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The Origin of Viruses and Somatic Diseases

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Abstract- A main genome is the genome of bacteria or, more precisely, the genome of single-celled prokaryotic microorganisms that appeared on earth 3.5 billion years ago, which marked the beginning of biological life on the earth planet. How the bacteria appeared - there are many assumptions, but the main one is that the earth, like other planets in universe, participated in this creative process. One of the intermediate biological products of the bacterial genome is a human. The action of creating multicellular mammals from single-celled microorganisms that have "gray" matter and are capable of thinking has been going on for millions of years and is still going on today. The question remains: where does this process go - from Homo sapiens to Homo degrading or Homo natural? The significance of the relationship and interdependence between the main genome and the human genome has become particularly acute with the appearance of the SARS-CoV-2 coronavirus (disease X?). Here we will discuss the mechanisms of the emergence of coronavirus as one of the crucial stages of the adaptation process of virus formation from adaptogens and its impact on the further development of mammals, including humans.

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INTRODUCTION

The virus has been initially discovered in the late 19th century as the causative agent of an infectious disease in the tobacco plant¹. After this discovery, all subsequent findings of viruses from plants and animals have been related to the pathologies that they caused. As a result, if a new virus has been discovered, it was necessarily associated with a plant or mammalian disease. It has been thus established that the virus is an etiological factor that causes the disease and that it must will be fought as a source of infection. However, the virus cannot be the source of infection since it is its consequence or marker, that is, an indicator of violation of certain protective functions of the whole organism in a mammal, including in humans^{2,3}. Thus, the virus is a signal of what has already happened and is spreading. It have been assumed that the virus appears from adaptogens (Fig.1) circulating in prokaryotes (bacteria, archaea, etc.) in the form of complexes of molecular motifs designed to adapt mammals to changing environmental conditions. Prokaryotes, as is known, in addition to the external environment, live in the mammalian body - in the intestines, on the skin and mucous membranes, including the respiratory tract⁴. In humans, the number

of prokaryotes is being determined by the ratio: one human gene – some million genes of bacteria, archaea, etc.^{4,5}. If we take into account that bacteria multiply within a few minutes and are also under the control of the immune and hormonal systems (a kind of filter) of the macro-organism, they both adapt (improve) and are a source of pathogens (viruses, bacteria), as well as somatic diseases (Fig.2). Thus, the origin of both infectious and somatic diseases of mammals are adaptogens or molecular motifs located in prokaryotes.

Bacterial molecular motifs adjusted due to external factors genetically adapt the mammalian immune and hormonal systems to the environment, which, as a rule, does not manifest itself as a disease (Fig.2, left half). Adaptive events occur constantly, according to the biological laws of development, and allows us to modify by changes in the environment, i.e., to adapt. At the same time, the damaged or altered immune (anti-infectious) and hormonal (anti-"somatic") systems of mammals are not able to fight and utilize prokaryotic molecular motifs or adaptogens at the genetic level (Fig.2, right half). In turn, the inability to adapt normally leads to the appearance of infectious disease and, in the future, to somatic diseases. How do disorders occur in the immune and hormonal systems of mammals? These are, as a rule, xenobiotic factors of both natural and anthropogenic origin, including medical, which often goes against the biological laws of nature development³.

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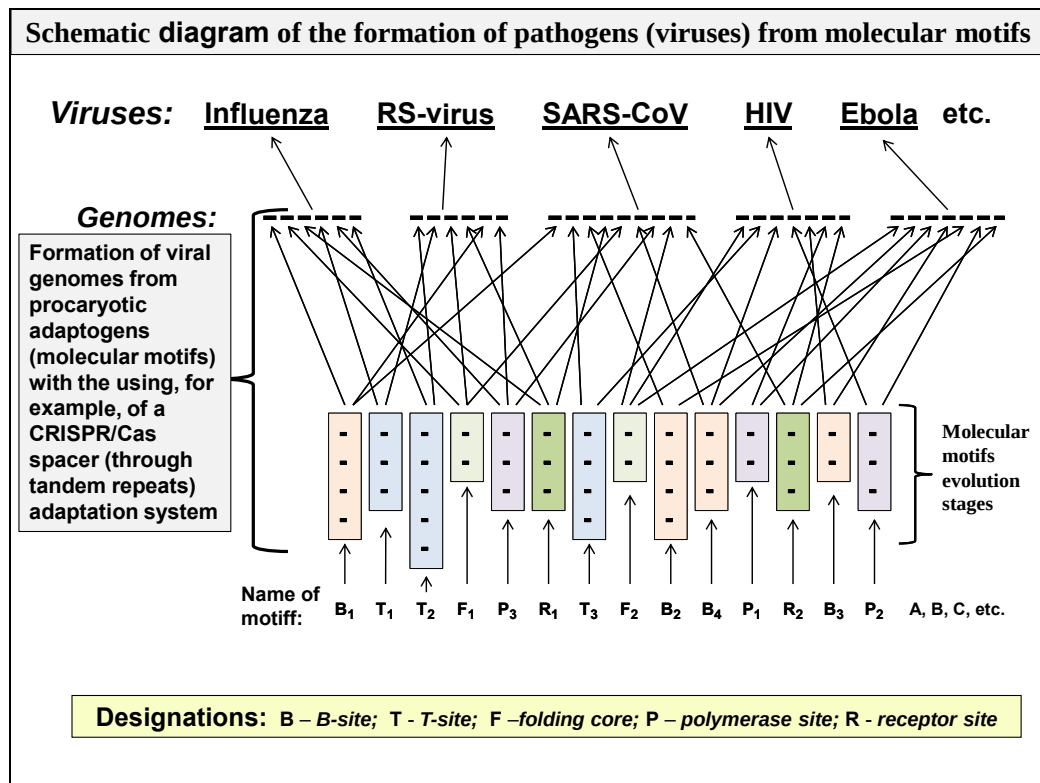


Fig. 1: Scheme for constructing of viruses from molecular motifs

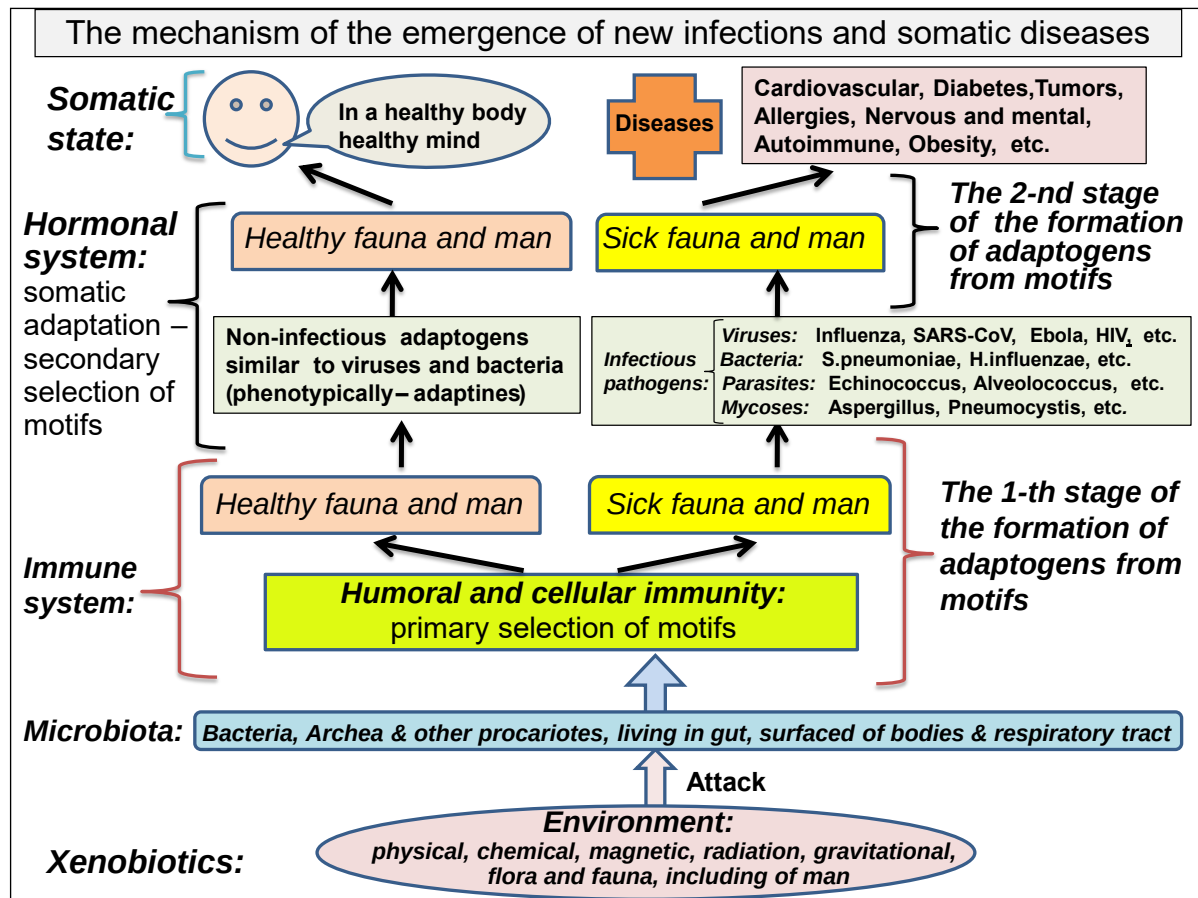


Fig. 2: Mechanism of appearance of infections and somatic diseases

The biological significance of the system of interrelation and interdependence between prokaryotes and multicellular (eukaryotic) organisms (flora and fauna) is the adaptation of eukaryotes to external environmental factors through the use of the prokaryotic microbiome. The mechanism by which modified molecular motifs are being transferred from prokaryotes to eukaryotes (from bacteria to mammals) is carried out, for example, by the CRISPR/Cas spaser adaptation system according to the retrovirus-like cut-and-paste principle^{6,7}. The loci where the molecular motif shall have been inserted are being marked by tandem repeats in the genomes of bacteria and mammals⁸. These repeats are being also found in viruses^{9,10}.

The main task of medicine is to learn the biological laws and use them for medical purposes. To realize this, it is necessary to correct the immune and hormonal systems of a particular person based on their characteristics. At the same time, the features of the immune and hormonal systems of each person depend on the prokaryotes that live in the intestine, on the surfaces of the skin and mucous membranes, as well as in the respiratory tract⁴. In this sense, prokaryotes manipulate molecular motifs (Fig. 1). Given that the ratio of molecular motifs in adaptogens (prokaryotes) and molecular motifs in even the largest viruses is always in favor of adaptogens, it is necessary to prevent the appearance of infectious and somatic pathology at the stage of pathogen formation.

Before attempting to carry out the genetic correction of prokaryotes at the level of molecular motives, it is necessary to determine the phenotypic markers of the immune and hormonal systems of a particular person. Objective methods of analysis (blood tests, ultrasound, computed tomography, biopsy, heredity, etc.) are being widely used to study the hormonal or "somatic" systems. But this is not enough to determine the existing somatic structural changes at the genetic level. A method for identifying somatic molecular markers will have been discussed below. As for the immune system, it is necessary to compare the molecular motifs of prokaryotes living in the macroorganism with the humoral and cellular defense systems adapted to them. Available diagnostic technologies make it possible to construct personal immunoantigenograms (IAG) based on the use of, for example, microarrays¹¹. Each microdroplet represents one molecular motif. The result is a unique matrix for each region or person, which can be used to analyze the infectious and somatic state of the environment or each person in specific geographical conditions¹².

With a high degree of probability, it can be assumed that the technology presented above for the analysis of the immune and hormonal systems of mammals, including humans, is relatively accessible due to its simplicity and has already been implemented in several closed laboratories over the past 15-20 years.

Medicine, whose task is to prolong the comfortable biological life of an individual person, does not always follow an individual approach. If this principle is still observed in medical (somatic) practice, then about prevention (vaccination), an individual approach has not yet been developed. The highest vaccination coverage is still considered preferable. In this case, as a rule, the vaccine is used against a specific infection, and all are vaccinated simultaneously (herd immunization) without taking into account the state of the immune and hormonal systems of a particular person. Moreover, vaccination of the population to eliminate the causative agent of the infection is inappropriate because the virus is not the cause but only the consequence of the disease. Thus, the fight against the result, and not against the cause, as a long-term practice has shown, exacerbated the medical problems declared in the form of "disease X"¹³.

One example of "disease X" is the coronavirus. This virus should have appeared because the ecological niche¹⁴, artificially created by humans for more than two centuries in the population of mammals, led to a gradual filling with molecular motifs that formed a prokaryotic adaptogen that manifested itself in the form of coronaviral infection. A feature of this virus that distinguishes it from other viruses, such as HIV, is that SARS-CoV-2 causes local immunodeficiency in the respiratory tract^{15,16}. As a result, chronic "smoldering" infections show their activity. In our opinion, these activated chronic bacterial infections cause a "cytokine storm." In this regard, it is clear why in the first wave of infection, older people get sick and die, and, with rare exceptions, children do not get sick. As a result of the current of the first wave, favorable conditions had been created to create a natural vaccine. Sexually mature young people who were asymptomatic with the coronavirus should have been a source of prokaryotic adaptogens for the elderly. At the same time, the closer the family ties and the same sex, the more effective the vaccine should have been¹².

Since this natural vaccination was not controlled for several reasons (isolation, antibiotics, antiseptics, etc., which prolonged and worsened the situation), the spread through the respiratory tract of inadequate adaptogens formed in sick and dying older adults in the form of genetically modified variants of coronavirus caused a second, more extensive wave of infection, involving middle-aged people and children. Subsequent waves of infection will mostly affect children and middle age, not so much in terms of the severity of the disease, but in terms of somatic consequences (Fig. 2, top right).

Vaccines developed using traditional technology based on neutralization and removal of the pathogen circulation from the population, even using different platforms, will have not a significant impact on preventing the development of coronavirus infection, especially with regard to somatic complications. The

harmlessness and immunogenicity of the preparation are not yet determining indicators of their effectiveness. Even medically effective vaccines against smallpox, measles, polio, yellow fever, etc., will eventually return to the human population in new infectious and somatic pathogens. Thus, epidemiological or ecological niches, artificially created as a result of vaccination using traditional technology and inconsiderate interference with the biological laws of nature, are filled with new infectious pathogens or their complexes, for example, disease X. In addition, the practice has shown, vaccines against AIDS, hepatitis C, and other infections cannot be developed using this technology.

However, the closest antigenic composition of the currently available adaptogen vaccines for SARS-CoV-2 is pneumococcus, so the available pneumococcal vaccine for individuals 60+ is currently more promising than the set of limited molecular motifs contained in the coronavirus itself¹⁷.

In the future, the obtained personal IAG will serve as a basis for introducing a new vaccine technology. The IAG encoded on electronic carriers, obtained during the analysis of blood serum during annual preventive examinations, can be used at a convenient time for a person to receive an aerosol (for the respiratory group of infections) or a yogurt (intestinal group) cocktail as a preventive vaccine against infectious and somatic pathology^{3,12}.

Therefore, the vaccine should not be viral against viruses and bacterial against bacteria, but prokaryotic adaptogenic or adaptive to correct the human immune and hormonal systems to changing environmental conditions. The number of molecular motifs involved in the construction of IAG are significantly limited due to the existence of common structures or molecular motifs in nature (Fig.1). Here the analogy with music is appropriate, where there are only seven notes and an infinite number of melodies.

As for the importance of using monospecific diagnostic genetic engineering and serological methods developed without considering the molecular motifs of adaptogens, the result, in most cases, cannot provide the complete and necessary information. It is especially evident with SARS-CoV-2 infection when the virus suppresses innate and acquired immunity in the respiratory tract and chronic bacterial infections (for example, pneumococci, enterococci, etc.) begin to activate, stimulating antibodies against other molecular motifs that do not coincide with motives of the virus (false-negative results). The situation is complicated when the diagnostic molecular motifs of the coronavirus and diagnostic motifs, for example, pneumococcus, are the same. For example, one of the immunodominant antigenic determinants localized in the lysine-rich domain of the SARS-CoV-2 phosphoprotein - at the position of amino acids 369-375 (KKDKKKK) - coincides with a large number of similar antigen-significant B-sites

located in the proteins of pneumococci, enterococci, staphylococci, and Klebsiella. Thus, it is not known which B-epitopes: coronavirus or bacterial stimulate antibodies? If it is bacterial, which most often happens with a coronavirus infection, then the treatment tactics based on the choice of an antibiotic will give a positive result, and there is no need to select antiviral drugs for a long time.

The possibility of analyzing the hormonal (somatic) state through the use of molecular motifs in the IAG had been confirmed by the publication of Tilson et al.¹⁸, where it has been shown that antibodies specific to the structural protein of the Ebola virus was detected in patients with aortic aneurysm. Thus, firstly, confirms the position that there are common antigenic structures and, consequently, common molecular motifs in viruses and humans. Secondly, it confirms the ability to diagnose the somatic state by serological methods. In Figure 2 (left part), adaptogens (the formed complex of molecular motifs) involved in the hormonal (somatic) adaptation of a healthy person manifest themselves as adaptins capable of inducing antibodies that serve as a marker of the hormonal (somatic) state. In result, if infectious pathogens are markers of disease, then adaptins are markers of the hormonal (somatic) state of mammals, including humans. It has to be assumed, molecular motifs found in animals in the form of 827,000 viruses (the data presented at the 68th Annual International Conference "Association of Wildlife Diseases," held on August 4-9, 2019 in Tahoe City, California (USA), Zoe Grange, et al.: "SpillOver - a new web tool to assess spillover risk of wildlife viruses") were non-infectious adaptogens or adaptins.

The main task of advanced diagnostic technologies is the epidemiological forecasting of new infections and somatic changes based on the construction of regional and personal immunoantigenograms with subsequent correction of the human immune and hormonal systems based on the use of biological laws of nature. In this plan, it is necessary to combine the existing methodological developments and improve them for the new tasks arising from the concept: "In nature, small fragments of genetic information (molecular motifs) evolve into large, structured formations called viruses. At the same time, the same motive can be found in different micro- and macro-organisms, that confirms the unity of the biological world, its close relationship and interdependence"³.

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