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The evolutionary view of coronavirus epidemics process

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Abstract

Every virus is a parasite that cannot exist on its own and is fully dependent on its carrier. This is the basic condition of its existence. The parasite must have its host, and thus is a living cell. Based on our long-term study of BLV and HIV, we conclude that the carriers of these viruses are bacteria or yeast. Viruses can exist in these carriers in the intestinal and respiratory tracts for months or years. Carriers are indifferent to the fact that the virus multiplies and mutates in them. The mutant can arise in patient, and given optimal conditions, it can reproduce and spread to other individuals. However, it is possible that a new mutant may have originated in several places. It is only a matter of time before mutations appear in one virus particle. From an epidemiological point of view, it can be assumed that in the case of coronavírus variant Omicron, it could take 10 to 20 years for more than 30 mutations to occur. This coincides with the period when the first SARS-CoV-1 infection occured in 2004. Consistent with the idea that the virus can survive in an infected body for months or years in its carriers, then the Omicron ancestor can date back to the first SARS-1 epidemic.

Key words: SARS-CoV-1, Omicron variant, bacteria, carriers, intestinal tract, elimination

Introduction

When working with the bovine leukosis virus (BLV), in addition to monitoring the infection by detecting antibodies against the virus in animals, we also investigated the mechanism by which the infection is transmitted from sick animals to healthy ones. After several years of research, a conclusion has been reached that the virus can be hosted by bacteria and through these carriers it is transmitted to healthy animals. This assumption was experimentally tested and confirmed by the results. Subsequently, the idea was elaborated on the HIV model in the laboratory of prof. Flossie Wong-Staal (UCSD, USA). It was found that the bacteria of HIV-positive people from the USA and Slovakia are hosts, carriers of HIV. Evidence was confirmed at the DNA level by hybridization and PCR using commercial, diagnostic primers [1-12]. By the sequencing of PCR products synthesized on the template of patient’s bacterial DNA using primers for env, gag and pol HIV-1 gene, homology for more than 90% with HIV-1 isolate HXB2 (HIVHXB2CG) were revealed [1-12]. At the protein level, HIV- like proteins were confirmed by Western blotting using commercial monoclonal antibodies against HIV antigens [4-12]. In throat swabs of HIV-positive children from Cambodia and Kenya, HIV was detected in commensal bacteria, but also in the yeast *Candida albicans*.[5-11].

The discovery that BLV and HIV use bacteria or yeast as vectors led us to focus on monitoring the presence of the novel coronavirus in the intestinal tract of infected individuals (13-17). Rectal swabs were taken from recovered patients at the Institute of Clinical Microbiology at the University Hospital Nitra (Slovakia) (16). The obtained results confirm that out of a cohort of 30 tested persons, only five patients (17%) did not show signs of presence of the novel coronavirus in their stool more than 12-28 days after being infected, as proven by RT PCR tests. This result also indicates that 2-4 weeks is long enough for the body to cleanse itself of the virus. The remaining 25 subjects (83%) still had presence of coronavírus in their stool more than 12-28 days after being infected. When comparing the RT PCR products of nasopharyngeal swabs with samples from the intestinal tract, no significant differences in measured levels were found. This suggests that the viral load detected in the throat has also been transmitted to the intestinal tract. The results show that the vast majority of patients who have overcome the infection, the virus is still present in the stool and their intestinal tract. This supports the assumption that these individuals may still be infectious and may pass the virus to other people. Based on these results, it was concluded that the carriers of many, if not all viruses may be bacteria, yeast, or other single-celled organisms. These organisms are characterized by a great willingness to accept foreign genetic information, which is the basis of evolution in general. Viruses use this successfully, although the benefit to the hosts is problematic in this case.

After transmission to humans, the novel coronavirus enters the cells of the respiratory tract, which contain the ACE2 receptor. Upon contact of viral tentacles with this receptor, the virus penetrates the receiving cell of the respiratory tract, where the process of tissue destruction occurs. After overcoming the infection and eliminating the virus in the recipient's lung cells by a conventional drug-based treatment approach such as ventilation and activation of the immune system, the infection is suppressed and the patient can be pronounced cured. However, carriers containing viruses in most cases travel and survive in the intestinal tract. The immune system does not allow them to penetrate into the body from there. Some people after having been infected may become carriers of the coronavirus and thus may infect others by secreting the coronavirus in the form of droplets, but also in faeces.

The coronavirus has been found in the stools of infected people in several laboratories, the official explanation being the virus was in the process of leaving the body which cleared itself of the virus. But that is not the case. In many cases, the virus does not disappear, it remains in the tract where it can survive for weeks or even months. The reason that carrier virus has not yet been detected in the intestinal tract of patients after their recovery is simply that fecal infection is not thought to be a significant contributor. However, history provides us with abundant evidence of the importance of disinfection and disposal of feces during epidemics. It is incomprehensible why, in the current epidemic, this possibility of transmitting infection is absolutely marginal and has not been considered. We have become better at successfully preventing the droplet aspect of this infection with face masks, social distancing and hand washing, however, but we are not yet sufficiently preventing rectal infection. It is necessary to introduce rapid disposal of excrement, disinfection of toilets and UV emitters and ventilation and encourage regular rectal hygiene, washing and disinfecting of hands. These measures must be introduced where toilets are public or shared - care homes, schools, workplaces, hospitals, airplanes, buses, but also in households. After all, it is this form of virus transmission that can answer the question of what can be the mechanism of causing new and new waves of infection.

Hypotheses about the origin of the epidemic

Currently, there are several hypotheses for the origin of the epidemic. Perhaps the most discussed is the one that links the outbreak of the disease to the wet market in Wuhan, where there was a natural transmission from an animal to a person. Another hypothesis claims that there was a virus leak from the laboratory. However, there is currently no conclusive evidence that the SARS-CoV-2 coronavirus was artificially created in a laboratory. Both of these alternatives are not sufficiently proven and convincing.

Our obtained results allow us to consider another alternative of the etiology of the novel coronavirus pandemic. If we approach the problem from a broader perspective, it is best to start with an evolutionary approach. SARS, or severe acute respiratory syndrome, is a viral respiratory disease of zoonotic origin caused by a coronavirus known as SARS-CoV-1. The syndrome caused the SARS epidemic between 2002 and 2004. More than 8,422 people from 29 different countries were infected and at least 774 people died worldwide with a gross mortality rate (CFR) of 11% [18]. No cases of SARS-CoV-1 have been reported worldwide since 2004. At the end of 2017, chinese scientists observed the virus spreading through Asian civets on cave bats in the Chinese province of Yunnan. Bats have been the initial reservoir of the pathogen.

SARS-CoV-1 was identified by throat swabs, but only people with evidence of severe infection were tested. The virus may have been much more frequent in the population than recorded. There have been many cases with a mild course of infection, however, these were analyzed and wrongly diagnosed as influenza. It can be assumed that the overall number of infections can be ten times more than official statistics show. Based on the above results, it is possible to consider the idea that the coronavirus, after overcoming the infection, may settle in the intestinal tract in most infectious patients, where it remains asleep for several decades. There it can gradually and uncontrollably change and mutate since no intervention takes place, remaining almost undetectable. However, at that time, the presence of the SARS-CoV-1 in the intestinal tract was not monitored. The new variant, Omicron, shows an unusual number of mutations - only on the "spike protein" there are more than 30 of them. From an epidemiological point of view, such a number of mutations required a longer time, probably up to 10 to 20 years. The precursor to the Omicron coronavirus variant has probably been around for a long time, much longer than thought.

The long-term presence of coronavirus in the population is also evidenced by the detection of antibodies against SARS-CoV-2, which were found in Italy (also the virus in wastewater samples), Spain and Portugal as early as 2019. This surprising finding was not sufficiently analyzed and substantiated. Antibodies to any virus can only be synthesized in the presence of the virus, so the coronavirus must have been there before. But no RT PCR test for SARS-CoV-2 were performed anywhere at that time. Based on these data and findings, we will try to estimate what process in the viral changes may have occurred and subsequently result in the SARS-CoV-2 pandemic. We can assume the following three alternatives:

1. SARS-CoV-1 mutated, which is common in viruses. And gradually a new variant was selected - aggressive SARS-CoV-2.

2. SARS-CoV-1, encountered a new carrier compatible with humans. The virus multiplied and mutated and one of the mutants - SARS-CoV-2 became prevalent.

3. A new aggressive SARS-CoV-2 mutant was selected from SARS-CoV-1 and obtained an optimal carrier, exceptionally compatible with humans.

The detection of new coronaviruses in the intestinal tract up to 28 days after overcoming the infection opens a new perspective on the etiology of the new coronavirus. Currently, we do not know exactly how many patients the virus survives in their intestinal tract. Based on our results, it can be even more than 50% of infected people. However, a much more comprehensive study is needed for this. Based on these findings, it is possible to assume that the new coronavirus could exist in the intestinal tract for a longer period of time and mutate without restriction.

Conclusion

The fact that new variants of the virus are still emerging may indicate that SARS-CoV-1 was significantly more prevalent in the population than it was originally assumed. Detection of novel coronaviruses in the intestinal tract up to 28 days after overcoming the infection opens up new alternatives of the etiology of the novel coronavirus. Based on these findings, it is possible to assume that the novel coronavirus can exist indefinitely in the intestinal tract and mutate without limitation. And the greater the prevalence, the higher the chance that new variants and mutants would emerge. These do not depend on the carrier, there are no restrictions. The mutant could have arisen in one or several individuals and given optimal conditions, it reproduced and was transmitted to more people. From an epidemiological point of view, it can be assumed that in the case of coronavírus variant Omicron, it could take 10 to 20 years for more than 30 mutations to occur. This coincides with the period when the first SARS-CoV-1 infection occured in 2004. This idea clearly needs to be proven experimentally.

The novel coronavirus has been found in the stools of infected people in several laboratories, which has been explained by the body cleansing itself of the virus (18-25). However, this is not the case. The virus can leave the body, but based on our results in the HIV and BLV system, it usually remains in the intestinal and respiratory tract of the carrier, where it can exist for a long time. Virus carriers establish themselves in the intestinal tract and become a component of the microflora. The immune system eliminates virus carriers that enter the body from the intestinal tract. If the infected person's immune system is weakened - colds, illnesses, infections, injuries - the carrier of the virus multiplies, penetrate from the tract into the infected organism and the latter can infect others. In the tract, viruses happily multiply and mutate in the carrier. Carriers containing virus, like all living organisms, die and constantly leave the intestine with feces. Since the intestinal tract of the vast majority of infected people contains carriers of the coronavirus, there are still large numbers of them in wastewater around the world, despite the fact that the epidemic is already on the decline. This finding may help in dealing with potential new epidemics caused not only by the coronavirus, but also by other viruses.

The virus can exist in the intestinal and respiratory tract practically indefinitely only in the carrier - bacteria, yeast, or other single-celled organism. The virus can stay there for years and recurrent infections can occur. This depends on many factors, especially the health of the person, the quality of his immune system and the composition of the microflora. If the virus carrier is not detected and removed, the infections may recur continuously and the body never eliminates the virus. In this way, the viral load, hidden in the intestinal tract in general, will constantly increase, which will represent a great danger for the human population in the future. The presence of viruses in general in the intestine can be the source of many health problems. By identifying the carriers of the viruses and their subsequent elimination, we also destroy the virus. Only then can we be sure that the virus is eradicated.

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Disclosure of conflict of interest

The authors declare that there is no conflict of interest.

Statement of informed consent

Informed consent was obtained from all individual participants included in the study.

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