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Origin of Covid-19: laboratory leak is the most likely scenario

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A Covid-19 epidemic (acronym for '*coronavirus disease 2019*') was officially declared in January 2020 in the city of Wuhan, then quickly turned into a pandemic spreading throughout the world. The rapid spread of the SARS-CoV-2 virus (for '*Severe Acute Respiratory Syndrome*'), responsible for this pandemic, led to lockdowns being imposed on everyone, regardless of age group or susceptibility to the disease. It has disrupted the lives of billions of people. But where did the virus come from? This three-part article aims to describe what is known about the origin of this virus and why it should matter to us, here and now. All those involved in this pandemic story are undoubtedly hiding part of the truth. In the first part, we explain the issue and why it may be of interest to us, even after the pandemic is over, and describe its main players. In the second part, we will review the history of this pandemic. In the third part, we will give the opinions of various institutions on its origin.

Where could Covid-19 have come from?

It is important to remember that a virus cannot multiply on its own, but only inside the cells of other species, which it must first be able to penetrate. There are two theories about its origin.

The first theory is known as the zoonotic origin theory (disease linked to animals in ancient Greek), according to which the virus was transmitted from animals to humans. This complex term actually covers two very different sub-theories.

The first sub-theory is that an ecosystem (swamp, cave, etc.) was colonised by humans who were then exposed to a virus they were not accustomed to and which spread among humans. It could also be that an animal, an intermediate host, was infected and facilitated the transmission to humans, for example through wild animals commonly eaten in China (pangolins, raccoon dogs, etc.).

The second sub-theory is linked to industrial farms in China, which mix thousands of pigs and tens of thousands of chickens. The risk that a virus specific to pigs could, by chance, be adapted to chickens and, at the same time, that there could be a chicken nearby is high in such a farm. Having been selected to jump a species barrier (from pigs to chickens), it will multiply all the more quickly due to the concentration of thousands of animals in the same enclosed environment. Such an origin is not natural, but industrial. Very often, the state imposes the slaughter of animals in the event of contamination, including small-scale outdoor farms, which do not present the same risks and are not sources of contamination. Thus, even this second sub-thesis (industrial farming) is

politically interesting and should not be overshadowed by the first. A zoonosis necessarily involves several passages back and forth between animals and humans, which generates a certain genetic diversity before any passage from humans to humans.

The second theory is that of a leak from one or more laboratories. It has been reported that researchers are conducting experiments known as '*gain-of-function*' (GOF) experiments to produce viruses that are more or less dangerous than the original virus[i].

What is a GOF?

In brief, GOFs refer to techniques that enable a virus to gain or lose a function. These are either genetic modification techniques (resulting in GMOs) or *in vitro* culture techniques in which viruses are exposed to cells of a type other than that for which they are adapted by evolution. *In vitro* cultures change the selection pressure so that the virus gains or loses a function as it is gradually multiplied. This is also known as '*serial passage*', where viruses are successively exposed to cells, culture media or animals with the intention of selecting a genetic change without producing it (as in the case of GMOs). For example, scientists genetically modify mice so that some of their cells have a human-type receptor. These are '*humanised*' GMO mice. They then inject these GMO mice with viruses adapted to bats. The viruses that survive are those that are more adapted to attack 'humanised' cells. Little by little, they select viruses capable of attacking humanised cells, and therefore human cells too. The most frequent case is a mixture of these two techniques.

Professor Simon Wayn-Hobson (virology department, Institut Pasteur, Paris) argues that "*the consequences of an accident could range from a few infections to a catastrophic pandemic*"[ii]. Professor Anton van der Merwe (Oxford University) argues in the Financial Times that "*researchers are doing and want to continue doing precisely those experiments that make laboratory leaks more likely. This includes GOFs*"[iii]. According to him, there are "*few justifications for such experiments except scientific curiosity and the desire for prestige*"[iv]. Proponents of these gains of function put forward the argument of preparing a vaccine to deal with any possible 'natural' passage of an animal virus to humans…

Can the intermediate host be found?

The SARS virus of 2002, different from SARS-Cov2, took five months to be isolated and sequenced[v]. The origin is SARS from bats, passed on by civets, then to humans[vi]. It should be noted that this first episode of SARS was of zoonotic origin. But the next two outbreaks, in 2003, were the result of laboratory leaks[vii], since all the people contaminated were working in a laboratory that was storing the virus[viii].

MERS appeared in June 2012. A Saudi doctor asked the Dutch virologist Ron Fouchier (a specialist in GOF), who obtained the sequencing of the virus published on 8 November 2012[ix], *i.e.* in five months. From the outset, the intermediate host was known to be the camel. Today's resources are non-comparable with those of 2003 or 2012. For example, a virus can now be sequenced in 4 or 5 days. SARS-Cov2 was sequenced at the end of 2019 in 5 days and released on 11 January 2020. However, 5 years after the official start of Covid-19, several intermediate hosts have been accused without justification. According to some, it weakens the zoonotic theory, without prohibiting it.

Who are the main protagonists?

Zhengli Shi did her PhD in Montpellier, then held several positions in the United States. For more than 10 years, she has run the P3 laboratory in Wuhan, designed by the Institut Pasteur and built with plans offered by France, and she co-directs its P4 laboratory[x] (the P4 type is the most closely monitored), receiving funding from the US government via a US NGO, EcoHealth Alliance. Unfortunately, even P4 laboratories are exposed to leaks from laboratories[xi]. In 2005, Zhengli Shi was part of the team that proved that the SARS outbreak of 2002 and 2003, which killed 774 people worldwide, was caused by a bat[xii].

Ralph Baric co-directs the virology laboratory in North Carolina (USA) with military personnel. It was Baric who taught Zhengli Shi how to genetically modify viruses.

Peter Daszak, President of the NGO EcoHealth Alliance, is a central figure. Over the past 20 years, he has collected more than 80 million dollars from research organisations in the United States to harvest viruses and carry out GOF experiments on them. He promises that, thanks to his virus collections and GOF work, other researchers will then find vaccines[xiii]. His funding goes mainly to the North Carolina laboratory and Ralph Baric, as well as the Wuhan Institute of Virology (WIV) and Zhengli Shi laboratories (P3 and P4).

Antony Fauci was public health advisor to eight US presidents and director of the National Institute of Allergy and Infectious Diseases (NIAID) from 1984 to 2022. He promoted major advances in the chemical fight against HIV. He defended the GOF, the zoonotic thesis and supported Daszak and Baric. He is the state guarantor of scientists like Daszak.

Tales from the prehistory of the SARS-CoV2 epidemic

In 2012, six miners (aged between 30 and 63) were working in a mine in Mojiang (Yunnan province, China) where bats were living. A few weeks later, they were admitted to hospital in Kunming with persistent coughs, fever and difficulty breathing. Three of them died. This mine is located 1,500km from Wuhan. A group of researchers (DRASTIC) has made this information public [xiv]. Between 2012 and 2015, researchers at the Wuhan Institute of Virology (WIV) identified 293 coronaviruses in and around the mine, including one called RATG13. All these viruses were sequenced and could be consulted in a database that the WIV made available to everyone on the Internet. According to the WIV and Zhengli Shi, none of them is suitable for transmission between humans; the miners died from an infection by a fungus[xv]. But while this database would have helped researchers get an idea of the viruses sequenced and the history of viruses obtained by the WIV, it denied public access from 3 September 2019. Why?

It turns out that RATG13 is, according to Zhengli Shi, the closest ancestor of SARS-CoV2, as it is 96.2% identical. But this is not enough to be an ancestor that would have evolved so '*naturally*' (3.8%) in only 6 years. Scientists can estimate the speed of mutation by natural reproduction. So, either it is not the real ancestor and we need to look elsewhere, or it did not evolve '*naturally*'. Furthermore, according to the zoonotic theory, if RATG13 is the ancestor, it would have travelled 1,500km from Mojiang to Wuhan without causing an epidemic. It would have miraculously reappeared six years later, having mutated much faster than in the wild, in the vicinity of the WIV, which was working on this very type of virus and carrying out GOF on SARS, or potentially in the Wuhan animal market, on the other side of the river, around 13.5km away...

We have therefore seen that the origin of SARS-CoV2 raises a number of questions and hypotheses, involves several key players and could come from techniques that create GMO viruses. In the second part, we will describe the practices of the Wuhan Virology Laboratory (WIV) and the prehistory and history of Covid-19.

i Hervé Le Meur and Caroline Lemerle, « Gain de fonction : l'art de créer des super viruses », *Inf'OGM, le journal*, n°164, July/September 2021.

ii S. Wain-Hobson, « The irrationality of GOF avian influenza virus research », *Front. Public Health*, Volume 2, 2014.

iii A. van der Merwe, « Scientists dismissed lab leak theory due to conflict of interests », *Financial Times* 10 March 2023.

iv Jamie Johnson, « Joe Biden may be forced to declassify intelligence into Covid-19 origins », *The Telegraph*, 10 March 2023.

v SARS appeared in November 2002. Its sequence is published in:
C. Drosten *et al.*, « Identification of a Novel Coronavirus in Patients with Severe Acute Respiratory Syndrome », *N Engl J Med*, Vol. 348, No. 20, 348:1967-1976, 15 May 2003.

vi Y. Guan *et al.*, « Isolation and Characterization of Viruses Related to the SARS Coronavirus from Animals in Southern China », *Science*, Vol 302, Issue 5643, pp. 276-278, 10 October 2003.

vii R. Ebright quoted in :
Y. Rui *et al*., « Wuhan Virology Lab Deputy Director Again Slams Coronavirus Conspiracies », *Caixin Global*, 7 February 2020.

viii "*The index cases were systematically described in people working in laboratories studying the virus responsible for severe acute respiratory syndrome (virology students, contract researchers). These index cases were the source of contamination for the other people affected (parents, nurses, etc.)*".
Wikipedia contributors, « Severe acute respiratory syndrome », *Wikipedia, the free encyclopaedia*.

ix Ali M. Zaki *et al.*, « Isolation of a Novel Coronavirus from a Man with Pneumonia in Saudi Arabia », *N Engl J Med*, Vol. 367, No. 19, pp.1814-1820, 8 November 2012.

x Laboratories handling viruses or infectious agents are classified in ascending order of safety standards, from P1 to P4. P4 laboratories are the only ones authorised to handle viruses that are lethal to humans and for which there is no vaccine or treatment. Even in P3 laboratories, scientists are provided with an individual air supply. But viruses are so small that mistakes are the rule, not the exception. *Inf'OGM* has already documented the very many leaks. In any case, military laboratories escape the law and rarely report on their leaks. A British military scientist, Geoffrey Bacon, died of the plague in January 1962 in the UK. We can assume that he was working on the plague bacillus.

xi Christophe Noisette, « Pathogènes en laboratoire : la sécurité absolue est un leurre », *Inf'OGM*, *le journal*, N°164, July/September 2021.

xii Wendong Li *et al.*, « Bats Are Natural Reservoirs of SARS-Like coronaviruses », *Science*, Vol. 310, Issue 5748, pp. 676-679, 28 October 2005.

xiii Annick Bossu, « Covid-19 : un expert de l'OMS parle juste avant la pandémie », *Inf'OGM*, 13 April 2021.

xiv Li Xu, « The Analysis of Six Patients With Severe Pneumonia Caused By Unknown Viruses », May 2013 (translated by Drastic in June 2020).

[xv] D. Stanway, « Explainer: China’s Mojiang mine and its role in the origins of COVID-19 », *Reuters*, 9 June 2021.

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