Biological Weapon or Biological Threat?

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Abstract: A hundred years have passed since viruses were first discovered and throughout this time humans overwhelmingly regard them as agents of infectious diseases. Based on the previously developed concept (1997) on the role of viruses in the origin and evolution of biological kinds, we found it necessary to discuss another point of view pertaining to the biological nature and function of viruses. Adaptogens are structures similar to a virus but differ from it by disseminated format in the macro organism by the principle of mixed co-viral system are proposed for consideration as a biological complex of molecular motifs designed to adapt humans, animals, plants, bacteria (essentially all flora and fauna) to changing environmental conditions to maintain species diversity. From this standpoint a virus is regarded as a consequence of environmental effects on adaptogens, and serves as an indicator or marker of disease rather than a factor of evolution. In this regard, we propose to revise the established provisions for the diagnosis, prevention and therapy of infectious and somatic diseases as well as the classification of viruses.

Keywords: Viruses, Adaptogens, Classification, Evolution, Diagnosis, Vaccination.

In 1892, the Russian scientist Ivanovsky D.I. discovered an invisible particle that upon filtering through a sterilizing membrane, application of the contents of the filtrate to tobacco plants caused changes in the mosaic of the leaves. This particle was called tobacco mosaic virus - the causative agent of the disease. Thus, the word "virus" has become associated with "disease" in the world of science and everyday life. After that, many other viruses were discovered to be associated with bacteria, plants, animals and humans, each with unique infectious processes and mortality outcomes. Sadly, the latter was exploited by humans for the development of biological weapons, especially when highly pathogenic viruses were discovered, such as the Ebola virus, Marburg, Lassa, Hendra, Nipa, dengue, CCHF.

In 2010, Frank Ryan, a physician and evolutionary biology professor at Sheffield University (UK) published the book “Virolution” [1] and written in the preface was: “The main idea of this book is shocking. All living things on the planet, including people, live in symbiosis with viruses, evolve with them and thanks to them ... survive. Viruses, their derivatives and closely related structures constitute at least forty-three percent of the human genome, which leads to the conclusion: natural selection in humans and their ancestors occurred in partnership with hundreds of viruses.” Since the discovery of viruses nothing has changed in terms of determination of virus’s positioning in nature - viruses and disease concepts are still monolithic. However, it should be noted - the viruses themselves are not the cause of the disease.

In this report we propose a different point of view regarding the biological nature and purpose of viruses. To do so, we offer our interpretation of the preface of the book “Virolution” with the following comments:

1. Viruses are the products of environmental adverse effects upon adaptogens [2]. Adaptogens (as opposed to the concept of “pathogens”) are very similar in structure to viruses, but differ from them in a wider range of nucleic and amino acid sequences and do not cause diseases in humans, animals, plants, or bacteria. Adaptogens are the main and determining factor in preserving the diversity of flora and fauna on the planet. The unit of evolution in nature is the molecular motif, of which adaptogens are formed through domains, and consecutively disease markers or viruses of humans, animals, plants, and bacteria are formed from adaptogens [12]. Thus, adaptogens are the basis of life on the planet, and viruses are a kind of disease marker, or the biological manifestation of adverse environmental conditions on adaptogens due to, for instance, urbanization — the impact of technological progress on nature. It is not the virus's fault that the adaptation sometimes ends in mortality or a serious illness. Adaptogens in everyday life, generally, “work” imperceptibly for the benefit of humans, animals, plants, and bacteria. Man, along with other representatives of flora and fauna, in terms of biological sense and evolutionary development is only a large biological library of molecular motifs.

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E-ISSN: 2311-8741/19

2. Viruses and their structures are not derivatives from man, but man is a small derivative of adaptogens (viruses). Initially on the earth which can be viewed as a cosmic incubator, amino acids appeared, followed by nucleic acids, ultimately giving way to proteins. From this perspective, evolution of proteins was a consequence of the primordial system adapting to changing environmental conditions. Man is not the terminal biological branch, but an intermediate one in its development. There are more evolutionary advanced biological systems and they should be searched for in a manner analogous to the development and prediction of chemical elements carried out by Russian scientist Mendeleev D.I. Nikola Tesla described the existence of such a biological system through the demonstration of global physical phenomena in nature. Thus, the nature or life (the mode of existence of protein bodies) continues to form from chemical elements under the action of physical factors. The biological component and the role of adaptogens and viruses in this evolutionary process remains to be investigated. The evolutionary branch of Homo Sapiens, whether we want it or not, will be continued in Homo Accommodations or Homo Adopticus (a person adapted or harmonized with nature). If this does not happen, then it is only due to man's fault, *i.e*. which subspecies of Homo Sapiens (Homo "Amoralis" or Homo "Normalis") will win.

3. The assertion that "viruses, their derivatives and closely related structures comprise at least forty-three percent of the human genome" is incorrect. Conversely, the human genome constitutes a very small part of the genetic material circulating in nature among bacteria. Man is only an epidemiological unit (and not the best) among all the flora and fauna on the planet [3].

4. Natural selection, as known, implies the survival of the fittest, *i.e*. loss of the weak. The assertion that "natural selection among humans and their ancestors occurred in partnership with hundreds of viruses" is erroneous, since, in general, no fight is waged between partners. More accurately, adaptogens can be defined as partners in natural selection from medical point of view.

Adaptogens adjust us (humans, animals, plants, bacteria) to changing environmental conditions, and man, mindlessly interfering with this unique and sensitive evolutionary forming system (draining swamps, cutting down forests, mining the introduction of any species of animals and plants in an unusual environment, technological accidents, etc.) introduces extreme confusion and thereby turns adaptogens into viruses. Unfortunately, this series also contain the main principle of preventive medicine "vaccination to eliminate the pathogen". In our opinion, this inevitably leads to the formation of environmental (epidemic) niches and the emergence of new, unknown, and most importantly, unpredictably dangerous "X infections" and somatic diseases. In this case, the principle of "vaccination in order to maintain adaptogens" ("individual vaccination" or "personalized immunocorrection") [4] is more appropriate. In fact, viruses are just a marker of an already occurring disease or an indicator of suffering system in humans, animals, plants, and bacteria.

However, before you can correct immunity, you need to know specifically what to correct. For this purpose, based on the use of molecular motifs (antigenic determinants), we propose constructing immunoantigenograms (IAG) for a specific person and a specific geographic area — the biocenotic habitat of micro- and macro-organisms [5]. Taking into account the fact that in the 20th century, the methodological and instrumental basis in this regard are well developed and implemented for viruses, it is proposed to correct them for adaptogens. The fact that this is relevant can be understood from the list of diseases published by WHO experts in March 2018, which, according to experts, may pose a threat to the healthcare systems of most countries in the near future [6]. "These are Rift Valley Fever, Zika, Ebola, Marburg, Lassa, MERS, SARS, Nipah, Hendra, CCHF. At the same time, the range of infections can be expanded with new pathogens unknown to date," - experts wrote. Disease "X" was the name of the new disease. According to them, "... this infection is so deadly and mysterious that we do not know anything about it, except that this may be the next global epidemic." And what about the long-known "non-dangerous" pathogens, such as tuberculosis [7], vaccinia virus [8] - there are no problems? Or with the rubella virus [9], where the elimination of the virus is still proposed in the 20s of this century? Are all problems with smallpox, polio or measles solved? To decipher epidemics "X", it is proposed to create such a surveillance system that will allow to conduct a higher-level epidemiological analysis (creating IAG based on molecular motifs) and, most importantly, to make an epidemic forecast on the

emergence of new infectious agents and determining the scale of epidemics. In order to prevent them, personalized immunotherapy based on IAG is proposed. As a result, a technology will be introduced that can be used to decipher, for example, an outbreak of an unexplained infectious disease in Uganda [10], where in August 2018, 9 people out of 23 cases died (malaria? Marburg fever?) or at least to understand what it was, *i.e*. how the virus in the survivors turned into adaptogens, and from them into molecular motifs (possibly somatic proteins), which can be analyzed to make prognostic conclusions in terms of diagnosis (prediction) and vaccination (adaptation) of a man to changing environmental conditions.

Regarding the need to create new technologies, this task is long overdue and follows naturally from a message to The Telegraph in 2018 by the Executive Director of the Research Council of Norway and WHO Advisor John-Arne Rottingen, who in his message suggested “to prepare and plan work flexibly from the point of vaccine development and diagnostic tests; we want to see “plug and use” technology platforms implemented that will “work” for anyone, or, in extreme cases, for a large number of diseases or systems that allow us to create countermeasures on the principle of rapid response” [11]. In our publication “Biological Safety and Viral Infections” [2], the concept of the origin and evolution of new and newly emerging viruses was once again discussed, where, from the point of view of biological safety, a new technology arising from the concept was considered. In our opinion, this concept acquires special significance from the point of view of cognition of what biological weapons are at the present stage, taking into account the general biological and emerging social factors.

In this regard, it is appropriate to reiterate this concept with the detail of individual points regarding the possibility of creating biological weapons: “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.” In the form of a diagram, this concept is presented in a 1997 publication [12], where different molecular motifs are cited. However, for understandable reasons, only one type of molecular motifs will be analyzed in this message - diagnostic or B-epitopes.

Since our publication on biological safety [2] mainly discussed and considered the first part of the concept, it is now appropriate to discuss the second part which states that “the same motif can be found in different micro- and macro-organisms, confirming the unity of the biological world, its close relationship and interdependence."

The origin of the concept of molecular motive is closely related to the diagnosis of dangerous infections and began with unpleasant moments for us. In 1987-1989, when the USSR existed, our pilots from Odessa provided assistance to Angola (South-West Africa) in the form of civilian freight. During the next flight to Angola, one of the pilots, arriving in Odessa, felt ill and died suddenly from an incomprehensible hemorrhagic fever. The biological material collected was delivered to our institute (Belarusian Research Institute of Epidemiology and Microbiology) to exclude particularly dangerous viral infections. A second part was studied by a group of specialists from the Odessa Sanitary and Epidemiological Unit (SEU) for malaria. According to epidemic indications, we were meant to exclude Lassa fever. However, in our tests (enzyme-linked immunosorbent assay and immune blot) samples were positive for this pathogen [13]. Odessa specialists found the causative agent of tropical malaria (*Pl. Falciparum*) in red blood cells. In the end, the conclusion of the doctors was not in our favor. But what about our results? Subsequently, 13 blood sera of patients with a diagnosis of malaria obtained from Leningrad (now St. Petersburg) were specifically targeted for the presence of antibodies to the Lassa, Marburg and Ebola viruses in two tests: immunofluorescence and enzyme immunoassay. It turned out that part of the sera reacted with one antigen, several sera with two, and one serum No. 1754 reacted with all these antigens in two tests [14], and also with human immunodeficiency virus in immune blotting [15]. Thus, the same B-epitopes or antigenic sites participate in the construction of proteins of different origin - viruses and parasites.

The fact that B-epitopes are one of a certain number of molecular motifs involved in the formation of adaptogens is confirmed by numerous publications, the most obvious of which can be considered the message of Rubin G.M. with coauthors [16], who found 177 of 286 human infectious genes in a common fly.

The somatic component of this general biological evolutionary process, based on molecular motifs, was analyzed using bovine serum albumin (BSA) as an example, in which, during bioinformatic analysis of amino acid sequences, three consecutive B-epitopes were found in the C-terminus of the protein similar to

the antigenic determinant of nucleoprotein hantavirus. Human serum obtained from a patient with hemorrhagic fever with renal syndrome (HFRS), specifically reacted with a fragment of BSA hydrolyzed by chymotrypsin [17]. In line with this finding, the data obtained earlier by Tilson *et al*. Showed that the serum of a patient with an aortic aneurysm reacts in immune blotting with the matrix (M-protein) of the especially dangerous Ebola virus [18].

Thus, under the influence of the environment (from chemical elements and under the influence of physical factors), amino and nucleic acids are getting re-formed each time. Re-formed amino and nucleic acids give rise to molecular motifs. In turn, molecular motifs give rise to polypeptides though domains. Polypeptides give rise to functional proteins, which form complexes with nucleic acids and finally assemble adaptogens designed to harmonize (adapt) humans, animals, plants and bacteria to the environment. Ecological niches created as a result of urbanization, increasingly began to manifest themselves in the form of new, previously unknown infectious diseases and not only in humans, but also in other representatives of the fauna. For example, in the laboratory of M. Salvato (USA, 2013), an analysis of the genome of the arenavirus isolated from python showed the presence of similar genes borrowed from bunyaviruses, filoviruses and somatic proteins (ubiquitin ligase) [19]. The authors of the publication concluded that the snake arenavirus was the result of the formation of an ecological niche. Therefore, new viruses are the result of exposure to adverse environmental conditions (the biocenotic system). They serve as a disease sensor, and manipulation with them (the creation of diagnostics, vaccines, chemotherapeutic drugs) only aggravates, causing confusion in the biocenotic habitat of humans, animals, plants and bacteria.

To the question: who develops biological weapons? The answer is obvious. And we should not imply that if there is something wrong with nature in the Eastern Hemisphere, then in the Western hemisphere it will not manifest itself. This can be confirmed by the recent outbreaks of West Nile fever (WNF) in Western and Eastern Europe. It can be assumed that this could have begun with a synchronous outbreak of WNF in the USA and Russia in 1999 [20].

Why information on molecular motives is not analyzed in most developed countries is unknown. Maybe because we are a planet of 7.5 billion inhabitants? Why the annual messages of WHO experts in relation to dangerous infections (the last time, disease “X"), offer all countries to deal with what is unknown? After all, in fact, the diagnosis of a virus is a clarification of the consequence. Vaccination to eliminate the virus is the same fight with the effect, not with the cause! On the other hand, how can viruses be classified – they are a kind of “miscarriage” by nature? How many “miscarriages” await the fate of being classified? Maybe it's time to systematize the molecular motifs (make a “biological Mendeleev periodic table”) and get involved in the adaptation process ourselves? After all, there are only seven notes in music, but melodies ...?

In terms of diagnostics and prevention of infectious and somatic diseases, our proposals in more or less complete form have been set forth in scientific publications over the past 15-20 years. In a more or less unified form - in publications of recent years [2, 5]. The starting point for these findings was published since 1982, when it was proposed to look for chemotherapy-resistant strains of the influenza virus in a virus population obtained from a chicken embryo cell culture in a single-cycle reproduction of the virus under an agar coating with the inclusion of a chemotherapy drug in it [21]. The more resistant plaques found under the agar coating reflects the more the environment is altered. The clues that nature performs this way are in nature itself. For example, a tobacco ringspot virus (TRSV) triggers an infectious process in a plant cell only after all its 4 virus particles assemble in a single cell. In a healthy body (with a normal immune and hormonal systems) an adaptogen formed from molecular motifs implements its genetic information for humans, animals, plants, and bacteria unnoticeably. While in case of an altered immune and hormonal systems a virus formed from molecular motives causes a disease and serves as an indicator of what is wrong with the body (respiratory tract, gastrointestinal tract, blood system, somatic problems, including oncology and autoimmune diseases, etc.). Therefore, on the one hand, if a virus appears, it is an indicator of a whole complex of problems in the organism or population, which must be dealt with in a comprehensive way (health care). On the other hand, and most importantly, it must be dealt with individually or personally. If we are talking about human prevention, it is important to have a “trained” immune (from birth to 2-3 years due to bacteria) and hormonal (puberty) systems. At a later stage, for example, for maintaining the immune and hormonal systems of the body, one needs to live a healthy lifestyle, if possible, despite the fact that a genetically large number of altered states - molecular motifs (adaptogens) have accumulated and stuck

around. There are many options how to return a state of correct adaptogens to a person. For example, drink structured (normal spring) water, breathe fresh air, engage in physical activities (moderate exercise, jogging, walking), based on the mobility of all joints (the inner surface of the joints is lined with chondrocytes that produce, among other things, a component of the immune system that promotes restoration of the native tertiary (3D) structure of protein molecules [22] according to the principle of chaperones, which, by definition, hinders the development of oncology and others, including autoimmune diseases). At the same time, if vaccination is used as a prophylactic against a number of infectious and somatic diseases, then polyoxidonium, a drug acting in the fashion of Freund's adjuvant, which mainly stimulates the B-lymphocytic immune system, can be considered a universal remedy. The mechanism of action of polyoxidonium is spied in nature and is close in impact to a particularly dangerous Ebola virus. Anti-influenza vaccines based on polyoxidonium include surface glycoproteins: hemagglutinin (HA) and neuraminidase (NA) of influenza viruses, predicted for the previous epidemic season. Separate molecular motifs (B-epitopes) that are included in influenza hemagglutinin and neuraminidase should not be included in the structure of these molecules, since the immune response to them as separate antibody clones already pre-exists in the body (from previous immunization or obtained from an adaptogen — another infection) and additional stimulation of this clone can cause harm to the body. This harm, as a rule, is expressed in form of tolerance of the organism to a given molecular motif, proposed by nature as part of an adaptogen. This deprives the body of the possibility to adapt to the environment. And what if while aging we accumulate a dozen of such disruptions? Hence, there can be autoimmune reactions, and cancer, and the formation of an ecological niche with the onset of Disease “X”, and an incorrect interpretation of diagnostic tests [5]. In this regard, polyoxidonium is not the worst alternative to the current system of influenza vaccination. This is not the worst case, since, in the already existing immunopathological states, general stimulation of the immune system may have side effects, but they are much smaller than with a polyoxidonium loaded with the glycoproteins that are not always necessary for a specific individual.

Based on the above, a new technology is proposed, based on the concept of molecular motifs. It suggests the development of diagnostic test systems taking into account regional features and personal immune and somatic data (construction of immunoantigenograms during medical examination) [4]. Diagnostic tests based on the use of “natural focal, dangerous and highly dangerous” molecular motifs (B-epitopes) of human adaptogens will allow not only the diagnosis of infectious and somatic diseases, but also to predict the possibility of the appearance of pathological conditions and epidemics in the near future or make recommendations regarding the best place to live. In this case, vaccination based on IAG will actually be personalized immune and somatic correction [4]. Ultimately, biological threats, created, unfortunately, by man himself as a result of urbanization, will stimulate the processes of self-preservation in the form of the introduction of new technologies into people's daily lives. Natural reserves and mechanisms (in humans, the genome is built from only a few tens of thousands of genes, while bacteria have millions of genes to adapt) in the form of molecular motifs offered to macro-organisms through retrovirus-like adaptogens, are still, fortunately, available.

The author acknowledges the staff of the laboratory of biotechnology and immunodiagnostics of high dangerous pathogens: Fomina E.G., Scheslenok E.P., Semizhon P.A., Tkachev S.V., Grigorieva E.E., Shkolina T.V. for supporting individual statements for the preparation of this manuscript and critical comments.

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Received on 28-9-2019 Accepted on 20-10-2019 Published on 1-11-2019

DOI: https://doi.org/10.12974/2311-8741.2019.07.07