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Xenobiotics: The Impact of SARS-CoV-2 on the Evolutionary Development of Human

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Abstract

The importance and role of xenobiotics involved in the development of the microbiota is a determining factor in the evolutionary development of mammals, the entire animal and plant world. This is confirmed by the emergence of new and emerging infectious agents. The gut microbiome (normal microflora) plays a decisive role in maintaining normal physiological "immune and hormonal" processes in the human body and is an "ambulance" or a kind of "adaptogen" that restores the natural course of positive evolution of living organisms when exposed to adverse environmental factors. Biological, chemical, physical and other factors adversely affecting the microbiome can lead to numerous medical problems, including the appearance of multiple endo- and exogenous infectious pathogens (bacterial, viral, parasitic, fungal diseases), as well as somatic diseases such as obesity, diabetes, autoimmune and oncological diseases, as well as disorders of the central nervous system. This report attempts to open up the natural mechanisms involved in the formation of new types of pathogens, including SARS-CoV-2, in order to use biological laws for medical purposes. Currently, the opposite happens, eliminating medical problems, a person negatively affects the process of his improvement, turning Homo Sapiens into Homo Degradatum, while including the whole plant and animal world in this negative process.

Keywords: Xenobiotics; Microbiota; CRISPR/Cas; Tandem repeats; Vaccination; Technologies; SARS-CoV-2; Evolution mammals

Introduction

The main element in the fight against pathogens at the present stage is vaccination. Since the discovery by the English scientist E. Jenner in 1796 (against smallpox) of a method of protecting against infection by vaccination, more than one century has passed, but the main requirements for vaccines - the elimination of the causative agent from the environment and the maximum coverage of the population with vaccinations - have remained the same. Are we all the same in immune and hormonal development to intervene artificially in these complex interconnected and interdependent life systems? The problem of finding new vaccination technologies arose especially acute due to several reasons: 1) not all pathogens can be applied to the old technology (HIV, hepatit C and others); 2) with mass vaccination, not all patients produce protective antibodies; 3) vaccination is carried out without taking into account individual (biological) characteristics of a person; 4) the possibility of “disease X” appearance is alarming, that was announced by WHO experts in March 2018 in Davos [1]; 5) in the biological problems described above, the dominant role belongs to xenobiotic factors - the main elements of the environment, often negatively affecting the animal and plant world due to human activity, which again returns to man.

If we look at the development of the biological world in general terms, taking into account the accumulated scientific information about the variability of the human genome [2], involvement of bacteria and archaea in the formation of viruses as pathogens and their influence on evolution processes [3-5], the role of xenobiotics in the formation of earth microflora [6], the participation of retroviral mechanisms, including a system of spacer adaptation of CRISPR/Cas micro- and macroorganisms to changing environmental conditions [7-9], the process of adaptation of mammals can be presented in the form of a scheme: xenobiotics → genetically changed bacteria, archaea → man → adapted bacteria and archaea, then again xenobiotics and further in a spiral. The mechanism for the development of nature in this direction arose from the concept of the origin and evolution of the biological world, published in the scheme form in 1997 [10] and described in a concise form later [11]. Concept: "In nature, small fragments of genetic information (molecular motifs) evolve into a large structured entity called viruses. At the same time, the same motive can occur in different micro- and macro-organisms, confirming the unity of the biological world, its close relationship and interdependence." Assuming that the bacteria adjusted to the xenobiotics form a new biocenotic environment around them. After that rapidly formed bacterial immunity is used by prokaryotes through retrovirus-like mechanisms, including the CRISPR/Cas spacer adaptation system, on the "cut and paste" principle, to edit the immune and hormonal systems of the macroorganisms (including human) to new environment factors [7-9].

For many centuries, adaptation of mammals to coronaviruses took place without clinical manifestations. Bacteria, archaea and other microorganisms involved in the formation of adaptogens designed to adapt specific species of mammals, as well as birds [12], than under the influence of immune (anti-infectious) and hormonal (anti-somatic) systems of animals form adapted intestinal microflora, what does not lead to the appearance of viruses (pathogens) from adaptogens [5,9]. If clinical manifestations arose in some cases, they were not epidemic in nature, and the disease occurred in the form of single respiratory diseases. For the first time, the most pronounced clinical effect with deaths from coronavirus SARS-CoV was happened in China in 2002 [13-15], then in 2012-2014 in the Middle East - MERS-CoV [16,17].

At the same time, it is possible that his individual pathogenic molecular motifs were found in other viruses earlier, for example, in 1918, when a pandemic of the influenza virus H1N1 (flu "spanish,") killed tens of millions of people. It can be assumed that the pathogenic molecular motifs of the influenza virus were genes encoding the structural ORF9b protein that suppresses congenital immunity (blocks cell mitochondria), and NS5p non-structural virus specific peptide, which inhibits the production of interferon and is now found in SARS-CoV-2 [18]. In epidemic cases, the adaptogens of bacteria and archaea filled the formed epidemiological (ecological) niche [19] and produced a new pathogen (virus). Due to biological features, coronaviruses, including SARS-CoV-2, suppress non-specific and specific immune defenses in the upper and lower respiratory tract on the early stage of infection. As a result, chronic respiratory bacterial (streptococcus, staphylococcus, leptospires, etc.) and may be parasitic and fungal infections are appeared [20]. This, in turn, leads to a "cytokine storm" and the production of the severe acute respiratory syndrome (SARS).

The mechanism by which the adaptogen is transformed into a pathogen (virus) is implemented using the bacterial CRISPR/Cas spacer adaptation system, using the same tandem repeats available in bacteria and archaea, as well as in viruses [21], including coronaviruses [22] and human [23-25].

The human gut is estimated to contain up to 100 trillion microbes, and types of microbes include not only bacteria, but also viruses, archaea, fungi, and protozoa [26]. It turns out that one of the 30,000 genes in humans accounts for more than one million genes of the intestinal microbiota! It is increasingly understood that the intestinal microbiome plays a decisive role in maintaining normal homeostatic processes in the body (immune and hormonal system). Biological, chemical, physical, etc. factors, which have negative effects on the microbiome, can lead to numerous medical problems, including the appearance of multiple endo- and exogenous infectious pathogens (bacterial, viral, parasitic, fungal diseases), as well as somatic diseases such as obesity, cardiovascular diseases, diabetes, autoimmune and cancer diseases, as well as disorders of the central nervous system [9,27].

Based on the peculiarities of the development of the infectious process in coronaviruses and taking into account the fact that SARS-CoV-2 causes human immunodeficiency in the respiratory tract, which in turn stimulates the development of bacterial pneumonia, traditional technology of vaccine development requires a significant revision. It is known that the targets for viruses that cause immunodeficiency (HIV, LHM, SARS-CoV-2) are different cells of the immune and non-immune system, so to fight them, it is necessary to carry out a specific immunocorrection based on the comparative analysis of molecular motifs of the intestinal microbiota of a certain region and specific immunoantigenograms of a group of people or a specific person living in the area. An alternative to the prevention of SARS-CoV-2, for the first time, may be the pneumococcal vaccine for adults, containing the main immunodominant antigenic determinants, which protects

against the development of severe pneumonia. As a last resort, those without immunopathology can also use intact polyoxidonium [5] or, for all, for example, a bacterial cocktail of normal microflora that restores the gut microbiota, the same bioyogurts, etc.

In the long term, as a new medical technology for the prevention of infectious and somatic pathologies, it is most realistic to carry out individual immunocorrection based on individual characteristics of humans or populations of animals grown in the same geographical conditions. Immunoantigenograms, built using multipeptide diagnostic methods, show different levels of antibodies available in a particular person. In the case of a high titer of antibodies to a specific B-epitope (a clone of antibodies), this peptide is excluded from the system of adaptogenic correction. This is necessary due to the possibility of developing tolerance or the appearance of autoantibodies, which can lead to the development of allergies.

Maybe multipeptide diagnostic test systems designed to build individual immunoantigenograms are frightening because of the exorbitantly large number of peptides included in the test system? However, given the fact that the same peptide is part of different infectious pathogens, and they are easily classified (according to the principle of the table of chemical elements of D. I. Mendeleev), this is not a super task. It is appropriate to compare it with music, where there are only seven notes, and there are infinitely many melodies, in this case there are a lot of viruses, and the number of molecular motifs formed by adaptogens is relatively small.

As evidence of the need for an individual approach in the immunoprophylaxis of infectious diseases, it is necessary to have in the form that the immune and hormonal systems are interrelated and interdependent. You can't regulate one without affecting the other. For example, in the population of people living in Southeast Asia (China, Mongolia, Japan, Korea, Vietnam), the somatic complex produced by hepatocytes and responsible for the utilization of an alcohol in the body (alcohol dehydrogenase - ADH and acetaldehyde dehydrogenase - AADH), differ in activity compared to Europeans and North Americans [28,29]. High activity of ADH (allelic gene variant - ADH1B*47His) and low activity of AADH (allelic gene ALDH2*2) are characteristic for citizens of Southeast Asia countries. Mortality from coronavirus in these countries (on October 20) ranges from 0.3 (China) to 1.3 (Japan) per 100 thousand population. In the inhabitants of Europe and North America, containing a highly active gene for ADH and a highly active gene for AADH (for example, the allelic gene ALDH 7), the mortality rate from COVID-19 per 100 thousand residents varies from 49.7 (France), and 69,2 (USA) to 73.4 (Spain). Mixed variants of AADH activity give intermediate mortality rates (Canada-25,7, Russia -17,2, Germany-12,1).

Conclusion

This communication raises the question: if you are immunizing against SARS-CoV-2 with a traditional vaccine, can you expect an increase in mortality in South Asian countries and only a slight decrease in European countries and the Americas? It's possible. However, the relationship between business or globalization and fundamental science should not be strained!

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