

## Indirect Coronavirus Elimination

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### Introduction

All viruses, including COVID-19, are parasites. They cannot exist by themselves and fully depend on their carriers. This is the basic condition of their existence that is the law, the axiom. What living cell carries viruses? After all, the parasite must have its host, a living cell [1]. The basic question is in what form the virus exists in the primary host. They must also exist in living cells, but they cannot be host cells, that is, bats or civets, because they would destroy their host. If we continue with this research, the question is in what form the virus passes into the secondary host [2].

### Description

It is generally claimed that a virus can exist for as little as 2 s-5 s during which it spreads to another species. However, it is contrary to the biological law that a virus cannot exist without a living cell. According to the generally accepted statement, he admits this [3]. In this way, the law is gradually limited, except that it is forgotten and we come to unauthorized closures. That is the situation we are in now. We did not respect the law, so we turned the parasite into a king. Tracking viral pathways is not easy and has not been sufficiently investigated. However, this is a key issue, the solution to which can lead to a fundamental reversal of the way we perceive viruses [4].

What living cell carries viruses? We have been looking for an answer to that question for over 30 years, when we started working on the diagnosis of leukosis in cows caused by Bovine Leukemia Virus (BLV) with the aim of its nationwide eradication in Czechoslovakia. A stable was set up to monitor the transmission of infection from BLV-infected cows to healthy animals. Finally, we concluded that the vectors of transmission of the virus and its hosts can only be bacterial cells. This conclusion was tested experimentally and the results were confirmed [5].

Consequently, based on the project for NIH was started analysing host cells of HIV in the laboratory of prof. In this model, too, the bacterial cells of the intestinal tract were found to be the host of the virus. Evidence was confirmed at the DNA level by hybridization and PCR using commercial, diagnostic primers and consequent sequencing. At the protein level, HIV-like proteins were confirmed by western blotting using

commercial monoclonal antibodies against HIV antigens. In the swabs of HIV-positive children from Cambodia and Kenya, HIV was found in commensal bacteria, but it is also often found in the yeast *Candida albicans*. Based on these results, it has been suggested that many, if not all, viruses, including coronavirus, can be transmitted by bacteria or yeast [6].

It should be ascertained whether the current pandemic has been caused by bacteria or coronavirus-containing yeast. It is likely that such coronavirus is transmitted to humans and travels further to the recipient cells of the respiratory and intestinal tract. Upon contact of the viral tentacles with the ACE2 receptor, the virus is released and penetrates the recipient cell of the respiratory tract and the process of tissue destruction begins [7].

A virus, like a parasite, is a specific biological form and is therefore difficult to fight. Its main weakness is that it is hosted by bacteria or yeast. Bacteria can be eliminated with suitable antibiotics. By destroying bacteria carrying a virus, the virus ceases to exist. Thus, many viral infections can be stopped. To verify this conception, a throat swab needs to be collected from an infected person. The swab is transferred directly applied to agar and incubate overnight [8]. Individual grown bacterial colonies will be determined by RT PCR for coronavirus. Subsequently, it will be analyzed to which antibiotics the bacteria containing the coronavirus are fully sensitive. The optimal antibiotic is administered to the patient. Under normal circumstances, it is expected that the results may be known within 10 days. Patients should be given probiotics and prebiotics after the antibiotic treatment. The proposed approach of identification and treatment of coronavirus infections is very rapid. The most important aspect is starting the treatment at the earliest opportunity. By finding a suitable antibiotic to kill the virus-containing bacterial cells, we can immediately intervene straight at the beginning of the disease process [9].

### Conclusion

Although we eliminate the virus in recipient airway cells by the classic drug-based healing approach, ventilation and the immune system, the virus-containing bacteria survive. They are stored in the respiratory and intestinal tract and under optimal conditions, they multiply, penetrate the body through the blood system and attack the recipient's cells. This reversal, also called the second wave of infection, is very likely. By applying

appropriate antibiotics, coronavirus-containing bacteria in the intestinal tract are eliminated, thus preventing the second wave of infection. Last but not least, the great advantage of the given treatment method is the fact that expensive vaccines, which are still being developed, are not needed.

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## References

1. Zajac V, Kovac M, Ciernikova S, Mego M, Rauko P, et al. (2005) Detection of HIV sequences in colon bacteria of AIDS positive patients. *Clin Microbiol Infec Suppl* 11: 53.
2. Zajac V, Mego M, Martinický D, Stevurkova V, Ciernikova S, et al. (2006) Testing of bacteria isolated from HIV/AIDS patients in experimental models. *Neuroendocrinol Lett* 27: 101-104.
3. Zajac V, Stevurkova V, Mátelova L, Ujhazy E (2007) Detection of HIV-1 sequences in intestinal bacteria of HIV/AIDS patients. *Neuroendocrinol Lett* 28: 591-595.
4. Zajac V, Matelova L, Liskova A, Mego M, Holec V, et al. (2011) Confirmation of HIV-like sequences in respiratory tract bacteria of Cambodian and Kenyan HIV-positive pediatric patients. *Med Sci Monit* 17: CR154-CR158.
5. Hainova K, Mego M, Wachsmannova L, Adamcikova Z, Stevurkova V, et al. (2013) Microflora of intestinal and respiratory tract in AIDS process. *J Antivir Antiretrovir* 15: 1-6.
6. Hainova K, Adamcikova Z, Ciernikova S, Stevurkova V, Krcmery V, et al. (2014) Detection of protein homologs with HIV-1 antigens in bacteria of positive patients-phase II. *Neuroendocrinol Lett* 35: 110-115.
7. Zaja V (2014) The fundamental role of bacteria and yeasts in AIDS progression. *J Vacc Vaccinat* 5: 238.
8. Wachsmannova L, Ciernikova S, Majek J, Mego M, Stevurkova V, et al. (2016) Internalization property of intestinal bacteria in colon cancer and HIV/AIDS patients. *Neuroendocrinol Lett* 37: 245-250.
9. Zajac V (2018) Evolutionary view of the AIDS process. *J Intern Med Res* 46: 4032-4038.