American Journal of
Biomedical Science & Research

www.biomedgrid.com
ISSN: 2642-1747

Mini Review

The Main Genome is the Source of Viruses

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To Cite This Article: *Vladyko AS* and Petkevich AS. The Main Genome is the Source of Viruses. Am J Biomed Sci & Res. 2023 20(5) AJBSR. MS.ID.002741,* DOI: 10.34297/AJBSR.2023.20.002741

Received: November 11, 2023; **Published:** November 27, 2023

Abstract

The appearance of coronaviruses, like other viruses in mammals, is provoked by environmental factors - xenobiotics, formed mainly due to unreasonable human activity and resulting from the formation of an ecological (epidemiological) niche filled with molecular motifs of the intestinal microbiota using, for example, CRISPR/Cas mechanism, when these motifs try to adapt the immune and hormonal systems. It all depends on how much xenobiotics damage the immune and hormonal systems. Therefore, viruses are not the cause, but the consequence of the disease. The fight against viruses with the help of vaccines prepared on their basis has disrupted and delayed the natural mechanisms of regulation of biological processes in plants and mammals for more than 200 years (since the discovery of the smallpox vaccine). Thus, viruses arise from bacteria, and adaptation ends with microbiota bacteria, which can cause disease or, as a rule, in a healthy organism, the stage of bacterial infection is asymptomatic. In the latter case, the molecular motifs of the microbiota are adaptogens, not apoptogens (viruses) and spread in the environment, adapting or infecting others. This mechanism is also applicable to somatic diseases, such as cardiovascular, autoimmune, oncological, etc. Structural and functional features of SARS-CoV-2 proteins suggest that its main property is the ability to suppress innate and acquired nonspecific viral immunity in the respiratory tract (unlike HIV, in which all immunity is suppressed). This led to the reactivation of chronic, mainly bacterial, respiratory infections - pneumococci, staphylococci, hemophiluses, however, fungal infections can also be observed – mucormycosis, aspergillosis, etc. This feature of the coronavirus prompted doctors at the beginning of the epidemic (2020) to use a pneumococcal vaccine, which, as it turned out, similarly to the coronavirus vaccine reduces the severity of the disease and mortality. We propose a technology of individual vaccination based on personal diagrams of human antibody clones specific to new circulating molecular motifs. Analysis of the profile of antibodies, namely their individual clones to the antigenic structures of the virus in humans before vaccination, should serve as a basis for excluding or including individual immunogens in a personal vaccine. In the future, the data from the antibody diagrams of each person can be transferred to a USB flash drive and used to obtain an aerosol or a nutritional cocktail formed from bifidobacteria adapted to infectious agents by a natural mechanism: xenobiotic (a new structure of the antigen) - a bacterium.

Keywords: Main genome, Nature of SARS-CoV-2, Molecular motifs, CRISPR/Cas system, Prokaryotes, Microbiota, Adaptogens, Apoptogens, Personal vaccination technology

Introduction

From the analyzed publications [1-6] it follows:

a) For 1 human gene (a person has 29-31 thousand genes, according to other data 20-25 thousand genes), there are approximately 1million molecular motifs (spacers, units of evolution) located in the genes of bacteria living in the intestine, on the skin, mucous membranes, etc.

b) The mitochondrial apparatus of mammalian eukaryotic cells, including humans, has the genetic code of bacteria

c) Approximately 300 bacterial genes are contained in the chromosomes of human somatic cells

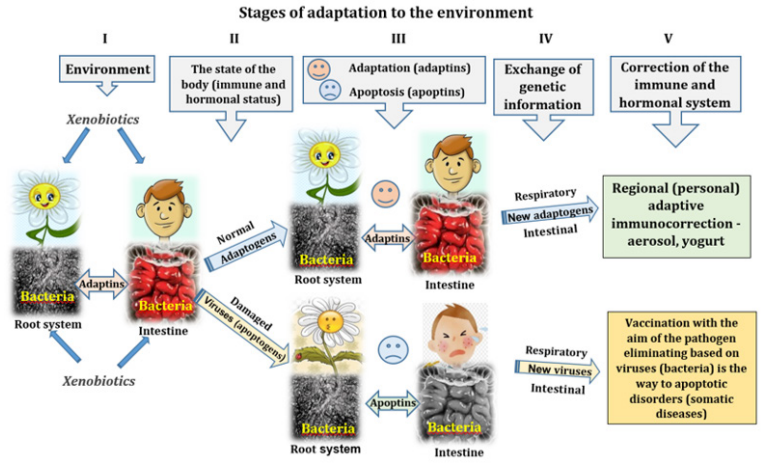
d) The reproduction cycle of bacteria is a matter of minutes, and they instantly genetically change under the influence of the external environment (ecology) and immediately transmit these changes through a retrovirus-like mechanism, for example,

through the CRISPR/Cas adaptation system, to the macro-organism.

It was previously shown [6]: *"Viruses, their derivatives and closely related structures make up at least 43% of the human genome, which leads to the conclusion that natural selection in humans and their ancestors occurred in partnership with hundreds of viruses"*. At the same time, as follows from our analysis [7], it is not viruses and their structures make up 43% of the human genome, but a human is a small genetic derivative of viruses or, more precisely, adaptogens, which are contained mainly in bacteria and are the source genetic material or the main genome that regulates the processes of existence and appearance of biological diversity (animals and plants). Bacteria, mentally and morphologically patronizing a person, constantly and every second transmit acquired changes to the human genetic apparatus, using a retrovirus-like mechanism formed over millions of years of evolution - "cut and paste". In addition to retroviruses, bacteria and archaea have such a mechanism - this is a CRISPR/Cas system for editing the genomes of macroorganisms based on tandem repeats available in all viruses, as well as one cellular and multicellular organisms [8-12]. Publications on this part give reason to hope for this mechanism in human and animal gene therapy [13-15]. For example, genome editing using the CRISPR/Cas9 platform precisely modifies endogenous gene targets in many human cell lines and animal models, which can serve as an effective clinical treatment method for patients with hematological diseases [14]. It is assumed that *the identity of tandem repeats in bacteria and humans is necessary for the exact entry of the spacers (molecular motifs) of bacteria into the human genome at the right time and in the right place to correct its immune and hormonal systems, thus, a person adapts to a changed environment*.

The Emergence of Adaptogens and Viruses

A person with a normal intestinal microbiota and, consequently, a healthy immune and hormonal system lives most of his life without serious infections and somatic diseases. In this case, a person exchanges "healthy" viruses with the external environment (natural vaccine or adaptogens). Conversely, when these systems are damaged by xenobiotics, and the microbiota is unable to restore the normal functioning of the immune and hormonal systems, the microbiome forms apoptogens (pathogenic viruses) that can cause diseases in weakened organisms and do not cause in strong ones. Figure 1 shows the scheme of the molecular motifs circulation (units of evolution) formed by the microbiota (bacteria) for the adaptation of multicellular organisms (plants and animals, including humans) to changing environmental conditions (Figure 1).



Note*: Xenobiotics (here)- substances of material and mental origin, foreign to the organism. **Adaptogens** (here)- genetic structures (molecular motifs) microbiota, initiating the synthesis of adaptin's proteins in the organism. **Adaptins** (here)- a group of proteins synthesized by the organism in response to xenobiotics in order to adapt one to a changing environment. **Apoptogens** (here)- genetic structures (molecular motifs) microbiota, initiating the synthesis of apoptin's proteins in the organism. **Apoptins** (here)- proteins synthesized in the organism by molecular motifs of the microbiota in conditions of damaged immune and hormonal systems. **Apoptosis** (here)- a multi-stage program of the organism's death, regulated by a group of special molecular motifs of microbiota.

Figure 1: Scheme of distribution of adaptive or apoptotic (viral) molecular motifs in plants and mammals depending on the state of the immune and hormonal systems (stages I-IV) as a basis for choosing the technology (method) of prevention and treatment (stage V) *.

*The authors do not pretend to consolidate a new interpretation of the given terms (to avoid overload during description and the appearance of new terms).

It can be seen the development of the infectious process can be divided into 5 stages. From 1 to 4 stages, depending on the immune and hormonal state of the organism, either adaptation (upper part) or disease (lower) is formed. In the first case, adaptogens (or non-pathogenic viruses) and their proteins are involved in the process, and in the second-apoptogens or pathogenic viruses and apoptins. At the 5th stage, options for correcting the immune and hormonal systems are being considered. If the correction is carried out with the help of adaptogens, there will be an improvement of the organism, if on the basis of a virus - distant somatic diseases.

Conclusion

The technology of creating vaccines, developed more than 200 years ago, based on the stimulation of virus neutralizing antibodies and pursuing the goal of removing the pathogen from circulation in the human population, is unattainable. First, the same type of vaccine stimulates the production of the same type of antibodies to ensure herd immunity, and it is easier for the pathogen to mutate in this monotony; secondly, why remove something that should not be removed, but should adapt according to the natural mechanism. There is still no vaccine against HIV, hepatitis C and a number of other dangerous infections. There are many questions about the existence of problems related to the somatic consequences of the use of vaccines against smallpox, polio, measles and a number of bacterial infections. Thus, the current vaccination system based on the introduction of a vaccine through a needle is barbaric and does not exclude the possibility of manipulation of genetic material, as well as violent. And this is at a time when the theory of the "golden billion" is being discussed!

We propose a technology of individual vaccination based on personal diagrams of human antibody clones specific to new circulating molecular motifs. Analysis of the profile of antibodies, namely their individual clones to the antigenic structures of the virus in humans before vaccination, will serve as a basis for excluding or including individual immunogens in a personal vaccine. In the future, the data from the antibody diagrams of each person can be transferred to a digital chip or USB flash drive and used in the cocktail device to obtain an aerosol or a nutritional cocktail formed from bifidobacteria adapted to infectious agents by a natural mechanism: xenobiotic (a new structure of the antigen)-a bacterium. Thus, we do not offer a vaccine preparation, but an easily accessible technology that takes into account the peculiarities of both a particular country and the individual biological characteristics of each person.

Acknowledgement

None.

Conflict of Interest

None.

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