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COVID-19 and its possible origin

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Abstract

The struggle between man and infectious diseases dates back to the very beginning of civilization, where the increase of infectious entities is closely associated with poor human actions and management of ecosystems. The objective of the present research was to outline the possible origin of the new coronavirus officialized as SARS-CoV-2 causing COVID-19. A series of aspects about the possible origin of the new pandemic are presented, broken down as follows: Where does this virus come from? probable theories about how this virus spread to humans, what do we know?, what don't we know?, and what can we do now?. It is concluded that this is a highly infectious entity with a high probability of zoonotic transmission, where bats and the mammal known as pangolin stand out as potential reservoirs, but the possibility of synthesizing this virus at laboratory level should not be ruled out, so we do not know if the virus will become endemic, recurrent year after year or finally be controlled; What we do know for sure is that the joint efforts of all human beings living on this planet are needed to win the battle against this new coronavirus.

Keywords: Anthropogenic; Coronavirus; COVID-19; Origin; Pandemic; Zoonotic

1. Introduction

The struggle between man and infectious diseases dates back to the very beginning of civilization [1]. Throughout history, mankind has suffered the scourge of an infinite number of entities with varied etiological diversity (viral, bacterial, fungal and parasitic), which have spread death and incapacity among millions of the planet's inhabitants [1-4]. The increase in re-emerging and emerging diseases in recent decades has greatly complexified the epidemiological picture at the global level [3,5,6], where the occurrence of several epidemic and pandemic outbreaks has been evident, with marked repercussions on human health and that of other animals [7-10]. It must be taken into account that this increase in infectious entities has not been, nor is it something casual, but rather the consequences of human mismanagement of ecosystems [4,10,11]. The current situation that the planet is experiencing due to the new coronavirus is one more effect, derived from the mismanagement of anthropogenic activity, accumulated over thousands of years [11-13].

The new coronavirus (2019-nCoV) identified on December 31, 2019 in Wuhan, China, currently officialized as SARS-CoV-2, produces COVID-19. Moreover, this virus is the first of its family to be declared a pandemic by the World Health Organization (WHO) on March 11, 2020 [14] Global epidemiological studies of coronavirus (CoV) over 15 years have shown that bats in Asia, Europe, Africa, America and Australia are reservoirs of a wide variety of viruses, harboring and spreading these infectious agents quite easily, increasing their transmission capacity [15-17].

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The truth is that we do not yet know whether the virus will become endemic, recurrent year after year or eventually be controlled [20-24]. Nor does it prevent, in addition to disease, also infection. The pace of vaccination is slow, with economic interests and irregular distribution, which has given way to the emergence of new waves, and the appearance of mutations that could hinder the efficacy of current vaccines [18,19,21,24].

1.1. Where does this virus come from?

There are approximately 6 400 species of mammals on our globe. Bats and fruit bats make up 20% of the mammal population. There are 1,000 different types of bats and fruit bats, and they are the only mammals that can fly, which explains their wide range of movement. Bats and fruit bats harbor a large number of viruses. Bats and fruit bats in developmental history have probably been the entry point for viruses into the mammalian pedigree [16,17,26].

There are numerous dangerous viruses that have spread from "bats" to humans and are responsible for many diseases: measles, mumps, rabies, Marburg fever, Ebola, and other rarer and no less dangerous diseases. In other mammals, viruses derived from "bats" have repeatedly caused massive deaths in pig, chicken or poultry farming [16,17,25].

These are biological processes that are millions of years old. The DNA of healthy individuals also contains remnants of viral gene sequences that have been "incorporated" over millennia. SARS and MERS have intensified research on coronaviruses precisely because a new coronavirus epidemic or pandemic was expected soon [16,25,26].

Twenty-two of the 38 known and by no means definitively classified coronaviruses have been extensively studied by Chinese researchers (see publications by Peng Zhou on the epidemiology of "bat coronaviruses in China"), and other publications by US authors mentioned above. Peng Zhou predicted an upcoming new coronavirus epidemic in March 2019 for the following reasons:

- high biodiversity in China;
- high number of "bats" in China;
- high population density in China = close coexistence between animals and humans;
- high genetic variability of "bats", i.e. a high probability that the genome of individual types of coronaviruses can change spontaneously as a result of random mutations;
- highly active genetic recombination of coronaviruses means: Coronaviruses of different types exchange genomic sequences with each other, which can make them more aggressive to humans.

The fact is that many of these viruses - coronaviruses, but also Ebola or Marburg viruses - live together in these "bats" and can accidentally exchange genetic material. Although unproven, Peng Zhou also addressed Chinese eating habits, which increase the likelihood of these viruses being transmitted from animals to humans. Peng Zhou warned of a corona pandemic in his March 2019 article. And he wrote, that he could not say exactly when and where this pandemic would break out, but that China would likely be a "hot spot." So much for scientific freedom. Peng Zhou and his Wuhan group continued research, and it was they who identified the COVID-19 genome, on January 7 and shared it with the world [25,26].

1.2. Probable theories as to how this virus spread to humans

- The COVID-19 virus has been transmitted directly from a bat to humans. However, the structure of the virus that is in question and that genetically matches 96% of the current "COVID-19" virus cannot bind to the "angiotensin-converting enzyme" (ACE) type 2 in the lungs. However, the virus needs this enzyme in order to penetrate lung cells (and heart, kidney and intestinal cells) and destroy them.
- A COVID-19 virus jumped to humans from the pangolin, a dandruffed mammal from Malaysia that was illegally imported into China, and which initially did not cause disease. As part of consecutive human-to-human transmissions, this virus has adapted to general human conditions through mutation or adaptation, and was eventually able to attach to the ACE2 receptor, and penetrate cells, which "started" the pandemic.
- There is an original strain of these two viruses COVID-19, which unfortunately so far has not been detected.
- It is a synthetic laboratory virus, because this is exactly what was investigated and the biological mechanism of the excitation, and described in detail in 2016.

The virologists in question denied this possibility, of course, but they also cannot rule it out in the "Nature Medicine" just published: "The proximate origin of SARS-CoV-2" by Kristian Andersen [26].

What is special about these facts is that coronaviruses can live together with the Ebola virus in the same "bat" without the bat getting sick. On the one hand, this is scientifically interesting, because perhaps immune mechanisms can be found that explain why these bats do not get sick. These immune mechanisms against coronaviruses and Ebola virus could provide important information for *Homo sapiens*. On the other hand, these facts are worrisome, because one can imagine that due to high and active genetic recombination, a supervirus can form, which has a longer incubation period than the current COVID-19 virus, but with similar lethality to the Ebola virus [26].

SARS had a lethality of 10%, MERS lethality was 36%. It was not due to *Homo sapiens* that SARS and MERS did not spread as fast as COVID-19 now. It was just luck. The claim that a virus with a high mortality rate could not spread because it was killing its host too fast was correct at the time when a caravan of "infected" camels had left X'ian for the Silk Road and that is why the high mortality did not spread to the next caravan. Today it is very easy. Today everyone is massively networked. A virus that kills in three days still goes around the world. Everyone knows Beijing and Shanghai. I have known Wuhan for 20 years. None of my colleagues and acquaintances have ever heard of Wuhan, but have you seen how many foreigners there were in Wuhan, in a city that "nobody knows", and how they went to all regions of the world at lightning speed? That is the current situation.

1.3. What do we know? What don't we know?

1.3.1. We know

that it is an aggressive virus;

- that the average incubation period lasts five days; the maximum incubation period is not yet clear;
- that asymptomatic carriers of COVID-19 can infect other people, and that this virus is "extremely contagious" and "extremely resistant" (A. Lanzavecchia);
- we know the populations at risk;
- that in the last 17 years it has not been possible to develop a vaccine or a monoclonal antibody against coronaviruses; 5. that it has never been possible to develop a vaccine or a monoclonal antibody against coronaviruses;
- that it has never been possible to develop a vaccine against any coronavirus;
- that the so-called "flu vaccine" has minimal effect, contrary to popular publicity.

1.3.2. What we do not know

- Whether or not immunity exists after passing an infection. Some data indicate that humans can develop class G immunoglobulins after day 15, which should prevent re-infection for the same virus. But this has not yet been definitively proven;
- how long a possible immunity could protect;
- whether this COVID-19 virus remains stable or whether a slightly different COVID-19 spreads again worldwide in autumn, analogous to the usual flu wave, against which there is no immunity;
- If higher temperatures in summer help us because the COVID-19 casing is unstable at higher temperatures. It should be mentioned here that the MERS virus spread in the Middle East from May to July, when temperatures were higher than we have ever experienced;
- How long it takes for a population to become so infected that the R-value is <1:

If 1 million people in Zurich are tested at a given time, COVID-19 12% to 18% are said to be positive at this time. To deprive the pandemic of its pandemic character, the R-value must be <1, i.e. about 66% of the population must have had contact with the virus and developed immunity. No one knows how long, how many months it will take until the infection, currently assumed to be 12% to 18%, has reached 66%! But it can be assumed that the spread of the virus from 12% to 18% to 66% of the population will continue to generate seriously ill patients.

- 6. So we do not know how long we will be dealing with this virus. Two reports, which should not be publicly available (US Government COVID Response Plan and a report from Imperial College London) independently arrive at a "shutdown" phase of up to 18 months;
- 7. and we do not know if this virus will occupy us epidemically / pandemically or perhaps even endemically;
- 8. We still do not have a recognized and widely applicable defined therapy, and we have never been able to present one of these therapies in the case of influenza.

Perhaps the authorities and the media should put the facts on the table instead of presenting every other day reports of a seemingly successful vaccine, and that is still a long way off.

1.3.3. What can we do now?

I also cannot answer the question and give the best solutions. It is not known whether it is possible for Switzerland to contain the pandemic or whether the infection will not be affected because all measures have been done and implemented too late.

If so, one can only hope that we will not pay for this "policy" with too many dead and critically ill people. And that not too many patients will suffer the long-term consequences of COVID-19 infection, such as that "thanks to" COVID-19 I suffer from pulmonary fibrosis, altered glucose metabolism and new cardiovascular diseases. The long-term consequences of having suffered a SARS infection are documented up to 12 years after the alleged cure. Hopefully, COVID-19 will behave differently.

Lifting the "lockout," or a return to what we perceive as normal, is surely everyone's wish. What steps will have negative consequences in returning to normalcy? With an outbreak of the infection rate, no one can predict. Every step toward relaxation is basically a step into the unknown. We can only say what is not feasible: an active infection of non-risk groups with the COVID-19 virus is surely an absolute fantasy. It can only come to mind for people who have no idea about biology, medicine or ethics:

- it is certainly impossible to deliberately infect millions of healthy citizens with an aggressive virus, about which we really know nothing, neither the extent of acute damage nor the long-term consequences;
- The greater the number of viruses per population, the greater the probability of accidental mutation, which could make the virus even more aggressive. Therefore, we should definitely not actively help to increase the number of viruses per population.
- The more people are infected with COVID-19, the more likely it is that this virus will become "better" adapted to humans and become even more disastrous. It is assumed that this has happened before.
- With government reserves of supposedly 750 billion, it is ethically and morally reprehensible to infect millions of healthy people for mere economic considerations.
- Deliberately infecting healthy people with this aggressive virus would acutely undermine one of the fundamental tenets of all medical history of pure short-term economic "concerns": the principle of "primum nil nocere." As a physician, I would refuse to participate in such a vaccination campaign.

The determination of the concentration of COVID-19 IgM and IgG antibodies in the blood apparently goes hand in hand with the neutralization of the COVID-19 virus. The quantitative and qualitative diagnosis of these antibodies has so far only been investigated in a small clinical study with 23 patients. It is currently not possible to say whether the determination of the mass of antibodies in the blood will make a controlled "blockade" safer by allowing only infectious and infectious persons to move freely. It is also unclear when this method will be clinically valid and widely applicable.

2. Conclusion

It is a highly infectious entity with a high probability of zoonotic transmission, where bats and pangolins stand out as potential reservoirs, but the possibility of synthesizing the virus at laboratory level should not be ruled out, so we do not know if the virus will become endemic, recurrent year after year or finally be controlled; what we do know for sure is that we need the joint efforts of all human beings living on this planet to be able to win the battle against this new coronavirus.

Compliance with ethical standards

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Disclosure of conflict of interest

No conflict of interest to be disclosed.

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Authors short Biography

