi Zhengli's group routinely did with bat coronaviruses, as their publications show, the virus could already be ready to infect someone in the lab and go out inside that unknown person to conquer the world.

What I reject is the possibility that the virus was intentionally designed, produced intentionally, or intentionally released, because the evidence does not support those possibilities at all, even though the web burns with people claiming it, including some Nobel laureate.

I doubt an international investigation could reveal that the virus escaped the Chinese from a lab, but it could reveal whether evidence has been destroyed. I think the Chinese would not allow such an investigation, but with their policy of concealing the truth it is they who encourage speculation of all kinds.

