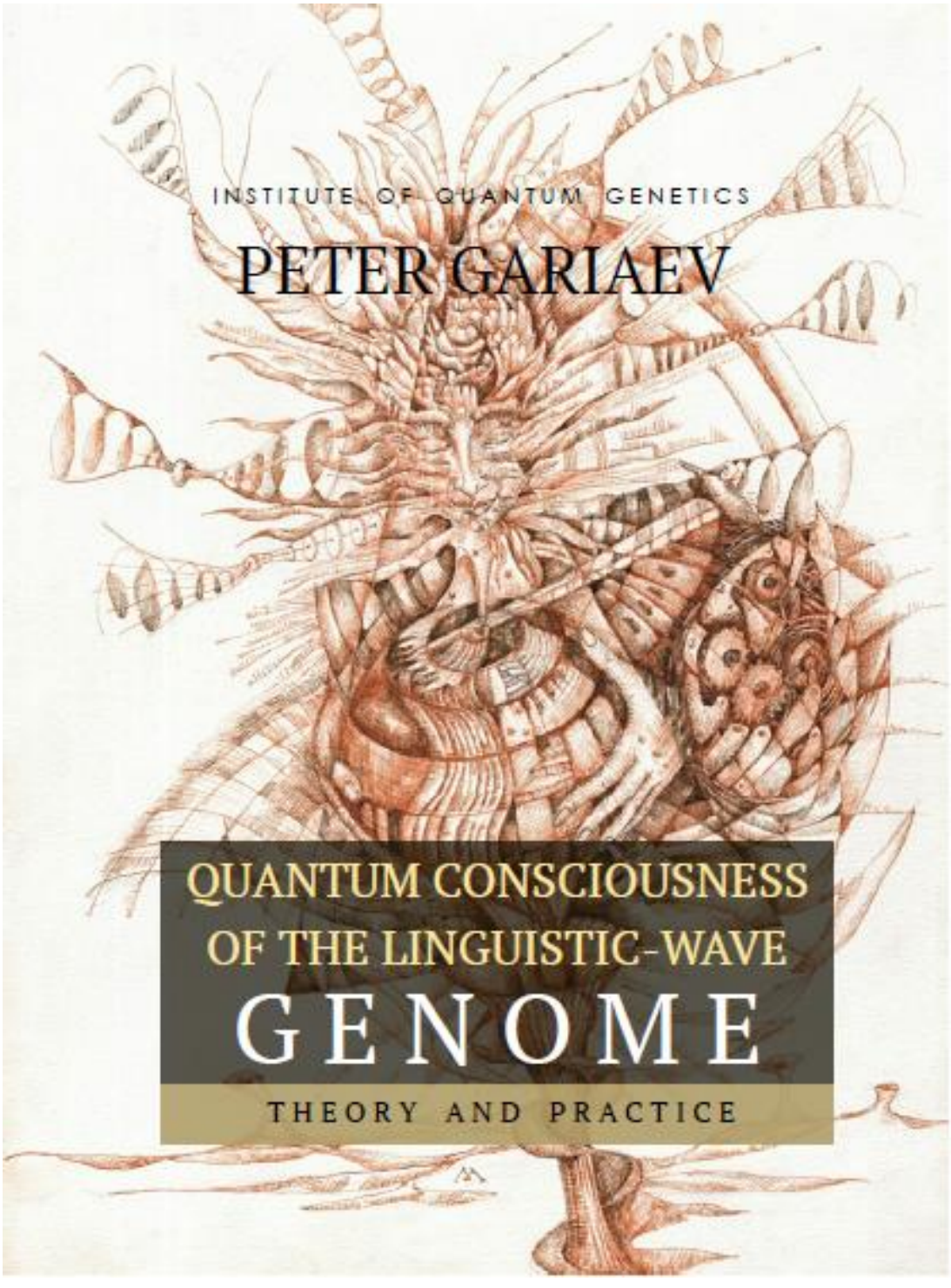

INSTITUTE OF QUANTUM GENETICS

PETER GARIAEV

QUANTUM CONSCIOUSNESS OF THE LINGUISTIC-WAVE GENOME

THEORY AND PRACTICE

P.P. GARIAEV

Quantum Consciousness of the Linguistic-Wave Genome

THEORY AND PRACTICE

Institute of Quantum Genetics

Gariaev P.P.
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EDITOR'S COMMENT

"A fascinating book, demonstrating new principles of genome operation. The application of these principles will have world changing consequences."

Peter Gariaev is a Russian scientist, pioneering researcher and leading expert in the field of Wave Genetics. In his book "Quantum Consciousness of the Linguistic-Wave Genome", Peter Gariaev outlines and explains the flaws in the current Genetic Code Model. Peter Gariaev explains why the translational machinery must operate with quasi-intellect and that amino acid selection is contextual and linguistic, based on whole mRNA scanning, and not verbatim codon by codon dogmatic mechanical selection.

Peter Gariaev, elaborates on his own research and critically analyses other's research, he lays the foundations of a new field of science – the study and application of the quantum and electromagnetic nature of the genome, as a holistic continuum, facilitating instantaneous metabolic control throughout an organism. The newly discovered principles outlined in this book pave the way for far reaching world changing technologies in medicine, agriculture, computing, and communications. This includes what humanity has long dreamed about: distant and non-operative healing, organ regeneration, significant extension of human lifespan, and quantum computing, to name a few.

Graham Ross McCallum
Editor of the 1st English edition of
"Quantum Consciousness of the Linguistic-Wave Genome"
Bachelor of Science in Molecular Biology and Biochemistry
(Australian National University)
Associate Diploma of Applied Science (Biology)
(Canberra Institute of Technology),
Graduate Diploma in Information Technology
(Charles Sturt University)

REVIEWS

I have known P.P. Gariaev since my student years, when we both studied at Moscow State University, he was in the department of Molecular Biology, and I was in the department of Embryology. Back then, we made our first attempts to understand the molecular mechanisms of zygote transformation into an adult organism. Like then, now, I am working with homeotic proteins that direct differentiation of embryonic cells and induce either apoptosis or forced differentiation of malignant cells. Their biological role is enormous, as evidenced by the work of numerous research groups around the world, as well as our experimental data. More is understood about the mechanisms of cytodifferentiation, but not everything. Publications of P.P. Gariaev and his co-authors, including his monographs "The Wave Genome" (1994) and "The Wave Genetic Code" (1997), and this, his third monograph, allow us to open new perspectives for understanding the mechanisms of embryogenesis and cell differentiation. These works are aimed to solve one key problem – to understand the functioning of the genetic apparatus. Without rejection of classical ideas, P.P. Gariaev persistently, and on a new modern platform, develops the ideas of Russian scientist Alexander Gurwitsch, about the wave nature of the chromosomes operation. Understanding the wave function of the genome is the scene of hot debate, which indirectly indicates the enormous potential value of these works. P.P. Gariaev and his colleagues have made significant theoretical and experimental contributions to this complex area of natural sciences.

I am interested in the wave principles of chromosomes, and I resonate most with Gariaev's ideas on morphogen functions, and especially homeotic proteins as their main component. In this monograph P.P. Gariaev lays the foundations for linguistic genetics. The starting point is an in-depth critical analysis of the basic provisions of genetics – the triplet model of the genetic code, proposed by F. Crick more than forty years ago. This model allowed us to make breakthroughs in terms of understanding the functions of the genetic apparatus of all living beings inhabiting the Earth. However, canonized by biologists, this model has become a hindrance for the development toward a deeper understanding of genome function, as was demonstrated by P.P. Gariaev and his co-authors. Logical consequence of this theoretical analysis of the genetic code resulted in a profound statement that DNA, RNA and proteins

represent texts, not in a metaphorical sense (as it was essentially postulated earlier) but texts in a real sense. Multiple studies led to this idea, this includes the works done by P.P. Gariaev and his co-authors that made comparative mathematic-linguistic analysis of the texts of DNA genes and human speech, independent of the language used to create the texts. Key arguments lie in the in-depth theoretical and practical analysis of the genetic code model that led to the conclusion that the genome on the level of synthesis and application of DNA-RNA-protein texts, is actually a quantum biocomputer. This idea cardinally changes our understanding of protein functions, especially of the cerebral cortex proteins as correlates of consciousness and intellect. Biochemistry, involving proteins, plays a leading role in the function of the organism now may and must be understood as an intelligent quasi-speech biosystem control. The role of homeotic proteins in embryogenesis, as factors of intelligent organization of the developing embryo, becomes clear. Any fundamental idea in this area is of great interest and requires further experimental and theoretical development.

Hopyorskaya O.A.
Ph.D. in Biology

In the book "Wave Genome. Theory and Practice" P.P. Gariaev touches upon the fundamental questions of the genetic code related to the structure, function, and, if I may say so, "origin" of chromosomal DNA.

It is clear how far we are from complete disclosure of all the secrets of genetic code, however, the ideas of Prof. Gariaev and his colleagues, give us an opportunity to see absolutely new perspectives of operation of the chromosome apparatus in living cells, in particular, a new scientific and practical direction, which could be called "genetic-wave navigation and regulation in biosystems". This new direction is introduced by the author within the framework of theoretical models, confirmed by his own research and independent experimental research. The quantum component of genetic cell operation is of extreme importance. It is clear, that metabolism of cells, tissues, and organisms as a whole, which is extreme in its complexity and scale, needs some regulation. The author introduces a new substantial idea of genetic quantum biocomputing.

Such an approach is of interest to optical-radio electronics, radio technology, computing, navigation and management systems. Moreover, wave mechanisms of cell operation directly relate to nanoelectronics. Living organisms clearly demonstrate examples of nanobiotechnologies, effectively utilizing their own wave biocomputer regulation on nanostructures such as enzymes, ribosomes, mitochondria, membranes, cytoskeletons and chromosomes.

Nanotechnological mechanisms of cell operation and their genetic apparatus, need theoretical and biological consideration, and physical-mathematical analysis to develop, amongst other things, not known before, principally new laser-radio wave technologies for genetic regulation of multicellular organism metabolism. Application of such technologies by Gariaev's team has produced impressive results. The author has correctly and comprehensively demonstrated remote (over many kilometers) wave transmission of directive genetic information from a Donor (living tissue) to the Recipient (organism). Until recently such transmission was considered to be principally impossible; now this is a fundamental fact.

Now we have found the opportunity to build completely new unique molecular-optical-radio-electronic equipment that should be able to perform complex navigation-regulatory functions for positive control of genetic-physiological functions in organisms. The task for the creation of the genetic laser is under investigation. Proof of laser pumping of DNA

and chromosomes *in vitro* was demonstrated and published by Prof. Gariaev and his colleagues in 1996 and was confirmed by Japanese researchers in 2002. Such a laser will perform many previously unknown functions of the genetic apparatus to solve many problems in biology, medicine and agriculture. Other opportunities for this work is application of the coherent states and radiation of living cells and their information structures for developing biocomputers, based on the principles of holography, solitonics, and quantum nonlocality. In fact, the prototype of such a biocomputer was created by Gariaev's team that allowed the collection of unique results on quantum gene transmission and remote wave genetic bioregulation. Chromosome laser and biocomputer application is not limited by the aforementioned, and extends beyond the biosystem's limits - to space communication, regulation of super complex technical processes, aircraft navigation, etc.

This book points out a number of unresolved problems, including the investigation of DNA wave replicas and laser-radio wave processes during scanning and transmission of quantum biological information from donor to recipient.

I believe that the publication of P.P. Gariaev's monograph will promote further investigation of one of the divine mysteries - mysteries of the genetic code and will lead to the application of new ideas for the benefit of the Humanity.

V.A. Matveyev

Doctor of Technical Sciences,
Professor of Moscow State Technical University named after N.E. Bauman,
Dean of the Faculty "Information and Management Systems",
Honored Scientist of Russia,
Laureate of Prizes of the Russian Government and the City of Moscow

What characterizes today's genetics and molecular biology? No doubt, it is the great progress in methodology and research technical equipment. An expensive and long-standing "Human Genome Project" is a good example of this. This program helped to discover the sequence of the 3 billion letters in human chromosomal DNA. This is, certainly, a wonderful event. However, one would expect much more out of such a titanic work. Why is it so?

In the first part of his monograph P.P. Gariaev makes a long-awaited, deep, and most importantly, honest theoretical analysis of the actual causes for the failure of this program. The causes, oddly enough, are found in the biologists conventional canonized genetic code model. Relying on pure logic and on a great experimental work of the huge global scientific community, the author leads the reader to believe that in reality only a small part of the functions of the genetic apparatus is known and understood. The model of the genetic code, developed by Noble Prize Laureate F. Crick, is incomplete. 'The model does not fully explain some of Crick's own postulates', - Gariaev says.

These postulates (the so-called 'wobble hypothesis') are very important in order to understand rules of nucleotide pairing during anticodon-codon recognition in the process of protein biosynthesis. Following 'the rules of 'wobble hypothesis' we see another (previously missing) fundamental characteristic of the genetic code – its homonymy, - Gariaev states. This is the second vector of degeneracy of the triplet code (Synonymy is the first vector of degeneracy), i.e., the code's unambiguity for selection of different codons was detected immediately. It is well understood and well-examined in the functions of isoacceptor transfer RNA (tRNA). Homonymy is about the code's ambiguity of the first identical two nucleotides in these codons. The third nucleotide's "wobble" (the 3rd nucleotide may be any of the 4 bases) and that is why they are not involved in the coding of amino acids. In other words, the ribosome reads the messenger RNA according to the "Two-out-of-Three" Rule. In 1978, this was found by Swedish researcher, Ulf Lagerkvist, but then, disregarded by the scientific community. It is obvious, that when a ribosome follows this rule, it creates the ambiguity in homonymous codon reading. For this reason, there is a risk of selecting the wrong amino acid or a stop codon. This can lead to incorrect protein synthesis and death of the organism. However, the synthesis of proteins is a very accurate process. Why do ribosomes never fail and make a mistake? Experiments indicate that the protein synthesizing cellular apparatus uses the linguistic mechanism of

context orientations for correct ribosome reading of the homonymous codon. This brings up the question (which Gariaev raises too): is the term "reading" relating to ribosome reading (in a complex with transfer RNA) of messenger RNA a metaphor (as is considered in genetics) or an intellectual process, actual reading and understanding? One can assign an accurate meaning to a homonym, only if one understands the meaning of entire text (the context). So, does it mean that a cellular ribosomal apparatus reads and understands the RNA in non-metaphorical sense? A definite answer to this question is a stumbling block. It is not easy for biologists to accept the idea of quasi-consciousness, quasi-intellect of the genome. Gariaev thoroughly analyzes this theoretical and in the larger sense, philosophical dead-end, and defines a genetic and biological role for homonymous degeneracy of the triplet code. According to Gariaev, the codes homonymy is a factor which takes the ribosomal apparatus operation, and the entire cell, to a quasi-consciosness level, and hence, to other multi-dimensional semantic realms. In fact, the case of coded effects of mRNA contexts is retroactively recognized by molecular biology as a "second genetic code", without any explanation of what kind of code it is. Here, the author explains and demonstrates the significance of homonymy with the example of a global danger of reckless use of transgenic manipulation with chromosomes in genetically modified foods. What namely do transgenic "engineers" do? They introduce foreign protein genes into the chromosomes of organisms, and this automatically changes the genetic contexts. This leads to misunderstanding of homonymous codons and incorrect transposition (e.g. jumps) of ribosomes on the mRNA. This leads to distortion of the second (linguistic, according to Gariaev) genetic code. As a result, erroneous proteins with abnormal functions are synthesized. There are formidable and global warnings: such transgenic manipulations are already leading to the extinction of honeybees in the United States. The bees collect and feed themselves with nectar and pollen from transgenic crops – this is a reason, and probably the main one, for their death. 'Is Human population next?' - asks Gariaev. Misunderstanding of the second genetic code mechanisms, misunderstanding of the real (non-metaphorical) linguistic nature of DNA leads not only to the misinterpretation of proteins biosynthesis but also of embryogenesis, and this is not less dangerous than the curse of "transgene magic".

Gariaev's theoretical studies are not limited by the critical analysis of the triplet code model, they go further, to the quantum mechanisms of chromosomes. This part of the theoretical work is performed by Gariaev in

close collaboration with major physicists and mathematicians from the Lebedev Physical Institute of the Russian Academy of Sciences, Moscow State University, Institute of Control Sciences named after V.A. Trapeznikov, Russian Academy of Sciences, and foreign scientists from Canada, England, Germany and Austria. All this laid the foundation for the consideration of chromosome operations as a quantum biocomputer. To Gariaev and his co-authors, genomic quantum computing applies the principles of chromosomes coherent radiation, the principles of bioholography and quantum nonlocality of genetic information.

The experimental part of the monograph confirms the theoretical ideas of the author and his colleagues, the most important of which is that genetic information may exist and work in a form of physical fields, from photon level to radio wave level. The author and his associates conducted experimental research in this field in Russia and Canada. They were the first in the world, who performed remote (over many kilometers) transmission of wave genetic information for regeneration of the pancreas in animals and discovered the phenomenon of wave immunity.

This monography contributes to, and clearly demonstrates that genetics and molecular biology need to transcend to a significantly higher level of development, moreover, it contributes to this transcendence.

V.N. Volchenko, Ph.D.
Professor of Moscow State Technical University named after N.E. Bauman, Russian Academy of Natural Sciences

THE GENETIC CODE IS MORE COMPLEX THAN ITS TRIPLET MODEL

Nowadays (what a paradox!) the situation in genetics as the basis of biological knowledge, makes an impression of an elaborately painted and beautiful, although dangerous mirage. And this is after the failure of the famous "Human Genome Project", when the average man, the taxpayer, was persuaded that finally we "have read all" the genetic information of the human chromosomes. One could hear exclamations about the breakthrough successes of transgenic engineering, cloning of animals and Human cloning about to come next. However, what is the true reality? The result of the "Human Genome Project" took us to "new heights" of official genetics. Now we know the sequence of 3 billion nucleotides in our chromosomes. And so, what? We still do not understand the most important, strategic and ideological: how are Humans, and all Life coded by their chromosomes? Here is a typical statement written by Emmanuelle Thevenon in the *LABEL France* journal in the article "The Sciences About Living Organisms: The End of Almighty Genetics?": "Despite considerable investment, the therapeutic results of genetic studies leave much to be desired, to such an extent that researchers are beginning to reconsider the very concept of the discipline, which has been leading the biological sciences for already fifty years". The "moment of truth" was postulated: 'everything is programmed in the genes'. And this has been the paradigm for decades. The discovery of the DNA double helix set the following theoretical scheme: the DNA structure has regions, defined as genes, which with coding proteins as well as RNA, determine the appearance of the living organism and controls its behavior.

Like an almighty demiurge, the genome appeared to be the creator of the organism, which should explain everything about it. Such understanding of the "almighty genetics" was reinforced with the launch of the international 'Human Genome Project', involving

the USA, Great Britain, France, Germany, Japan and China. *A priori* it was considered that everything is recorded in the triplet code of the protein genes. And therefore, it would suffice to localize an "undesirable" gene to neutralize its undesirable function. On a daily basis the mass media kept us informed about the progress of the research, saying that this would lead to the creation of new cures. However, 10 years after the sequencing of the HIV virus genome, no vaccine is in sight. Genetic therapy, had evoked unprecedented hope, so far has led only to extremely small results. Out of hundreds of clinical trials, conducted in many countries around the world, only one led to real healing: French doctors, directed by Marina Cavazzana-Calvo and Alain Fischer (INSERM U429, Necker Hospital in Paris) cured ten children, suffering from severe combined immune deficiency (SCID). However, even this success was short-lived: in October 2002, a side effect in the form of leukemia was found in one of the children and led to a halt of clinical trials. At the same time the United States also stopped part of their development programs for gene therapy. Today, geneticists are pinning their hopes on the fact that the human genome will identify thousands of genes, characterizing every human being. Approximately ten to twelve thousand genes have already been identified, but the specific features were stated only for 5,000.

Here is one example: in 2001, the deciphering of the genome of Drosophila melanogaster was declared with great fanfare, and at the same time in Europe, there were only two specialists capable of comparing and identifying the 3,000 different species of Drosophila. The discrepancy is obvious. To get out of the epistemological dead-end, that genetics was facing, two French scientists, molecular biologists, Jean-Jacques Kupiec and Pierre Sonigo offered to apply Darwin's theory to their discipline, thus, breaking with modern determinism. In their recently published book *'Ni Dieu ni gène'* [Neither God nor gene], they explain that the community of the body's cells is determined not by genetic programming, but competition, going on between the various components of a living organism in order to obtain external resources, without which they cannot live. Molecules emerge in an arbitrary manner, and the

principle of "natural" selection encourages livable combinations. As in most of higher organisms (plants, animals, etc.), those molecules and cells survive and develop, which are able to find resources thrive better than others. This theory probably explains the fact that genetics still cannot develop a vaccine against HIV. It cannot be developed, because it is supposed to do the impossible: to quickly react to billions of changes per minute in billions of individuals. It's as pointless as studying the structure of the automobile, atom by atom, in order to improve road safety. So, what do we have as a result of this ambitious program? The sequenced genomes of six people (one male and one female from each of three different races, plus Craig Venter's genome, the leader of the "Human Genome Project"). Some differences were found among them; however, a consensus sequence could not be identified. The majority of genes are almost identical in all organisms, from *E. coli* to Humans. In other words, the "mountain brought forth a mouse". Disappointment, confusion and vacillation settled in genetic scientific circles. The gene - the basic element of genetics, surprisingly, is gradually going beyond the scope of its understanding. The voices of scientific panic-mongers call to discontinue the study of the genome and replace it with the study of all known proteins, creating a discipline of proteomics, instead of genomics. Roughly speaking, they describe it like this: "since we cannot understand how the genetic apparatus and DNA molecule actually work, let's step aside and engage in a detailed study of all the proteins. Then, we will certainly understand, how the body is formed, and according to what kind of principles." However, this is not more than a repeat of the same mistake made with the genome, as the proteins are polyamino acid DNA replicas. Again, the future crisis can be foreseen, but it is no longer genomic, but proteomic. And again, with a huge waste of finances and scientific effort. Is this money laundering in a "scientific fashion"? Renowned biologist, Bruce Lipton, is unambiguously explicit and direct in his article:

"The Human Genome Project – “A Cosmic Joke that has the Scientists Rolling in the Aisle”[1]. He foresees a revolution in biology as a consequence of rejecting the concept of genes as biosystem regulatory structures. He sees this revolution as the analog to the one in physics, which had to make a shift from a Newtonian outlook to quantum. Here comes the era of quantum (wave) genetics.

[1] https://www.brucelipton.com/resource/article/the-human-genome-projects

THE ORIGIN OF ERRORS

Why can't genetics and biology leave behind the vicious cycle of misunderstanding actual chromosome coding mechanisms? How is the gene understood nowadays? Has anything changed here, since the discovery of the DNA double helix? To answer these questions, let's turn to "official" molecular biology and genetics, by taking a fundamental and relatively new textbook, one of the co-authors of which is a co-creator of the DNA double helix model, a Nobel Prize laureate, James Watson: *"Molecular Biology of the Cell"* (James Watson, Bruce Alberts, Alexander Johnson, Julian Lewis, Martin Raff, Keith Roberts, and Peter Walter. Garland Publishing, Inc. New York & London, second edition). Note, that at the time of this analysis (2008), no fundamental changes in the understanding of the genetic code had taken place in official genetics, and hence, we'll find the same in the textbooks. None of the basic provisions in this discipline were revised by official biology, although much has been found that could potentially destroy its basis. What is so threatening to official genetics in these old and recent studies?

Let's analyze its classic provisions first-hand, as is written in a classic university textbook. The Wolpert theory of positional information [Wolpert, 1971], is the theory that for over 30 years has been the basis for explanation of how the molecular (genetic) regulation of 4-dimensional (spatial and temporal) construction of multicellular organisms is performed. It says: *"In many developmental systems a small patch of tissue in a specific tissue acquires a specialized character and becomes the source of a signal that spreads into the neighboring tissue and controls its behavior. The signal may, for example, take the form of a diffusible molecule secreted from the signaling region. Suppose that this substance is slowly degraded as it diffuses through the neighboring tissue. The concentration then will be high near the source and decrease gradually with increasing distance, so that a concentration gradient is established. Cells at different distances from the source will be exposed to different concentrations and may become different as a result. A*

hypothetical substance such as this, whose concentration is read by cells to discover their position relative to a certain landmark or beacon, is termed morphogen. Through the morphogen, the signaling region can control the patterning of a broad field of adjacent tissue. Morphogen gradients are a simple and apparently a common way of providing cells with positional information." [Alberts et al, 1989, 2nd edition, p.913]

"Although there are many examples of signaling regions ... there are remarkably few cases where a morphogen has been identified chemically. In most cases all that is known is that when the presumed signaling region is displaced, by grafting or otherwise, the pattern of the tissue nearby is correspondingly altered. It is not possible to tell from this sort of observation how far the pattern is due to direct responses of individual cells to a morphogen and how far it is dependent in addition on interactions between the responding cells. In most instances it is probable that the initial morphogen gradient imposes only the broad organization of the pattern and that local cell-cell interactions then generate the details... a morphogen gradient might engender in a field of cells reacting individually... in the absence of {morphogen}...the transient, position-dependent influences can have effects that are "remembered" as discrete choices of the cell state and thereby define the spatial pattern of determination. The choice of cell state represents the cells memory of the positional information supplied. This record, registered as an intrinsic feature of the cell itself may be called its positional value." [Alberts et al, 1989, 2nd edition, pp.913-914]

Thus, in accordance with the above, the embryo development is determined by some hypothetical morphogens, the identification of which is an extremely rare event, and the nature of which is not necessarily related or identical to genetic structure, that is, DNA or RNA. And there is a very mysterious statement, that morphogens can act in "a field of cells". What kind of "field" is not specified. There are unexplained concepts, for example, "remembered" positional information on the level of "the cells memory" with the formation of a "positional value". What is "the cells memory", again, is not explained. But the fact that it is "crucial" is emphasized, as "the mechanisms for supplying

positional information in an animal embryo generally act over only small regions, or morphogenetic fields, on the order of a millimeter long (or about 100 cell diameters) or less". This is what makes it necessary for the authors to introduce the unexplained term of the "cellular memory". The authors write: *"...the distinction between head and tail has to be established when the rudiments of the head and the tail are no more than about a millimeter apart. The circumstances that gave rise to that distinction are ancient history by the time the animal is a centimeter or a meter long; if the distinction between the head and the tail is to be maintained, it must be maintained through cell memory"* [Alberts et al, 1989, 2nd edition, p.914]. Let's remember these key words, expressions and terms, introduced in this passage, but unexplained: "cell memory", "field of cells", "remembered positional information", and also important for the future consideration the fact that morphogenetic information acts in the embryo at a distance of not more than a millimeter.

"The final cell state is arrived at by a sequence of decisions." [Alberts et al, 1989, 2nd edition, p.915]

Another term, casually introduced by the authors – "cell state decisions" but without any comments about who and how makes these decisions.

"This makes it very likely that retinoic acid is the natural morphogen. The receptor for retinoic acid has recently been identified as a protein homologous to the receptors for steroid and thyroid hormones; it regulates gene transcription by binding to specific DNA sequences." [Alberts et al, 1989, 2nd edition, p.917]

This is an illustration of the above mentioned - morphogens do not necessarily take the form of nucleic acids, i.e. in fact, they are not genes. Mainly these are proteins and sometimes these are such simple compounds as retinoic acid.

Further on, the authors make a showdown, persistently ignored by "official" genetics: *"The molecular mechanisms that underlie this crucial form of growth are unknown."* (Intercalary regeneration) [Alberts et al, 1989, 2nd edition, p.919]

And what is even more surprising: *"The structure of an organism is controlled by its genes: classical genetics is based on this proposition. Yet for almost a century, and even long after the role of DNA in inheritance has become clear, the mechanisms of the genetic control of body structure remained an intractable mystery. In recent years this chasm in our understanding has begun to be filled. … Studies on Drosophila have revealed a class of developmental control genes whose specific function is to mark out the pattern of the body… They … are called homeotic selector genes… The products of these genes act as molecular address labels, equipping the cells with a coarse-grained specification of their positional value. A homeotic mutation … causes a whole patch of cells to be misinformed as to their location and consequently to make a structure appropriate to another region."* [Alberts et al, 1989, 2nd edition, pp.920-921]

Another concept is introduced without any explanation - the "molecular address labels" of homeotic selector genes. It sounds good, but it is not clear. How do the products of selector genes, i.e. proteins, play the role of addresses for moving embryonic cells, which at the same time by unknown commands are converted into other cells - muscle, bone, nerve, and so on? Furthermore, please remember, that a morphogen's action in the embryo is for not more than the distance of 1-2 mm. How can molecular addresses of morphogens work in the embryo, when their action is so restricted in space? There is no answer. There are only declaratory and contradictory statements, which reaffirm the lack of understanding of the key point in the genome operation: how the structure of an organism is encoded.

"Several representatives of each of the groups of segmentation genes have been cloned and used as probes to locate the gene transcripts in normal embryos by in situ hybridization". [Alberts et al, 1989, 2nd edition, p.926]

The transcripts of the *bicoid* gene and other genes, involved in organizing the structure of the developing embryos, were obtained in this fashion. Further we read: *"…the bicoid gene transcripts are the source of a positional signal: the transcripts are*

localized at one end of the {Drosophila} egg, even though the effects of a mutation in the gene are spread over a large part of the embryo." [Alberts et al, 1989, 2nd edition, p.927]

Here is another glaring contradiction between the experimental and "official" theory. Let's explain what we mean. RNA-transcripts of morphogenesis genes, and respectively, their protein-products are synthesized locally in certain limited embryo sites, and the morphogenetic action of the proteins extend far beyond the location of these proteins biosynthesis, to most parts of an embryo. This means, that we see the apparent inconsistency of the theory of positional information about the "gradient-limited" action of morphogens. Contradicting to themselves, the authors, however, present great illustrative experimental data on the localization of morphogens in one location of the embryo and the manifestation of their action at distances fantastically remote from the location of their origin and the location of morphogen diffusion. In other words, obviously, there is a strangely ignored, long-range action of the selector proteins of morphogenesis. This reveals another fundamental genetic (embryonic) phenomenon – nonlocal action of morphogenesis proteins. To put it in a simple way, protein (or proteins), managing the spatial (and temporal) organization of the embryo, are initially at the same location of the embryo field, but their action can be observed in a completely different remote site of the embryo, where they cannot diffuse at a sufficient speed to directly provide the regulatory action. In other words, their function is realized nonlocally. So, the spatially-remote action of protein factors of embryogenesis is revealed. This is a fundamental fact, but it is not noted by a major part of "official" embryology / genetics, so once again, we are at a logical dead-end. Why is it so? The answer is simple: the explanation of this phenomenon, as well as many other "anomalous" characteristics of the genome of multicellular organisms, inevitably leads genetics and biology in general, to substantially different interpretations of chromosome operation.

Let's take our critical analysis further. A similar effect of nonlocality was observed with the *Krüppel* gene. The authors write:

"By analogy with Bicoid, it can be assumed, that Krüppel protein as a diffusible morphogen expands from the site of Krüppel transcription, although the observed expansion of the protein is not as extensive as required in accordance with this hypothesis." This refers to the hypothesis (theory) of morphogen gradients by Wolpert. The process of simple diffusion of morphogenesis proteins is too slow to explicitly explain: the protein is located here, and its action takes place at a remote site, where it has not penetrated. This is an important acknowledgment. And again, we see the distance factor consistently ignored: fast, non- diffused, remote transmission of embryonic information, the nature of which is unclear to the authors. The following fact is ignored: the exit of proteins (as large molecular structures) beyond the cell is not a simple act of diffusion (as in the case of gases or solutions), but a complex, energy and time-consuming process of exocytosis. The protein, once released from the cell to reach its site of local (material) action, should again be captured by another cell, which is a barrier for the protein journey to the place of its action. This capture of protein (endocytosis) is also a complex and lengthy process. Thus, the passage of morphogens (at least, of protein nature) through the cellular layers to the place of action is a complex, lengthy and multi-step process, eliminating what we see in reality – actual, fast, remote transfer of programming activities of protein-morphogens. Why don't the authors ask a simple question: what if semantic, textual constructs of protein-morphogens are the goal for wave transmission over long intracellular, interstitial distances? This is quite logical, when there is no evidence of direct organizing morphogenesis acts by homeotic proteins. Homeotic proteins enter into the cells cytoplasm and perform obscure (from the point of view of its mechanisms) embryonic-regulatory functions. Then, they bind with specific sites in chromosomal DNA to activate protein synthesis of the next protein-morphogen. The latter, after making its regular, seemingly aimless, voyage around the cytoplasm, again reactivates the next selector gene, that produces the next protein-morphogen, etc. One can see the picture of cascading hierarchical (fractal) regulation of morphogenesis genes

activity. The picture is beautiful, however, puzzling: how does it work, the morphogenesis-programming function of homeotic proteins, and why is it remote? Embryologists complete helplessness on this key issue is well demonstrated, for example, in the review of the famous researcher L. Korochkin. All considerations here are, in fact, reduced to a simple statement about activities of certain morphogenesis genes, synthesizing certain protein products. The key driving forces of the morphogenesis process, and their nature, are left behind. It looks as if we were trying to understand a painting by analyzing how many paints and of what chemical composition were used to create this painting. The result of such analysis would be miserable: Mona Lisa would be seen as 200 grams of various oily substances, smeared on textile in specific ways. Is this an allegory of the "Human Genome Project"?

Exploring further…

"… The hierarchy of positional signals should correspond to a hierarchy of regulatory interactions among the genes, governing the pattern. This can be confirmed by studying how a mutation in one gene affects the expression of another. The antero-posterior patterning genes are found to form a hierarchy with five major tiers, such that the products of the genes in each tier regulate the expression of the genes in the tiers below. Egg –polarity genes stand at the top, followed by gap genes, then pair-rule genes, then segment-polarity genes, and finally, homeotic selector genes. For example, one can take a mutant embryo that lacks the normal Krüppel gene product and test the expression of the normal ftz gene by in situ hybridization with a cloned ftz gene probe. The usual ftz stripes fail to develop in just that region of the blastoderm corresponding to the defect in the Krüppel mutant. Thus, the Krüppel product, directly or indirectly, regulates ftz gene expression. On the other hand, in a ftz mutant the distribution of the normal Krüppel, the ftz product does not regulate Krüppel gene expression. … Some of these interactions… have a relationship of mutual inhibition… they are expressed…with a sharp boundary {of their products}". [Alberts et al, 1989, 2nd edition, p.928]

In this quoted passage, you can see one highly characteristic aspect, common to all studies related to regulation of morphogenesis genes. They talk about anything but the main point. And the main point is about strategic motives and mechanisms of embryo genetic functions of morphogenesis genes products, i.e. the corresponding proteins. What are the embryo programming functions of these genes? What is the specific function of these proteins? There is no answer. Instead they present complicated and, it should be noted, the exact hierarchy, showing how genes sequentially turn on and turn off each other by means of their own protein products. This automatically leaves the impression that these "turn on-turn off" operations of morphogenesis proteins is their only regulatory-metabolic purpose in cytoplasm of embryonic cells. Are they truly their only purpose? Clearly, this is not the only purpose, as their resulting activity – embryogenesis, which of course, cannot be reduced to the "turning on and off of the genes" and their network connections. This is a typical situation of the so-called black box, where input is represented by Gene (protein), and the output - by Function/Feature. We would like to look inside the black box and therefore, we ask the question: what is the main function of these genes and their products, the proteins, in the organization of embryogenesis? We also can and should take it to a broader perspective: what is the origin and evolution of the chromosomes encoding functions? There is no answer and will be no answer until we revise the existing dogmatized provisions of genetic coding. The situation has become even more complicated. *Hox*-genes, which were considered to be the key in the process of ontogenesis, are in turn regulated by micro RNA-transcripts. They are encoded by DNA regions, located between *Hox*-genes that were considered purposeless. Some micro RNA directly strengthens or weakens the expression of the *Hox*-genes, some indirectly affect the operation of other transcription factors. Besides that, micro RNAs can regulate both neighboring and distant *Hox*-genes [Lemons, McGinnis, 2006]. So, what is the main regulator-programmer of embryogenesis? Below regulatory micro RNA (in the hierarchy), there are only low molecular weight metabolites and ions. *Causa*

finalis is unclear. Are we going back to Aristotle-Driesch entelechy?

Compelling reasons to amend and supplement the understanding of genetic functions are obvious and are already sketched by unambiguous maxims of the respected authors of the mentioned textbook. However, most biologists reluctantly give up the illusions, even if they are presented, as here, by a recognized authority, Noble Prize laureate - Watson *et al*. In addition, in science, as in any market, there is a powerful system of commercial brands. Unfortunately, this is relevant to the triplet genetic code as well. Many years of extensive analysis of the world literature on genetics and molecular biology demonstrates that there is a very limited number of scientists publicly trying to reconsider the seemingly settled canons of genetics. In addition to our research, there are the works by Jiang-Kanzhen [Jiang Kanzhen, 1981, 1991, 1994-1996, 1998, 1999, 2000] and the academic school of Acad. V.P. Kaznacheev [Kaznacheev V.P. et al, 1973; Kaznacheev V.P., Mikhailova L.P., 1985]. To some extent, works by Mosolov [Mosolov A. N., 1980], Richard A. Miller [Miller, 2003] and Popp correspond with this direction, as well as research by Burlakov [Burlakov, 1999; Burlakov et al., 2000]. Richard Alan Miller should be mentioned separately. In 1973, Miller and Webb were the first ones to express the idea that genetic apparatus can operate on the principles of holography [Miller, Webb, 1973]; for this statement Miller remained the "genetic anathema" for many years.

What is the origin of errors in genetics, in this seemingly well-doing and successful field of biological knowledge? It seems that the beginning of the crisis, paradoxically, was set by the triumphant discovery of the DNA double helix and its functions by Watson and Crick in 1953, followed by the efforts to develop the principles of protein encoding. Indeed, it was a major breakthrough toward the understanding of chromosome function. In fact, this was only half of the truth, or even less. The euphoria of these findings, followed by their "branding" for many decades has blocked understanding of the additional main genetic functions of

DNA. They lie in other *linguistic*[2] realms of the genome - wave, quantum nonlocal, and textual [Gariaev, Tertyshniy, Tovmash, 2007; Gariaev, Kokaya, Mukhina et al., 2007; Gariaev, Kokaya, Leonova-Gariaeva, 2007]. However, this part of the genetic ideology and experiments are the subject of further analysis, see below.

[2] *Important translator's note*: Throughout this book the word *"linguistic"* (esp. when in *Italics*) refers to "linguistic sign". "Linguistic sign" is a term from linguistics, and has two parts: a signifier, the form; something signified, what is referred to, the meaning. According to Ferdinand de Saussure, language was a system of signs, in which each formed part of an interdependent whole. This is one of the central most important terms in this book, used by the author many times. It implies that genome codes actually represent "linguistic signs" - they are the forms that hold the meanings or semantics (like words in the language), and together they make contextual whole (sentences).

ULF LAGERKVIST FIRST INDICATED THE DEFICIENCIES OF GENETIC CODE TRIPLET MODEL

So, what were misunderstandings of the genetic code about? They were about excessive rigidity of the triplet code model as a purely physical-chemical system of ribosomal machinery operation and the unjustified attribution to the triplet model code of all genetic attributes. These false assumptions are based solely on the principle of complimentary interaction of bases of messenger RNA (mRNA) and transfer RNA (tRNA), when adenine "complements" uracil, and guanine "recognizes" cytosine in the process of codon-anticodon "reading" by a ribosome from mRNA. The protein code is understood as a universal and unique vector of all genetics and embryology. The canonical genetic code table has become a kind of fetish, a sacred cow, or, if you like, Caesar's wife, which is above suspicion. Only once there was a published work that gently threw a shadow of doubt on the model of the triplet code, however, it didn't attract any attention. The Nobel triumph of Watson-Crick and all following successes in the study of protein synthesizing apparatus seemed to be leading to the shining heights of the human and all other genomes complete understanding.

The aforementioned work with the first doubts (in relation to genetic code) was published in 1978. It covertly demonstrated complications and incompleteness in the triplet model of the genetic code, however, the study was clearly underestimated in scientific circles. To be precise, it was simply ignored. This was an article by Ulf Lagerkvist, called "Two out of three. An alternative method for codon reading" [Lagerkvist, 1978]. Let's take a closer look at it.

Lagerkvist writes: *"The genetic code is a universal, highly degenerate, three-letter code in which the first two positions of the codon are read by the anticodon strictly according to the rules of classic*

base pairing. The third position in the codon, however, introduces complications."[3] Thus, there is a discrepancy between the large number of codons in a degenerate code and the limited number of anticodons which are able to read these codons. To bridge this gap, in 1966, F. Crick introduced his ingenious hypothesis (1). In this classic paper, Crick proposed or, to be precise, stated that the nucleotide at the 5'-position of the anticodon is in the wobble position and it can actually interact with 3'-position of the codon ignoring the rules of classic, thermodynamically beneficial, base pairing.[4] Later Lagerkvist also gives examples of such "incorrect" base pairings, confirmed experimentally in cell-free ribosomal systems, as well as examples of such pairings that ignore even the Wobble Hypothesis. Based on these studies, he asks the natural and sacramental question: is this anomalous behavior (in pairing of 3'-5 'nucleotides in codon-anticodon pairs) applicable to the synthesis of proteins *in vivo*? The obvious answer is that the Wobble Hypothesis rules should work in all situations involving wobble positions, but this automatically leads to errors in protein synthesis. For example, for amino acids Phe/Leu, codons group (UUU, UGC, UUA and UUG) on anticodon with 'G' in a wobble position cannot recognize the codons UUA and UUG, which leads to errors and the introduction of Phe instead of Leu into the synthesized protein.

For better illustration, we present a table of the genetic code, provided and rearranged by Lagerkvist according to codon families based and oriented towards the first two working

[3] There is one confusing simplification, when they write and speak about – the 1st, 2nd and 3rd nucleotides in codons and anticodons. Considering anti-parallel nature of the triplets, the 1st, 2nd and 3rd nucleotides in the codon (mRNA) pair with the 3rd, 2nd and 1st nucleotides in the anticodon. From the standpoint of physics and chemistry of the nucleotides interaction via hydrogen bonds, the 3rd "wobbling" nucleotide of the anticodon is the 3'-nucleotide, and complementary to it 1st nucleotide of the codon is the 5'-nucleotide of the codon.

[4] Pairing according to the rule: adenine-uracil, guanine-cytosine.

nucleotides:

Genetic Code - Table 1.

UUU Phe	**UCU Ser**	**UAU Tyr**	**UGU Cys**
UUC »	**UCC »**	**UAC »**	**UGC »**
UUA Leu	**UCA »**	**UAA Och**	**UGA Umb**
UUG »	**UCG »**	**UAG Amb**	**UGG Trp**
CUU Leu	**CCU Pro**	**CAU His**	**CGU Arg**
CUC »	**CCC »**	**CAC »**	**CGC »**
CUA »	**CCA »**	**CAA Gln**	**CGA »**
CUG »	**CCG »**	**CAG »**	**CGG »**
AUU Ile	**ACU Thr**	**AAU Asn**	**AGU Ser**
AUC »	**ACC »**	**AAC »**	**AGC »**
AUA »	**ACA »**	**AAA Lys**	**AGA Arg**
AUG Met	**ACG »**	**AAG »**	**AGG »**
GUU Val	**GCU Ala**	**GAU Asp**	**GGU Gly**
GUC »	**GCC »**	**GAC »**	**GGC »**
GUA »	**GCA »**	**GAA Glu**	**GGA »**
GUG »	**GCG »**	**GAG »**	**GGG »**

Lagerkvist placed amino acid codes in nucleotide triplets (codons) in compound groups of four codons, which share the first two nucleotides, and the third nucleotide (3') interacts via hydrogen bonds with the first (5') nucleotide of anticodon, wherein this 5' nucleotide of anticodon "is wobbling", i.e. *de facto* it is accidental. To be more precise, the 3' codon nucleotide is not involved in amino acid coding, although it was determined by chromosomal DNA. If we ignore the reality, the 3' nucleotide may be any of the four possible nucleotides, but only for the given encoded protein. However, since this DNA sequence may encode other proteins (reading frame shift), then, codon nucleotide voluntarism for DNA is excluded. When all four codons are distributed via similar amino acids, then, these four form codon families. But there is a nuance in this distribution via similar amino acids: the same amino acids fall into different families. E.g., Leu (leucine) falls in two families (if the family is determined not by amino acids, but by the first two

nucleotides in a codon)- these are the families of family of UU and CU. The amino acid Ser (serine) falls into the families of UC and AG. Amino acid Arg (arginine) falls into the families of CG and AG. However, there is an advantage of such a classification of codon families: it becomes obvious that the model of triplet encoding of amino acids in the primary protein is inconsistent. In fact, this encoding is a doublet, in no ways it could be a triplet. Lagerkvist writes: "*...The data discussed so far indicate that it is possible for the translational machinery of the cell to read codons by the "two out of three" method, disregarding the third nucleotide. This is certainly so under the conditions of protein synthesis in vitro and possibly also in vivo*." He stated, in general, obvious to everyone the principle of codon reading as "two out of three", but no one before Lagerkvist had ever focused attention on this important fact. And that's a pity. If the above is true, the protein-synthesizing system has a source of potential errors when both the ribosome and tRNA share the "two out of three" rule for reading mRNA codons by tRNA anticodons. Table 1. shows that the same amino acid may be encoded by fours of codon families. For example, the four of CU-family encodes leucine. The four of GU-family encodes valine, UC - serine, CC - proline, AC - threonine, GC - alanine, CG-arginine, GG - glycine. Right on the surface, immediately noticeable, there is a fact of degeneracy, i.e., information redundancy of the code. If you borrow linguistics terminology for the protein code (which has been widely and commonly used for a long time), the degeneracy of the code can be understood as synonymy. It is also unanimously accepted. In other words, the same object, for example, the amino acid, has a number of ciphers - codons. Synonymy doesn't hide any danger for the accuracy of protein biosynthesis. On the contrary, such redundancy is good, since it increases the reliability of the translational ribosome "machinery".

However, Table 1. shows another fundamental, gene-linguistic phenomenon, which is kind of unnoticed and ignored. The phenomenon is that in some codon families, the fours of codons, namely, their meaningful identical doublets of nucleotides encode not one but two different amino acids as well as stop-

codons. Thus, doublet UU-family encodes phenylalanine and leucine, AU-family - isoleucine and methionine, UA-family - tyrosine, Och-family and Amb-family - stop-codons, CA-family - histidine and glutamine, AA-family - asparagine and lysine, GA-family - aspartic acid and glutamic acid, UG-family – cysteine, tryptophan and Umb stop-codon, AG-family - serine, and arginine. Continuing the analogy with linguistics, let's call this phenomenon – homonymy of the first two coding nucleotides in some codon families.

Unlike synonymy, homonymy is potentially dangerous, as was noted by Lagerkvist, though he did not introduce the term of "homonymy" in relation to the protein code. Seemingly, such situation should have resulted in ambiguous encoding of amino acids and stop-codons: the same codon doublet (within some of identified by Lagerkvist families) encodes two different amino acid, or various stop-codons. These special codon families are presented in Table 2.

Table 2.

UAU Tyr	**UUU Phe**	**CAU His**	**UGU Cys**
UAC »	**UUC »**	**CAC »**	**UGC »**
UAA Och	**UUA Leu**	**CAA Gln**	**UGA Umb**
UAG Amb	**UUG »**	**CAG »**	**UGG Trp**
AAU Asn	**AGU Ser**	**GAU Asp**	**AUU Ile**
AAC »	**AGC »**	**GAC »**	**AUC »**
AAA Lys	**AGA Arg**	**GAA Glu**	**AUA »**
AAG »	**AGG »**	**GAG »**	**AUG Met**

To better illustrate, we have rearranged these codon families in Table 3. The final rearrangement of doublet codon families and ambiguously encoded by them amino acids (as well as stop-codons), clearly illustrates homonymy of the triplet code in general. Out of eight codon families (arranged according to meaningful doublets), five families are homonymous. This displays the indisputable and ignored fact of the second, homonymous, multivalent plane of the triplet code. The code is *linguistically* homonymous-synonymous.

And this is fundamental.

Table 3. Synonym-homonymous vector protein genetic code.

UAU Tyr UAA Och UAC » UAG Amb	UUU Phe UUA Leu UUC » UUG »	CAU His CAA Gln CAC » CAG »
UGU Cys UGA Umb UGC » UGG Trp	AAU Asn AAA Lys AAC » AAG »	AGU Ser AGA Arg AGC » AGG »
GAU Asp GAA Glu GAC » GAG »	AUU Ile AUA Met AUC » AUG »	

Synonymy (redundancy, noise immunity)

Homonymy (DNA-RNA real textual resources)

It is crucial to understand: if synonymy of the code is good (information redundancy), then homonymy is potential evil (information uncertainty, ambiguity). This evil is imaginary as the protein synthesizing apparatus easily bypasses this difficulty, see below. If we automatically follow the table/model of the genetic code, the evil becomes real, non-imaginary. And then, it is obvious that the homonymous code vector leads to protein synthesis errors, since ribosomal protein synthesizing apparatus when meeting with the homonymous doublet and following the "two out of three" rule, must select one and only one amino acid from two different but ambiguously encoded by identical doublet-homonyms. Besides amino acid selection, it has to decide (in the case of UA-family) whether it should stop the synthesis of peptide chain (select stop-codon) or include tyrosine in its makeup. If the selection is inaccurate (and the genetic code table does not indicate how to make accurate selection) – it will result in errors in protein synthesis. Potentially dangerous homonymy, leading to inaccurate "reading" of codon by anticodon, stems from random nature (*non-linguistic*) existence of 5'-nucleotide of anticodon which bind with the 3'-codon in homonymous codons. This random nature is challenged by many, appealing to the Crick's Wobble-rules of codon-anticodon pairing. So now let's dot the "i".

F. Crick tried to remove the strangeness of the non-

canonical behavior of the 3'-5' pair with the help of the so-called "Wobble Hypothesis" [Crick, 1966]. The "Wobble Hypothesis" introduces the concept of ambiguous matching of codons to amino acids in gene-encoded proteins and suggests the possibility of non-canonical and random pairing of 5' nucleotide of the anticodon of transfer RNA (tRNA) with the 3' nucleotide of the codon of messenger RNA (mRNA) during its translation into protein. Simply speaking, sometimes during protein biosynthesis, there is a possibility of non-strict matching of codon-anticodon nucleotides in these conditions. This means that non-canonical base pairs[5] are formed, which do not differ significantly by geometrical parameters (Uridine-Guanine, etc.). Moreover, the Wobble hypothesis, and Crick's model in general, automatically implies that in codons (triplets) of the genes, only the first two nucleotides (doublet) encode amino acid sequences in protein chains. 3'-codon-nucleotides are not involved in encoding of amino acid sequences in proteins. These 3'-nucleotides, although being strictly determined by the DNA molecule, allow arbitrary, random, non-canonical pairing with the 5' nucleotide of anticodons of transfer RNA carrying the amino acids. And therefore, these 5'-nucleotides of anticodons can be any of the possible four. Hence, 3'-nucleotides in codons and pairing with them 5'-nucleotides in anticodons do not have *gene-linguistic* character and play the role of "steric crutches", filling "empty spaces" in the codon-anticodon pairs. In short, 5'-nucleotides in anticodons are not random, but "wobbling". This is the main point of the Wobble Hypothesis. If we accept the idea of "steric crutches", then it is clear that the 3'-nucleotide in homonymous codons of mRNA is not involved in encoding of amino acids for this protein. At first sight, there is a genetic-semantic arbitrariness, and it looks like, the triplet code model loses its logic and obvious meaning. To confirm this, let's cite the words of the actual author of the theory of the triplet code, Francis Crick, written

[5] Canonical thermodynamically beneficial base-pairing - adenine/thymine, guanine/cytosine (for DNA), adenine/uracil, guanine/cytosine (for RNA)

by him in his autobiography shortly before his death [Crick, 1989, p. 98]: "*An important point to notice is that although the genetic code has certain regularities—in several cases it is the first two bases that encode one amino acid, the nature of the third being irrelevant—its structure otherwise makes no obvious sense."*. Let's specify. The 3'-nucleotide in the codon can theoretically be any of the four possible bases, as it pairs with the 5'-nucleotide of the anticodon randomly, and this pair, as already mentioned, is not involved in encoding of amino acids for this protein. But, once again, in reality the 3'-codon nucleotides are determined in the original DNA and do not break genetic canons. These are exactly the 5'-anticodon nucleotides which are complementary to the 3' codons nucleotides that "violate" the canons. Surprisingly, F. Crick saw the synonymous degeneracy of the code, but he did not see the homonymous. Although his phrase *"…makes no obvious sense"* tells us that genius brain of F. Crick was aware of limitations of his model and the ambiguity, associated with the 5'-"wobbling" anticodon nucleotide, when ribosome reads mRNA codon-by-codon together with tRNA according to the "two out of three" rule. So, this 'ribosome-mRNA-tRNA' complex inevitably has to solve the typical linguistic semantic problem of homonymy. Otherwise, errors in protein synthesis are inevitable.

F. Crick saw "*no obvious sense"* in his model. Why didn't he? He also wrote: *"although the genetic code has certain regularities."* Why only certain regularities? It is clear that regularities stated by him are in synonymy for codon families, grouped by the identical first two bases (the third can be any), i.e., for a half of all codon families, namely for CT, GT, TC, CC, AC, GC, CG, GG synonymous families. Each of them encodes one out of twenty different amino acids, or is a stop. Wherein, the 3'-nucleotide paired with the 5'-nucleotide of anticodon are not involved in the encoding, and this is what provides synonymy. However, and this is important, F. Crick did not say anything that he can put his finger on, neither here, nor in the Wobble Hypothesis about another half of the codon families. These are TT, AT, TA, CA, TA, GA, TG, AG families, where in each of them two different amino acids or a stop function are encoded.

The role of the 3'-5' codon-anticodon' pair was not commented in any way by F. Crick. It seems that the uncertainty of encoding in this strange family confused F. Crick and made him mention the absence of obvious sense in his model. He does not describe anywhere, what happens outside of these synonymous "few cases". And outside of these few cases there is a strange "non-obvious" codon family - TT, AT, TA, CA, AA, GA, TG, AG. There is nothing you can find in Crick's works about this. In such a way F. Crick implicitly raised the question of encoding the "non-obvious." And he hasn't responded to it. There is nothing on this important subject in the modern studies either. The answer to be found in the hypothesis of contextual orientations of genetic apparatus (quantum biocomputer) during its work with the non-obvious (homonymous) family.

“TWO-OUT-OF-THREE” AS A SIGN OF GENOME QUASI-CONSCIOUSNESS

Let’s ask the following questions: “wobbling” is a synonym of randomness, but is “wobbling” itself random? It appears that “wobbling” is pseudo-random. Let’s justify the fundamental importance of the pseudo-randomness of 5'-nucleotide in anticodons in situations of homonymy during protein synthesis by ribosome. A pair of 3'-5' codon-anticodon nucleotides in a situation of homonymy intentionally does not represent the element of a *gene-linguistic* structure of the ribosome mRNA “reading” technique. The reason for this is that protein code *inter alia* is a mental structure. This construct deals with mRNA texts, the texts which are not metaphorical (that’s why we omit quotes in this case), but real texts, which represent thoughts and commands. Mentioned pseudo-randomness is biologically necessary. It makes the code flexible, in the course of natural selection allowing the biosystems to perform adaptive – explorative searches for the right protein, synthesizing trial proteins to adapt to changing environment conditions. The protein code is synonymously generous, rich and redundant. However, via its homonymy it also penetrates into other semantic realms of genetic coding at the mRNA texts level and, possibly, pre-mRNA.

So, we have two protein vectors: synonymous and homonymous. The first one provides information redundancy in amino acid selection. The second one helps in ambiguous situations of amino acid selection, looking for solutions in the fundamental attribute of genetic information - its textual and linguistic character. If organisms automatically functioned within the canonical framework of Nirenberg-Crick’s model of genetic code, then, life on Earth would have been impossible. Although, as we can see, everything is fine in this respect. Protein synthesis is a very accurate process, borrowing its practices from linguistics and logic, i.e. intelligence. The ribosomal apparatus and the entire genome represent a quasi-intelligent system, which reads mRNA text triplet

by triplet (e.g., locally, piece by piece) and at the same time, reads it as a whole, e.g. continually, nonlocally. This nonlocal reading, ability to comprehend the read text, eliminates the problem of codon homonymy. How does it work?

Again, let's return to the half-forgotten and underestimated article by Ulf Lagerkvist. In this case, we are not going to criticize the triplet model of protein code again and again. It has played its nowhere near weak role in the evolution of genetics and biology. Now our goal is to consider the protein code as a dualistic *linguistic sign* system, operating by blind physics and chemistry on one hand, and operating by quasi-semantic constructs of DNA and RNA texts and quasi mental functions of the genome on the other hand. Moreover, the triplet code, is only one of many subsystems which code and create the dynamic blueprint of the future organism, namely, the lowest subsystem. Failure to acknowledge this fact leads to senseless and expensive research projects. Ulf Lagerkvist was the first to state the inconsistency in the protein code triplet model, but he couldn't find the reason [Lagerkvist, 1978]. He tried to get the model out of its dead-end but failed. There was nothing he could oppose to the obvious and strange fact that the "two out of three" rule is also valid for the ribosomal translation machinery under *in vivo* conditions, moreover, *"with a frequency that is not negligible."*. Then, Lagerkvist writes: "*If this is so, the cell would be faced with a certain probability of misreading which could mean a threat to translational fidelity if the "two out of three" method were to be used inappropriately-i.e., anywhere outside the codon families, where it could lead to mistakes in protein synthesis."*. However, what the inappropriate usage of the "two out of three" rule truly means, remained a rhetorical question to Lagerkvist. And why *"outside the codon families"*? And not all codon families, but particularly in homonymous, not synonymous codon families. Lagerkvist didn't understand that either. Although, he tried to explain it this way: *"…those places in the code (Gariaev: in mRNA) where the "two out of three" method could lead to translational errors are exclusively occupied by low-probability codons. This organization of the code and the competition with tRNAs having anticodons able to read all three*

positions of the codon would effectively prevent the "two out of three" method from being used when it might compromise translational fidelity." This abstract is in contradiction with the actual situation, since 50% of codons are homonymous. So, the author explained only those codons "reading all 3 positions" of nucleotides in codons, i.e. synonyms, leaving behind the other half of codons (homonyms). The remaining half, the codon-homonyms cannot be considered occurring with "*low probability"*. Immediately recognizable is that the UUU codon-homonym is able to bring chaos into protein synthesis. In short, the logical contradictions of the model, which are visible even to the naked eye, are simply disregarded by Lagerkvist as well as scientific circles even today. Such disregard is encouraged by the fictitiously soothing and well-known fact that ribosomes *de facto* hardly make any errors during amino acid selection. All this led to the temptation to consider triplet model of the genetic/protein code correct. Nonetheless, the open fractures of the conventional model of the code become larger and more noticeable.

To overcome the homonymy dead-end, we need to consider a very simple but very important aspect: refer to linguistics and borrow the notion of context, which will resolve this problem. A homonym loses its ambiguity only within its context, i.e. a role of a part becomes clear when you can see it within the whole. In this sense, the idea of the mRNA context (the whole text) is nowhere near metaphoric. Little by little, *post factum* molecular biologists and geneticists acknowledge this fact, coming up with the idea of *"the secondary genetic code"* [Ovchinnikov L.P., 1998]. Let's cite L.P. Ovchinnikov, one of the prominent molecular biologists: "An initiator codon is recognized only within a certain context. If we ask a question "Is it possible to write an amino acid sequence of the protein encoded in mRNA, if/when we have 1) a sequence of nucleotides of some mRNA, 2) the table of genetic code and, 3) we know that mRNA translation goes from 5'- to 3'-end, while the peptide chain grows from the N(amine)-end to the C (carboxyl)-end?"; then, we'll have to give a negative answer to this question... To recognize a codon as the initiator, not only the codon itself is

important, but rather the context is important which assigns the initiator's role to this codon. Initiation with eukaryotes occurs... mostly from the first AUG, however, only in cases when AUG is in the optimal context: a purine (A or G) should be located just two nucleotides before it, and G should be located immediately after it. If the first AUG in eukaryotic mRNA is not in the optimal context, it is bypassed, and initiation starts with the next AUG. In the case of such initiation of translation in eukaryotes, the mRNA sequence is scanned (from the beginning of mRNA) to locate an AUG codon in its optimal context."

As we see from this long, but extremely important citation, to resolve the problem of the genetic code model, classical molecular biology (in here represented by RAS academician L.P. Ovchinnikov) was forced to borrow this idea of context in homonymous codon situations. And he introduces the second, no less important point, that there is a factor of remote influence by certain mRNA-blocks (cap, poly-A and UTR's (Untranslated Regions)) on remote sites in mRNA, where ribosomes integrate the first certain amino acid into a synthesized peptide chain. This is where the idea of "reading-scanning" an entire mRNA, i.e. mRNA context, was required. My team had predicted all these explanatory factors long before, including the mechanism of polynucleotide scanning via soliton excitations of RNA and DNA [Gariaev, 1997].

Let's point out another important moment of codons recoding depending on the context, this moment doesn't fit into the Procrustes' bed of the canonized triplet model either. The factor of mRNA frame shifts reading by ribosome is long familiar. It is clear, that such mRNA frame shifts (as well as codons contextual influences and "reinterpretations") cannot be explained from the points of view of mere physics and chemistry. To explain them, we need to acknowledge new *linguistic* realms of the genome, we need to see genome as a quantum biocomputer [Gariaev P.P. et al, 2001], to see its mathematical logic which involves ultimate, purely intellectual operations including the abstract concept of null [shCherbak, 2003]. These are cardinally new ways of understanding biology and genetics.

It's indicative [Ovchinnikov, 1998]: *"...that reading of mRNA within a single cistron is not always continuous. Originally, it was assumed that the nucleotide sequence in mRNA is always read continuously from the initiator codon to the stop codon. However, it turned out that in the course of translation of Phage T4 Gene 60 mRNA, a considerably long sequence can be bypassed. In such a case a ribosome makes kind of a 50 nucleotide jump along mRNA from one GGA glycine codon located before UAG stop codon to another GGA glycine codon. The mechanism of this phenomenon is not absolutely clear yet."*

This is one of numerous examples of genome operation, going beyond the existing canons and dogmas. Sure enough, such ribosome "jumps" should stem from the real, not metaphorical, reading and understanding of mRNA meaning: one should know from and where to jump. This leaves no chance for any allegory or metaphor. All these deviations from the canons of the triplet model L.P. Ovchinnikov called *"the secondary genetic code"* [Ovchinnikov, 1998].

What type of code is this? What principles is it based on? I guess, the clue is in the linguistic potencies of DNA and RNA molecules, which are, in fact, real intelligent constructs. Only acknowledging that this is not a metaphor, we can explain true meaning of the mentioned deviation from the common rules for genetic information translation from mRNA texts. An ardent desire to find different codes in DNA has already led geneticists to propose that there are dozens of codes in the genome. Eduard Trifonov writes about this in a funny and biting manner as a pandemonium of the Second Genetic Codes[6]. This is a declaration of confusion about chromosomal coding complexity, especially knowing that the first genetic code (discussed above) is not yet understood.

Let's make an intermediate summary about discovery of these new fundamental phenomena within the framework of

[6] http://trv-science.ru/2012/01/17/stolpotvorenie-vtorykh-geneticheskikh-kodov/

Nirenberg-Crick's first model of genetic code, the phenomena stated (but not yet understood) by official science:

a) distantness contextual influence by remote mRNA sequences on the accurate codon's reading by a ribosome, and on the codon's recoding,
b) nonlocal scanning of long mRNA sequences,
c) semantic mRNA reading frame shifts,
d) long-distance ribosome "jumps" along mRNA,
e) recoding of codons.

Let's try to understand what happens in contextual situations, including homonymous situations with coding doublets, while keeping in mind Lagerkvist's "two out of three" method, resulting from Crick's wobbling hypothesis of the 3' – nucleotides in codons. Acknowledging the thesis of genome's quasi-intelligence, we must interpret genetic homonymies in the same manner as linguistics. Namely, the informational content of the homonym becomes clear only after reading and comprehension of the whole text (or sufficiently large part of it), i.e. the context, regardless whether it's a human or genetic text. For example, we cannot understand the meaning of such homonyms as "band" and "spring" without knowing the whole phrase or sentence. Similarly, the ribosomal translation quasi-intelligent system must read and comprehend the whole mRNA text or its larger part 1) to make an accurate decision about the selection of any of the two homonymous codon doublets, coding different amino acids and /or stop-signals; or 2) to decide about ribosome "jumping" on a certain distance along mRNA strand. The same applies to the situations of codons recoding, but in this case, the notion of context has a larger semantic scope, going beyond the framework of linguistics, for example, in case of amino acid starvation or heat shock situations. In such situations, the biosystem sees "contextual" situations in critical ecological-biochemical emergencies, which require immediate or time-consuming evolutionary adaptations followed by introduction of new amino acids and synthesis of new trial proteins. Anyway, it is high time for geneticists and molecular biologists to change their attitudes towards protein synthesis. This process can

no longer be seen from the points of view of purely physical-chemical interaction between DNA, RNA, enzymes, ribosome proteins, amino acids and other metabolites. Here we have one of numerous examples of multi-dimensional intelligence of the whole organism and its tissues, cells, and genome.

Historically, linguistic terminology in relation to the protein code has been commonly and long applied. Namely, from the early 1960's, when F. Crick and M. Nirenberg first called DNA molecule a text. It was a brilliant anticipation, however, F. Crick and the majority of others, using this term until now, understand the textual aspect of DNA, RNA and proteins as a metaphor, borrowing its semantic origin from linguistics. Let classical geneticist assume for a moment that these terms in relation to the chromosomal apparatus are not metaphoric. Then, logic will strongly suggest that the protein synthesis system and genome have a minor consciousness and intelligence or their equivalent in a form of biocomputing [Gariaev P.P. et al, 2001]. Real physical-chemical and quantum acts in one super-sophisticated metabolic network of protein synthesis originate from one intelligent source of nature.

Although the idea of genome computing *in vivo* is nothing more than a model, this model is considerably more developed in comparison to understanding protein biosynthesis merely from the view of chemistry, physics and biochemistry. A genome is intelligent in its own fashion. This ideology traces its origin back to Aristotle with his entelechy postulate[7], later followed by Driesch[8]. Classical genetics is not yet ready to take this turn, namely, return to a new level of the "*causa finales*" formula. Thus, classical genetics slows down biologists thinking, and this is quite counterproductive. This is stagnation, and we all see results of it: conventional genetics followed by medicine are not and will not be

[7] http://www.bibliotekar.ru/brokgauz-efron-ch/166.htm

[8] http://vikent.ru/author/2259/

able to solve the problems of cancer, tuberculosis, AIDS, aging, etc., applying the old theoretical base. However, there is a way out. It is with the serious consideration of new, bio-semiotic or epigenetic models of the genome, discussed in this book. And a lot has already been done in this direction. The bio-semiotic aspect of genetics was magnificently presented by the studies of Sedov, Chebanov's and some foreign researchers[9]. They see not only textual aspect in the genome but also its aesthetical aspects: *"In many DNA regions, they found refrains or "tunes with variations", rhythmical and semantic iterations, resembling homonyms, poetical rhymes and musical themes"*.

DNA-protein musical phenomena deserve special attention. In the Western world production and marketing of such DNA and protein "music" has reached a mass scale. Nucleotides and amino acids in DNA and protein sequences are associated with different notes according to certain algorithm, resulting not in cacophony but actual music. They even try to use this music for therapeutic purposes. Any existing search engine in the Internet will provide a long list of links for "DNA music" or "Protein music". In other words, moneymakers ignore genetic science and irresponsibly and recklessly exploit the beginners understanding of the wave, musical and *linguistic sign* functions of genetic structures. We believe that uncontrolled listening of such "music" might be dangerous as we have no idea about possible consequences, introducing into our metabolic "DNA-protein cauldron" wave information vectors of little-studied action.

Let us introduce another example, demonstrating some genome intelligence, notably in the field which is considered to be the firing range of pure randomness - natural mutation - in the natural mutation process, where (as believed) chaos and stochastics prevail. Though, let's point out that the notion of chaos, as an absolute randomness is a thing of the past. Prior to the discovery of

[9] http://www.zanoza.lv/blog/gordon/430

DNA, a chaotic mutation process allegedly forming the basis of the evolution, was called *"hypothesis of indefinite variability"* of the organism, and represented the *"raw material"* for evolution, according to Darwin. Let's recall that at the end of his life Darwin realized and admitted that seeing random variability as the only basis of evolution is a fiction. If the protein code contains and employs strictly semantic structures such as text, reading, recognition, decision making, etc., then, it is natural to assume that both genome and protein code was created by thought, and the genome itself is intelligent. Stochastic processes in operation of chromosomal DNA are optimized. We assume, there is a compromise between stochastics and determinism. The stochastics in genome mutations has been long and well-studied. Random DNA mutations are mainly detrimental in cases when they affect protein and RNA-coding chromosome regions (euchromatin), or they are neutral, in case of allegedly "non-coding" chromosome DNA (heterochromatin) mutations. Surprisingly, mutations (when the cell controls the mutational semantic aspect) turn out to be beneficial, thus, they contribute to intelligent, non-Darwinian evolution. Such mutations, specially selected and implemented by the biosystem itself, can hardly be called random. These mutations are not the result of natural selection during long-term evolution, they are put into action fast, fitting within a single life cycle of the biosystem. The combinatorics of these mutations is intentionally set by the organism. It is clear from the results of immunogenetic research, where amino acid sequences of antibodies (referred to as Wu-Kabat variability coefficient or plot) are intelligently and preventively selected by B-lymphocytes [Kabat E. A. et al., 1977]. The combinatorics of amino acid sequences is the result of hyper-variability of V(D)J genes of antigen-binding regions of immunoglobulin antibodies. This mutation hyper-variability is, as one would assume, intentionally preprogrammed by the genome for recognition of antigens at the molecular level. At first, the cell and its genome in a mysterious way scan the antigen, then, it decides about V(D)J genes' mutation combination for the desired selection of coded amino acids which make up Wu-Kabat variability. V(D)J

genes' behavior contradicts neo-Darwinian dogma, which states that germ line gene variability is pre-existent before any selection is made. Let's keep in mind, that there is no accurate and instantaneous "decision" about amino acid selections (there is no full determinism), though, there is not absolute stochastics either, since mutations are regulated (programmed) by an organism itself. In other words, there is back and forth communication between the trial mutation combinations and the structure of antigen-binding regions of immunoglobulins antibodies. Here randomness and regularity are in balance.

The protein code was created by Intelligence. Following Spinoza and Nalimov, let's consider the Universe to be "*causa sui*", to be linguistic, i.e. intelligent [Spinoza, 1677; Nalimov, 1989]. Then, immune-competent cells (with their genome) intentionally and intelligently use randomness, creating desired genetic texts with certain semantics, resulting in an adequate immune response. Naturally, such genome intelligence operates within certain narrow limits of immune response, and its scope and magnitude is incomparable to the intelligence of the Human brain. This is the observation of the general principle of biosystem fractality, including gene-cell-tissue-organ and organism dimensions of intelligence. In other words, we see non-linear, fractal iteration of the same phenomenon, function and structure in different dimensions. Herewith, intelligence, consciousness, thinking is the manifestation of the biosystem reflecting its environment for self-regulation to sustain its integrity, survival and evolution. Speech (brain/cerebral cortex) and quasi-speech (genome) reflection is one of the things that make it possible.

The above suggests a simple and seemingly right, inspired by pantheism, thought, that the genetic apparatus as well as all organisms are the action result of the Creator (Nature). And therefore, everything in the organism is intelligent. And we could have set our minds at rest at this point. However, such an answer is too extreme since it is an answer to everything in general and at the same to nothing specific. It's a universal "black box". Any question could be black box input, though the same answer will be provided

in the black box output. We cannot accept this. This requires real studies of chromosome function, based on Linguistic Wave Genetics (LWG). There have been promising results already, snapshots of which can be found at *www.wavegenetics.org*.

For example, there has been successful regeneration of the retina of the eye and recovery of vision, and now it is feasible to regenerate injured spinal cords and cerebrums to their full functionality. All these achievements are aligned with the main strategy - programming of the stem cells' genome, based on completely different understandings of genetic apparatus operation. The potential prospects of this go far beyond medicine: engineering of a quantum biocomputer, operating on chromosome quasi-intelligence; creation of a bio-internet; development of deep space communication, etc. All these achievements and opportunities are possible due to not only the linguistic aspect of genetic information but also to its quantum, wave otherness. The ability to operate with wave equivalents (phantoms) of DNA and RNA as the highest information system of the genome-quantum biocomputer, is an inherent attribute of the chromosomal apparatus of biosystems.

The correct meanings of homonyms are determined when the ribosome-nanobiocomputer (with the rudiments of thought-consciousness) perceives the text of the entire mRNA (the context). This is the key hypothetical point of Linguistic Wave Genetics (LWG). The following is essentially important in our hypothesis. Transcending the narrow scope of understanding of genetic processes as only physical and chemical and realizing that they also have the quality of thought-consciousness, is a leap to deeper levels of understanding of the genome as a quantum biocomputer, which is able to read and interpret genes as real text-programs. Who or what has created these programs? This is a separate big question. There was a splendid study done by V.I. shCherbak [shCherbak, 2003]. To some extent, it is close to our study, since it proves not only quasi-intelligence of the genome, but also from the perspectives of physics, mathematics and philosophy justifies the intelligent source of creation of genetic information, which is

critically and strategically important. V.I. shCherbak, analyzing quantitative ratios of atomic nucleuses of encoded amino acids and codons within the triplet genetic code, suggested that in the process of protein biosynthesis, there is a system of arithmetic operations, and this at the same time demonstrates some aspects of genome quasi-intelligence. Within the protein code V.I. shCherbak found the system of genetic computation, using the null function. This is a very important finding as null is a purely intellectual and extremely abstract concept, which sets and lays the foundation for co-ordinate thinking and consciousness, making possible quantitative measurements of the external world. These measurements are then interpreted by the internal organismic genetic computing consciousness. So, digits (along with letters) become an integral part of the genetic (protein) code. And therefore, according to V.I. shCherbak, arithmetic regulation in linguistic and/or textual genetics is real.

Experimental study executed by Eidelman provides a good evidence for the above statement. Eidelman employed fast re-associating along "sticky-ends" DNA fragments as a main factor for artificial DNA-computing technology *in vitro* in a demonstration for the solution of the so-called "Travelling Salesman Problem" (TSP) [Adleman L.M. 1994]. However, it's not the best example. In fact, Eidelman's DNA-computing is performed by people, where they make the final decision, choosing out of billions of potential "solutions", presented by re-associating sticky-end DNA fragments [Gariaev P.P., Makedonsky S.N., Leonova E.A. 1997; Gariaev P.P. et al., 2001]. Developing his ideas further, V.I. shCherbak wrote: *"If that is the case, some cell organelles should work as biocomputers. Thereby, we have to discover the number systems with which they work"*. Then he continued: *"it seems that the genetic code is connected more closely to abstract notions of arithmetic than with notions of physics or chemistry"*.

We assume that both statements are not quite right. The chromosomal continuum already represents a biocomputer. Perhaps, it is not self-sufficient, and it is incorporated into cellular and tissue computing via additional cell organelles. V.I. shCherbak

considers the binary logic of digital computing of the genome to be the primary, determining factor for its operation. The "translation" of digital DNA-RNA "conscious reading" into analogue form is considered by him as secondary or subordinate. If this is true, this is only somewhat true. The strategic line of genome functions is about operation with holographic and textual images. In a conventional computer, all information is recorded in the form of combinatorics of one and zero alterations. This is the information code or cipher, it represents ciphered wealth (a resource of digitized information) which is to be deciphered into words and images. The chromosome quantum biocomputer does not need to strictly operate with ciphered wealth (e.g. numerical digitized operation), it operates with wealth directly (via holographic blueprints), in cases when it is working on building the whole organism and not just synthesizing proteins. The chromosome quantum biocomputer uses the principle of holographic processing of information in the form of ready holographic blueprints of the inner state of cells, tissues and organs; the organism achieves its inner self-vision and self-regulation via this state communication from genome holograms. Binary digital logic is not fully set aside. It is required, for example, when turning protein and RNA genes on and off, which is also important, especially for building protein phrases or texts[10].

At the same time, V.I. shCherbak's studies are fundamental. They are important ideologically, as for the first time ever, they provide inexorable and clear mathematical evidence that protein code is a quasi-intelligent system and at the same time the result of the Universe's semantic nature. One can explain the origin of the protein code only when seeing it as a conscious act rather than a consequence of the blind Darwinian evolution. Read below what V.I. shCherbak had to say about this (clarifying his statements from the article [shCherbak V.I., 2003]), as well as in a personal letter: "There are concentrated data, not the hypothesis, in this article.

[10] The concept of protein phrases was postulated and will be developed by us.

The presented data put a fundamental (I emphasize this word) ban on the speculative models of physical-chemical evolution of the genetic code, and, hence, life. This ban is dictated by the abstract symbolism of arithmetic (the core of mathematics), that was found within the code. Previous attempts failed to declare the model of physical-chemical evolution insolvent because all the efforts were reduced to manipulation with a negligible probability of the accidental introduction of the cell information system. Pay attention to the paradox: these attempts leave a loophole for physical-chemical evolution, honestly admitting that a negligible probability still exists! According to many people, billions of years is enough to realize this probability. This means that physical-chemical theory of evolution can be defeated, if a long desired, ban of Darwinian evolution becomes fundamental. Such a ban is dictated by the abstract symbolism of arithmetic within the genetic code. Simply speaking, no interaction between molecules in physical-chemical evolution - no matter how long it takes! under any natural conditions is able to produce the abstract number concepts and its *sign* representation in a positional computational system, using the extremely abstract concept of null. The game should now proceed according to different rules. This new code organization suggests searching for its origin within the realm, which as it seems to us, is operable with intellect only. ... It's the newest weapon against the theory of Darwinian evolution, not just "thermonuclear" but a weapon of "annihilation." The article presents the facts and not speculative models...".

THE ROLE OF NON-CODING (“JUNK”) DNA

Historically, the majority of the genome, which is not directly related to the triplet code, has been called “junk”. This is absolutely wrong. Now, three decades later, it was confirmed [Shabalina, Spiridonov, 2004]. The detailed list of protein-coding genes was made after the completion of projects on sequencing the mouse and Human genomes. In general, the protein composition of the mouse is similar to the Human, and approximately 99% of the protein-coding genes in the mouse have a homologue in the human genome. The total amount of protein-coding genes in the mammalian genome is estimated to be approximately 30,000. Such an estimate is surprisingly close to the number of protein-coding genes in the genome of nematodes. The function of non-coding DNA remains poorly understood, and perhaps, interspecies comparison is the only way to demonstrate that well conserved DNA sequences that have been developing slowly as a result of competitive selection, are functionally important. In general, non-coding regions are less conserved than protein-coding parts of genes. Comparative analysis of non-coding regions in genomes of higher eukaryotes shows mosaic structure alternation of highly conserved and distinct segments. Conserved elements, the so-called phylogenetic footprints, make up a significant proportion of noncoding DNA. Comparative analysis of the Human and mouse genomes showed that approximately 5% of the genomic sequence consists of highly conserved segments of 50-100 base pairs; this proportion is much higher, than can be explained only by the presence of only protein coding sequences. The average number of intergenic regions in the mouse and Human (15-19%) does not differ from the number of nucleotides in introns and intergenic regions of nematodes (18%). Some short intergenic regions of mammals represent mandatory sites for known transcription factors and regulatory proteins, while others have no known biological function. The fraction of protein-coding DNA in the genome is reduced with increasing complexity of the organism. In bacteria,

about 90% of the genome encodes proteins. This number decreases to 68% in the yeast, 23-24% in some nematodes, and 1.5-2% in mammals. Various mechanisms for increasing the diversity of proteins include: the use of multiple segments at the beginning of transcription, alternative binding of pre-mRNAs and their processing, polyadenylation, as well as post-translational protein modification. However, these methods of increasing the diversity of proteins also failed to explain why mammals and lower biological systems (insects, worms) vary so greatly in the volume of "non-coding" DNA, having the same sets of genes and proteins as well as similar mechanisms for their diversification. There is no answer to the question: if it is not the genes or proteins, what determines the complexity of highly organized organisms? We can certainly say that the complexity of organisms correlates less with the number of protein-coding genes, than with the length and diversity of non-coding DNA sequences. In general, the complexity of organisms correlates with the increase of the following parameters:

1. with a transcribed, but non-translated part of the genome;
2. with the length and number of introns in the protein-coding genes;
3. with the number and complexity of cis-control elements and with the increased number of involved complex and multiple promoters for single genes;
4. with the number of genes for protein-encoding and for non-coding RNA genes;
5. with the complexity and length of noncoding regions of 3' – ends of mRNA;
6. with the ratio and the absolute number of transcription factors within the entire genome.

In other words, the structural and physiological complexity of the organism is highly dependent on the complexity of regulation of gene expression and on the size and diversity of the transcriptome. The reason for this is that single-stranded RNAs have unique properties, which ensure regulatory functions. These are their ability to recognize DNA sequences via complementary

interactions; their conformational elasticity, and the ability to be translated into proteins. Thus, the complexity of organisms is related to the RNA pool, which acts differently in evolutionary different taxa? But what does it mean, "acts differently"? This is another pretense of an explanation of how the genome operates and creates an organism from itself. And this is the version offered in the cited paper. However, as the authors point out, the paradox of the growing share of the non-coding part of the genome with increasing complexity of biosystems still challenges both genetics and biology, although, since the discovery of non-coding DNA, 40 years have passed. As we can see, even the recent studies come to nothing with the strange fact: the higher the biosystem in evolutionary terms, the more “junk” it has in its genome, up to 98% in humans.

PROBABLE LINGUISTIC SIGN FUNCTIONS OF "NONCODING" OR "JUNK" DNA

From general consideration, it is clear that almost the entire genomes of higher organisms cannot be a useless "selfish" load. Evolution would never tolerate this. “Junk DNA” also performs genetic coding functions [Akifiev, 2004], but what are they? We assume (and experimentally prove to some extent) that these functions are realized at another level of *linguistic* organization of the genome. This is a mental-wave level, involving the principles of quantum physics. This part of the genome operates based on laser radiation, holography, linguistics and, probably, quantum nonlocality. We see the total DNA-chromosomal continuum as an inseparable whole with the entire organism. This continuum functions as a biocomputer quasi-intelligent system [Gariaev, Birshtein et al, 2001]. The genome-computer combines two hypostases of physics. The first hypostasis of the quantum genome continuum uses combined interphase chromosomes as liquid crystal formations in the form of dynamic multiplexed polarized holograms. Physical-mathematical formalism of bioholography was presented by us in the following works [Tertyshniy, Gariaev et al. 2004; Tertyshniy, Gariaev, 2007]. Polarization holography provides gradients of endogenous light fields, which are calibrating and blueprinting the dynamic space-time of growing and adult organisms. Such wave functions also include generation of text-holographic directing vectors for morphogenesis. The second hypostasis of the quantum genome is the usage of its own entangled (quantum nonlocal) photon-polarized (spin) states. This is necessary for instantaneous analysis-synthesis of a current biochemical-physiological state for the billions of cells and tissues of the organism as well as for making adequate “decisions” on biosystem regulation.

THE GENOME AS A LINGUISTIC, SPEECH CONSTRUCT

Above we have discussed the idea of the "second genetic code" in the light of contextual orientations of the ribosomal apparatus and other semantic motives of its behavior. Let's ask ourselves why the genome is speech-like (not in a metaphorical sense) and whether the "redundancy and junk" of the majority of the human or other genomes could be explained by the textual-holographic attributes of the genetic apparatus? The strategic statement, underlying the idea of a speech-like genome, was given by V.V. Nalimov [Nalimov, 1989], who considered the Universe to be conscious, linguistic and, like Spinoza, identified Nature with the Creator God. We adhere to the same positions and do not personify God as some kind of personality. Just as thousands of years ago, we ask: where do we come from, humans, animals, plants, and all Life? Modern science, including genetics and molecular biology, as a display of the Laws of the Nature-Creator, has stored a vast amount of data. Analysis of this data could hasten and facilitate the understanding of DNA as a speech-like material-wave dualistic structure.

Let's cite the Bible: *"In the beginning was the Word, and the Word was with God, and the Word was God .... In him was life, and the life was the light of men ... And the Word was made flesh, and dwelt among us "*[John, 1:14]. And further - *"And the whole earth was of one language and of one speech"* [Genesis, 11:1]. We note here the key points, corresponding to the logic of our study. The Word of the Creator (His Speech), as well as isomorphism of the Creator and the human, are the primary elements, constructing everything inanimate and animate, all Life (including Man) according to the matrix principle: ideal - material. It also corresponds to Hegel's Absolute Idea. Are there now (and not just *"in the Beginning"*) in the human body and in other organisms, animals, plants and other biological forms, any references of a Universal speech common to all Life? In other words, how is the semantic (linguistic) Universe represented in biological systems? Such speech representations

exist in DNA, as well as in DNA matrix re-representations, such as the isomorphic languages of RNA and Proteins. This is probably true for DNA's wave replication of itself, discovered by us [Gariaev et al, 1991; Gariaev, 1994; Gariaev, Tertyshniy, Tovmash, 2007]. Such wave replication is the first direct experimental evidence for the existence of wave DNA equivalents. The highest forms of DNA material-wave matrix functions are speech-like and holographic controls of biological system construction. They determine the potential body forms and as well as intelligence-thinking. The combination of these factors can be considered as permanently operating directives in the construction of the human body and spirit. In contrast to the mortal body of all living creatures, DNA, as a germ plasma, is immortal. Its continuous extension through time and space is provided by hereditary transmission of chromosomes from parents to children. DNA of all Life on Earth is immortal. Even the death of all organisms, due to possible catastrophes does not mean the end of the genetic (natural, cosmic) information. It has multiple levels of nonlocality, including proposed by us - quantum nonlocality [Gariaev, Tertyshniy, 1999; Prangishvili, Gariaev et al., 2000 (b); Gariaev, Birshtein et al, 2001; Gariaev, 2003; Gariaev, Gariaev, Kokaya, Leonova-Gariaeva et al., 2007]. Genome quantum nonlocality means that a chromosomal quantum biocomputer (aka genome) is a single organismic (and partially inter-organismal) system in a so-called entangled state. One can say that the genome contains all of the current genetic-metabolic information of all the cells, tissues and organs of the biosystem. Moreover, such knowledge occurs instantaneously and at any given moment in time. The carriers of this knowledge are endogenous photons and radio waves[11]. In this sense, genomic information goes beyond the chromosome, beyond the Earth. Quantum genomic information of the entire Earth's biosphere, probably is also nonlocal and, therefore, on a universal scale it is eternal, fertilizing more and more new worlds, where physical and chemical conditions are

[11] Gariaev P.P., "Wave Genome" – 3 (is being prepared for publication)

adequate for the birth of life. Note, that the factor of transmission of such information is the Word (Speech), Light and radio waves. And we see that these two fundamental and primary creative elements are present in chromosomes. *In vitro* and *in vivo,* genetic structures generate super-weak *linguistic* acoustic and electromagnetic (including light) fields, as references of the Light and the Word. From a viewpoint of quantum physics, the genome is a superposition of coherent entangled (unmanifested) states, morphogenesis is a system of "objectifications" (manifestations) of a genomes planes in a decoherence-ontogenesis process[12]. You can take an even bigger perspective. All dynamic parts of biological systems are to some extent are entangled, nonlocal, and immaterial, just as Intention is non-material and ideal (an intention of any biological system to evolve and adapt to changing conditions). However, these dynamic parts of the biological system manifest through material biochemical and physiological acts, are a result of instantaneous understanding of their own "on-line" state. In this sense, the zygote contains a potential image of the adult organism in a form of an ideal entangled nonlocal state, which materializes with decoherence. Such perspective allows explanation of the incomprehensible, such as thermophiles survival at the temperatures above 100 degrees Celsius, when supposedly DNA, proteins, and membranes should break down. Thermophiles survive probably due to rapid transitions between local and nonlocal states.

Let us take a closer look at the genetic coding problem from the position of speech and symbolic constructions. This is a knot of contradictions in modern biological science, which also manifest on the social level in the form of persecution of researchers who are trying to get out of the narrow confines of the triplet protein coding model. The materialistic geneticist's ideas, who believe that the genetic code is based only on matter and can be reduced only to the program of protein biosynthesis, still prevail. Those materialistic

[12] The term was suggested by S.I. Doronin ("Quantum Magic", StP: IG "Ves", 2007, p. 336)

scientists are directly or indirectly opposed by other scientists, who rely on new scientific ideas and data and believe that the genetic code is a much broader concept.

The idea of DNA as a text (speech), as a metaphor, was first expressed by F. Crick and M. Nirenberg, the creators of the triplet code model. This was an ingenious foresight; however, it was vulgarized by the spirit of allegory and, therefore, devalued. This led to immutable contradictions within classical genetics. In his memoirs, F. Crick's [Crick, 1989] admitted his realization that his genetic protein-coding model is ambiguous, inaccurate or inconsistent. Where is the deficiency of the Triplet Code Model? We have already reviewed some issues. Developing this critical analysis, we can say, the coding possibilities of the cell, of chromosomes and DNA are not confined by the *linguistic* nucleotide triplets. As speech-like structures, nucleic acids *in vivo* can form meta-languages via fractalization methods. That's why encoding of the protein pool may pass through large blocks, these blocks encode not only the inclusion order of individual amino acids to the growing peptide chain, but possibly they also encode the creation sequence of protein domains, sub-units and even the structural and functional assemblies of enzymes, e.g., of the electron transport chain. So, in this case, the fractality can also be seen as follows: specific coding fragments of the DNA-RNA-protein relationship represent multilingual unambiguous texts of nonuniform scale. Whatever is "a phrase" or "a sentence" in one scale, will be "a word" in another, larger scale. If you keep enlarging the scale, this "word" will become an "alphabetic character". This generalized approach suggests seeing these multiscale semantic blocks of genetic structures as information-intensive signs (hieroglyphs), representing the substrate as a kind of "cellular information metabolism" on mental-material-wave level. This construction of metalanguages is common to mathematics. We have no reason to think that the genome does not use this mathematical technique to the maximum, building new, increasingly complex, semiotic-semantic realms, with their constant re-identification at different levels of biosystem's organization in the process of its own

development. At least, as was already discussed, the triplet code already reveals mental vectors, using mathematical techniques, including the maximally abstract concept of zero [shCherbak, 2003]. Moreover, the function of most synthesized proteins, carbohydrates and lipids is in dynamic realization of metabolic networks, implicitly encoded in DNA with a quasi-verbal component. This reasoning supports the ideas of V.V. Nalimov, who considered all life as a part of Semantic Universe [Nalimov, 1989]. According to V.V. Nalimov, the human is a variety of texts, the grammar and semantics of which, we are trying to embrace with a single, probabilistically given, outlook. Personality, from such perspective, is a self-reading text, with the ability of self-modification.

Let's reduce the scope of genetic consideration to the human, taking into account fractality of text structures of human DNA. Then, we can assume that the re-representation of the human within its own genome (like the representation of any organism into its chromosomes) is of isomorphic text-like character. The proposed argumentation was intended to show how we can push the limits of the Crick model of genetic code. The model had a seizure at the level of weak understanding of spelling rules for the protein "words" "writing" with amino acid "alphabetic characters". This is a clear hindrance towards development of the understanding of the essence of genetic coding.

The fake metaphorical nature about the implicitly present linguistic element of the standard genetic code model, inevitably leads to a dead-end, and this is still the case. Preference is temporarily given to the analysis of the material mechanisms of protein synthesis accuracy, but ignoring the main principle of this accuracy - the mental (semantic) principle of unambiguous selection from coding doublets-homonyms as components of real (non- metaphorical) mRNA texts. This unambiguity is ensured by resonant wave and contextual (semantic, associative, holographic), the so-called background mechanisms. Until now, these mechanisms laid beyond experimentation and reason, however, it is a high time to recognize them now. The homonymous (ambiguous) nature of a code can be resolved in the same way as in natural

languages, by the logical placement of a homonym as part into the whole, into the complete phrase, into the context. It is the meaning of the context that decrypts and assigns a unique meaning to the homonym, making it unambiguous. That's why, messenger RNA (mRNA) as a kind of "phrase" or "sentence" in protein synthesis should work as a functional coding unit to specify the amino acid sequence at the level of aminoacylated tRNA associates, which complementarily interact with the whole mRNA molecule. Wherein, the role of ribosome A, P-sites is to accept these associates (protein precursors followed by enzymatic stitching of amino acids into protein). In this case, the only correct homonymous doublet-codons will be chosen by context-oriented unambiguous selection, that ensures the highest accuracy of protein synthesis, and hence, life on the Earth. Conscious selection, that is, of intelligent origin - is a quasi-thinking genome prerogative only, although for ease of comprehension, we must resort to other terms to explain the consciousness-intelligence elements of the genome, considering it as a biocomputer [Gariaev, Birshtein et al, 2001]. Note, such delegation of conscious-intelligent functions to the genome also does not fully reveal the nature of the genetic information. What is Consciousness and Intellect? An eternal problem of humanity, which will never be fully resolved.

Remembering the common basic provisions of the genetic (protein) code: it is a triplet, non-overlapping, redundant, and it doesn't have "commas", i.e. codons are not separated from each other in any way. The code is universal. It does not have an intelligent origin, and everything happens automatically within the framework of physics, chemistry and biochemistry. What is missing from this list of provisions now? Virtually nothing. However, in fact, the code is a two-, three-, four-, ... n-symbolic fractal and hetero-multiplet formation. The genetic (protein) code is overlapping, i.e. several proteins may be encoded within a single gene. The code has commas, since hetero-codons can be separated from each other by sequences with other functions, including punctuation functions. The code is not universal. There are 18 codes for mitochondrial proteins, and other types of organisms [The Codes, 2000]:

The Standard Code
The Vertebrate Mitochondrial Code
The Yeast Mitochondrial Code
The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code
The Invertebrate Mitochondrial Code
The Ciliate, Dasycladacean and Hexamita Nuclear Code
The Echinoderm and Flatworm Mitochondrial Code
The Euplotid Nuclear Code
The Bacterial and Plant Plastid Code
The Alternative Yeast Nuclear Code
The Ascidian Mitochondrial Code
The Alternative Flatworm Mitochondrial Code
Blepharisma Nuclear Code
Chlorophycean Mitochondrial Code
Trematode Mitochondrial Code
Scenedesmus Obliquus Mitochondrial Code
Thraustochytrium Mitochondrial Code

Surprisingly, all these codes are agreed to be the result of blind physical-chemical evolution, although the probability of the accidental creation of any of them is practically zero. How should we understand the genetic code, considering the contradictions above and our proposed line of reasoning?

Following our reasoning, a good, simplified, primary version of the Creative material-wave control is the semantic alignment order of amino acids and aminoacylated tRNA associates as precursors of protein-linguistic constructs. From this position, it is easier to understand the operation of the genetic protein code as one of a multitude of hierarchical programs in biological-system material-wave organization. In this sense, the protein code is the lower link in organism construction programs, since the language of the genome is creatively multidimensional, pluralistic and by no means is limited to the task of protein synthesis.

The inability of the early concept of the genetic code to be consistent, seemingly should have encouraged the search for new ideas. Instead, preference was given to analysis of mechanisms of protein synthesis accuracy, ignoring the main motive of this accuracy – the unambiguous selection of coding doublet-homonyms. Below is an example of such argumentation (though useless in relation to the problem in question), but necessary to illustrate the pseudo logic in the evaluation of the genetic code's bottom line: "*The fidelity of the decoding process depends on the accuracy of the two adaptor mechanisms …: the linking of each amino acid to its corresponding tRNA molecule and the base-pairing of the codons in mRNA to the anticodons in tRNA. …Two fundamentally different mechanisms are used to reduce errors in the two steps… Many aminoacyl tRNA synthetases have two separate active sites: one that carries out loading reaction {of amino acid attachment to tRNA} … and one that recognizes an incorrect amino acid attached to its tRNA and removes it by hydrolysis. … A more subtle "kinetic proofreading" mechanism is used to improve the fidelity of codon-anticodon pairing. … once tRNA molecules have acquired an amino acid, they form a complex with an abundant protein called an elongation factor (EF), which binds tightly to both the amino acid end of tRNAs and to a molecule of GTP. It is this complex, and not free tRNA, that pairs with the appropriate codon in an mRNA molecule. The bound elongation factor allows correct codon-anticodon pairing to occur, but prevents the amino acid from being incorporated into the growing polypeptide chain. The initial codon recognition triggers the elongation factor to hydrolyze its bound to GTP (to GDP and inorganic phosphate), whereupon the factor can dissociate from the ribosome without its tRNA, making it possible for protein synthesis to proceed. … the elongation factor thereby introduces a short delay between codon-anticodon base-pairing and polypeptide chain elongation, which provides an opportunity for the bound tRNA molecule to exit from the ribosome. An incorrect tRNA molecule forms a smaller number of codon-anticodon hydrogen bonds than a correct one; it therefore binds more weakly to the ribosome and is more likely to dissociate during this period."* [Alberts et al, 1989, 2nd edition, pp. 215,217]

Commenting on this passage, we can say that the emphasis it placed on mutual “recognition” of tRNA and amino acids via aminoacyl-tRNA synthetases. Again, the metaphor “recognition” was used without clarification of what “recognition” means. Moreover, the accuracy of the “recognition” of the codon by anticodon is illusionary because of the “wobbling” of the third nucleotide, that we already discussed above.

The homonymous (ambiguous) nature of the code can be resolved in the same way as in natural languages through context-orientation. Therefore, mRNA as a “phrase” or a “sentence” in protein synthesis should perform as one functional coding and semantic unit, which quasi-intelligently sets the amino acid sequence at the level of aminoacylated tRNA associates. And they complementarily interact with the whole mRNA molecule within context. Wherein, the role of ribosome A, P-sites is to accept these associates (protein precursors followed by enzymatic stitching of amino acids into protein). Knowing this, one can predict that interaction of aminoacylated tRNA with mRNA is of a collective phase character similar to re-association ("annealing") of single-stranded DNA during the drop of temperature (in PCR) following the "elongation" of the native polynucleotide. Is there any experimental data that could be interpreted this way? Continuing our discussion about the role of contextual orientations within mRNA for protein synthesis, we can introduce the following facts below.

It is known [Ter-Avanesyan, Inge-Vechtomova, 1988] that the correct recognition of termination codons by tRNA molecules depend on their contextual environment, namely, whether a stop codon is followed by uridine. In addition, Goldman [Goldman et al., 1995] clearly demonstrated the following: *insertion of nine consecutive low-usage CUA leucine codons after codon 13 of a 313-codon test mRNA strongly inhibited its translation without apparent effect on translation of other mRNAs containing CUA codons. In*

contrast, nine consecutive high-usage CUG leucine codons at the same position had no apparent effect, and neither low- nor high-usage codons affected translation, when they were inserted after codon 223 or 307. Additional experiments demonstrated that the strong positional effect of the low-usage codons could not be accounted for by differences in stability of the mRNAs or in stringency of selection of the correct tRNA. The positional effect could be explained if translation complexes are less stable near the beginning of a message: slow translation through low-usage codons early in the message may allow most translation complexes to dissociate before they read through.

As we see, the interpretation of their experiments involves cumbersome assumptions about *dissociation* of translation products, assumptions which in no way result from their work, assumptions which require special and exquisite research. In this respect, the idea of contextual orientations in protein synthesis regulation is simple, logical and functional. The cited work well highlights the strategic line: the impact of strictly-defined, remote regulation (from the location where peptide bonds from codon insertions in mRNA are formed) of the inclusion or non-inclusion of a particular amino acid in the composition of synthesized protein. This is a distant influence, but the cited paper just mentions it without any comment and clarification as, apparently, researchers had no idea how to explain it. And there are more and more studies like this. The paper that we discuss here presents a half a dozen similar results, which are hardly explained. The reason is the incompleteness of the standard model of the genetic code. This is also true, since there is evidence about the existence of the so-called "swollen anticodon" [Ter-Avanesyan, Inge-Vechtomov, 1988]: *the interaction of mRNA with tRNA in the A-site of the ribosome includes not three but a larger number of base pairs. This means that commonly accepted postulate of the triplet nature of the code is not valid here anymore.* The cited paper presents data on tRNA-tRNA interaction within the ribosome, and these data corresponds to our idea about aminoacylated tRNAs associates as protein precursors. Speaking about this, they say that the effect of mRNA context on unambiguous inclusion of amino acids into peptides represent some

fundamental but so far poorly studied principles of genetic information decoding in protein synthesis, wherein there is a chance for numerous normal and rarely erroneous shifts, and reading frame overlaps. The errors occur when doublets or quadruplets of bases are read as triplet-codons. Frame shift mechanisms of the reading frame are practically unexplored. Many studies showed that an erroneous translation of proteins by the ribosome are caused by various negative factors - antibiotics, temperature changes, certain concentrations of cations, amino acid starvation, and other environmental conditions. Increased ambiguity of codon translation, localized in a particular context, has biological significance and results in non-random distribution of “erroneous” amino acids along the length of the synthesized polypeptide. This non-random distribution leads to modifications of protein functions related to the mechanisms of cellular differentiation, and therefore, mRNA contexts represent a substrate of a natural selection. The optimal level of translation "errors" (if these are real errors) are regulated by unknown mechanisms and is ontogenetically and evolutionary justified. These potent statements, discussed by Ter-Avanesyan and Inge-Vechtomova, correspond well to our understanding of genome operation - wave *linguistic* interactions in the watery-liquid-crystal environment of the cell and its nucleus, where the protein-synthesizing apparatus is involved.

The genetic role of mRNA is dualistic. This molecule, as well as the DNA molecule, signifies a turning point in understanding – the complementary stratification of material and wave-genetic information. The ambiguity of material coding is overcome by the precision of wave coding, which is actualized through mechanisms of collective mental, associative-holographic and contextual effects in the cell-tissue continuum. In this context, the universal context is represented by the Semantic Universe, according to V.V. Nalimov [Nalimov, 1989]. The leap towards a more developed Genetic-Protein Code model is wave regulation of “RNA → Protein” translation and is accompanied by a partial or total waiver of the principle of canonical pairing of adenine with uracil (thymine) and

guanine with cytosine, inherent to DNA replication and RNA transcription stages. Such a waiver is energetically unfavorable on a microscale, though it is necessary and inevitable from an information perspective, and energetically favorable on the level of the whole organism. From this position, macrocontexts of pre-mRNA and contexts of mRNA can be seen as a semantic background (contextual) source of information, which provides a dramatic increase in the signal and selection of a particular one of two homonymous aminoacylated tRNAs.

The idea of the Semantic Universe was originally developed in the works of S. Berkovich, who believes that DNA within the genome is only a barcode, which is connected to some universal computer [Berkovich, 2001]. Let's apply these provisions within the scope of genome operation as a biocomputer (genome-biocomputer). How does the quasi-intelligent ribosomal system behave, when dealing with homonymous situations in mRNA? Let's give a simple example to explain this. Assume, you are to select one word out of the two in some sentence. These words are analogues of homonymous nucleotide doublets in ambiguously coding mRNA triplets. Here mRNA represents a phrase or a sentence. The words ***maX1***, ***maX2*** with the wobbling third letter ***X***. ***X1***, ***X2*** can randomly take the meaning of the letters ***N***, ***P*** (***man***, ***map***). Let's compose a sentence: "A ***ma(X?)*** has a ***ma(X?)***" Clearly, the choice of two letters ***N*** and ***P*** and assigning to homonymous doublet "***ma***" exact semantics of the words "***man***" or "***map***" depends upon a whole sentence, on the context, which serves as a semantic background, allowing to distinguish the signal from the noise of uncertainty, i.e. to select/identify the necessary word. If we ignore the context, semantic errors become possible. Though in fact, even if these letters are placed incorrectly, contrary to the context, the context (background) provide information redundancy, still leaving it clear to interpret the homonymous "***ma***" in the whole sentence.

The homonymous doublets in codons are in a similar situation. The 1st wobbling (random, either) nucleotide in anticodons, together with the 3rd nucleotide in codons, in this case represents, as we have said before, a kind of "steric crutch" that

supports physical and chemical integrity of the codon-anticodon bond. This makes it possible to integrate new amino acids into protein texts, although not always. Why not always? The given example with a sentence provides a good illustration. mRNA is informationally redundant, and we do not know how many context changing mutations are necessary for NORMAL contextual orientation of homonymous doublets to become ANOMALOUS during protein synthesis. This is a quantitative aspect, which is not clear so far. And it will remain unclear for a long time, since the SEMANTIC WORK of the genetic apparatus is a *terra incognita*. Calculate, how many substitutions or deletions of letters are necessary to make in the above sentence, to make the semantics of the homonymous doublet “ma” no longer clear. Perhaps, these calculations are possible although rather challenging. And what about mRNA? This is completely different territory. So, the introduction of the second genetic code table is still far away. For a start, we need to be able to interpret the whole problem.

Perhaps, pre-mRNA and introns, and partially "junk" DNA play a similar (contextual) role. This hardly understood genetic mental economy can be interpreted as a mobile contextual background for interpretation (and re-interpretation) of protein genes. These are different levels of gene-contexts, which need to be somehow "read" and "interpreted" by a living cell together with ribosomes. "The reading subject" may be represented by a multi-faced soliton family (specific undamped solitary waves - optical, acoustic, conformational, and rotational-vibrational, etc.), excited at the level of DNA and RNA. In this respect, it is interesting to take a look at non-linear dynamics of soliton rotational-vibrational nucleotide motion around the sugar-phosphate RNA frame and around single-stranded DNA segments. Such soliton waves move along polynucleotides, furthermore, solitons change their behavior (dynamics, radiation) depending on the nucleotide sequence, which represents a physical reference of “reading” [Gariaev, 1994; Gariaev PP, 1997].

Here we have given a detailed critique of the canonical genetic code model. The main focus is on its linguistic component.

Another facet of genetic coding has remained unaddressed - the function of a genome as a quantum biocomputer, where its "working medium" operates on the principles of laser radiation, holography, solitonics, and quantum nonlocality. This is a topic for a separate discussion, which should be based on experimental results on distant wave transmission of genetic-metabolic information, and how this distant wave data transmission provides for the strategic regulation of genetic and physiological functions of the organism. [Gariaev, Kokaya et al., 2007; Gariaev, Tertyshniy, Tovmash, 2007; Tertyshniy, Gariaev, 2007; Gariaev, Kokaya, Mukhina, Tertyshniy et al., 2007].

MORE ON THE CENTRAL DOGMA OF MOLECULAR BIOLOGY. PRIONS.

Prions represent a specific class of parasitic proteins of various strains which cause neuro-dystrophy in animals and humans. Stanley B. Prusiner, who in 1997 received a Nobel Prize for research in this area, in the early 1980's called these proteins prions or *Proteinaceous Infectious Particles* [Prusiner, 1996]. Prions cause diseases such as *"scrapie"* (in sheep) and *bovine spongiform encephalitis* (BSE mad-cow disease). In Humans prions cause *"Kuru disease"*, *"Creutzfeldt-Jakob disease (CJD)"*, *"Gerstmann-Sträussler-Scheinker disease (GSS)"*, *"Alpers' syndrome"* and *"Fatal familial insomnia (FFI)"*. Significant progress has been made in this field, although the main subtle mechanisms for the development of pathological conditions of this kind are still unknown [Weiss et al, 1997]. Mice with a knockout of PRNP (PRioN Protein) gene are resistant to PrP^{sc} infection, which requires PrP^{c} to be present for the development of spongy encephalopathy. RNA aptamers (RA) were isolated that could accurately recognize the recombinant prion of hamster protein bound to glutathione S-transferase. In addition, RAs were sensitive to certain amino acid sequences. A characteristic feature of these RAs is the presence of a guanine-rich RNA bend with a formation of 4-coiled RNA motifs with repeating guanine quartets, which were named G-quadruplexes or G-tetrads. Notably, these structures are typical for chromosomal telomeres too. Weiss et al. (1997) mentioned the following: *Among the selected RNA aptamers, eight (40%) could be grouped into three classes based on their homology within the three single-stranded loop regions. While individual members of each class had identical putative G-tetrad and loop regions, they showed significant covariation in the Watson-Crick helix* [Weiss et al, 1997]. The mentioned Weiss et al (1997) paper raises questions related to the proposed idea of genome operation on different principles (see below).

The raised questions are as follows:

(i) How do RAs recognize prion proteins?

(ii) How do RAs bind to prion proteins?

(iii) Is RA recognition of prion proteins in brain homogenates of infected and non-infected animals accurate enough?

Prion proteins (PrP^{sc}) are strain specific like bacteria and viruses. Phenotype and function of the latter are determined by their genomes. But when prions are isolated from diseased tissues in their pure form, no nucleic acids are found in their composition. Once in the stomach (or other tissues), prions migrate to the brain in some mysterious way, and then, breed there, causing brain morphological and functional degradation. It is unclear how they travel the Stomach-Brain distance, separated by the blood-brain barrier. This remains a puzzle, although there are some assumptions, that the lymph serves as an intermediate step in transport of PrP^{sc} to the brain, and it is assumed that this protein via nerve endings can retrogradely travel along axons into the spinal cord and to the brain. The latter mechanism, although not explained or proven, finds some justification in the new theory of nerve impulse. Humans, animals and yeast organisms synthesize normal non-infectious prion-like proteins (PrP^{c}), similar in their amino acid sequence to prions. Special genes, responsible for PrP^{c} synthesis, were found too. Besides the fact that they are not pathogenic, the secondary structure of PrP^{c} is different from PrP^{sc}. In the brain or *in vitro,* in the presence of PrP^{sc}, PrP^{c} converts into PrP^{sc} with a reduction of the proportion of α-helixes and growth in the proportion of β-Sheet. All subsequent PrP^{c} synthesized in the brain also acquires this structure and, thus, the function of PrP^{sc}. The function of "normal" PrP^{c} remains unknown, though there are assumptions that it has a role facilitating normal activity of Purkinje cells.

The yeast prions (Psi + and Sup35) in *Saccharomyces cerevisiae* led geneticists to a dead-end, since it was found they transmit genetically inherited features without the participation of DNA or RNA [University of Chicago Medical Center press release, 1997].

In our opinion, the most incomprehensible and key fact in understanding the nature of prions is their virus-like strain specificity in pathogenesis, caused by various types of PrP^{sc} (there are more than 20), in the apparent absence of corresponding DNA or RNA or a genetic apparatus. Genes of different PrP^{c}'s slightly differ in nucleotide sequences. Mutations of these genes can cause PrP^{c}>PrP^{sc} conversion, followed by PrP^{sc} accumulation and subsequent disease. There are unexplained cases of spontaneous formation of prion strains in older people and older animals. Prion propagation takes time. For mice, depending on the strain, incubation period may be from 50 to 500 days. In humans, it takes years. Development of prions is accompanied by a macroscopic and 'life incompatible' accumulation of PrP^{sc} polymer filaments in the brain, which when stained with Congo red dye show green birefringence with polarized light. This means, that prion plaques cause divergence of rays of right and left polarized light. This seemingly insignificant and unrelated fact of prionic syndromes is not accidental in relation to the pathogenic nature of prions.

TELOMERES AND TELOMERASE

Recent years were marked by a growing interest in telomeres and telomerase in relation to aging (see, e.g., Biochemistry (Moscow), v.62, issue 11, November 1997; the volume is entirely devoted to the issue of telomeres and telomerase). The following on telomeres is derived from this source.

In 1961, L. Hayflick and P.S. Moorhead showed the limitation of the replicative ability of normal human fibroblasts. When normal human embryo cells grow in the most favorable conditions, their aging and death inevitably arrives after ~50-70 cell divisions. The observation was reproduced by numerous other studies. At the same time, cancerous cells, developing in identical "ideal" conditions, are immortal. What are the reasons for mortality of some cells and immortality of others? In 1971, A.M. Olovnikov suggested, that the cause of aging and death at the cellular level is a result of chromosomal end (telomeres) underreplication by DNA-polymerase during cell division [Olovnikov, 1996]. This is due to the use of RNA-primers during DNA synthesis from the 5'-end to the 3'-end, followed by their removal. Moreover, the 5'-end of the replica remains under-replicated. With each chromosome replication act, their ends are shortened in length by the distance from the front of the DNA polymerase molecule to its catalytic center, this length is a "dead zone", where there is no replication of single-stranded DNA during cell division. And when chromosome shortening reaches a critical length, vitally important DNA coding sequences adjacent to telomeres are negatively affected. Some researchers see such chromosome shortening as a synonym to aging. The number of telomere shortenings serves as a replication-meter, determining the number of divisions to be made by a normal cell. As soon as the minimum critical number of repetitive telomeric TTAGGG sequences is reached, cells lose their ability to divide. At least it had been widely thought so, until quite recently...

However, it turned out that the situation is much more complicated. There are mechanisms that oppose the "dead zone" effect. One mechanism was found by C.W. Greider and E.H. Blackburn in *Tetrahymena*. It was these researchers, who discovered terminal transferase - ribonucleoprotein enzyme, called “telomerase”. It was found that after each cell division, telomeres are resynthesized by telomerase. The enzyme extends the 3 '- end of telomeres and by doing so compensates for the “dead zone” effect, and sometimes over compensates by a significant amount. Telomerase turned out to be an unusual reverse transcriptase, i.e. an RNA dependent DNA polymerase with its own RNA template for synthesis of the short repetitive sequences of terminal chromosome DNA. The RNA template region of *Tetrahymena thermophile* is the most well-studied. This region has 9 nucleotide residues in positions from 43 to 51 (5'-CAACCCCAA-3'), out of which only 7 nucleotide residues (43-49) belong to the template, they form an active part of telomerase and determine the catalytic function of the enzyme. Later, telomerase was found in the extracts of immortalized human cells. Unlike normal mortal cells strains, the abnormal immortal cell lines do not age and produce telomerase. Therefore, telomeres of immortalized cells are not shortened during successive passages *in vitro*. Such protection from DNA shortening is most efficient in cancer cells. Normally, similar processes are found, for example, in the fetus and testicular tissues.

An additional characteristic in the telomere preservation mechanism, which (similar to the case of prion synthesis in the brain during some forms of kuru disease) is unclear and is the subject of our analysis. As you know, immortalization of human cells in culture is usually associated with expression of telomerase activity. However, in some cases, no telomerase activity is apparent, although comparison of terminal restriction fragment (TRF) patterns, before and after immortalization, shows that telomere elongation has taken place. The extreme heterogeneity of telomere lengths and differences in dynamics of telomere maintenance in telomerase-negative lines in comparison to telomerase positive lines, indicate that these cells use one or more alternative (ALT)

mechanisms of telomere lengthening (ALT - Alternative Mechanism for Lengthening of Telomeres). Remarkably, all ALT cell lines, examined by now, have a similar TRF pattern. That possibly proves a common ALT mechanism. All telomerase-negative immortalized cell lines, examined so far, have the signs of ALT-activity, which is consistent with the hypothesis that maintaining telomeres with telomerase or ALT is necessary for immortalization. The nature of the ALT mechanism (or mechanisms) is currently unknown, although there is an assumption, non-experimentally based, that there may be a mechanism of recombinational elongation of telomeres at work here.

Thus, one has to conclude, that within the framework of ALT-activity, there might be an unusual phenomenon of DNA synthesis, occurring “without” copying a material complementary DNA or RNA template. This complements the list of similar “anomalies”, which began with the mysterious prion’s brain penetration and the distinct virus-like behavior of prion proteins in the apparent absence of DNA or RNA. This means that, in this latter case, the information about prion genetic strain characteristics is preserved without any gene-structures. The “anomaly” of yeast prions, where some of the genetic characteristics are also transmitted without DNA or RNA templates, fall into this category too.

QB-REPLICASE

And finally, let's discuss the third phenomenon, belonging to the studied family of "non-template anomalies" in polynucleotide synthesis. This is the functioning of Qb-replicase, an RNA-dependent RNA-polymerase of Qb coliphage. *In vitro* Qb-replicase can operate as a machine, self-replicating RNA molecules. This was shown a relatively long time ago [Spiegelman et al, 1965; Mills et al, 1967]. This enzyme turned out to be able to synthesize certain sequences of short RNA without an RNA template [Sumper, Luce, 1975]. Similar "template-free" RNA synthesis applies for T7 bacteriophage RNA-polymerase [Biebricher, Luce, 1996]. The same result was obtained for *de novo* RNA synthesis by DNA-dependent RNA-polymerase of T7, T3 and SP6 phages. These experiments again demonstrated the violation of the seemingly unshakable central dogma of molecular biology and genetics, postulating: DNA ⇒ RNA ⇒ PROTEIN. This canonical statement that only material RNA or DNA molecules can be the templates for DNA or RNA synthesis. But one point of this dogma has already been modified. The flow of strategic information (well-known since the discovery of reverse transcriptase) looks different: DNA ⇒ RNA ⇒ PROTEIN. Given the "anomalies" in the reproduction of prions, it is quite possible to make one more amendment: DNA ⇒ RNA ⇒ PROTEIN, which we will discuss below.

Discovery of "template-free" RNA synthesis led to reconsideration of the genetic apparatus operation (at least for lower biological systems) and ongoing active discussions about the accuracy of "free-template" experiments in the scientific literature. The high integrity of Qb-replicase experiments in relation to artifacts associated with the presence of extraneous trace impurities of RNA in reagents and laboratory glassware, was well demonstrated in Sumper and Luce works [Sumper, Luce, 1975]. It was demonstrated that decreasing nucleoside-triphosphate concentration below 0.15mM, RNA (template-free) synthesis terminates, while template-dependent RNA synthesis occurs

normally. Synthesis kinetics in "template-free" conditions have a very long lag period in contrast to the short lag period with the template-dependent synthesis. However, there were still some doubts. It was only after the series of brilliant studies of Christof K. Biebricher, Manfred Eigen and Rüdiger Luce in 1981-1987, "template-free" RNA synthesis was finally proven.

Nevertheless, in some studies, where they failed to achieve the required experimental integrity, they present the methodological flaws in the research setting as advantages. For example, upon discovery of homologous to 23S RNA of *E. coli* and *B. subtilis* fragments as well as homologs of RNA fragments from Qb phage among the products of "template-free" RNA synthesis, the group of A.V. Chetverin argued that all experiments in this field can be explained by contaminating exogenous RNA from laboratory air present in the reaction mixtures, as was the case in their setting. Their winning argument was with the demonstration of petri dishes with agarose, containing the Qb-replicase system. The dishes were incubated uncovered in open-air from 0-10 minutes to one hour. The RNA reaction products were stained with ethidium bromide. After that, observations of increasing amounts of RNA were recorded, indicating the inoculation of contaminating foreign RNA's from laboratory air and their autocatalytic reproduction [Chetverin et al, 1991; Munishkin et al, 1991]. The fact that absolutely anything may get onto laboratory glassware from dirty air, including RNA, is not surprising. But this is not relevant to those experiments, which are carried out at a high methodological level. Another point is surprising here. Biebricher and his colleagues, who over 10 years have been obtaining irreproachable fundamental results for "template-free" RNA synthesis in purified systems *in vitro*, do not consider this phenomenon to be a violation of the central dogma of molecular biology and genetics. They believe that the process of enzymatic ribonucleoside-triphosphate Qb-polymerization (without a template!?) *in vitro*, is autocatalytic, the 6S RNAs that are synthesized act as templates for themselves, and, at the same time, mutate. Mutational variations are subjected to natural selection in the spirit of Darwin's theory, and after

several rounds of replication, microevolution of synthesized RNA terminates on the RNA with the greatest autonomous fitness. Probably, for Biebricher and many others, giving up the central dogma means a complete change or a significant amendment to the chromosome's strategy of operation. Apparently, so far, they have not found any significant ground to do this. They also fail to explain their own results, and above all, the fact of RNA synthesis without an RNA template. They admit that they do not understand the biological role of stably synthesized 6S RNA fractions in such systems.

In biosynthesis *in vivo*, during the reproduction of Qb phage in *E. coli*, 6S RNA is also formed. Like *in vitro*, it is also heterogeneous in nucleotide sequences and variable in number: from 100 to 200. In each template-free or normal synthesis, different sets of RNA are produced. And only some of them are replicated in (-) strands. Hence, the templates are selected for reproduction from the very beginning - they are not accidental or random due to their "texts" (semantics). 6S RNA's biological role cannot be explained as it is proteins coding and it is not involved in the infectious process. This limitation in understanding nucleic acid functions is dictated by the existing rigid paradigm that state that genetic structures operate exclusively on a material level, which is disputed by modern data. An important detail is the very long lag period of 6S RNA synthesis, taking up to 16 hours in the case of DNA-dependent RNA-polymerase from T7, T3 and SP6 phages, and this fact also has no explanation. And there is another non-trivial fact. Qb-replicase is composed of 5 different protein subunits, four are named I-IV or subunits α, β, γ, δ, and the fifth is named the "host factor" (HF). Subunit I is identified as the ribosomal protein S1, and subunit III and IV are translation and elongation factors, EF-Tu and EF-Ts. Subunits I, III and IV are operated in ribosomal protein synthesis, but, in this case, are used by Qb phage for RNA synthesis. There is an opinion that 6S RNA, replicating itself in bacteria as a "molecular parasite", is a "selfish RNA" [Jan van Duin] The Bacteriophages, Chapter 4. Single-Stranded RNA Bacteriophages. p.133-135. (Ed. Callendar R.). Plenum Press, New

York - London. (1988)]. In other words, 6S RNA can be considered analogous to eukaryote's "selfish DNA", whose role is also not quite clear. Another version of "selfish DNA" function has been proposed and is seen as a way for material-wave coding of an organism's space-temporal structure as a biological application of the principles of holography, solitonics, linguistics, resonant-wave interactions and laser processes [Berezin, 1997; Gariaev, 1994]. It is possible that the same mechanisms in a simplified version are valid for 6S RNA functioning in bacteria. Moreover, 6S RNA possibly works as a kind of "antenna system", receiving external physical fields as a regulatory genetic-wave factor.

Thus, all three discussed phenomena - prions, telomeres and Qb-replicase share a common strategic characteristic. It is their unusual ability to replicate proteins, DNA and RNA, seemingly, in a template-free (nonmaterial) and so far, inexplicable way. For prions - this is about the mysterious penetration into the brain from the stomach and the unexplained strain-specificity without a genome; for telomeres – this is a mysterious ALT mechanism of terminal chromosomal DNA synthesis; and for Qb-replicase – this is about mysterious " template-free" RNA synthesis.

As a possible explanation, we propose the hypothesis that prion-like parasitic proteins have a virtual genome, "borrowed" from the host-cell at the time of reproduction of these proteins. This reproduction occurs not only and not so much due to $PrP^{c} \Rightarrow PrP^{sc}$ transition, but due to the virtual genome, which may work in two ways (see. Figures 1 and 2).

Keto-groups of protein PrP^{sc} amino acids can react with the OH-groups of ribose residue acceptor ends of the respective transfer RNA (tRNA). This is a catalytic process. During the corresponding enzymatic reactions, the produced poly-tRNA-continuum spaciously brings anticodons together, forming a covalent discrete "imitation of informational RNA" (piRNAs). This stage is almost contrary to ribosome protein synthesis. And, perhaps, it occurs on A-, P-sites of the ribosome. Then, there is the reverse-transcriptase DNA synthesis on piRNAs. It requires a corresponding reverse

transcriptase capable of working with the covalent-discrete piRNA template.

There is another way (Figure 2), when restrictases "cut" the anticodon poly-triplet continuum of tRNA, followed by enzymatic "stitching" (ligation) of triplets. This also provides the RNA-template for DNA synthesis. This generates a clone of DNA molecules, which can replicate (reproduce) or be transcribed into normal messenger RNA (mRNA), responsible for the PrP^{sc} synthesis.

This hypothesis raises a question of mutual recognition of tRNA and protein amino acids. The same question was raised by Weiss et al. [Weiss et al, 1997]) about the ability of RNA aptamers (RA) to recognize prion proteins. There is no answer to it yet, but in the context of our version of a prion-genome, there is another, more important point: RA's are principally capable of recognizing certain amino acid sequences, and this indirectly confirms the idea of tRNA's ability to recognize the protein amino acids. And this is necessary for building of a linear tRNA-continuum and all subsequent acts of the prion temporary virtual genome generation.

In our given examples, the genome (or rather part of the protein-synthesizing apparatus of the host cell) is "borrowed" by PrP^{sc} proteins for the time of DNA-RNA-template synthesis. Because of such temporary coexistence of PrP^{sc}-RNA-DNA complexes, nucleic acids are not found in composition of PrP^{sc} during their preparative extraction in a "pure" form. "Borrowing" of this kind is archaic, however, under pathological conditions of the biological-system, it allows to bypass energetically and organizationally difficult pathways of a permanent reference to chromosomes for synthesis of parasitic proteins. Virtual genomes of PrP^{sc} and of similar protein-parasites makes them virus-like and strain-specific – the properties which are dependent on the specifics of polymerase systems of the host cell. Perhaps, such mechanisms of protein reproduction were evolutionary precursors of viral infections and precursors for reproduction of the first organisms. Apparently, this paleo-biochemical process of protein cloning has been preserved and may take place in many pathologies

(immunodeficiency, rheumatism, etc..). Also, there could be an even more complex version of reading information from the protein associates, presented in Figure 3.

If our hypothesis is confirmed, it will require further amendments to molecular biology dogma about unidirectional flow of the strategic information in biosystems: DNA ⇒ RNA⇒ PROTEIN. The first amendment was made by the discovery of reverse transcriptase. And the scheme has become different: DNA ⇒ RNA⇒ PROTEIN. Probably, the next step will be the following modification: DNA ⇒ RNA⇒ PROTEIN. We believe that in the case of parasitic prion proteins, the ribosome, essentially, functions as a protein-dependent mRNA-polymerase. Figure 4 presents the general scheme, modifying the central dogma of molecular biology and genetics, based on the above considerations.

We assume that for the penetration of PrP^{sc} into the brain from the stomach, bypassing the blood-brain barrier, biosystems utilize material-wave mechanisms of genome memory, distant soliton and other wave transmission of genetic information (suggested by us earlier). Indirectly, material-wave DNA memory is evidenced by the data on "no-DNA" prion protein synthesis in yeast. It may be also possible that there is a neural-wave pathway of information transmission about the primary structure of mRNA-prions in higher biosystems via the inner vibrational structure of soliton packages of nerve impulses, travelling from the stomach fibers into the brain. This method of RNA information conversion into the spectrum of Fermi-Pasta-Ulam resonances (pre-modulated by RNA text) and its spectrum transfer into the structure of the action potential spike in nerve conduction was proposed by Berubbers [Berubbers, 1997].

The phenomenon of telomere ALT-lengthening and *de novo* synthesis of 6S RNA in the Qb-replicase "template-free" system can also be seen as material-wave mechanisms of DNA synthesis.

What do material-wave Memory Information Mechanisms (abbreviated as "MIM") represent in genetic and other regulatory

organismic structures? Their study has just begun. Probably, the storage and formation of material-wave image-templates (image-programs) involves holographic and/or linguistic-background genome memory [Gariaev, 1994; Gariaev, 1997]. Presumably, ways of information biopolymers MIM replication are diverse and originate from the level of elementary particles, and in the first approximation, may be classified as follows:

1. Electron MIM or “the hole". This is the first classic example from quantum electrodynamics, when the removed object (electron) leaves in the place of its residence a field (vacancy), equivalent to it, but with the opposite positive charge. This vacancy Paul Dirac called “the hole” [Dirac, 1930]. This “hole” behaves like a proton but is not identical to it. The "holes" carry positive charge, which is essential for semiconductors in the so-called PN junctions.
2. Associatively-holographic MIM-reflections. Here the image of the object, which was placed within the two interfering coherent fields can be reproduced in the form of wave fronts in the absence of the object. This phenomenon has been studied in detail and is widely used in engineering and the arts.
3. Phantom leaf effect (leaf MIM). Discovered in 1975 by V. G. Adamenko through a Gas-Discharge Visualization Technique (GDV). The effect was reproduced in many laboratories around the world, including by the author of this monograph [Gariaev, 1994]. When a leaf of a live plant is placed into a high-intensity electromagnetic field with strictly defined parameters (rarely but fairly reproducible) it is possible to register the glow (spark image) of the whole leaf, even when a certain part of the leaf (no more 10-15%) was cut off. The mechanism of this phenomenon has a quasi-holographic nature, inherent to genetic apparatus of higher biosystems [Gariaev, 1994; Gariaev, 1997]. Phantom or MIM pains, are sometimes experienced by people who lost limbs as a result of injury, are related to the holographic memory of the brain’s cortex.

4. MIM signal structure, distributed in the background (see [Gariaev, 1997] for the Background Principle). For example, information about the precise meaning (semantics, signal) of the homonyms like "spring", "band", "bank" is found in the context of the message, where they appear. The whole text (context) acts as a background within which there is accurate information about the part or the exact semantics of the homonym. Homonymous ambiguity is very typical characteristic of the so-called genetic code – practically, of the protein code. We have discussed this in a detail above. We would like to add that this highly probable erroneous (random as a result of homonymous *linguistic* mRNA codon doublets) resolution of homonymous uncertainty owes to background-contextual, associative orientation of the ribosome, which takes into consideration the whole mRNA sequence or, in other words, its context (background). The Background Principle is an extremely important theoretical provision for practical biology, medicine, agriculture, and especially wave genetics. For example, in medicine, application of this principle leads to fundamentally new treatments to oncogenes and the HIV genome: it brings a possible explanation to why these *linguistic*-genetic structures suddenly begin to function only within a strictly defined contextual nucleotide environment, resulting from oncogenes and HIV genome transpositions and/or from "metabolic context" variations. They are homonymous: without a certain background nucleotide environment, the organism cannot "read" and "recognize" them as pathogenic elements. In this respect, the monumental challenge of explaining genome transpositions becomes transparent, as a factor of multidimensional manifestation of specific semantics for temporary homonymous and/or temporary null (like pseudogenes) *linguistic* nucleotide sequences. If we extrapolate the Background Principle onto the telomere ALT-recovery-mechanism, we can see the loss of the

telomere end as an extreme case of homonymy, known in linguistics and information theory as Shannon's theorem. To this theorem, when some words or letters (signals) in a text were lost or distorted, they can be restored taking into consideration the whole text (the context), including the background-associative principle (of which the Shannon effect is a special case) [Prangishvili et al., 1993]. To some extent, this is similar to the reproduction of the object's full image from the part of the hologram, since the image of the object (the information about it) is not localized in any one part of the hologram but distributed throughout its space. In the ALT-mechanism, the reproduced signal is the information about the lost sequence of telomere nucleotides, and the background (context) is the text of chromosome DNA adjacent to the missing part of the text. Even if we assume that the telomere recombination-mediated elongation principle is involved in ALT, then, this principle also requires "to know" what DNA fragment should be inserted in place of the missing one. This "knowledge" is related to the background-associative genome memory, close to the holographic memory of the chromosomal continuum, that we had postulated earlier.

5. DNA MIM. This phenomenon was discovered in 1985. In its short version, it was described in a publication of 1991. [Gariaev et al, 1991] It was examined in more detail in 1994 [Gariaev, 1994]. Similar results were obtained independently by the group of American researchers led by R. Pecora in 1990 [Allison et al, 1990]. The external manifestation of DNA MIM is about the strange effect observed during *in vitro* study of the light scattering by DNA products with laser correlational spectroscopy. A new factor, not covered by the theory of light scattering, is at work in this light-scattering study. The nature of the phenomenon is not clear. The group of R. Pecora characterizes DNA MIM as "... mimicking the effect of dust" (MED-effect), that is, the effect imitating dust, although the researchers made special arrangements

to ensure that DNA preparations had no foreign particles. The group of R. Pecora found this phenomenon applying to correlating laser spectroscopy involving not the total large-polymer DNA fractions (as in our experiments) but involving restriction DNA fragments of a certain length. And in this restriction case, DNA also behaved in an "abnormal" way: probing photons were diffracted not only by the polynucleotide strands, but also by "foreign particles", these particles were definitely not part of the preparation. This effect, was left unaddressed by Pecora's group and didn't allow for any explanation of the unusual nature of DNA light scattering from the perspective of the seemingly well-developed Rouse-Zimm model on the influence of polymer dynamics by a probing light beam (including a laser beam) in aqueous solutions.

Similar, but not identical, data received by Matsumoto et al. [Matsumoto, 1992] when they recorded a directly observed effect of "abnormal" Brownian motion of fluorescently-labelled native DNA molecules. Translational diffusion coefficients for fragments of DNA (56μm long), calculated according to the Rouse-Zimm theory, turned out to be significantly different from the visually observed and quantitatively evaluated DNA diffusion dynamics. However, the model gives a good correlation with experiments on other polymers, for example, synthetic polymers like Dacron, polyethylene, etc.

We may postulate that in DNA laser light probing experiments, light scattering involves MIM principles: i.e. light scattering occurs not only on the real material DNA molecules, but also on their virtual wave equivalents (trace structures), produced by the Brownian motion of these super-information biopolymer molecules. This can be compared to a hologram, when a material object, is in a specific way probed by a laser, is then "recorded" in the light scattered by the objects light field and its own wave (virtual) copy is created, which then exists independently from its prototype. It is possible to explain MIM effects by the theory of physical vacuum [Shipov, 1993], which fundamentally justifies the idea of the generation of torsion (axion-clustered) equivalents of

physical bodies. Let us consider that genome MIM-effects have long been known in cattle breeding (and not only) as a Telegony factor, when the characteristics of the first male parent are inherited, even when the same female produces offspring from the second, third, etc. fathers.

As for DNA dynamics "abnormality", as discovered in Matsumoto's studies [Matsumoto et al, 1992], in their experiments' case, there could be an acceptance of external photon physical fields affecting quasi-spontaneous DNA dynamics. The authors disregarded this possible contribution, that is why the discovered anomalous effect stayed beyond their comprehension. This kind of background physical field influence mechanism on nonlinear proteins dynamics was proposed earlier [Gariaev et al., 1996 (a); Gariaev et al., 1996 (b)]. It is based on the interaction of external physical fields with metal ions that comprise the active centers of many proteins. Probably, there are similar cases where external (background) and internal (endogenous for biosystems) physical fields affect DNA dynamics, since the sugar-phosphate DNA backbone contains various associated metals, whose role is not clear and might be exactly related to exogenous wave *linguistic* genome bio-orientations.

ARE THE GENOMES OF MULTICELLULAR ORGANISMS QUANTUMLY NONLOCAL?

A. Einstein and his co-workers, B. Podolsky and N. Rosen, [Einstein, Podolsky, Rosen, 1935] expressed the idea, the main point of which can be explained by the example of the elementary particles... Quantum objects, which may be represented by a pair of entangled photons, during their separation reveal some resemblance of information connection (or entanglement). Moreover, the quantum state of one photon, for example polarization or spin, can be instantaneously transferred to another photon, which becomes the analogue of the first one, and then collapses, disappears, and vice versa. There may be any distance between the photons. This event was called Einstein-Podolsky-Rosen (EPR) Paradox. The term "Quantum Nonlocality" is the synonym of this phenomenon, emphasizing the instantaneous spacious distribution and nonlocality of quantumly entangled elementary particles. This seems to violate the principle of causality - the cause and consequence are not separated by time, if we see time as enabling linear event sequencing. Therefore, Einstein and co-authors, at those times, not knowing about the complex structure of time (for example, about its fractality), considered their purely theoretical, but nevertheless strictly formalized model, as one that can never be applied experimentally. This contradiction of their theory with actual physical reality has persisted for about 30 years. Then, D. Bell [Bell, 1964; Bell, 1976] developed the EPR idea at the contemporary level with an active contribution of Ch. Bennet and colleagues [Bennet et al, 1993]. Their main challenge was not to in their theoretical analysis violate the main principle of quantum mechanics, proposed by Heisenberg, the dual material-wave state of quantum objects. This principle of uncertainty states that it is impossible to correctly measure the properties of a photon as a wave and as an elementary particle at the same time. Now, after the discovery of the "entangled" state of elementary particles, this is no longer the problem.

It is possible that such "entanglement" is an elementary base for transmission of genetic (and mental) information between organisms, which can be seen as a continuum of elementary particles, where macro-level properties repeat the properties of the micro-level. In this entangled state, both particles are a part of the same quantum system, so that whatever you do with one of them predictably effects another. Bennett and his colleagues believe that entangled particles, after their separation in space, can act as mutual "carriers" of their states (and, hence, information) to each other, since the state of the particle is already the information. However, in this case the information should be understood in the broadest sense as “any change”. Experimental execution of the EPR-Paradox required co-existence of three photons. This experiment was carried out by two research groups, one in Vienna, headed by Anton Zeilinger, and another group in Rome, directed by Francesco De Martini. The experiments of Zeilnger group [Bouwmeester et al, 1997] proved EPR principles to be practically feasible for optical fiber transmission of polarization states between two photons by means of the third photon within distances up to 10 kilometers. Since this discovery, leading countries have been discussing powerful programs to apply this effect for the creation of quantum optical computers with photons as information carriers. The speed and data processing power of such computers would be thousands of times greater than existing computers.

The idea that biological-systems use quantum nonlocality is very attractive in the overall global-outlook and in practical terms. This refers to our data about the wave *linguistic* role of gene-metabolic-information and mental realms in biological-systems. An initial feeble attempt to realize EPR application in biological systems had been made earlier [Josephson, Pallikari-Viras, 1991]. In their paper, theoretical analysis is basically reduced to the statement that organisms’ perceptions of reality are based on another more effective principle than the principle used by more formal procedures in science. According to the authors, in some circumstances, this principle is realized in "non-physical" inter-communicational *linguistic* interactions of a non-statistical nature

between spaciously separated biosystems, i.e. telepathy. Let's once again pose a question, this time in a narrower sense, not yet getting to telepathy: is the phenomenon of quantum nonlocality involved in operation of genetic apparatus of higher biological-systems? If it is involved, then, in what way? It is clear, that even assumptions made here are 100% tentative, however, it is high time for the introduction of at least a working hypothesis. In cases of genome wave-operation [Gariaev, 1994, 1997], the EPR effect is a desirable (but not compulsory) link, which may logically cement the chain of reasoning about MIM-functions of the genome. The proposed wave operation of chromosomes explains how wave and semantic vectors of heredity apparatus direct the organization of higher biosystems space-time structure. Such vectors involve chromosomal continuum holographic memory mechanisms and quasi-speech mechanisms of DNA-RNA-Protein construction. Here reading-scanning of the genome-biocomputer is performed via endogenous laser radiation and soliton gene-structures excitations. The genome's nonlocality (encoding and emanating the chromosomal continuum's gene-information) is already preprogrammed in its holographic functions. This information is distributed in the genome in the form of a hologram and/or quasi-hologram and simultaneously in the form of a fractal. This distribution of information is possible if we see the genome from purely material perspective. At this level of gene-information, quantum wave nonlocality does not yet function. When such gene-holograms are being "read" in a wave manner, the matter of chromosomes emanate *linguistic*-like wave fronts as directive vectors for morphogenesis. This is essential for maintaining the stable space-time structure of the biosystem. For this purpose, the genome generates step by step, layer upon layer, an "ideal" (wave) model - the template for potential material structures of the organism. This is an example of MIM directing the organization of the multi-dimensional structure of biosystems. When put this way, the model of material-wave biological system organization is not yet complete and requires further development.

The EPR-mechanism could be an essential amendment, at least at the level of photonic-laser and radio-wave processes in chromosomes and organismic proteins. Such a mechanism for regulation of vital processes attributes fundamentally new potencies to cells and tissues - the ability to practically instantaneously transfer vast pools of information between all cells and tissues of the biosystem via photons and polarized radio wave channels. If this mechanism is used, then it becomes clear why strategic *linguistic* biomolecules - nucleic acids and proteins - have L-isomer components, helical twists and, therefore, pronounced abilities of optical rotatory dispersion, circular dichroism and birefringence. This fact of the isomeric quantumness of bioorganic molecules can be explained in a different way. The asymmetry of atoms in bioorganic molecules, and the resulting isomerism, enable the biological-system to perform fast automatic scanning of polarization, holographic and other material-wave information regarding the state of its own metabolism and its current short-term space-time structure.

From this perspective, the following fact becomes unexpectedly important in explaining the mechanisms of prion pathogenesis: the birefringence of PrP^{sc} aggregates (see above), i.e. the biosystem's abnormal modulation of polarization vectors of its own informational photonic currents by means of the growing protein PrP^{sc} mass in the brain.

Note that the success of experimental quantum teleportation was possible due to waveguides (optical fibers), UV-pumped lasers and polarizers used for photon generation, photon separation in space and photon "programming". Formally, the above listed components have biological analogues in the form of microtubules within the cell nucleus and cytoplasm, and the coherent radiation of DNA and chromosomes. Chromosomes also represent the information bio-polarizers of their own laser radiation; and the fact that DNA and chromosomes are laser-active mediums was shown by our direct experiments [Agal'tsov, Gariaev et al., 1996]. Japanese researchers also confirmed our results,

though they carried out experiments in a slightly different fashion [Kawabe et al, 2002].

Let's assume that *in vivo* the EPR-factor works as a factor controlling an adult organism's state from the micro- to the macro-level. But how is this control implemented in embryogenesis? Perhaps, it mediates internal and intercellular transfer of DNA-RNA wave copies in different phases of their highly complex operation. It is possible that MIM effects on DNA preparations, obtained by us in 1985 and 1991 (and obtained independently by the group of R. Pecora in USA in 1990) are the result of local quantum teleportation, spontaneously occurring during laser scanning of DNA gels in spectroscopy by the dynamic light scattering method. Apparently, in this case of coherent photon interaction with biostructures, the latter could act as a liquid-crystal system of optically active fibers, distributing polarized photons in space, followed by information exchange between them. This same system reveals another effect as a new type of memory of genetic structures based on the Fermi-Pasta-Ulam Problem. This effect is characterized by appearance of isomorphic time autocorrelation functions of light scattering and MIM-effects during the study of DNA preparations and 50S ribosome subunits of *E. coli* and collagen [Gariaev, 1994].

If the EPR factor works in biological systems, it is logical to ask, why don't organisms limit themselves to such an effective form of instantaneous biological information communication? Why does the biosystem also need very slow nerve impulses? We can only make an assumption that the nervous system was required to help higher organisms slow these information processes, to which the current evolution of the biosphere is not yet ready. Most likely, the functioning of the nervous system and the functioning of the genome's quantum nonlocality are complementary and co-exist, sometimes expressed in forms of paranormal abilities, such as human-calculators or in telepathy.

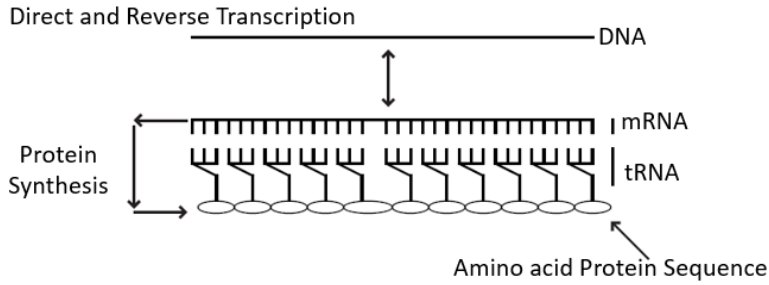


Fig. 1. The first method of cloning parasitic proteins *in vivo*.

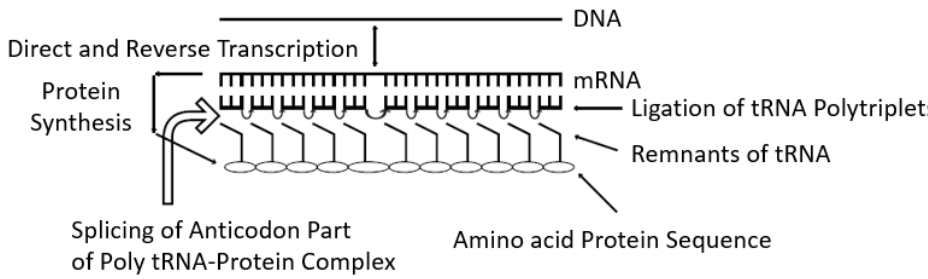


Fig. 2. The second method of cloning parasitic proteins *in vivo*.

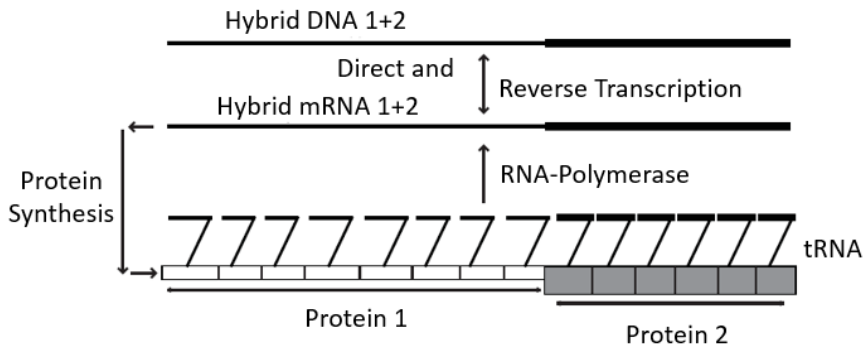


Fig. 3. Path of cloning associates (hybrids) of parasitic proteins *in vivo*. Proteins 1 + 2 – non-covalent association of subunits, e.g., in such complex proteins as an RNA polymerase.

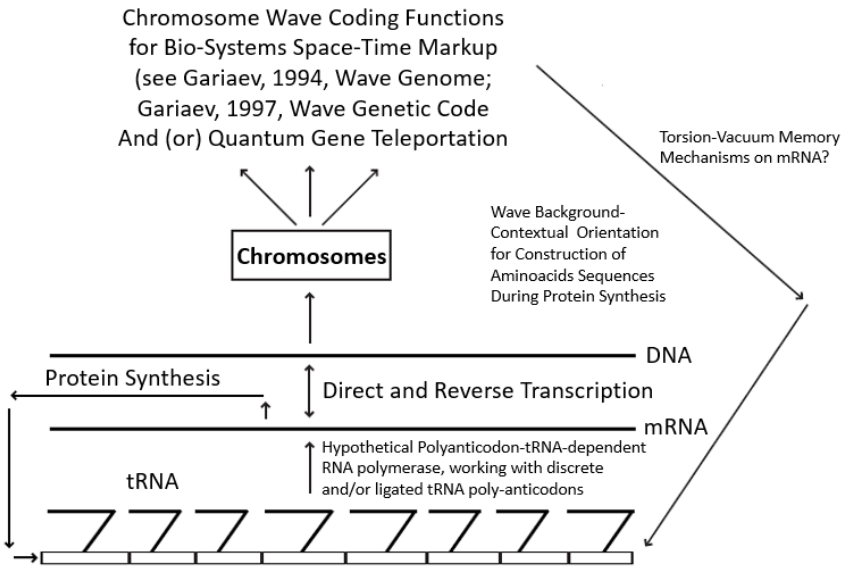


Fig. 4. The generalized scheme for the modified Central Dogma of molecular-wave biology.

WAVE BIOCOMPUTER FUNCTIONS OF DNA

In 1985, one of the authors recorded unusual oscillation modes of DNA, ribosomes and collagen “*in vitro*”, through applying a dynamic laser light scattering technique. This has recently been confirmed by us, and in addition, we have detected the phenomenon of laser light transformation into radio waves [Gariaev et al., 1997; Prangishvili, Gariaev et al., 2000]. Probably, such transformation is related to quantum nonlocality and may be recorded by a method developed by us. There is reason to believe that the genetic apparatus of higher biosystems can be quantumly nonlocal. This enables the cells, tissues and body to be in an ultra-coherent state. The above-mentioned results, prove our Wave Genes Theory once again, but this time at a higher level [Gariaev, 1994; Gariaev, 1997]. The key provision of this theory is that the biosystem chromosomal apparatus can simultaneously function as a transceiver (transmitter and receiver) of gene-*linguistic* laser, soliton and holographic fields. Moreover, the chromosome continuum of multicellular organisms resembles a statico-dynamic multiplex space-time holographic lattice, containing the compressed time and space of the organism. But even this is far from the full potential of genetic structures. DNA nucleotide sequences, forming holographic and/or quasi-holographic lattices, also form text speech-like structures, that fundamentally change our understanding of the genetic code. Biosystem evolution has created genetic "texts" and the genome-biocomputer as a quasi-intelligent "subject", which is able to “read and understand” those texts at its own level. To substantiate this elementary "intelligence" of the genome, it is extremely important to understand that natural human texts (regardless of what language) and genetic "texts" have similar mathematical-linguistic and entropy-statistical characteristics. Among other things, this applies to the concept of fractal frequency distribution density of letters in natural and genetic texts (nucleotides represent “letters” for genetic "texts”) [Maslov, Gariaev, 1994]. Below we will describe the results of our

research on commonality of such fractals for genetic and natural texts.

More evidence for the linguistic interpretation of genome code function was obtained by the American researchers [Mantegna et al, 1994]. Working with "coding" and "non-coding" DNA eukaryote sequences (within the framework of the old gene ideology), the authors conclusion contradicts existing dogma: linguistic functions are focused only in the protein-coding DNA regions. They carried out statistical analysis of natural and musical texts (Zipf-Mandelbrot law) and applied the Shannon principle of textual information redundancy, calculated as a text entropy. The results of the analysis show that non-coding DNA regions are more like natural languages than coding regions, and that possibly, non-coding sequences of genetic molecules are the basis for one (or more) biological languages. The authors also developed a statistical search algorithm for coding DNA sequences, which revealed that the protein coding regions have considerably less long-range correlations compared to non-coding zones separating these regions. The distribution of DNA-sequences turned out to be so complex that applied methods could no longer satisfactorily work with lengths over 103 base pairs. Zipf-Mandelbrot distribution for the frequency of "words" with a number of nucleotides from 3 to 8 bp showed more consistency with the natural language of non-coding sequences compared to those of coding. Again, we would like to emphasize, that the authors see coding as a recording of information about an amino acid sequence only. And this is the paradox, which made them say that non-coding DNA regions are not simply “junk” but are structures created for their specific purpose (unknown to us yet). Authors also failed to explain the long-range correlations in these structures, although they have discovered growing complexity of non-coding sequences in biosystem evolution. These data are fully consistent with our ideas that non-coding DNA sequences (which represent 95%-99% of the genome) represent strategic information content of chromosomes. In our opinion, this content has a material-wave nature, it is multidimensional and, as a matter of fact, acts as an associative-

image, and linguistic-wave embryogenesis program this being the meaningful continuation and logical end of any biosystem. Intuitively feeling this, the authors with a nostalgic melancholy bid farewell to the old and well served genetic code model, however, proposing nothing in return.

GENETIC CODE AS A WAVE LINGUISTIC STRUCTURE

Our understanding of the genetic code must change significantly, otherwise, we will never be able to create a DNA computer. For this purpose, we have postulated the mechanism of context-wave ribosome orientations as a solution to the problem of correct amino acid selection [Gariaev et al., 1999]. This problem arose immediately after the creation of the genetic code model in regard to the uncertainty in the selection of the third nucleotide in the triplet encoding some amino acids (F. Crick wobble-hypothesis). To understand how the cell's protein-synthesis apparatus solves this typical linguistic problem of homonymous uncertainty, it is necessary to introduce the concept of a background principle: associative- holographic memory of the genome and its quantum nonlocality [Prangishvili, Gariaev et al., 2000; Gariaev, Tertyshniy, 1999; Gariaev et al., 1999; Prangishvili, Gariaev et al., 2000]. This means that the genome can simultaneously represent a material and an ideal (mental) structure, i.e. a quantum object.

Endogenous physical fields of a very low power act as a universal information mediator in storage-compression-decompression-reading of the linguistic regulatory structures of the genome-biocomputer. These fields produce a chromosome apparatus and they represent a fast wave genetic informational channel, connecting the chromosomes of individual cells in a body into an integral continuum, working as a biocomputer. In short, the main provisions of the Wave Gene Theory (including genome quantum nonlocality) could be formulated as follows:

1. Soliton and laser fields of DNA and chromosomes are optical-acoustoelectric non-linear-wave processes, responsible for storage, reading and transmission of genetic and other regulatory field information in the organism space-time,
2. In biological systems, DNA, chromosomes and proteins work in "antenna" mode, receiving external acoustic and

electromagnetic fields, wherein the properties of such antennas change to perform regulatory body functions.

The liquid-crystal chromosome continuum is a non-linear optical medium and under certain conditions can function as a laser with alternating wavelengths as well as a soliton-laser (on the so-called Fröhlich modes [Agal'tsov, Gariaev et al., 1996]

3. Chromosomal DNA as a transceiver of laser radiation, linguistically polarizes its image, and simultaneously performs its conversion into radio waves. The radio waves, formed according to a quantum nonlocality mechanism (teleportation), are isomorphically (linguistically) polarized in accordance with photons polarizations. These radio waves can carry genetic-metabolic information from (both) within and outside of the biosystem.

PHOTONS CHROMOSOMAL BIOCONVERSION INTO A BROADBAND ELECTROMAGNETIC FIELD. LOCALIZED PHOTONS.

These provisions should be considered in a hypothetical biocomputer model, operating on genetic molecules. Let's have a look at "*in vitro*" photons conversions into gene-structure radio emission (where genetic structures are preparations of DNA liquid crystals). Apparently, in our experiments, [Prangishvili, Gariaev et al., 2000] we observed the so-called localized or entangled coherent photons, followed by their permissively-teleportational conversion into radio waves. This process involved a single-frequency He-Ne laser with an output power of 2mW, with a wavelength 632.8nm, and a stable resonator, controlled by an electronic thermostatic element [Priority on a patent to international patent application №99 / 01 / A of 06.01.1999]. When the laser beam interacted with DNA liquid crystals (or with any other objects), the laser generated radio signals, differing in nature (Fourier spectrum) depending on the type of the samples researched and depending on the methods of their preparation. The "three-mirror scheme" is one of the main conditions for DNA-linguistic bioactive radio wave generation. According to this scheme, the scanned object (DNA) reflects the laser beam back into the laser resonator. As a rule, during this process, the specific radio-signal modulations correlate with time variations of the two-dimensional speckle-patterns of light, scattered by DNA preparations.

In these experiments, we obtained preliminary data about the potential long-term recording of biologically active dynamic polarization-laser-radio wave genetic information from DNA preparations on 1) *the laser mirrors of the laser itself* as well as 2) *on the external laser mirrors*, *which are not parts of the laser* (see below). We assume that this phenomenon is associated with localization (compression) of photon fields in correlated scatterers system of

laser mirrors. Under conditions, when the material has poor absorption of its radiation from scatterers, the external light field can be retained in the system for a long time without dissipation into other forms of energy. The localization is caused by interference of multiply scattered waves. An external electromagnetic signal (in our case, this is a laser beam, polarizationally pre-modulated by DNA preparation), is localized ("is recorded") in a system of metal-containing the inhomogeneities of the laser mirrors. Later, this signal can be "read" (without significant loss of information) in another form of isomorphically polarized radio waves (isomorphic in relation to photons). Theoretical studies on the compressed states of localized photons provide more evidence toward our conclusions [Maximenko, 1999 (a); Maximenko, 1999 (b); Maximenko, 1999 (c)]. If "recording" on the mirrors is real, then, the metal-atoms-containing liquid-crystal DNA layers of the chromosomal apparatus (analogues of mirrors) can also represent a fractal medium for accumulation of localized photons. A medium which creates a coherent continuum with a quantumly nonlocal distribution of polarization-wave genetic information. To some extent this corresponds to our idea of genome quantum nonlocality, namely, one form of its nonlocality [Gariaev et al., 1999; Gariaev, Tertyshniy, 1999; Gariaev et al., 1999]. Probably there are other mechanisms of how light quanta (as solitons) can convert into radio waves. The study of Tuszinski et al [Tuszinski et al, 1984] demonstrated how two seemingly independent theories relate and complement each other. These theories introduce two physical models explaining unusual behavior of biological systems. These models were introduced by Herbert Fröhlich and Alexander Davydov. The so-called *Davydov Soliton* describes excitation, delocalization and electron motion along peptide chains of protein molecules in a solitary wave (soliton) form. Davydov's model is complemented by the well-known Fröhlich model [Fröhlich, 1968 Fröhlich, 1972 Fröhlich, 1975; Fröhlich, 1977] — developed in our work Blagodatskikh, Gariaev et al., 1996] — about the potential of a highly polarized (coherent, laser-like) state of oscillating dipoles of informational bio-

macromolecules. These dipoles manifest during the phonons Bose-condensation of the proteins electromagnetic waves (10^{12}-10^{13} Hz), DNA (10^{9} Hz), membranes (0.5×10^{11} Hz). In the above mentioned 'Tuzhinski et al' paper, the Davydov Hamiltonian is transformed into normal coordinates, and the Fröhlich Hamiltonian is canonically transformed into equivalent form in terms of the Hartree-Fock (HF) approximation method. The authors believe that the Hamiltonian model is able to link the two theories, which are mathematically equivalent. Moreover, both models complement each other physically. Bose-condensation of biopolymer vibrational modes correspond to the distribution of polarizations of a soliton wave. And vice versa: the soliton transport of the boundary energy along the peptide chain is accompanied by Bose-condensation of lattice vibrations of biological structures. It follows that a soliton generates an electromagnetic field, and probably this is a mechanism of the phenomenon observed in experiments, where the oscillating optical breather-soliton, representing DNA soliton excitations, generates optic-resonantly enhanced radio waves. Another idea drew our attention: in the biological system, the conversion of endogenous coherent photons (generated by chromosomes) into radio waves may occur according to a "three-mirror" or "multi-mirror" scheme on numerous reflecting membrane surfaces, similar to our model experiments. In this case, the cell nucleus (chromosomes) act as a laser light source, and the membrane of the cell nucleus and cytoplasmic membranes act as semi-transparent mirrors. Domain walls of cellular liquid crystal structures may also act as "mirrors", and both being the scanned objects at the same time. In this case, it becomes possible to "*in vitro* and *in vivo*" manipulate with light laser beams. These light laser beams are transported by a very complex network of living cell fibers and probably are, within cellular structures transformed into radio waves, carrying information about structural-metabolic alterations. Localization and "recording" of this kind of photonic-radio-wave information may lay the foundation for the creation of artificial biocomputer memory. Building on the momentum and stirring up scientific controversy, we would like to propose creation

of memory cells on DNA liquid crystals. “Reading” of information from such memory cells is accomplished by a laser beam, in modes, developed by us. As mentioned above, we have already obtained the preliminary experimental results in this area.

"IN VITRO-IN VIVO" NONLOCALITY OF GENETIC INFORMATION

The genetic wave information from DNA preparations, recorded in entangled photon polarizations, being quantumly nonlocal, transforms (unfolds) into a broadband radio wave spectrum, which is isomorphic to photon polarizations. These modulations of "photon-radio-wave" polarization by optically active DNA molecules carry quantumly nonlocal morphogenetic and, more broadly, metabolic wave information. Since the Fourier-Transform of the radio spectra substantially depends on the type of the scanned substance, we suggested that this phenomenon may lay the foundation for a new type of spectroscopy – "*polarization-laser-radio wave*" (*PLR-spectroscopy*) [Prangishvili, Gariaev et al., 2000]. The following observation was fundamental: photonic-radio-wave characteristics of various objects (PLR- Fourier-spectra of crystals, water, metals, DNA, etc.) are memorized by laser mirrors and "live" for some time. Notably, that these "mirrored spectra" (PLR-memory) are dynamic in time as well as equivalent to the spectra of the directly scanned object. These highly complex and very strange non-linear "memory" dynamics demonstrate spectral patterns that recur through the passage of time. It is possible that this is the manifestation a soliton type of Pasta-Ulam-Fermi return event, the one that we have already seen in the case of non-linear DNA dynamic light scattering on gel [Gariaev, 1994]. Characteristic recurrence of induced radio wave radiation spectral images of DNA preparations is shown in Figure 4. This is the first example of a relatively static, multilayer recording medium (laser mirrors) that is able to store the dynamic spectral information about recorded objects. This discovered phenomenon can afford a real basis for the development of a fundamentally new type of video recording as well as a new type of cinema.

Further studies revealed high biological (genetic) activity of radio waves that were generated by DNA preparations under the described above conditions. Using such DNA-radiations we induced

ultra-fast growth of potato tubers in soil-free conditions (the shoots grew up to 1 cm/day) and they had dramatic changes in its morphogenesis, where small tubers grew from stems, not as usual from stolons. These DNA-radiations induced statistically-valid "restoration" of old dead seeds of *Arabidopsis thaliana*, taken from the Chernobyl zone in 1987. Control seeds, radiated by polarized radio waves with no DNA information, were biologically inactive [Gariaev, Tertyshniy, 1999]. This series of experiments once again proved the potential existence of genetic information in a form of a polarization-laser-radio-wave physical field. For over 70 years biologists have been arguing about this possibility.

We assume that the main information channel in these DNA experiments is represented by bio-linguistic entangled modulations of photon and radio waves polarizations during "photon ⇔ radio wave" transitions with preservation of information between them as a case of quantum nonlocality (see below). This is why a well-known fact is now seen from another perspective: information bio-macromolecules - DNA, RNA and proteins - have a pronounced ability for optical rotatory dispersion and for circular dichroism. These can be observed in the discriminating (dependent on the wavelength and on the properties of the sample) rotation of electromagnetic photon vectors and in different photon absorption by samples (depending on the sample type and depending on the right or left rotation direction of the photon field electric and magnetic vectors). Low molecular weight components of biological systems, such as sugars, nucleotides, amino acids, porphyrins and other substances, have the same capacity. So far this had made no biological sense. Now, the phenomenon of optical activity can be understood as the basis for receiving rich information about the metabolism of the body. The information is read by the endogenous laser chromosome radiations, which then transforms into regulatory ("semantic") radio-radiation of the genome-biocomputer. The contradiction between the lengths of radio waves of such transformed radiations and the size of organisms, cells and subcellular structures is resolved. In this situation, the semantic resonances in biosystem space-time occur not at the level of

wavelength but at the level of frequencies and rotation angles of polarization modes. This also lays the foundation for the artificial laser-radio-wave "*in vitro* and *in vivo*" scanning of organisms and their components as a new type of spectroscopy [Prangishvili, Gariaev, 2000].

It appears that the given case of chromosome quantum nonlocality – the manifestation of nonlocality of genetic information - is a special case. Nonlocality of genetic information is highly characteristic for multicellular organisms and manifests on many levels:

1st level – Organism. Here nonlocality manifests as capacity for regeneration, for example, in *planarium* worm. When you cut this worm into pieces, any part of its body can regenerate into a whole organism. In other words, in this case, the common pool of the genetic information is not associated with any part of the biosystem. The same goes for plant's vegetative propagation.

2nd level – Cellular. It is possible to grow a whole organism from any cell, not only from a zygote. For animal biosystems it is complicated, but still possible. Any cell is a potential continuum of the organism.

3rd level – Cellular-Nuclear. Enucleation of nuclei from somatic and gametal cells, followed by injection of other nuclei into these cells, does not prevent normal development of the organism. Such cloning has already been implemented with higher biological systems like sheep. Each cellular nucleus is also a potential continuum of a biosystem. There is no localization of genetic potencies on any individual cells.

4th level – Molecular. The ribosome "reads" messenger RNA not only codon-by-codon but is also is able to see the meaning of the whole mRNA context, that means, nonlocally, continually.

5th level – Chromosome-Holographic. The genome has holographic memory [Gariaev, 1996], and is typically distributed (nonlocal) associative memory. On this and the following levels, nonlocality acquires a new quality, a dualistic material-wave character, since

holograms (like any material substance) “can be read” by electromagnetic and/or acoustic fields, which carry gene-wave information beyond material substance of chromosomes. On this level physical field(s), calibrating, laying out the future space-time of the organism, show up on the stage. It seems that it also pertains to the holographic memory of the brain cortex, assigning mental, semantic and conceptual scope, calibrating potential actions of the higher biosystems. And this is the highest, socio-genetic level of genome operation.

6th level – Quantum nonlocality of the chromosome continuum. Up to level 6, the nonlocality of genetic information is realized in the space and time of the organism, wherein the time and space are constant, without any gradients or distortions. Level 6 has a special character and a new quality. It manifests itself a form of quantum nonlocality, namely, in a permissive form, postulated in our work [Prangishvili, Gariaev et al., 2000]. In this case, nonlocality is realized both along the space of the biosystem and along the “compressed" to zero space-time of the biosystem. Instantly distributed in this way gene-wave programs, isomorphic to material, are simultaneously active "here and there" in the organism, so the semantic construction of “first and then” loses its meaning. This is a strategic factor, an extremely important evolutionary achievement for multicellular biosystems. The organism’s billions of cells must instantaneously "know" everything (or at least main strategic information) about each other.

Without the phenomenon of "wave information instantaneousness" the giant multicellular continuums of higher biosystems would be unable to holistically coordinate metabolism, physiology and other functions. Intercellular diffusion of signaling substances and neural processes have too much inertia to do this. Even if we assume that linguistic electromagnetic fields with instantaneous/light speeds are involved in intercellular transfer, which is quite probable, then, it is still insufficient. The very mechanism of quantum radio wave nonlocality is necessary here. And this mechanism is applicable to the genetic apparatus, which can act as an instantly distributed quantum (wave) object,

isomorphic to compressed material information of the chromosome continuum. Due to nonlocality, the genetic apparatus of the higher biosystems produces an interesting phenomenon: in certain linguistic situations in a "compressed" space-time of the biosystem, "here and there", "first and then" work as continuity, providing organisms with the qualities of super-coherence, informational redundancy, super-awareness and, as a result, integrity (survival). A good example of the above is the regeneration of organs and tissues in lower organisms (hydra, worms, amphibians, lizards, crustaceans), this ability, largely lost by a man. But it can be activated, if we start employing proposed by us the principles of biosystem's wave self-organization. A good example of this is the first-ever successful implantation of donor alloplants into a blind man, resulting in partial restoration of vision, performed by E.R. Muldashev [Muldashev, 2000]. Our studies, including the studies carried out together with E.R. Muldashev [Prangishvili, Gariaev et al., 2000], laid the ideological foundation for this kind of surgery, and the regeneration process. However, the theoretical-experimental research in this field is still in its infancy and requires further physical and mathematical consideration and development.

When applied to biocomputers, the analogues of such nonlocal processes and PLR-memory may become the basis for the development of computational technology in general. This will represent a profound revolution of silicon-based hardware components, and in some way, a new turn in the evolutionary development of computational technology towards a completely different qualitative level: Analogue ⇒ Digital ⇒ Image, where "Image" level is represented by the semantic nonlocal wave DNA-based computer.

WHAT IS THE "DNA COMPUTER" OF L. ADLEMAN?

However, the logic of studies in this field took another direction. They began to use DNA molecules as purely material structures, performing “parallel computation operations”. It started in 1994, when Leonard Adleman, a professor of computer science at the University of Southern California, proposed to solve "Travelling Salesman Problem” (TSP) with an algorithm implemented on a molecular (DNA) level [Adleman L., 1994]. This problem is an instance of the directed Hamiltonian path problem (HPP), and it is associated with the iteration of multiple alternate solutions to find the optimal one. Using "DNA-computing" Adelman solved the problem for 7 cities with 13 roads between them, when it was necessary to find the shortest route for a single visit to each of these cities. It took only one week to get the answer, whilst at the time a traditional computer would have taken a few years. It employed a fundamental property of the DNA molecule - its single strand complementary mutual recognition, so that in a solution (or inside living cell) any fragments of both DNA strands find their proper complimentary strand and form a normal double helix. This is also, a manifestation of the self-assembly properties of highly organized biological polymer molecular-supramolecular structures. *In vitro* or *in vivo*, ribosomes, membranes, chromosomes, viruses, and phages are self-assembling. And this is also valid for single-strand DNAs. The efficiency of the spontaneous mutually complimentary search of DNA strands (halves), as a part of self-assembly, ensured the high-speed search for the TSP solution. Until recently they could not explain the accuracy and efficiency of complementary DNA strands mutual recognition. And this is critical for the creation of a DNA-computer, so we write about it below.

Let us provide more details for Adleman’s model, as his logic is fundamentally different from ours. As we (and not only we) believe, the method chosen by Adleman and his numerous followers, employing DNA as a "computing" structure, is incorrectly understood by them as DNA-computing. David Gifford, a major

authority in computing, who was the first to support Adleman, said that "this is not the molecular computer", and that this technique "...can only solve some kinds of combinatorial problems, this is not a universal or programmable computer like an IBM PC". To understand why we and Gifford are right, let us examine Adleman's method further. The single-stranded DNA segments of 20 bases long with random sequences represented the cities. The complementary single-stranded DNA segments of 20 bases long, which cover half of the paths between the cities, represented roads. At the same time the canonical rule of base pairing in the double-stranded DNA is adhered to: Adenine-Thymine, Guanine-Cytosine. The path between 7 cities begins with a fragment of double-stranded DNA that connects any two cities. It is important that there can be more than one DNA fragment, designating any single city. Then, more than 100 billion radioactively labelled "DNA-cities" and "DNA-pathways" were mixed in the test tube and multiplied with enzymatic DNA-amplification. Adelman believes that "DNA computing" stops at this point. Then, to obtain the solution – to find the optimal pathway (certain DNA fractions), the reaction mixture with a "solution" was separated by electrophoresis to see all possible pathways from "start" to "finish". Then, they selected the DNA that passed each of the 7 cities only once; these represented the paths between 7 different cities. These fractions of "DNA-pathways" found at this stage were considered the most optimal or the "winning". This is what the TSP "solution" was about. Billions of parallel fast complementary spontaneous (non-programmable by a man) acts of "recognition" of single-stranded DNA and billions of spontaneous enzymatic replications of these molecules were involved in the process of searching for solution. Moreover, in a short time and energy consuming fashion, it produces a kind of "genetic soup." Such efficiency, high speed and accuracy of molecular processes is inconceivable for equivalent operations in digital electronic computers, using deterministic vectors of data processing. "DNA computing" involves non-deterministic acts of parallel mass-data processing of numbers-letters (4 nucleotides of

DNA). Adelman's algorithm for solving Hamiltonian Path can be summarized as follows:

1. Random paths are presented by graph.
2. Only those paths are retained that start (in case of cities A, B, C, D, E, F, G) in the city A and finish in the city G.
3. If the city has n cities, only paths to n cities are retained (n = 7).
4. Only those paths are retained, which pass all cities only once.
5. All retained paths are solutions.

Molecular-biological steps of obtaining the solution boil down to the following operations:

a) single-stranded DNA (ssDNA) synthesis;
b) their division by length with isolation and selection of a 20-base ssDNA;
c) mixing them in test tubes;
d) DNA strands with known sequences selection;
e) complementary double-stranded DNA re-association selection;
f) DNA PCR-amplification (multiplication);
g) cutting of the DNA with restriction enzymes;
h) ligation of DNA, complementary by "sticky" ends;
i) determining of the presence or absence of the labelled DNA in the test tubes.

How efficient is such a "computation" system? "DNA computer" performs 2×10^{19} operations per Joule, whereas a digital computer executes 10^9 operations per Joule, so it is 10^{10} times more efficient. Information can be stored in DNA molecule at a density of 1 bit/nm^3, whereas electronic storage density is approximately 10^{12}nm^3 contains 1 bit [Bass, 1995].

And yet, can the DNA operation in this method be called a computer operation? No, it cannot. In this version of experiment, there is massive processing of possible "DNA-pathways", including the right (optimal) ones. Only then, the actual computing begins,

but this computing is performed by people. Intelligent retrieval of DNA fractions represents a solution process for the TSP. Here, the computers role is performed by a person, and there would be no solution without the human intelligence. What makes this common with digital computing is non-participation in DNA programming. DNA is already naturally "preprogrammed" for complementarity for the cause of living system evolution. Single stranded DNA is innately capable of mutual recognition. Notably, Adenine-Thymine, Guanine-Cytosine complementarity is provided by close acting hydrogen bonds of the nitrogen bases only during the last stages of pairing. Preliminary sighting "calibrations" between single-stranded DNA, between tRNA-mRNA antibody-antigen, etc. is performed on the level of the distant wave interactions ("recognitions"). This DNA property can be called elementary potency for image recognition, and therefore, for computing. But this phenomenon is of a completely different nature, namely, this is wave-DNA computing. The principal difference between wave-DNA computing from electronic-digital computing, is that wave-DNA computing operates with images and quasi-speech constructions [Maslov, Gariaev, 1994]. This biocomputer does not work with a number as equivalent of wealth (for example, currency is a numbered equivalent of wealth, or 0s and 1s as an equivalent of information), but with the wealth itself. As mentioned above, the TSP problems are successfully and spontaneously solved without human contribution in the process of *in vitro* and *in vivo* self-assembly: in the biogenesis of ribosomes, viruses, membranes, multi-subunit proteins, as well as in the processes of self-organization of the chromosome apparatus after mitosis and meiosis. Moreover, the living cell applies these mechanisms to find coupling paths in antigen-antibody, tRNA - mRNA, protein-receptor, etc. reactions. These acts have achieved fast processing and search for optimal wave vectors of biosystem self-organization, where bio-morphogenesis represents the supreme manifestation of self-organization.

Parallelism and amplification of DNA restriction fragments with the multiplication of the "solutions" mass in Adelman's "computing" model may be also seen as an example of the "DNA-

semantic” realms artificial nonlocality, which is created in the space of reaction tubes, since the correct TSP solution has absolutely no time or space reference. Locality (space reference) is achieved only upon the choice of the correct solution made by the human mind, after selecting certain "DNA-winning" fractions.

It is impossible to correctly and efficiently use DNA as a basic information element of the potential biocomputer without recognition of new genetic molecule functions within biosystems. It would seem that DNA’s role was crystal clear - the genetic code was discovered a long time ago and there are a half dozen of Nobel Prize winners. It would seem that the success in genetic engineering is obvious. However, recent years demonstrated that it was not so rosy. Right now, genetics and embryology have moved to a new level, where the available knowledge about DNA as the carrier of the famous protein triplet code can no longer meet the needs. As it was decades ago, we still do not know the most important thing: how the information about the structure of our body is recorded in chromosomes and how this information is read. The conventional model of the genetic code is just an attempt to understand the construction process of the organism. The very fact that the model sees most of DNA as "junk", i.e. not performing any role, casts doubt in its accuracy. It is this "non-coding" part of the chromosomal substance that requires a different mindset, particularly for the creation of a DNA-computer, and not to mention the long sought-after solution for the origin-of-life conundrum.

LINGUISTIC PLURALISM OF THE GENETIC APPARATUS AND MODELLING OF LINGUISTIC-WAVE PROCESSES IN CHROMOSOMES. APPROACHING DNA BIOCOMPUTING.

Remember, the chromosome apparatus as a system, recording, storing, altering and translating genetic information, can be seen at the same time at the level of Matter and at the level of well-studied Physical Fields, which molecular continuum of DNA, RNA and proteins operate with, these physical fields are the carrier of the genetic and regulatory information. Our studies demonstrated that previously unknown types of memory (soliton, holographic, and polarization) are involved and the DNA molecule can work as a bio-laser and as a laser signal recording medium [Agal'tsov, Gariaev et al., 1996; Gariaev, 1994]. Furthermore, we have found that DNA is able to emit a laser-induced broadband electromagnetic radio wave field (see above). The genetic code will look principally different from this perspective, compared to the old "canonical" and inaccurate model. The previous model of the genetic code can explain only the protein biosynthesis mechanisms of living organisms. Therefore, the old model only interprets the initial segments of a far more complex hierarchical chain of material and wave holographic system, the semiotic-semantic, image/blueprint-like, encoding and decoding functions of chromosomes. As a gene-linguistic continuum of any biosystem, DNA molecules form pre-images or blueprints of biological structures and the entire organism, a kind of registry of dynamic, successive "wave copies" or "matrixes", isomorphic to architectonics of organisms. This continuum is a calibrating field for the construction of biological systems. In this regard, the mechanism of single-stranded DNA fast and accurate mutual recognition, as used by Adleman for the solution of the TSP, is only one method of the biosystem's self-organization. To be more specific, mutual recognition becomes possible because of unique super-stable acoustic-electromagnetic waves – solitons, born within DNA. Some

types of such waves are explained by the phenomenon of Fermi-Pasta-Ulam (FPU) - recurrence, discovered in 1949. Such DNA solitons have memory, peculiar to FPU-recurrence: non-linear systems can remember the initial excitation modes and periodically "return" to them. Remember, that the DNA liquid crystals in chromosomes represent a typical non-linear system. Another memory type of the DNA-continuum in the organism is quasi-holographic and fractal, since any hologram represents a fractal. Such memory is a representation of genome nonlocality (see above) and is associated with a fundamental property of a biological system - to restore the whole from its part. This property is well-known (plants grafting, lizards' tail regeneration, entire organism regeneration from the egg). The most advanced form of such memory is holographic (associative) memory of the cerebral cortex, i.e. neurons. All these results are given here only because it is futile to talk about a DNA-computer (even after solving the TSP with DNA molecules), if we do not take into consideration new logic in understanding of DNA wave-linguistic encoding bio-functions.

DNA solitary waves (solitons), running along the DNA's length, may act as "reading subjects" of the genome linguistic structures. This role is performed by the waves of nucleotide's rotational vibrations in single-stranded DNA segments as well as in RNA [Blagodatskikh, Gariaev et al., 1996]. Linguistic vibrational dynamics of such nucleotide rotation, probably, is one of many nonlinear-dynamic semiotic genome structures. As for the term "DNA texts" (borrowed from linguists for metaphorical use), it turns out that the text structure of DNA, indeed, is akin to human speech. Our mathematical-linguistic studies [Maslov, Gariaev, 1994; Trubnikov, Gariaev, 1995; Gariaev, Leonova, 1996] demonstrated that the key parameter of fractality is the same for DNA and human speech. It is well-illustrated if you compare Fig. 1a, representing the density matrix of a chaotic demonstration of some English text projection, and Fig. 1b, representing a similar matrix of nucleotide sequence encoding the primary structure of casein protein. These observations correlate with early works in this field (see, e.g., works of N. Chomsky on universal grammar or M.M. Makovskiy

monograph "Linguistic Genetics" (1992)). Using these theoretical developments and our own data on physicochemistry of DNA, we managed to experimentally prove the possibility of genetic information compression into the form of soliton wave packages, described by physics–mathematical formalism of Fermi-Pasta-Ulam (FPU) Recurrence Phenomenon. Such wave packages with artificially induced bio-information, generated by the FPU – radio-electronic devices (developed by us), can informationally resonate with the genetic apparatus of animals, plants, and probably humans, followed by dramatic and directed changes of their metabolism. It turned out, that the very substance of heredity - DNA - is a generator of FPU-soliton acoustic-electromagnetic fields. That is why the FPU-generators can introduce wave information into chromosomes by means of electromagnetic resonance mechanisms. The efficiency of FPU-generators are orders of magnitude greater with practical application of the mathematical commonality of DNA "texts" and human speech fractal structures [Maslov, Gariaev, 1994]. The grammar of genetic texts is probably a special case of universal grammar within all human languages. Therefore, physical-semantic resonances of DNA soliton structures and artificial linguistic FPU-soliton fields are realized similar to natural FPU-chromosomal fields. By introducing certain coded verbal commands via FPU-generator into the genetic apparatus of radiation damaged wheat and barley seeds, we managed to significantly reduce the number of chromosomal aberrations, i.e., to practically block the damaging effect of X-ray irradiation. Moreover, it was found that it is possible to prophylactically protect plants genomes from hard X-ray radiation with relevant wave commands (directives). Control experiments, where chaotic verbal constructs (commands) were introduced via FPU-devices into a biosystem's genome, revealed that these commands do not affect chromosomes. These effects were predicted and verified according to the Wave Gene Theory, using mathematical computer models, which simulated "reading" gene-texts by DNA solitons and simulated re-translation of these texts into other cells and tissues. Figures 2 and 3 represent the results of numerical modelling of DNA

conformational perturbations dynamics [Blagodatskikh, Gariaev et al., 1996]. The results demonstrated the dependence of solitary (soliton-like) waves to a DNA nucleotide sequence (from which this solitary wave originated). Our other physico-mathematical models and experiments justify the so-called antenna effect during excitation of selected collective macromolecules' modes by electromagnetic fields. This is directly related to the Wave Gene Theory's *in vitro* experiments of two-photon pumping of gene-structures, followed by DNA laser radiation. This is also consistent with ability of DNA liquid crystals to memorize an infrared impulse laser signal [Gariaev, 1994].

Let's return to the hypothetical biocomputer that uses DNA material-wave linguistic functions. It is obvious that the experimental results of Adelman and his follows are far from answering all the questions for the development of DNA biocomputer. For DNA and/or chromosomes to realize their potential *in vitro,* they must be in their natural environment - in a water solution, simulating karyoplasm, and in a liquid crystal state. Actual gene-structure regulation (including computing) can be discovered in conditions maximally close to those in a living cell. The DNA biocomputer is an extreme case of a living cell, however, an artificial analogue of the cell is currently impossible. Now, we can only make some models, that try to copy or approximate the wave-linguistic states of DNA in a living cell, for example, when we recorded DNA-wave information on laser mirrors or when we applied DNA-radio-waves for regeneration of radiation damaged seeds (see above). To move forward, it is necessary to start practically applying wave-memory types of gene-structures, and for this purpose, to invent memory units (cells), based on FPU-resonances and/or on the ability to record holograms, and also be based on the ability to record polarization-laser-radio-wave-DNA-information on localized (entangled) photons. Such memory will be by orders of magnitude superior in volume, speed, and "intelligence" compared with the memory of existing magnetic, optical discs and holographic storage units. The second principle opportunity is related to the listed memory types and is at the same

time greatly magnified by the chromosome's ability to be a laser-active medium. In this case, chromosome preparations simultaneously act as memory units (cells) and as lasers, reading their own (and induced) holographic, FPU-memory and memory stored on the localized photons. And finally, the last goal attainable at present, is the employment of quasi-speech DNA characteristics. It is possible to create a DNA-laser that will highlight and "speak" both natural genetic texts and artificial (synthesized by man) linguistic polynucleotide sequences, and which will simulate natural quasi-speech genetic programs. However, this is a very dangerous path, and it is necessary to impose safeguard measures (controls) on the creation of artificial wave genes. The operation of potential DNA-computers means entering into new semiotic realms of the human genome and the entire biosphere, the realms used by Nature for creation of human life. This idea is well substantiated: such as the theoretical works on the collective symmetry of the genetic code, carried out by Manfred Eigen in the Max Planck Institute in Germany. The studies of Eigen school show that the key part of information, recorded as quasi-speech in the chromosomes of all organisms on our planet, have an artificial nature. This is also confirmed by our experimental data: the chromosomal continuum and DNA of any biosystem acts as a kind of antenna to receive additional (possibly, exobiological) information from the external environment [Gariaev, 1994]. One might think that the genomes of Earthly organisms (at least partially) is a testing range for semantic exobiological influences, in this respect, it is significant that we already have the first entry points into this semiotic-semantic realm. The above leaves the following prospects for linguistic manipulations with genetic-structures as a main biocomputer substrate:

a. the creation of artificial memory based on genetic molecules, memory with a truly fantastic volume, speed and efficiency;
b. creation of a DNA-biocomputer, based on wave-principles, its methods of processing information are comparable to the human brain;

c. distant regulation of the key information processes in biosystems via artificial biocomputers (treatment of cancer, AIDS, genetic deformities, socio-genetic processes regulation and, ultimately, human lifetime extension;
d. active protection from destructive wave influences via the discovered information-wave channel;

e. establishment of exobiological contacts /connections /communications.

After all, let's ask: is there anything robust in Adelman's and others' experimental DNA-computing logic? Their logic is crippled, since it is based on a simplified understanding of chromosomes as merely a material substrate. Wave linguistic functions of genetic structures are not considered. One-dimensional thinking in relation to the invention of a DNA biocomputer will inevitably lead to a dead end. To be effective, such a computer must simulate how a genome operates with wave information: to be able to create images (blueprints), including quasi-speech images (blueprints), and be able to recognize them and manipulate them as commands. DNA-computer wave linguistic structures will have tremendous biological, and perhaps even intellectual activity. If these ideas are accepted, a different investment strategy is needed in genetics, embryology, genetic engineering, as well as in DNA-computing. DNA-wave computers will be able to manage super-complex processes, practicably comparable with metabolism and thinking. The fact that a genome (as we shown before) uses the effects of quantum nonlocality makes this even more realistic. The EPR-mechanism plays a fundamental role here. As a mechanism of vital processes regulation, it gives fundamentally new potencies to cells and tissues – the ability to instantly transmit the pools of genetic and metabolic information between all cells and tissues of a biological system, for example through the polarization channel of photons and radio waves, as mentioned above. If this is true, then, it explains why strategic linguistic biomolecules (proteins and nucleic acids) have an L-isomer composition, a helix twist and, hence, a pronounced ability for optical rotatory dispersion, circular dichroism and double refraction. Knowing this, we can see in a new

light the isomeric quantumness of other bio-organic molecules too. The asymmetry of their atoms and resulting isomerism and optical activity allows a biosystem to quickly and automatically “read” (scan) polarization, holographic and other material-wave data about the status of its own metabolism and the state of its current momentary spatial-temporal substructure.

We are convinced that an artificial DNA-wave computer will denominate a real revolution in not only in biological processes regulation, but it will also be used in social technologies, regardless of whether we like it or not. And this represents great potential danger for destructive use of such technologies.

WAVE DNA-REPLICAS

We have discovered that *in vitro* DNA samples can produce multiple replicating images - replicas of the DNA itself and replicas of the nearest surrounding objects. Such replicas appear in response to certain electromagnetic fields, typically, radiation in UV-IR range. These replicas may appear horizontally, to the left or to the right, they can also move in complex trajectories and remain for a certain period, even after the equipment is turned off and the initializing DNA radiation is discontinued [Figures 1- 4].

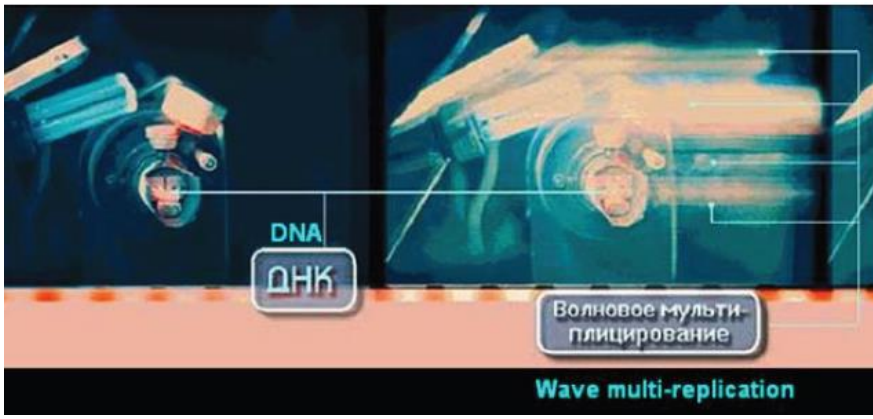


Fig. 1. The effect of wave replication of DNA and the nearest surrounding objects (control - left, experiment - right). This is the second method of wave DNA replicas identification.

In the control photographs, when the sources of UV-IR electromagnetic fields are turned off, you cannot observe the described phenomena, and you cannot observe it when the equipment is working as there is no DNA sample. In the first method of our experiments (see the next chapter “Methods”), during an exposure time of 1 second, the wave DNA replicas move in space and multiply, their trajectory is unpredictable and discrete. Replicas are generated only under conditions when the camera, DNA sample and the source of the initiating electromagnetic waves

are stationary in relation to one another. Disturbance of the DNA sample (the second method of the experiments) causes the vector of the replicas special distribution to shift exactly in the opposite direction (left to right) and then to fully dissipate. (Fig. 5 (a, b, c)). Moreover, there are cases when not only DNA sample is multiplied but also the surrounding objects multiply as well (Fig. 1, 5 (a, b).

To analyze the color impression on the film emulsion we present the images (obtained during film scanning) with the distribution of brightness in different color spectra - red (R), green (G), and blue (B): see Fig. 2(b), 3(b), 4(b).

Fig. 2 (a, b) shows that practically whole brightness scale of replicas is in the red spectrum, whereas the replicas are hardly distinguishable in green and blue color spectrums. Brightness histograms Fig. 3(c), that accompany Fig. 3b, show similar dominance of the red spectrum. The attention is drawn to the part of the histogram with the replicated image: a sector of brightness within the range of 128 to 255 is the distinctive peak of red in this part of the histogram compared to almost steadily declining of green and blue in the same histogram section. It is possible that such brightness distribution points are due to the fact that the photographed discrete track is a multiply repeated replica (mediated by DNA sample) of the light matrix of the "Duna-M" apparatus of red and infrared light (position 8, Fig. 8) – the apparatus on where the DNA sample was located during replicas generation. "Duna-M" is a lamp and represents a matrix of 37 alternating diodes (21 – red and 16-infrared diodes). In this experiment, a DNA sample was placed into an Eppendorf tube, which overlaid 5 diodes. This correlates with the 5-fold longitudinal patterns on the replica's track. (Fig. 3a).

An important property of wave DNA replicas is their relatively long lifetime after all initiating electromagnetic fields sources are disactivated. (Fig. 4). However, the lifetime of the replicas may also depend upon sensitivity of the photographic film (taking replica pictures) as well as on the film's spectral selectiveness.

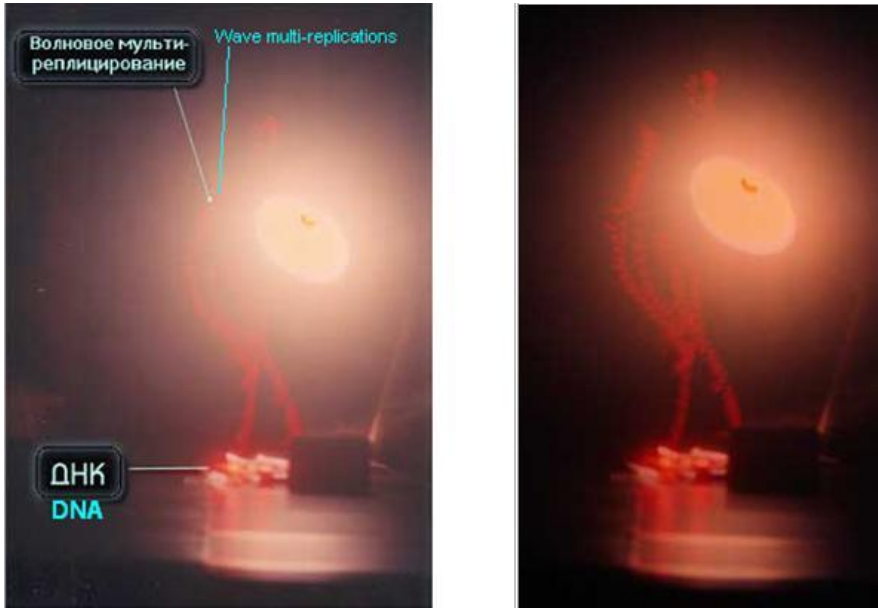


Fig 2 (a) Discreteness and complexity of the trajectory of wave DNA replicas (the original image - left, contrasted - right). This is the first method of wave DNA replicas identification.

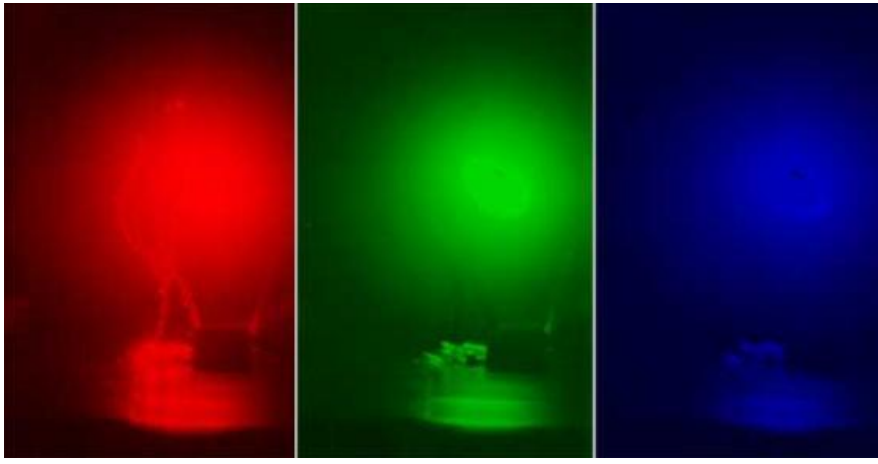


Fig 2 (b). Brightness distribution in red, green, and blue spectra.

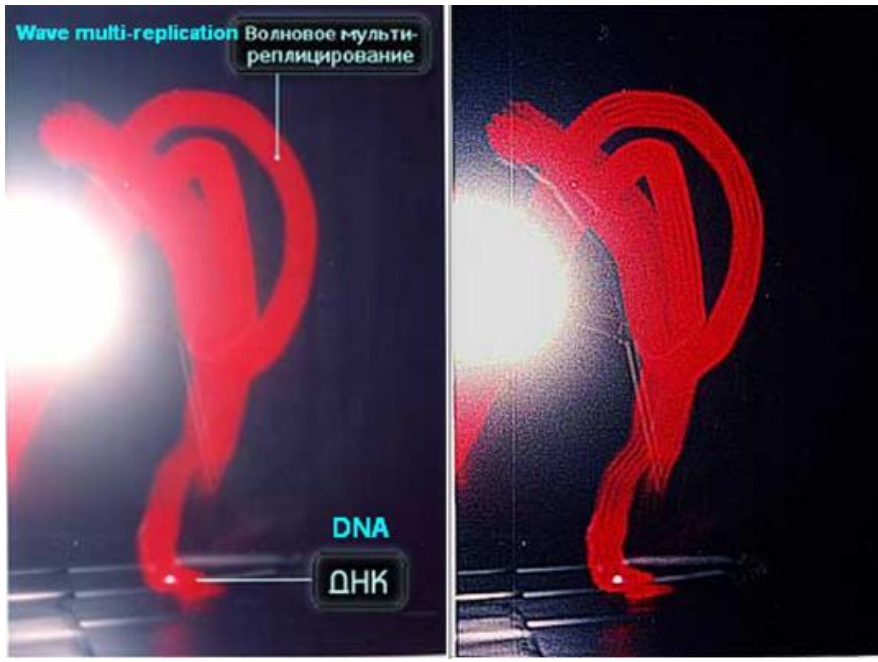


Fig 3 (a) Spatial dynamics of wave DNA replicas. Pay attention at the fine 5-fold longitudinal pattern of the track trajectory.

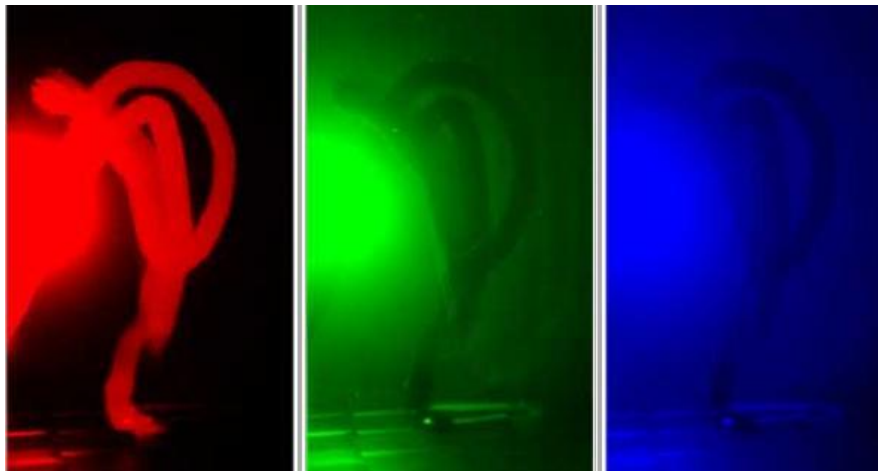


Fig 3 (b). Brightness distribution in red, green, and blue spectra.

Fig 3 (c). Histograms of brightness distribution in red, green and blue spectra.

Fig 4 (a). A long-lived wave DNA replica from the experiment in Fig. 3 ("phantom") after switching off the initiating electromagnetic fields.

Fig. 4 shows a clear difference in brightness distribution by color spectra between the image of wave DNA replica and its "phantom", which sustains itself after the source of light is turned off. Comparing the images in Fig. 4 (b) with their histogram images in Fig. 4 (c) shows that the image of replica's phantom in red spectrum is distributed through the whole range as well as through the brightness values. On the contrary, in the green and blue spectra, the values are localized within the narrow range from 70 to

120, there is a distinct peak, which explains the brightness of DNA replica, color tones and halftones, especially in the green spectrum.

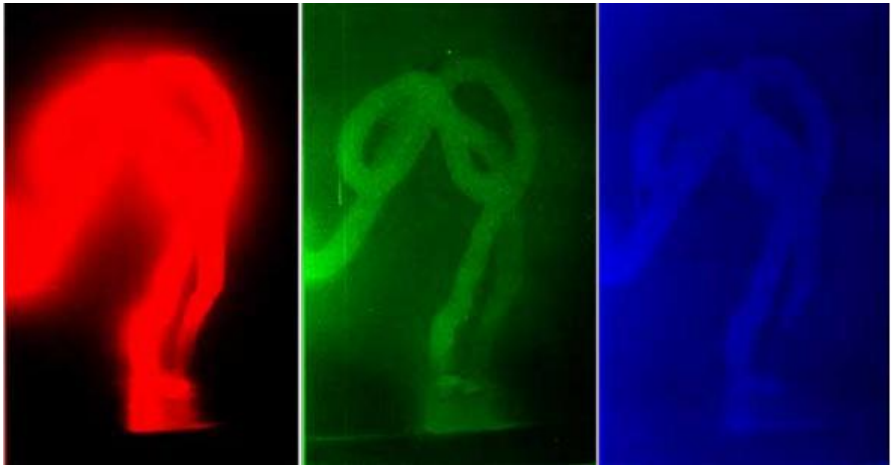


Fig 4 (b). Brightness distribution in red, green, and blue spectra.

Replicas generated in each case vary depending whether the method is stochastic (the first method of experiments) or deterministic (the second method of experiments) in space-time.

Induction of wave replicas of surrounding objects using a DNA sample (according to the first method) resulted in multiplication or triplet image of the BS(UV-B) lamp (Fig. 6).

To test the wave replica generation capability, we used various control substances: sodium chloride (crystallized *NaCl*); sodium chloride (1M solution); crystallized tartaric acid; racemic tartaric acid (1M solution); air-dried starch; crystallized glycine; air-dried calciferol; air-dried tocopherol; air-dried chlorophyll; double-distilled water; air-dried interferon mixed with *Bacillus subtilis*. None of these mentioned substances produced any wave replicas.

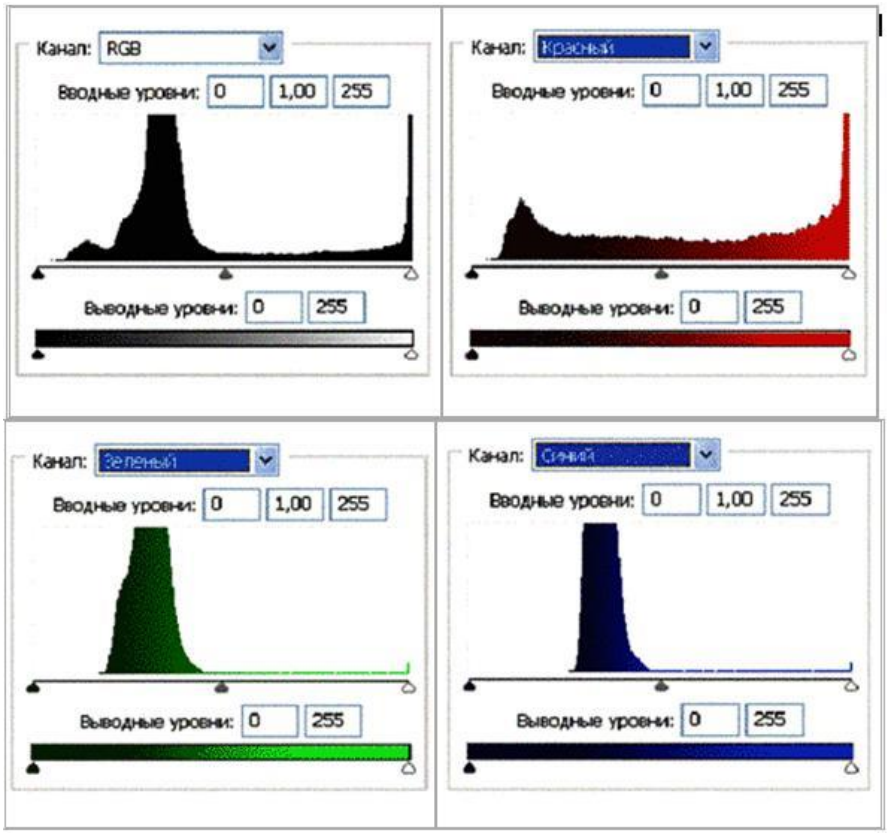


Fig 4 (c). Histograms of brightness distribution in red, green and blue spectra.

Fig 5 (a). The moment of DNA sample disturbance. The second method of wave DNA replicas identification.

Fig 5 (b). Immediately after disturbance, wave DNA replicas shift to the left. Note: sharpened color and brightness are not related to operation of the camera shutter.

Fig 5 (c). Disappearance of DNA replica formation effect after 5-8 seconds following the disturbance of DNA sample. All equipment, initializing the replicas, is on.

Fig 6 (a). Multiplication of the triple image of BS (UV-B) lamp. Original.

Fig 6 (b). Multiplication of the triple image of BS (UV-B) lamp. Contrasted.

Variation of the experiment shown in Fig. 5 (an old DNA sample was replaced with a new one). Refer to film frames #3 and #4 above. Frame #4 reveals replicas of the "Duna-M" diodes, shifting to the right. Pay attention at replicas of perforation, followed by replicas of exposed parts of the film.

Refer to film frames #11 and #12 above. From frame #4 to #11, the replicas of Duna-M diodes are absent, however, on frame #12 they appear again.

Refer to film frames #13 and #14 above. Frame #14 shows replicas of the Duna-M diodes. Pay attention how these replicas ‘enter’ the forbidden area of inter-shot space. These replicas disappear again on frame #14.

Refer to frames #23 and #24 above. From frame #14 to #22, the replicas of Duna-M diodes disappear, and show up faintly again on frames #23 and #24.

Fig 7. Matrix with red and infrared diodes (apparatus “Duna-M” or “Duna-T”). Contains 37 diodes: 21 red (650 nanometers) and 16 infrared (920 nanometers).

We applied two methods in our experiments. The first is presented in Fig. 8, the second is quite simple and is shown in Fig. 5(c). To generate and observe wave DNA replicas according to the first method, we operate as follows. Moderated by a time relay, different lamps are switched on in various combinations (Fig. 8), they are:

- BS Lamp (UV-B) or an incandescent lamp in blue spectrum (“General Use Lamp BS75”) made of CL98-1 glass type (see position #5 in Fig. 8)
- a matrix with red and infrared diodes (see position #8 in Fig. 8),
- a mercury anti-bacterial lamp or Compact electronic CEST26E27 Black (UV-C) lamp (see position #6 in Fig. 8), or BS (UV-B),
- and Cold Cathode Vacuum Thyratron Tube MTX90, (see

position #4 in Fig. 8).

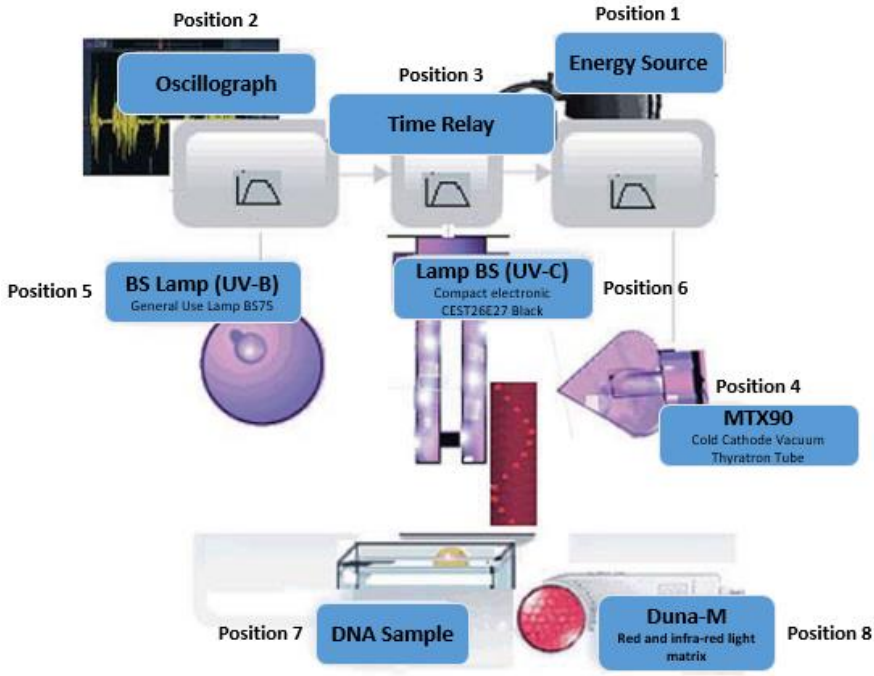


Fig 8.

Dehydrated DNA sample from bull's spleen (*JSC "Reachem"*, brand A, chemical plant *"Biolar")* in amount of approx. 100 milligrams in a sealed plastic conical Eppendorf tube (4 cm long and 0.9 cm in diameter in its upper end) or 3 milliliters of DNA water solution (or 1mg/ml) are placed in the active radiation zone in 1mm-50cm from the light emitters. The whole duration of the experiment is photographed, using Fuji 24-27 DIN film. At the same time, the oscillography electrodes (see position #2 in Fig. 8) register electromagnetic fields within experimental zone and record the average normal electromagnetic background noise/interference in the room, determined by the oscillograph's sine-wave. After 10 minutes of the experiment, the time relay switches off the UV-C lamp, and the camera captures the dynamic specific wave structures

(invisible to the eye but recorded by the photographic film) of multiple replicas of DNA and the nearest surrounding objects, directly related to the photonic influence of DNA. In other words, the DNA preparation image is multiplied, being spatially distributed in complex trajectories (the first method) or horizontally (the second method). The same images multiplication refers to the surrounding objects, related to DNA excitation.

To generate and observe wave DNA replicas according to the second method, we operate as follows (see Fig. 5 (c)). Dehydrated DNA sample, in amount of approx. 100 milligrams is placed on an aluminum foil holder; this time it is open to the air (not sealed). The BS (UV-B) lamp, Compact Electronic CEST26E27 Black (UV-C) lamp and "Duna-M" apparatuses are turned on and off with intervals of 2-3 seconds. 5 minutes later, photograph filming begins. In this method, we observe the replicas of the DNA sample and immediate surrounding objects, where they are distributed strictly to the right. When DNA sample is disturbed mechanically, the replicas distribution vector changes its direction to directly the opposite, shifting strictly to the left. From five to eight seconds after mechanical disturbance (although all replica excitation equipment is still on) the replicas dissipate (or cannot be registered by the used film type).

Despite of the advancements in molecular genetics and cellular biology, the fine mechanisms of the linguistic functions of the genetic apparatus are not yet known. This became pronounced after Pruitt's team's study that elegantly proved that Mendel's Laws sometimes do not apply and cannot explain everything in genetics, moreover, a gene's behavior defies common sense [Lolle et al, 2005]. Namely, adult *Arabidopsis* plants phenotypically expressed the *Hothead* ancestral gene, which was not present in the starter seeds (homozygous mutant in this gene). The *Hothead* gene, originally absent in the chromosomes of the planted seeds, in 10% of cases was found in adult plants. So far there's no explanation to this phenomenon. There was an assumption that the normal gene was stored as its revertase (reverse transcriptase) RNA-copy. This is a weak and evidence-free explanation which has no experimental

proof. This phenomenon of ancestral gene re-acquisition, inexplicable from the viewpoint of classical genetics, brought up a whole chain of unresolved fundamental issues in genetics and embryology. These issues are short-listed below:

a) Wobbling of the 3rd nucleotide in a codon makes the canonical table of the genetic code an arena of potential errors in protein synthesis, since it automatically attributes homonymy to significant doublets in codons (when pairs of identical doublets code different amino acids) [Lagerkvist, 1978]. At the same time, the third nucleotide in a codon can be any of the four, which was postulated by F. Crick [Crick, 2004]. Despite of the above, the probability of error in amino-acids selection is very low and this is truly an inconceivable fact;

b) The situation when 98% of the eukaryote's genome is considered to be either "junk" or (in the best-case scenario) playing a secondary, assisting role in the triplet code, or is a "graveyard" of virus genomes;

c) The remaining 2%, the gene coding DNA of the human (about 40,000 genes) turned out to be very similar to the ones of pigs, donkeys, flies and even *E. coli*;

d) For inexplicable reasons the genes are transposed in the 3-D chromosomal continuum;

e) For inexplicable reasons the genes are divided into Introns and Exons;

f) Template-free synthesis of RNA sequences by Qb-replicase of *E. coli* bacteriophage and the same synthesis of RNA sequences by the polymerase of T7 *E. coli* bacteriophage [Biebricher et al, 1981; Biebricher, Luce, 1996] violate the canonical principle of purely material DNA↔RNA replication;

g) Leaf phantom effect, when a fragment of a living leaf of a plant reproduces its own whole image in Kirlian, gas-discharge visualization (GDV) [Choundhury et al, 1979; Gariaev, Junin, 1989];

h) Inexplicable mechanisms of distantly functioning of morphogenesis selector genes, when their products are synthesized in one location, yet, the action is instantly detected at a remote location of the developing embryo.

All these and other inexplicable phenomena of chromosome linguistic functions encourage us to think and to prove that genetic memory has other significant attributes, significantly complementing the protein code. And it is likely that these attributes are of a wave nature. These contradictions and inaccuracies of the triplet protein code (which fail to explain the coding of the time-space structure of multicellular biosystems) forced us to see the genetic apparatus as a system of highly organized linguistic emissions of electromagnetic and acoustic fields. It appears that the results of our experiments with wave DNA replicas discussed above represent a good example of wave DNA functions.

The very first evidence of DNA wave memory was obtained by the author in 1985. This was the phenomena of the so-called "DNA phantom effect" [Gariaev et al., 1991; Gariaev et al, 2001], which was thoroughly described in the given works [Gariaev, Junin, 1989; Gariaev, 1994]. Such DNA memory expresses in the following way. Applying dynamic laser light scattering (DLS) to DNA solutions and DNA in rigid gels, within the spectrometer cuvette one can observe hypothetical structures (objects) that disperse light in a specific way after the cuvette with DNA sample has been removed. This phenomenon was called the 'DNA phantom effect'. Control measurements, prior to placing the DNA in to the spectrometer, produce only background light-dispersion.

Insufflations of the spectrometer's cuvette with nitrogen gas results in dissipation of the phantom effect, however, 5-7 minutes later it can be registered again. A similar effect was observed at Stanford University [Allison, Sorlie, Pecora, 1990]. The authors also applied the DLS method to study restrictive fragments of DNA. They discovered anomalous light-scattering of these DNA fragments, which, according to well-known theory, cannot be the

case. The authors called the phenomena *'mimicking the effect of dust'* (MIM). However, in their experiments the effect was not the result of any form of dust contamination, but rather the result of influence of other than DNA "objects", which performed like "dust particles", scattering light. And this occurred under conditions when DNA solutions were perfectly clear, pure and free from any contamination?! The performance of these dust-like-particles demonstrate attributes contradicting the classical models of light-scattering process for linear polymers [Hagerman et al., 1981; Zimm, 1956; Rouse, 1953; Tertyshniy, Gariaev et al, 2004].

These experiments [Gariaev, 1994; Gariaev et al, 2001; Allison, Sorlie, Pecora, 1990] have something in common: namely, the DNA samples were irradiated by light in the visible spectrum - 632.8 nm and 488 nm. And that is exactly what we did to initiate wave DNA replicas in our experiments. During production of wave DNA replicas, the emitter that has a wavelength equal to the wavelength of DNA's absorption and plays the dominant role. This is a source of UV light. You cannot exclude that in discussed DNA-phantom experiments, there were wave DNA replicas which distorted classical light scattering for linear polymers. It is also possible that wave DNA replicas play a certain role in the process of genetic wave communications among cells in ontogenesis and in the adult state of the organism as well as in between organisms.

Within the scope of the given experiment, wave DNA replicas are characterized by the common quasi-genetic process *in vitro*: a DNA sample creates wave replicas of itself and the objects (devices, equipment) involved in the initiation of replication, located in immediate proximity to DNA sample (Fig. 1-3, 5 (a), (b), 6 (a), (b)). This aspect of DNA behavior, if extrapolated to multicellular organisms *in vivo*, is a key in our wave genome model. According to this model, every single cell and the entire biosystem is continuously wave-scanning its own structural-genetic-metabolic state. In other words, chromosomal DNA *in vivo* (by means of its own coherent radiations) in a polarization-holographic manner is reading-scanning itself and intercellular metabolic space within the frequency range of 250-800 nm. This means, it is copying or

creating wave replicas of its structural-functional state at any given moment in time [Tertyshniy, Gariaev et al, 2004]. It is possible that the frequency range is much larger, however, the current level of technology can only record within mentioned frequency range. Presumably, such replicas produce the so-called “entangled” state and nonlocally and (instantly) unify the biosystem on information level.

Replicas registrations on photographic film is characterized by the following:

1. Replicas appear and disappear from one frame to another. For example, on Fig. 5: replicas are present on frame #3, on frame #4 they disappear; replicas are present on frame #11, on frame #12 replicas disappear again. Same is true for frames #13 and #14.

2. You can also see replicas of film perforations and light exposures (see frame #4).

3. You can see replicas overrunning interframe space, including the neighbor frames (see frames #13 - #14 and #23 - #24).

Below are the preliminary explanations of the above facts. The observed phenomenon of image shifting from one frame to another and film exposure in perforation areas can be explained by the fact that planar waveguides selectively chose the wavelength from a wide spectrum. They form in between the upper and lower borders of the width division of the film layer and between the film base and film emulsion. Under conditions

- of multiple reflections and light-scattering of the low-quality planar waveguides on the photo-emulsion grain,
- when planar waveguides have no focus
- and when “shifting” images (reflected from the opposite film borders) overrun each other,

we observe images interference (superimposition) followed by their dissipation. The images of the film perforation remain sharp since the holes are relatively large. By large here, we mean incommensurability of the size of perforation holes with the size of the photo-emulsion grains. Large and contrasted objects do not

require focus, when the images are transmitted to short distances commensurable with the size of the image itself. This also explains why relatively large images of the diodes luminescence "enter" onto the interframe space.

Irregularity of frame-to-frame replicas' registration can be explained as follows. The DNA strands experience respectively long UV- "pumping", and once DNA sample has received a critical amount of the stored energy, subsequent re-radiation takes place. This re-radiation takes some time, though its duration takes much less time. When the moments of frames capturing (filming) do not coincide with the moments of re-radiation of the pumped energy, no records of DNA or surrounding objects replicas are registered. When these moments match, replicas are registered by the film. If we find the optimal time interval for replicas registration, when frames capturing/filming moments match the moments of re-radiation of the pumped energy by the DNA waveguides, the registration will be continuously reproduced from one frame to another. DNA *in vivo* and *in vitro* is a hologram-generation medium [Gariaev, 1994; Gariaev, Junin, 1994.] Acknowledging this, we can assume that using a photo sensitive DNA medium (for example, collagen/gelatin) one can artificially record holograms in blue and UV spectra. In this case, when we use blue and UV lamps as a radiation source, there is an auto-recording of the DNA sample on itself, and a recording of the surrounding objects on the photo-sensitive quasi-cylindrical structures of the DNA sample (DNA sample is in a state of a rigid cholesteric gel). Then, each of these cholesteric domains is scanned by red and IR-radiation, this results in reading of a multiple diffraction-blurred (thus, distorted) images, where the first set of images is brighter and subsequent sets get fainter, and the images are shifting against each other. This holograms registration in UV light, followed by reconstruction in red and IR spectra, leads to blurring and dissipation of replicas' images. This blurring occurs due to the images multiple spatial distribution and due to the fact that each DNA fiber produces a few image sets. The blurring also occurs due to DNA's own acoustic vibrations according to the Fermi-Pasta-Ulam recurrence

phenomenon [Gariaev, 1994]. Such recurrence can provide the reproduction of the wave DNA replicas.

Possibly, such phenomena take place during significant exposure to UV radiation say of the skin surface (for example, when sunburnt), which leads to the generation of pathological programs of aberrant holographical regulation when read by red and IR-sunlight spectra. This, in turn, under the condition when the tissue is exposed to the excessive brightness of the reconstructed holographic images, may lead to appearance of some malignant tumors, like melanomas.

High exposure of UV radiation, simultaneously with the registration of holograms, occurs as an effect of electrons being liberated and damaging the structure of DNA. The accumulation of such electrons creates a free capacitive charge on the surface of DNA strands. The accumulated charge creates the effect of spatial redistribution of DNA strands, which in turn affects the predominant distribution of the reconstructed images-replicas. The shift of images of the reconstructed diffracted sets to the side opposite to the original diffraction, can be explained by the capacitive effect of charge polarity alteration – e.g. minus to plus or plus to minus. This spatially-distributed capacitor (condenser) – due to leakage and alteration of charge polarity as well as their mutual allocation – led to the discovery of an effect of the predominant appearance of right or left diffraction order in regulated DNA structures. This effect can be observed in Fig. 5 (a, b) and it can be used for creation of regulated spatial DNA nanostructures, for example, in the processes of human organ and tissue regeneration, by means of purposeful holographic regulation (primary results of which have been already achieved [Gariaev et al.., 2007 (a); Gariaev et al., 2007 (b)]).

POLARISATION ASPECT OF BIOHOLOGRAPHY

In this chapter, we introduce an example of bio-information photons operation *in vitro*: application of our optic-radio-electronic equipment for distant transmission of regulatory genetic signals. Here, we also try to explain a similar operation of chromosome photons *in vivo*. All this is related to bio-linguistic polarization of laser light, i.e. holographic. The described photon functions occur when the beam of a special bimodal laser scans (reads) the genetic donor-nanostructures. At the same time, biosystems are capable of self-scanning and self-correction (self-computing) by coherent radiation of their own chromosomal continuum in the range of 250-800 nanometers. We simply reproduce these endogenous nanotechnologies *in vitro*. This computing, irrespective of whether it is natural in a living organism or artificially reproduced by man, generates a pool of wide-spectrum wave data, which organisms use for their self-regulation, and which we use for constructive purposeful regulation of the biosystems metabolism.

We introduce a mathematical model of polarization-dynamic actions of desired biosystems metabolic regulation by means of laser holographic-computing *in vivo* and *in vitro*. We discuss the general mechanisms of these actions of natural and artificial regulation of biosystem metabolism and detail the methodology and equipment required for practical work in this direction [Tertyshniy, Gariaev, 2007].

The concept and term of ‘holography’ takes its origin from two Greek words: “whole” and ‘image’. Until recently, the essence of holography was reduced to the technical method of full-size space-projection (3D) and space-time-projection (4D) of objects. Now, the concept of holography has cardinally expanded and is also refers to the structure and functioning of the cerebral cortex [Pribram, et al, 1974] as well as the genetic apparatus. When we speak of genetic memory, we imply that the chromosomal continuum, as a quantum biocomputer, operates with 4D wave

images of itself to regulate its 4D structure and metabolism [Gariaev et al, 2001].

Phase (transparent) structure of the holographic object produces its full and detailed holographic image in space. Dennis Gabor was the first to propose this holography method in 1984. Since then, it has been substantially developed by Soviet scientists. The method is based on interference of any coherent radiation. Two beams (waves) of light of the same light source – the "object wave", scattered by the object, and the "reference wave", circumventing the object - are simultaneously directed at the photo film. The resulting interference pattern of these waves, containing information about the object is registered on the photosensitive surface and is called the hologram. When the hologram or its part are irradiated (illuminated) by the "reference" wave, you can see the dimensional image of the whole object. This holography is widely used in physics and in different areas of technological equipment (especially, for image recognition and information coding), in acoustics (for detection of internal defects in critical metal structures, for example, in nuclear power plants) and so on. Holography also opens great possibilities for production of 3D cinematography and television.

By saying "gene-holographic bioregulation", we mean strategic regulation of morphogenesis, biochemistry and physiology of developing and adult organisms, which involves regulatory chromosomal activities of acoustic, light or electromagnetic, of a genetic blueprint nature. This is an example of genome operation as a biocomputer. *In vitro* and *in vivo* regulation of Biosystems involves the transmission of holographic information from the donor to the recipient. In 1997, conducting our laser-holographic experiments on plants, we provided the rationale of donor-recipient holographic information transmission [Gariaev et al., 2000; Gariaev et al, 2001 (a); Gariaev et al, 2001 (b); Gariaev et al, 2004] The key point of this phenomenon is that a special laser beam passes through semi-transparent biological tissues and cells, representing the donors of the wave equivalent of genetic-metabolic information. Here, the donors act as holographic modulators of

scanning light. It is this modulation that represents the polarization-phased holography of the structure and dynamic metabolic (incl., genetic) status of the donor. It results in a complex dynamic registry of 4D -commands, operated by a quantum biocomputer to regulate/affect recipient organisms. This artificial quantum biocomputer actually *in vitro* (in a significantly simplified form) reproduces *in vivo* operation of our genetic apparatus as a natural DNA-wave biocomputer. [Gariaev et al, 2001]

To ensure stable and clear (without distortions) memorization of scanned information *in vivo*, we proposed to consider the optical nature of the cell's nucleus as vibration-resistant polarization-sensitive transducer of dynamic holograms. The physical mechanism of this transducer is based on the principle of redundant coding of each amplitude-phase scattering point of an object in a form of polarized Newton quasi-rings.

In our experiments on rat pancreas regeneration (see the next chapter for more details) we performed vibration-resistant transmission of dynamic polarization holographic information from the donor to the recipient. Under the condition of a sufficiently long and targeted near-resonant exposure of the recipient, we managed to holographically regulate the recipient's conditions by means of artificially transmitted holographic data, emanated from the donor tissues and cells. This allows the recipient's stem cells to receive an informational impulse to commence differentiation for post-embryonic morphogenesis, leading to full pancreas regeneration in rats. We do not know what type or types of stem cells were involved - this is a subject for further experiments. In our experiments, we found that the main pool of biohолographic data resides in dynamic-polarization modulations of the Euler angles. We explain this in the following way. Partial laser beam reflections/scatterings, pass through every point of the donor bio-samples, and create light cones of dispersed radiation, where orthogonal-circular polarization (emanating from the laser) transforms into a polarization space-cone distribution. The key event here is the interaction of the scattered radiation of the light cones with the polarization reference wave. This wave is synthesized by the

sensor-transducer, that can be represented by associates of the polarization-active cell nucleus. This interaction produces distributed in space polarization Newton quasi-rings. Living cells always represent a metabolically and polarization time-varying medium. Nonetheless, the light dispersed by such a medium, produces Newton quasi-rings, which are practically motionless in relation to one another and in relation to the beginning coordinates which usually set in the donor-object space. The above is possible because donor points are relatively "entangled" with each other. Variable Euler angles are conditioned by microscopic amplitude vacillations of the donor's points, corresponding to the living biological object cells' dynamic state. These variable angles represent the angles between straight lines, which are tangential to transient polarization quasi-rings, and the axes of coordinates, within which the donor's points are examined.

Moreover, it turns out that it is possible to transmit donor information into recipients at a remote location. By remote location, we mean a distance considerably exceeding the wavelength of the laser scanning signal. To explain and realize this process, we developed the concept of cell nuclei being polarization quasi-lenses. The physics and the mechanism of such lenses is that they simultaneously act as polarizers and sources of coherent light (250-800 nanometers). Located in cell's cytoplasmic cellular continuum, they perform scanning of their own and cytoplasmic polarization modulations. And this is the main contribution towards biohologram synthesis, and, is also the least explained phenomenon.

The same factors solve the problem of dynamic stability of polarization holograms, which turned out to be especially important when working with living organisms. With any micromotion of a) the laser beam in relation to the scanned donor-sample or b) of the donor in relation to laser beam (for example, due to seismic mobility of the laser foundation and/or due to instability/disturbance of the donor), the same relatively stable system of polarization Newton rings appear along donor cells. In other words, the donor laser-scanning produces polarization of

bioholographic objects that are stable, non-blurred, and thus, are recognized by the recipient system as regulatory. Performing holographic coding and information transmission, we managed to preserve the information redundancy. Here, the redundancy is related to direct and indirect Fourier-transform. This transformation is comprised of, firstly, of formation and registration of Newton quasi-rings from every point of the donor, and, secondly, of their indirect Fourier-transform.

The direct Fourier-transform produces a system of Newton quasi-rings for every point of donor's cells. The indirect Fourier-transform transforms these rings into identical points on a remotely located recipient. Finally, the redundancy is achieved due to the fact that, while passing through cellular-quasi-lenses, every donor cell structure transforms into the aggregate of 3D polarization cones of the standing light intensity wave. In case of partial erosion or vibrational dispersion of the Newton quasi-rings, corresponding to a certain point on the recipient, the remaining part of quasi-rings turn out to be sufficient for the correct formation of the required (missing) point of the donor.

These are the main differences and advantages of the introduced method and technology for holographic regulation of biosystem cell states. Listed above solutions allowed achievement of polarization-dynamic holographic transmission of information without geometric or scale distortions.

Note, that in order to produce a hologram, it is also possible to use non-coherent radiation. However, in our case, we used coherent light to provide multiple feedbacks, which, in the end, ensure that transmitted holographic-modulated information remains biologically active when transmitted via light, electromagnetic, or acoustic channels. Moreover, the "working" signal, outgoing from a donor, carries polarization hologram, modulated by vibrating Newton quasi-rings. The light beam modulated by the donor's bio-tissue is transmitted by the square photo detector inbuilt into the laser tube. This enables the modulated light beam to be transformed into a variable

electromagnetic signal. Notably, modulating vibration of Newton quasi-rings (rings of intensity) depicts a coded polarization-phased dynamic of each donor's micro fragments, for example, Liquid Crystal Chromosomes. In turn, micro dynamic vibration of these rings (and straight lines, which are tangential to them) depict the dynamics of the Euler angles. All this linguistic dynamic (holographic and "key–to–lock") resonantly affects the recipient's biosystem, for example, it affects the Liquid Crystal Chromosomes by reprogramming them isomorphically with the donor.

Thus, dynamic polarization modulation of the light beam, represented by Newton quasi-rings, during their motion is transformed into electromagnetic signal. This electromagnetic signal modulates the carrier frequency of the harmonics of the generator of impulses, regulating micro-shifts of the mirrors of the laser resonator. The maximum modulation depth of the working signal is in the range of 0.5 MHz to 1.5 MHz, which can be easily detected and received by any medium-wave radio.

Furthermore, by reproducing these audio signals, we have discovered that they are biologically active. This is true for many recordings on any medium from both animate and non-animate donor objects. More results of our observations will be presented in the coming publications.

THE THEORETICAL SUBSTANTIATION OF POSSIBILITY OF STORAGE, RECORDING AND READING OF DYNAMIC POLARIZATION HOLOGRAMS FOR APPLICATION ON INFORMATION BIOPOLYMERS

Earlier we successfully carried out a remote (tens of meters) laser-radio-wave transmission of morphogenetic signals from bio-donor (preparations of pancreas and spleen of rats) to bio-recipient (rats sick with type-1 diabetes), which caused regeneration of the pancreas in the body of the sick rats and subsequently their complete recovery (the rats in the control group, who did not receive the treatment, died) [Gariaev et al., 2007 (a)]. This phenomenon requires a bio-theoretical and bio-physical explanation, since the proof of the possible existence of active genetic information in the form of an electromagnetic field is of critical ideological importance.

It is known that the primary information polymers of cells – DNA, RNA, proteins and many other organismic metabolites contain asymmetric atoms of nitrogen, which makes those metabolites optically active and allows them to polarize light. It is also known that abiogenic nitrogen-containing polymers are, with high diffractional efficacy, capable of recording dynamic polarized holograms [Baklanova et al., 2005]). In this respect, it is attractive to examine informational bio-polymers – DNA, RNA and proteins as viable storage units and recording substrata for polarized-biholographic information, considering the fact that DNA, RNA and proteins are also nitrogen-containing polymers. It is possible, due to this similarity, DNA, RNA and proteins are able to absorb quanta of light with transitions between stable trans-isomer and cis-isomer conformations in polypeptide chains and polynucleotide strands. The DNA molecule is of particular interest as a "custodian" of polarized-holographic genetic information [Tertyshniy, Gariaev et al., 2004] and as an analog of abiogenic nitrogen-containing polymers [Baklanova et al., 2005]. The main contribution to the

intricate network of energy levels of such polymer molecules for relatively slow processes ***(~10^{-3} c***) is brought by their primary stable conformational states. For DNA this are A, B and Z-forms of its conformations.

Possible photo-isomerization of DNA, RNA and proteins, taking place in a bio-recipient's cells, when the recipient is irradiated by a polarized-holographic image, may lead to alteration of the orientation of absorbing transition as well as to the cross section of the absorbing chromophore and its hyper-polarization capability. In turn, a photo-induced change in isomer concentration and their spatial orientation alter optical properties of the environment, in particular, the diffraction index and absorption coefficient. We assume that the effectiveness of photo-isomeric transition is defined by the properties of the nitrogen-containing nucleotides sequences of particular DNA, RNA, amino-acid sequences of particular proteins and also the isomers' absorption cross section, quantum yield of trans-cis-isomerization and influencing light parameters, which is modulated by the indicated bio-polymers of the bio-donor's cells. This new polarized state of the light wave, radiated from the bio-donor's tissue, controls the intensity and polarization of the informational polymers in the bio-recipient cells.

A holographic information-laser transducer was used to remotely transmit wave genetic signals and/or triggering wave structures [Gariaev et al., 2007 (a)]. In this transducer, reciprocal orthogonal nature of the polarized modes of the scanning laser irradiation allows to increase the probability of maximum alignment or congruence with the large DNA molecule axis and with orientation of DNA liquid crystal directors in the chromosome composition. Optical response of the cis-isomer is considered to be isotropic. The composition of the polymer matrix along with nitrogen-containing composites may also include non-photoactive neutral fragments, contributing as a background to optical properties of the compound in question [Prangishvili, 2000]. Photo-induced DNA restructuring may result in structural reconstruction of the entire DNA polymer sequence. Light induced anisotropy of

3D nucleus distribution in DNA liquid crystal continuum (in chromosomes) will, very likely be more long-lasting and, therefore, may be an important factor for analysis of processes which are responsible for stable long-term storage of holographic information recorded in DNA liquid crystal topological-forms.

During the experimental transmission of holographic information obtained from cells/donor-tissues to the cells/recipient-tissues the following effect is observed: around every cell-hologram of both participants, in the near-field, there is a layer of neighboring cell-holograms which exchange holographic information with one another and with the central cell [Budagovsky, 2004]. Then, each cell, along with its own polarized-holographic structure and its dynamic properties, also contains holographic information about the nearest, neighboring cells. This is another very important reason for provision of redundancy and multiple duplication of holographic information in biosystems.

A physical-mathematical description of the dynamics of the described processes (which are analogues to photo-isomerization and re-orientation of DNA molecules) is given in terms of the function of angular distribution density. We will assume that all three molecular groups being part of DNA: trans-isomer, cis-isomer and neutral molecules, are independent. From the paper [Baklanov et al., 2005] we know the system of balancing equations. This system describes the dynamics of distribution functions of isomer abio-genetic polymers with high polarizational activity. This, to a certain extent, corresponds to processes taking place in DNA molecules during irradiation by circularly-polarized light, taking into account the effect of the non-photoactive fragment of the polymer matrix:

$$\frac{\partial n_l}{\partial t} = R_1 n_l + \frac{1}{4\pi} R_c \left(1 + 5SP_2 + \frac{1}{6} D P_2^{(2)} \cos 2\varphi\right)\left(N_0 - \int n_1 d\Omega'\right) \\ - -D_l \Delta_\Omega \left(n_l(t,\Omega) - n_l^0(\Omega)\right); \qquad (1)$$

$$\frac{\partial S(t)}{\partial t} = -\frac{1}{5}\frac{U_{hl}}{kT}\frac{1}{\tau_h}\left(S(t) - \frac{a_{20}(t)}{5a_{00(t)}}\right) - 6D_h(S(t) - S_0);$$

$$\frac{\partial D(t)}{\partial t} = -\frac{1}{5}\frac{U_{hl}}{kT}\frac{1}{\tau_h}\left(D(t) - \frac{6a_{22}(t)}{5a_{22}(t)}\right) - 6D_h D(t);$$

$$n_c(t) = \frac{1}{4\pi}\left(N_0 - \int n_l(t,\Omega')d\Omega'\right).$$

Angle $\Omega = (\theta, \varphi)$ the solid angle of the angular distribution density function of the dynamics of photoisomerization processes and the reorientation of molecules in the holographic structure of biosystem's photoinduced morphogenesis.

Coefficients $\boldsymbol{R_l}$ and $\boldsymbol{R_c}$ characterize the rate of isomerization intensity change. In more detail their values may be represented as follows:

$$R_l = \frac{I}{\hbar\omega}\sigma_l^{\parallel}\gamma_l\left(\varepsilon + \frac{1-\varepsilon}{1+a^2}\varsigma(\theta,\varphi)\right); \qquad (2)$$

$$R_c = \frac{I}{\hbar\omega}\sigma_c\gamma_c + \frac{1}{\tau_c}$$

Where *S(t)* – cis-isomers distribution function in a DNA molecule during irradiation by elliptically polarized light, n_l – current value of diffraction index of a DNA molecule during irradiation by elliptically polarized light, $n_c(t)$ – current absorption coefficient value in a DNA molecule under irradiation by elliptically polarized light, ***D(t)*** – distribution function of trans-isomer parts of DNA under irradiation by elliptically polarized light, $\boldsymbol{I}$ – light intensity value. $\varsigma_l(\theta,\varphi) = a^2 sin^2\theta cos^2\varphi + cos^2\theta$ - ellipticity of light factor. Here, $\boldsymbol{a}$ – degree of ellipticity, $\varepsilon \equiv \frac{\sigma_l^{|}}{\sigma_l^{\parallel}}$ - trans-isomer asphericity coefficient, $\sigma_c, \sigma_l^{|}, \sigma_l^{||}$ - trans-isomer and cis-isomers absorption cross-sections along and perpendicular to molecular axis; γ_l and γ_c- quantum yields of photo-isomerisation reaction; $\boldsymbol{P_2}$ and $\boldsymbol{P_2^{(2)}}$- associated Legendre functions; $\boldsymbol{a_{20}(t)}$ and $\boldsymbol{a_{22}(t)}$ – coefficients of expansion functions $n_l(t,\theta,\varphi)$ in a series of spherical functions; $\boldsymbol{D_l}$ and $\boldsymbol{D_f}$ - rotational diffusion coefficient of trans-isomer molecules in polymer matrix; $\boldsymbol{U_{hl}}$- intermolecular interaction potential; τ_h - polymer matrix relaxation time.

It was found that neutral molecules also influence the change dynamics of the order parameter of the polymer matrix as a result of photo-orientation. The polarized light effect on the polymer causes re-orientation of the molecule's nitrogen-containing parts, which, in turn, provoke redistribution of their molecular surroundings and, hence, a change of the order parameter of the nematic domain. The nematic domain is a structural formation, which is a part of a liquid crystal, within which all molecules have spontaneously induced uniform orientation. Sizes of such domains vary within the range of 10^{-3} – 10^{-5} centimeters [Soviet Encyclopaedia, M. 1980. P. 442]. In relation to the above, we would like to repeat the most important fact: chromosomal DNA has a liquid crystal structure [Du Praw 1970]. This fact ensures low-energy consumption orientation of the liquid crystals directors of this polymer under the influence of weak external and endogenous polarized electromagnetic radiation. This results in formation of various linguistic topological structures, of which donor's holograms are a specific case. It probably also relates to 'wave regeneration' of pancreas in rats *in situ* [Gariaev et al., 2007]. This regeneration is achieved by means of multiple transits of the polarized wave of the scanning laser beam, which has been modulated by the donor's cells' hologram. The result of laser scanning of the donor is transmitted and memorized by the liquid crystal continuum of the recipient, providing it with the required registry of directing holograms. The other explanation, complementing the previous: the triggering wave signal, modulated by the donor, is received by a hypothetical photoreceptive-site of the recipient (for example, photoreceptive-site of stem cells). Such a photoreceptive-site launches pre-existing genetic programs according to the "key to lock" scheme resulting in activation of certain differentiations and post-embryonic morphogenesis. All this leads to the regeneration of pancreas.

Modulation of the light beam by donor bio-tissue is transmitted by a quadratic photodetector. This photodetector is built into the laser tube. This is how modulation is transformed into an alternating electromagnetic signal. Importantly, modulating

vibration of Newton rings (intensity rings) reflects coded polarized-phase dynamics of each donor's micro fragment, e.g. liquid crystal chromosomes. In turn, micro dynamic vibration of these rings (and of lines in tangent to them) transmit the Euler angles dynamics. All these linguistic dynamics (holographic and "key to lock") resonantly effect the recipient's biosystem, e.g. on liquid crystal chromosomes, reprogramming them isomorphically to the donor.

Thus, polarised-dynamic modulation of the light beam, represented by Newton quasi-rings, is transformed during their motion into the electro-magnetic signal. The signal which modulates the carrying frequency of impulse generator harmonics, which regulate micro-shifts of mirrors in the laser resonator. The maximum modulation depth/index of the useful signal is allocated within a range of frequencies from 0.5 MHz to 1.5MHz. These bio-donor signals are transduced via a radio-receiver into the acoustic spectrum, which, according to the preliminary data, are biologically active. The same is applicable to abiogenic donors, e.g. some minerals.

The registry of the wave images, which appear in the holographic scenario, reflect in real-time and with high resolution the genetic-metabolic status of the bio-donors. It is this registry that represents the dynamic directive for the stem cells of the recipient, following the principle "repeat after me/do as I do", and is supplemented by the "key to lock" triggering option. Actually, both vectors of artificially activated regeneration represent a simplified model of endogenous processes during natural posttraumatic acts, for example, regeneration of a lizard's tail or regeneration of planaria. Natural endogenous reconstruction occurs due to inner reserves, that is "inner marking" (and triggering) radiation of cells, surrounding the damaged cells. During endogenous regeneration, dynamic-polarised information from healthy cells is continually transmitted from one spherical layer of cells-holograms to another layer. It is worth repeating that chromosomes and DNA *in vivo* emit coherent light in the range from 250 to 800 nanometres [Biophotonics and Coherent Systems. Proc., 2000, 2-nd A. Gurwitsch Conf. and Add. Contrib. Eds by

L. Beloussov, F.A. Popp, V. Voeikov, R. van Wijk. Moscow State University Press], i.e. they are capable of being a laser-active medium. The latter was proven and demonstrated by our direct experiments on creating DNA and chromosomal coherent emitters *in vitro*, this is when we were working on a quasi-genetic laser [Agal'tsov, Gariaev et al., 1996]. These data, in a slightly modified version, were confirmed by Japanese researchers [Kawabe et al, 2002]. Chromosomal liquid crystal continuum (as the primary operating element of the genome-biocomputer) acts as a unity of the two fundamental attributes: a medium for recording and storage of the dynamic 4D-holograms and, at the same time, a medium of coherent light emission. One could say that genome is a self-emitting and self-scanning system, a quantum biocomputer. Our task therefore is to, at least partially, reproduce these attributes of the genome *in vitro*, primarily relying on already known laser and hologram technologies as well as the theory of these processes, whenever possible extrapolating them on (to) the operation of the chromosome apparatus.

The idea of holographic management of growth and development of biological tissues was confirmed by American scientists with the example of the model for motion regulation of neuronal growth cones under the influence of slowly moving laser spot [Ehrlicher et al., 2002]. Bioholographic management was also demonstrated during wave transmission of morphogenetic signals onto plant calluses [Budagovsky, 2004].

Denisyuk's works deserve special attention to understand the principles of holographic information-laser transducer (in fact, a quantum biocomputer) operation [Denisyuk, 1974 (a)]. He developed the basis for holographic imaging of material structures, including dynamic structures, moving in space and time (for example, Doppler holography). This is especially important for our theoretical constructs and their application in specific devices, since in terms of holography, organisms are unstable constantly changing mediums. Applying Denisyuk's principles, we managed to experimentally prove its application in biosystem function. Application of space-holographic transmission of modulated

information, performed in a few ways in biological and physical objects, gave the impulse for further development of a management theory for biological and physical objects. The essence of this phenomena is based on the hypothesis of the unity of wave and material processes, occurring in closed-looped and open-cyclic systems [Denisyuk, 1974 (b)]. Transmission of modulated information from the donor-object to the recipient-object is carried out by means of rectilinearly distributed mutually interpenetrating waves, carrying multilayer modulating information.

One of the theoretical grounds for the method of holographic bio-management is the physical-mathematical model that we used to find a method for generation of non-coherent dynamically polarised biological holograms. These biological holograms employ the optical properties of cell nucleuses (chromosomes) as spherical lenses (quasi-lenses) – optically-polarised components in a form of DNA liquid crystals–cholesterics in the composition of cells nucleuses.

Let us review the formalised description of this process, proposed for registration of colour holograms without lasers [Alexandrov, 1998]. Note, in this process, chromosomes cannot to be literally viewed as lasers. What they have in common with lasers is that chromosomes are the source of coherent optical radiation. Adapting this proposed formalism to the biological system, we are going to describe intracellular processes. After that, we will present the mathematical substantiation of non-coherent polarised-holographic amplitude-phase quasi-lens functionality, and this will allow us to explain the essence of this method of distant wave-management in organisms. A biosystem, in a sense, is a complex association of optically active substances, rotating the polarisation plane of optical radiations (passing through these substances), and this fact is very well-known [Stephen Ross et al, 1997; Mae-Wan Ho.]. However, the principles of bioholographic management with polarised light have never been considered before.

To substantiate the method of obtaining non-coherent polarised-dynamic holograms (including biohologrames), generated

with the quasi-lens, let us present the final formula of light intensity distribution $\boldsymbol{I}$ in the hologram registration plane from Alexandrov's physical-mathematical model [Alexandrov, 1998].

$$I = I_0 T cos^2 \left[\frac{\alpha_0}{L}\left(\sqrt{L^2 + r^2} - L\right)\right] \quad (3)$$

For comparison, we will show the intensity of the distribution $\boldsymbol{I_1}$ in a normal coherent axial hologram of the donor's point, obtained as a result of interference of the object's spherical and carrying plane waves:

$$I_1 = 4 I_0 cos^2 \left[\frac{k_0}{2}\left(\sqrt{L^2 + r^2} - L\right)\right] \quad (4)$$

where: $\boldsymbol{I_0}$- light intensity, scattered by some point, located on the scanned biological donor-object; $\boldsymbol{T}$- intensity transmission coefficient; α_0 - a polarised light rotation angle while a normal light beam is passing through any optically active component of an organism. Such an active component, for example in the "near-field", could be represented by practically any metabolite or sub-cellular structure, including DNA [Mae-Wan Ho.]. $\boldsymbol{L}$ - is a distance between the point on biological object-donor to the registration plane of the recipient-hologram; and $\boldsymbol{r}$ - distance from the axial line (passing through the centre of the hologram "registrar") to the point onto which the light beam falls (originating from the point on the bio-object-donor); $k_0 = \frac{2\pi}{\lambda}$ where λ - the average wave length of the transmission signal, emanating from the source of light (in this case, these are cell's nucleus or their aggregates). For modelling of this process *in vitro* we use a special laser, monitoring the polarisation activity of the scanned bio-structures [Gariaev et al., 2007(a), 2007(b)]. From the formula (3) one can see that inside a circle of $\boldsymbol{r}$ radius, there will be $\boldsymbol{N}$ light (or dark) rings, which can be

defined by formula: $N = \frac{\alpha_0}{\pi L}\left(\sqrt{L^2 + r^2} - L\right)$.

Wherein, the impulse response function $h = (x, y, z)$ (or holographic point-spread function) can be represented by:

$$h(x, y, z) = T(x, y, z)cos^2\left(\frac{\alpha_0}{z}\sqrt{x^{2+}y^{2+}z^2}\right) \quad (5)$$

The holographic transmission function can be defined on the basis of Fourier transformation of the formula (5). The obtained hologram contains complete volumetric information about the spatial characteristics of the holographed object or about the spatial distribution of points of the donor's surface in relation to the hologram registration plane of the recipient.

Thus, the solution to our task is similar to the traditional one. At the same time, it is obvious that the method described above is critically different from other known interferential methods and has indisputable advantages.

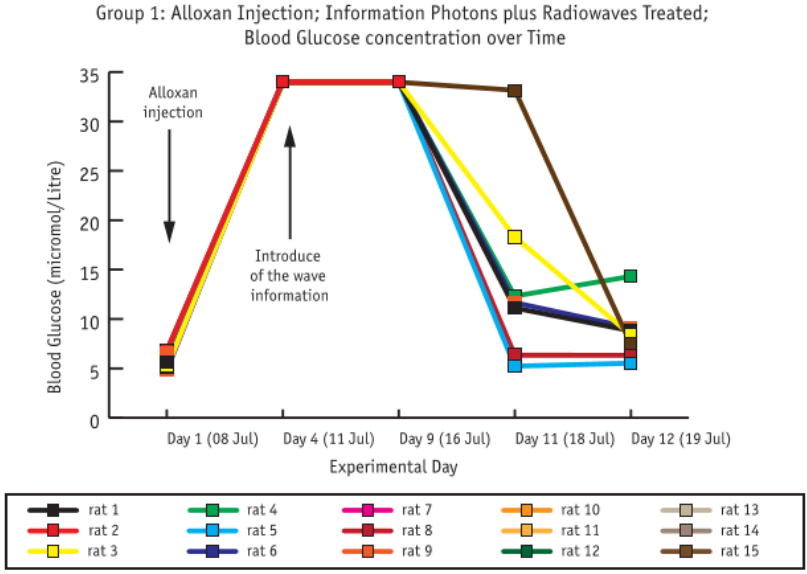
First, together with laser monochromaticity and coherence of the light of cellular nucleuses, (similar to the cases with endogenous bio-wave processes as well as induced signal transmission), rotary dispersion power of the optically active medium of an organism is used along with spatial locally-distributed polarised filtration via the quasi-lens for performance in the "remote-field". The above is sufficient (even under condition of donor dynamics being an unstable medium) for the recipient to receive the donor's wave bio-signal-image without distortion. The fundamental property of the cellular structures of a biosystem is to be optically active, i.e. to polarise light. Presumably, this property allows organisms to use even incoherent light for vibration-resistant hologram registration and reconstruction even without laser sources of light. It happens when biosystems, e.g. plants, use natural sunlight (on the entire spectrum from UV to IR) for their bio-morphogenesis. Vibration-resistance is defined by the value of polarization-optical rotatory power and, hence, by the thickness of

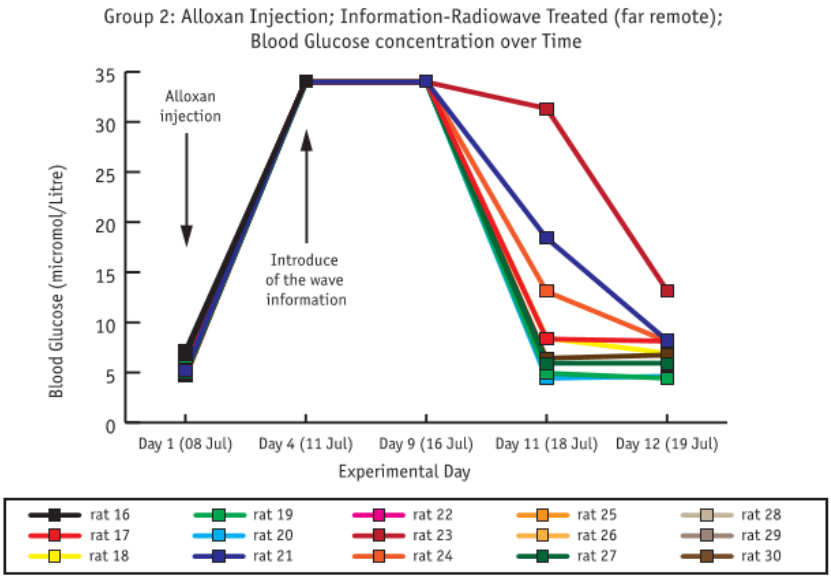
the optically active medium of cellular nucleuses for operation in the "near-field"; and the thickness of the optically active medium of quasi-lenses for operation in the "remote-field". It is known that the rotatory power of certain liquid crystals can reach 40000 degree/mm. When their power is used in the holographic information-laser transducer (the main component of the quantum biocomputer) it is sufficient for this method to be used for polarised-holographic transmission of genetic-metabolic information and for the biosystems' holographic management.

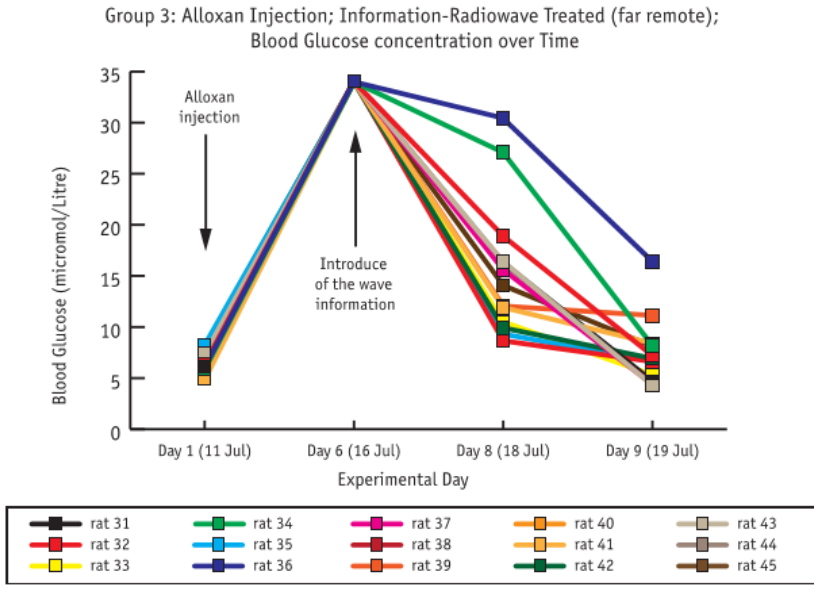
With the help of the proposed mathematical model, we have substantiated the model mentioned above of the liquid crystal cellular nucleus (or nuclei continuum) as a biological quasi-lens. It allowed us to develop the first biohолographic apparatus, practically, the quantum biocomputer, which performs the following real functions of biosystem-recipient's wave management:

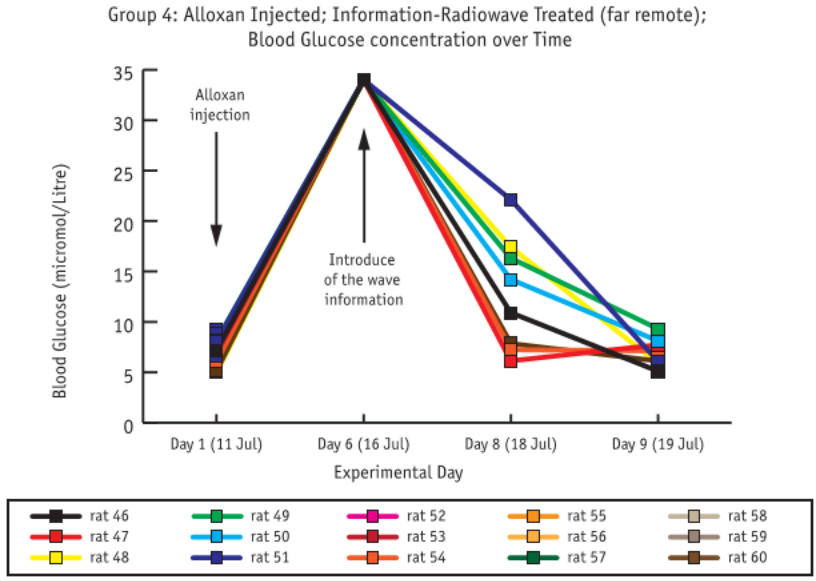
1. "Reading" from the biosystem/bio-structure the wave equivalent of genetic-metabolic information and/or triggering wave signals, which activate appropriate programmes in the recipient's biosystem.
2. Transmission of polarised-holographic dynamic modulated information from donor to recipient, located in a "remote-field", by means of specially developed and manufactured quasi-lenses.
3. Addressed introduction of this information into the recipient's biosystem.
4. Strategic management of the recipient's biosystem's metabolism.

EXPERIMENTAL VERIFICATION OF THE PROPOSED THEORY, BASED ON UNPUBLISHED EXPERIMENTS IN TORONTO, 2002









The graphs above present four experimental series: four groups (depicted in 4 separate graphs) of rats with diabetes (the pancreas was destroyed by previous alloxan injections) were

irradiated by modulated broadband electromagnetic radiation (MBER), containing information, scanned from "fresh" preparations of pancreas and spleen from newborn rats of the same line of species. The Y axis represents blood-sugar level, and X axis – number of days from the beginning of the experiment.

The first arrow on the first day represents alloxan injection (200mg/kg), the second arrow– irradiation by the by modulated broadband electromagnetic radiation. From the top to bottom (experiment):

Group 1 – laser beam and MBER irradiation at 1 cm distance;

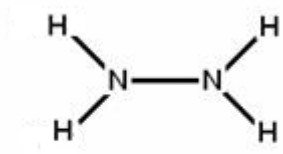
Group 2 – MBER irradiation at 3 m distance;

Group 3 – MBER irradiation at 15 km distance;

Group 4 – MBER irradiation at 15 km distance.

It is evident that by the 9th-12th days blood-sugar levels practically stabilised, returning to normal levels. All four groups survived. In a control group (60 rats), where MBER had not been performed, 95% of rats died through the 4^{th} to 7^{th} days. The results of the experiments were statistically analysed in accordance with the Student's t-test – the difference in blood-sugar level values within the groups is significant: $p<000.1$

ADDITIONAL THEORETICAL MODELS OF WAVE GENETICS AND EXPERIMENTAL DEMONSTRATION OF WAVE IMMUNITY



Hydrazine

Many researchers in their works point out the risk of hydrazine environmental pollution, which has a negative impact on human health and on ecology. Our present study demonstrates the principle possibility of developing technology, that allows biosystems to develop tolerance to the toxic effects of hydrazine by applying electromagnetic fields. Before starting to work in this direction, we performed several primary model experiments with alloxan. Alloxan is a cytotoxic agent, mainly affecting beta-cells of the pancreas and caused type 1 diabetes.

In previous experimental work [Gariaev et al., 2007 (a)], it was noted that modulated broadband electromagnetic radiation (MBER) generated by a helium-neon laser and modulated by healthy pancreas and spleen tissue, affects the course of experimental diabetes in rats induced by intraperitoneal injection of alloxan in a dosage of 200 mg/kg of animal body weight. Exposure to MBER resulted in an increased life span, normalization of blood glucose levels, and facilitated the regeneration of pancreatic tissue, of the animals in the experimental groups compared with the control.

The goal of this present work is to assess the induced resistance effect of animals to alloxan under the condition of preliminary MBER treatment. A special laser with interconnected complementary orthogonal polarizations of the light beam was used for this purpose. Generation of the BER (broadband electromagnetic radiation) was conducted in accordance with Fabry-Perot interferometer's scheme, where the operational laser beam passed multiple times through thin freshly prepared sections of pancreas

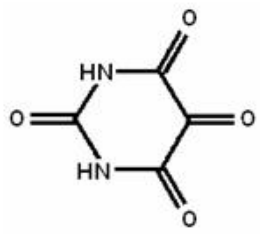
and spleen from a healthy newborn rat. We believe that preparations specifically modulate the laser beam in a way that the system reveals the following capabilities:

1) BER, that is emitted from the discharge interval of the He-Ne laser is reinforced;

2) BER is parametrically connected with the preparation-modulated laser beam and as a result it becomes highly biologically active;

3) biological effects can be observed at relatively long distances from the source of BER;

4) Electromagnetic transmission of directive genetic-metabolic information from biological-object-donor to the bio-recipient takes place. In this case, the information carrier is MBER (modulated broadband electromagnetic radiation).



Alloxan

The bio-structures, that can be probed by the laser beam in the given system, are: living and/or quasi-living organisms, for example, bacteria, viruses and active organs and tissues, metabolites and abiogenic substances.

RESEARCH METHODOLOGY. PHYSICS COMPONENT

To obtain broadband electromagnetic radiation, modulated by the biostructures, biotechnology is applied with a use of a helium-neon laser, developed by us earlier [Gariaev P.P., Tertyshniy G.G. 1999]. A Helium-Neon laser of 2mW power and a 632.8nm wavelength has two combined, orthogonal linear-polarized modes of emission, with a single-frequency for each of them. The laser beam scans the biological structures – in this case, freshly retrieved tissues of pancreas and spleen of a newborn rat of Wistar strain. Semitransparent preparations were placed onto glass microscope slides and then covered by a second glass slide and this "sandwiched" object was positioned in front of the optical axis of the laser. Adjustment of the glass containing the tissues was made to provide partial reflection of the modulated (by the tissues) laser beam back in to the laser resonator. This multiple-passage-mode allows the preparation to be an optical correlator [Mazur, Grachev, 1985] and therefore, affects distribution of the secondary modes of the laser emissions. Optical signals were registered and transmitted to an electronic circuit, which governs the generation regime of the laser, wherein, the frequency stabilization of the coherent radiation took place. In this mode the laser generates, apart from the red light, BER modulated by the preparations – that is – the MBER itself. Distance between the scanned preparation and the active laser element is 11cm.

RESEARCH METHODOLOGY. BIOLOGICAL COMPONENT

The experiments involved Wistar strain male rats matured to reproductive stage, 5-6 months old with average mass of 180-220 gram. Diabetes for the purposes of this experiment was induced by intro-peritoneal injection of alloxan in a dose of 200mg/kg body mass of the animal after a 24-hour fasting period with normal levels of blood glucose. The animals were divided into 4 groups:

- Group 1 control (n=20) – no BER irradiation;
- Group 2 (n=20) and Group 3 (n=20) – animals were subject to preliminary MBER;
- Group 4 (n=10) – placebo, where BER was not modulated by bio-structures and the laser beam passed through empty lab glasses without the pancreas and spleen tissue sections.

Group 2 rats were placed 20 meters from the source of MBER in the laboratory basement. In this group, alloxan diabetes was induced one month following from the last day of MBER treatment. Animals from Group 3 and Group 4 were placed 70 cm from the source of MBER. In these groups alloxan diabetes was induced one day after the last MBER treatment.

MBER treatment for Group 2 and Group 3 was carried out over 4 days, for 30 minutes each day, following the scheme: 10 minutes of MBER (modulated by samples of pancreas), 10 min of MBER (modulated by samples of spleen) and another 10 minutes of MBER (modulated by samples of pancreas).

Group 4 – placebo – was being irradiated by BER – not modulated by any samples (the laser beam passed through the empty lab glasses) for 30 minutes daily over 4 days.

Group 1 – control - was not subject to any radiation, neither BER nor was it MBER.

During the experiment, we assessed the general health conditions of the experimental animals, recorded the date of death

for the animals following the time of alloxan injection in all observed groups. The animals of Group 2 and Group 3 were observed for 1.5 months from the day of alloxan injection. When blood glucose level reached peak values following alloxan injection, eight rats (3 rats from Group 2 and 5 rats from Group 3) were assessed for reproductive function.

Measurements of blood glucose levels were performed by a *Ascensia Entrust* glucometer made by *Bayer*. The Measurement range of glucose levels were from 2.0 mmol/l up to 30.6 mmol/l. Measurements of glucose levels higher than 30.6 mmol/l were marked as *HI*.

Heart-, lung-, liver-, kidney-, spleen-, and pancreas- tissues were removed in order to perform microscopic investigation and histological analysis in:

Group 1 – control – day 3 and 4 after alloxan injection, corresponded to the highest death rate of the animals;

Group 2 and 3 on day 8 after the alloxan injection, and also on the 42nd day of the experiment after assessing reproductive function in male animals.

For histological analysis purposes, the tissues were fixed in 10% neutral formalin, dehydrated in spirits of increasing concentration and then sealed in paraffin wax. Paraffin sections of 5-7μm thick were obtained on a *Leica SM 2000R* microtome and were H&E (haematoxylin and eosin) stained, and then, analysed with a *Leica DMLS* microscope. We obtained video footage using *CCD*-cameras.

Statistical analysis was conducted on the experiment's results using *Stastica 6.0* statistical software and *MS-Excel*. The degree of accuracy (p) was determined with the Students T-Test, using confidence coefficient and number of degrees of freedom (1) according to the table. Calculations of all mathematical parameters were performed in compliance with commonly known formulas on a PC.

Research in this series of experiments revealed that

application of the indicated dose of alloxan in control and placebo groups triggered diabetes complicated with toxic damage of vital organs and systems. This led to a low survival rate of the animals in these groups. On the contrary, in Group 2 and 3 we observed increased tolerance to the destructive effects of alloxan in varying degrees.

Groups	Blood Glucose level over time, m mol /l			
	Day 1	Day 2	Day 3	Day 4
Group 1 (control), n=20	5,97±1,38 n=20	25,93±8,16** n=18	24,65±9,78** n=8	22,63±10,7** n=6
Group 2 (test), n=20	6,78±0,83 n=20	24,7±9,17*** n=20	18,99±8,0*** n=18	21,93±9,91*** n=18
Group 3 (test), n=20	5,23±0,69 n=20	8,00±6,32* n=20	6,44±4,39* n=20	4,88±2,90* n=20
Group 4 (placebo), n=10	4,9±0,85 n=10	26,97±6,85**** n=8	_ ^ n=1	_ ^ n=1

Table 1. Blood Glucose levels over time in animals after alloxan injection, dose of 200mg/kg of body mass.

* - blood glucose level in Group 3 on the 2nd, 3rd, and 4th day of initiating alloxan diabetes is reliably different ($p<0.05$) from the level of glucose in blood of the animals in Groups 1 and 2 on the 2nd, 3rd, and 4th day, and is also reliably different ($p<0.05$) from glucose level in blood from animals in Group 4 on day two;

** - blood glucose level in Group 1 on the 2nd, 3rd, 4th day is reliably different ($p<0.05$) from the initial level;

*** - blood glucose level in Group 2 on the 2nd, 3rd, 4th day is reliably different ($p<0.05$) from the initial level;

**** - blood glucose level in Group 4 on the 2nd day is reliably different ($p<0.05$) from the initial level;

^ - in Group 4 on the 3rd and 4th day of observation there was one surviving rat; the initial day was the day of alloxan injection.

Group 1 – control – survival rate after alloxan injection of the animals on day 2 was 55%, yet, by the day 4 it fell to 30% (Fig. 1). Glucose levels in Group 1 animals on day 2, 3 and 4 was reliably different ($p<0.05$) from the initial value (Table 1). Animals, dying in Group 1 (control) at terminal stage, were put down by

euthanasia (5 rats), organs were used for pathomorphological analysis. In Group 1 (control) there was no spontaneous reduction in glucose levels within the observation period. However, in this control group, there was one rat which expressed tolerance to alloxan, and its blood glucose level remained within physiological norms.

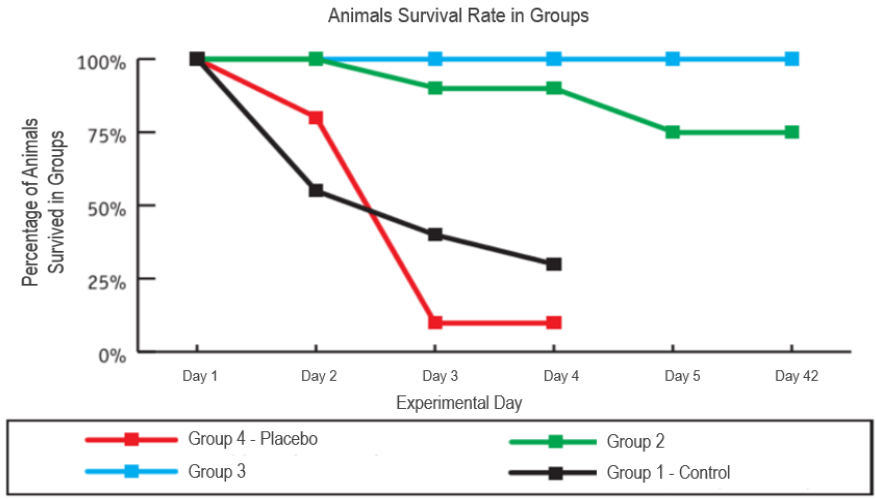


Fig 1. Animal survival rate (%) in researched groups during modeling of alloxan diabetes. All animals were injected with alloxan in a dosage of 200mg/kg of body mass. Group 1 – Control – BER and MBER treatments were not performed. Group 2 – MBER treatment was performed, animals were located 20 meters from the source of irradiation. Modeling of alloxan diabetes was performed 1 month after the last MBER treatment. Group 3 - MBER treatment was performed, animals were located 70 cm from the source of irradiation. Modeling of alloxan diabetes was performed 1 day after the last MBER treatment. Group 4 – Placebo – BER treatment was performed, not modulated by biostructures (laser beam was passing through empty lab glasses without pancreas and spleen preparations). Animals were located 70 cm from the source of irradiation. Modeling of alloxan diabetes was performed 1 day after the last BER treatment.

In Group 4 – placebo – after the preventive BER treatment, non-modulated by the tissues of pancreas and spleen, and subsequent alloxan injection in dose of 200 mg/kg, their blood glucose level on the 2nd day was reliably different from the initial

($p<0.05$). Animal survival rate on the 2nd day was 80% and dropped down to 10% on the 4th day. This was considerably different from what we observed in Group 2 and Group 3 and the survival rate was lower than in control Group 1 (30%). (Fig. 1)

Preventive MBER treatment significantly influenced alloxan diabetes progression in animals of Group 2 and Group 3 (Figs. 1, 2, 3, Table 1) and is accompanied by a cytoprotective effect. (Fig. 4). This was observed in both above mentioned Groups, despite of the fact, that diabetes modeling in Group 2 was induced a month after the last preventive MBER treatment, and animals during the treatment were located 20 meters away from the source of MBER in the laboratory basement.

Survival rate in Group 2 (n=20) reached 90% on the 3rd and 4th days after alloxan injection (Fig. 1) which is significantly different from survival rate in the control Group (30%) and in Group 4 (placebo) (10%). Wherein, it was marked by a reliable glucose level increase ($p<0.05$) in Group 2 animals on the 2nd, 3rd and 4th days in comparison to the initial value (Table 1). On the 4th day post alloxan injection, 13 animals in Group 2 (65%) showed blood glucose levels over 14.5 mmol/l, whereas 5 animals (25%) from the same group were observed with normal physiological levels of glucose (Fig. 2). Glucose levels in Group 2 on the 4th day was ($p<0.05$) significantly different from the initial level. (Table 1). By the 7th day post alloxan injection the survival rate in Group 2 decreased to 75% (out of 20 animals with severe hyperglycemia 5 animals died) and the remained at the same level up to the end of the observation period of one and a half months (Fig. 1). On the 8th day post alloxan injection, euthanasia was conducted on six animals from Group 2, the tissues of which were extracted for pathomorphological analysis. The other nine animals were observed for a period of 1.5 months. It is important to note that from day eight up to day 15 post alloxan injection, animals with severe hyperglycemia revealed a reduction in glucose level (Fig. 2). However, by day 18 post alloxan injection, 4 animals of Group 2 regained severe but stable hyperglycemia (more than 30.6 mmol/l) which remained for the entire observation period. The overall

health condition of these four animals was assessed as satisfactory. Similar results have been observed in our previous experiments [Gariaev, Kokaya et al, 2007]. The other 5 animals from Group 2 maintained glucose levels within physiological norms.

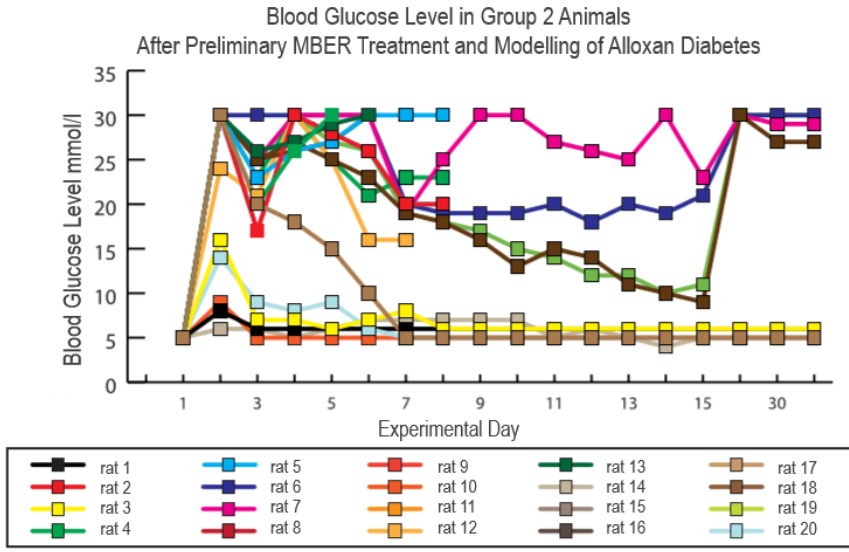


Fig 2. Preventive MBER treatment effect on alloxan induced diabetes progression of rates in Group 2. Animals were injected with alloxan with a dosage of 200mg/kg one month after preventive MBER treatment. Then irradiation was performed over four days each treatment being 30 minutes long. The distance from the radiation source was 20 meters. The animals were in the laboratory basement. MBER treatment scheme: 10 minutes of MBER (modulated by samples of pancreas), 10 min of MBER (modulated by samples of spleen) and 10 minutes of MBER (modulated by samples of pancreas). The initial day is the day of alloxan injection.

Reproductive function was assessed for three rats from Group 2 with severe hyperglycemia (glucose levels over 30.6 mmol/l). These animals gave birth to multiple healthy progeny. One and a half months after alloxan injection, tissues extracted from these animals were used for pathomorphological analysis.

A stronger effect from preventive MBER treatment was observed in Group 3, which was located 70 cm away from the source of radiation, and alloxan diabetes modeling was performed within

one day after the last MBER treatment (Fig. 1,3, Table 1). Every animal in this group survived. We observed 100% survival rate during the entire period. 90% of animals retained their normal physiological glucose level during the 1.5 months of observation, which is reliably different ($p<0.05$) from the control Group, Group 4, and Group 2. However, two animals from Group 3 on the day six of the experiment had glucose levels increase to over 20mmol/l with a subsequent reduction to normal level. On day eight of the experiment, six animals were euthanized for pathomorphological analysis. Reproductive function was assessed for five animals from Group 3. All the animals gave birth to healthy progeny. One and a half months later, tissues from six animals of this group were taken for pathomorphological analysis. Glucose was at normal levels. The health condition of all the animals from Group 3 was satisfactory during the whole observation period.

During histological analysis of the pancreas tissues from Groups 1, 2 and 3 several distinct features were observed (Fig. 4). The histological picture of the pancreas tissues from control group animals were characterized by clearly visible degenerative alterations of islets of Langerhans (Fig. 4b). The number and size of the islets were reduced, they were of unusual and irregular form. The quantity of β-cells was dramatically reduced, also in most of them, cytoplasmic vacuolation was also reduced, the nucleus size was decreased, chromatin condensation and in some cells karyopyknosis was observed. Lymphocyte infiltrate was detected around and inside of some of the islets.

In Group 2 on the 8th day, post alloxan injection, the histological picture of pancreas tissues was characterized by destructive changes of various degrees: the islets were of reduced size and of irregular form, β-cell reduction was observed, the total proportion of insulin apparatus in the islets was significantly reduced. Only a relatively small part of the islets apparatus maintained an intact structure (Fig. 4c).

The histological picture of pancreas preparations in Group 3 on the 8th day, post alloxan injection, was considerably different

from the control Group and Group 2. Along with the pathological changes in islets of Langerhans tissues of pancreas, also observed was a large quantity of islets of Langerhans, of large, medium and small sizes with lightened cytoplasm, of normal spherical form, with large round core nucleuses (Fig. 4e).

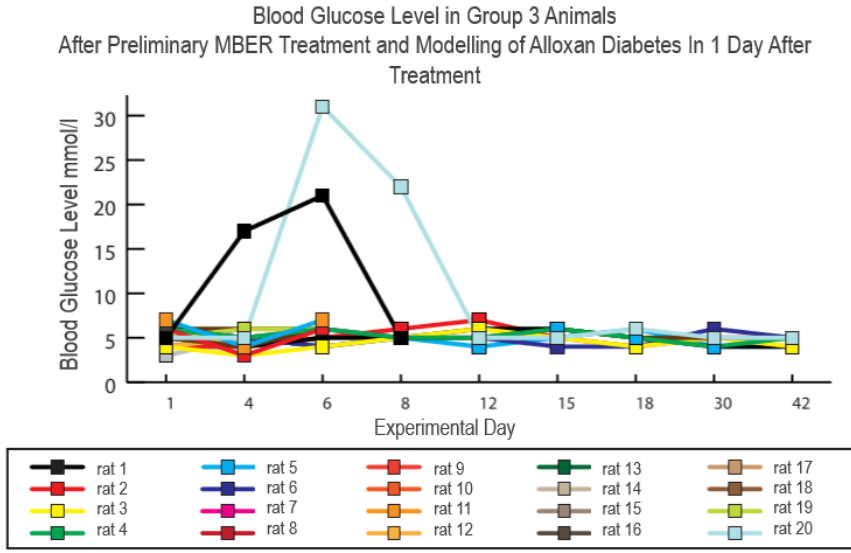
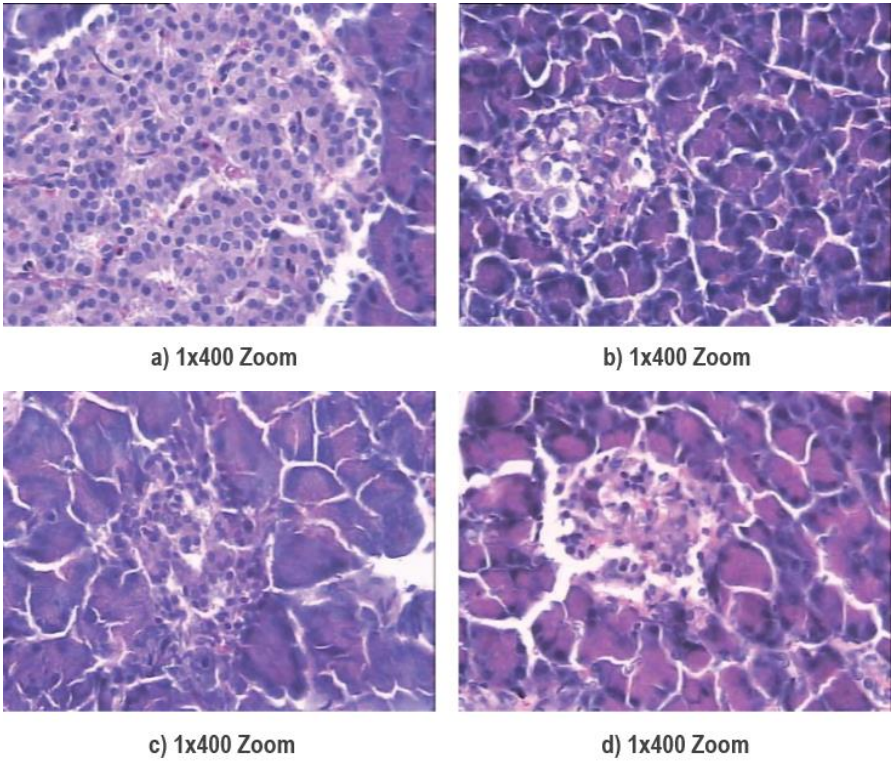


Fig 3. Preventive effect of MBER treatment on the progression of alloxan induced diabetes rates in Group 3. Animals were injected with alloxan in dosage of 200mg/kg one month after preventative MBER treatment. Irradiation was performed on four consecutive days for a duration of 30 minutes. The distance to irradiation source was 70 cm. The animals were located in the laboratory basement. MBER treatment scheme: 10 minutes of MBER (modulated by samples of pancreas), 10 minutes of MBER (modulated by samples of spleen) and 10 minutes of MBER (modulated by samples of pancreas). The initial day is the day of alloxan injection.

One and a half months after alloxan injection the histological picture of pancreas preparations in Group 2 was also characterized by degenerative changes in the islets of Langerhans apparatus (Fig. 4d)

As opposed to Group 2 and control Group, the histological picture of the preparations in Group 3, one and a half months post

alloxan injection, was characterized by signs of hypertrophy and hyperplasia of the pancreas. Numerous islets of Langerhans of varying size and normal spherical form were noted (Fig. 4f). Attention was drawn to the large number of small islands and discrete agglomeration of β-cells, and the large islets of Langerhans contained increased numbers of β-cells, located very close to one another. The structure of the islets of Langerhans and separate β-cells was unchanged, nucleuses in the cells were large and round, with clearly visible nucleoli.



a) 1x400 Zoom

b) 1x400 Zoom

c) 1x400 Zoom

d) 1x400 Zoom

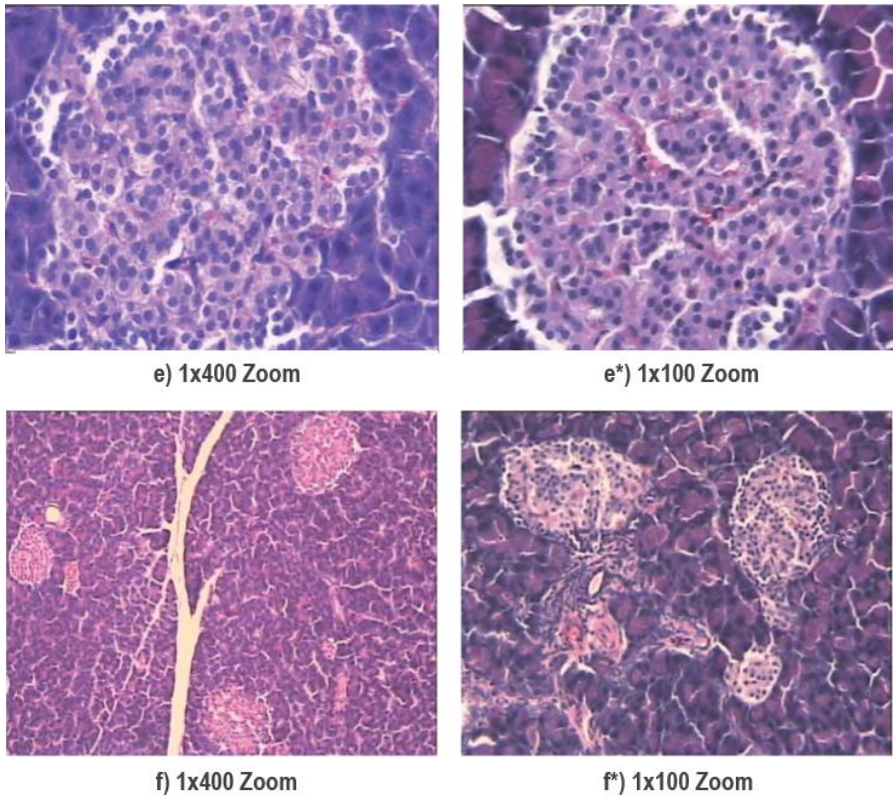


Fig 4. Pancreas tissue structure, islets of Langerhans: a – intact rats; b – Group 1 (Control), post 200mg/kg injection of alloxan; c – Group 2 on day eight post 200mg/kg injection of alloxan. One month prior to induction of alloxan induced diabetes the animals of this group had preliminary MBER treatment, being located 20 meters from the source of radiation in the laboratory basement; d – Group 2, 1.5 months post 200mg/kg injection of alloxan. One month before induction of alloxan diabetes the animals of this group had preliminary MBER treatment, being located 20 meters from the source of radiation in the laboratory basement; e – Group 3 on the day eight post 200mg/kg injection of alloxan. One day before induction of alloxan diabetes the animals of this group had preliminary MBER treatment, being located 70 cm from the source of radiation; f – Group 3, 1.5 months after 200mg/kg injection of alloxan. The animals of this group had preliminary MBER treatment at the distance of 70m from the source of irradiation. Zoom 1x400, Zoom 1x100, H&E stained.

It may be stated, that a positive effect was observed for preventive MBER treatment in Groups 2 and 3. Differences in the dynamics of blood glucose level and survival rates of the animals in these two groups point to correlation between the length of MBER treatment and induction of the alloxan diabetes. A biological protective effect by the long-range operation of MBER treatment, discovered in our previous experiments [Gariaev, Kokaya et al, 2007] was also confirmed in this series of experiments. This effect is revealed by blood glucose level dynamics in Group 2, as well as by the very fact of animal survival in this group in comparison with placebo and control groups. Despite of a significant ($p<0.05$) increase in glucose level in the animals of Group 2 compared to the initial value, and despite of the absence of any reliable differences in the glucose levels in Groups 1 and 2 on the 2nd, 3rd and 4th day post alloxan injection, the survival rate of animals in Group 2 was high. Severe hyperglycemia in 20% of the animals in this group did not lead to their death and the animals were in a satisfactory health condition for the entire observation period. The MBER treated animals in Group 3 developed tolerance to alloxan, and their blood glucose levels were within physiological norms for the entire observation period (and were reliably different ($p<0.05$) from data in Groups 1, 2 and 4). The survival rate in Group 3 was 100%. Analyzing the histology of pancreas preparations in different groups, one can state that preventive MBER treatment in Group 3 resulted not only in a cytoprotective effect on the cells of pancreas, but also encouraged hypertrophy and hyperplasia processes within it, which obviously had a compensatory nature. The present experimental results comply with the results of our previous experiments conducted earlier [Gariaev, Kokaya et al, 2007].

Thus, three phenomena of MBER treatment on animals with alloxan diabetes were discovered:

Firstly – the factor of survival with severe hyperglycemia during prolonged period of observation with preserved reproductive functions in animals;

Secondly – revealed in the previous experiment and once

again confirmed in the present one, that MBER encourages pancreas regeneration in sick animals *in situ*;

Thirdly – preliminary treatment of animals with MBER facilitates development of tolerance to alloxan.

Observed effects are related to the fundamental problem of "recording" and "transmission" of the electromagnetic component of genetic information during the post-embryonic growth with wave processes in the genome and the entire organism. MBER, parametrically connected with preparation-modulated photons, probably represents a carrier and transmitter of the bio-preparations information to the target biosystem, where the biosystem is able to addressably receive such information as a strategic directive. Apparently, MBER is a wave trigger, that initiates "standby" regenerative morphogenetic processes, information about which is contained in the genomes of every cell. Quantum mechanisms of the MBER effect on embryonic and post-embryonic processes remain unknown, although some ideas in this respect have been expressed in our earlier works [Gariaev, 1994; Gariaev, 1997; Prangishvili, Gariaev and et al, 2000 (b); Gariaev et al, 2001; Gariaev, 2003] and are being further developed currently. As for the protective and cytoprotective action of MBER, this is a very promising field with sound perspectives.

It is very likely that a factor of "weak influence" [Chukova, 2002] plays a specific role in the discovered protective-regenerative manifestations. In this respect it can be assumed that the discovered by us effects have endoergic character, when even weakly absorbed energy of coherent polarized laser irradiation feeds the increase of free Gelmgolc energy accumulated in chemical bonds of pancreas and spleen preparations metabolites. For example, the atoms of informational macro-molecules (DNA, RNA and proteins), while absorbing light, along with the energy of light quanta also gain their momentum of the motion quantity, which creates an inverse population of nuclear Zeeman levels (see Zeeman effect). This is a "chemical polarization" of the nucleuses. Thus, biochemical reactions in preparation, initiated by the polarized

laser irradiation, are able to generate electromagnetic radio fluctuations. In this situation pancreas and spleen preparations take the role of a molecular radio station, where every type of molecule has its own characteristic frequencies. And those frequencies can be amplified thanks to stochastic resonance due to the presence of broadband electromagnetic radiation of the laser gas discharge in the experiment.

Based on obtained experimental data, we propose to create a technology, that will allow development of animal tolerance towards the toxic effects of Hydrazine. We suppose that tolerance to Hydrazine and to many other toxic substances can be developed by affecting the strategic metabolic vectors, where the most important ones are the functions of genetic apparatus on the quantum level.

ADDITIONAL THEORETICAL MODELS

The obtained data has wider implications than demonstration of the capabilities of a possible wave defensive antidote-effect and require theoretical consideration since they relate to strategic (quantum) mechanisms of multicellular biosystems' genetic apparatus operation. We propose three formalized hypotheses of the wave processes for "reading or scanning" genetic-metabolic wave information from donor-bio-structures, remote addressed transmission of this information, and introduction of this information into the biosystem-acceptor and management of the biosystem's metabolism.

1. Endogenous polarization-holographic processes in biosystems

Wave informational scenarios – unfolding in the biosystem itself (as well as during their scanning by the laser beam) at the initial phase, occur at photon level. Let's consider this level in more detail. In our previous works [Prangishvili, Gariaev et al., 2000(a); Prangishvili, Gariaev et al., 2000(b)] we presented two- and three-dimensional models of biohолographic management for building the spatial structure of multicellular organisms during embryogenesis. From first sight, under relatively stationary conditions in the biosystems (final phases of morphogenesis), these models are quite realistic. However, in living organisms, statics and dynamics are paradoxically intertwined. An adult organism is relatively static spatially on the macroscopic scale, and significant changes on this level only are apparent at the stages of deep aging. This "relatively static" condition is provided through the internal space-time dynamics of metabolic processes at micro levels of biosystems organization. This is so, because metabolic processes are a mobile aggregate of bio-chemical-bio-physical space-time transformations of the microstructure of the organism. Taking into account non-stationary nature of biosystem's structure, we propose a more

advanced model of endogenous informational polarized-holographic directive processes in multicellular organisms, which mainly take place at the genome level. The model reflects the bioholographic aspect of metabolism in general and therefore, includes bio-morphogenesis as its specific case. The model utilizes existing physics-mathematical formalism for polarization holography, yet extrapolates it onto probable endogenic similar processes in the genetic apparatus of multicellular organisms.

The model also is founded on our experiments using a special double-polarized He-Ne laser (λ=632.8nm) with two orthogonal, interlinked optical modes, this was mentioned earlier. When the laser beam of a such quantum generator interacts with biological-tissues in the mode of dynamic holography of converging beams, previously unknown information about dynamic spinning-oscillating processes at optical and atomic-molecular levels is being simultaneously read and recorded. The data obtained in this fashion about genetic structures and/or living cells is of a special interest. All informational structures of an organism, including DNA, RNA and proteins, are optically active, e.g. they are capable of spinning the light polarization plane, and they are dichroic – there is a difference between absorption of right-hand- and left-hand-polarized light. Modulations of polarization that correlate with the structural-functional condition of any metabolite, represent a uniqueness in their capacity for storage of information about metabolism and its dynamics. At the same time, they represent a channel of intercellular photonic bio-linguistic contacts. Such peculiarities of processes of polarized-holographic nature, apparently, are inherent to genome operation as a biocomputer. The above makes it possible to modulate these processes with the above-mentioned laser. This laser can perform polarized-holographic recording, scanning, remote transmission and "injection" of wave directive genetic-metabolic information from one biosystem to another. Besides, such a laser performs a conversion of photons, scanning the biosystem, into a broadband electromagnetic spectrum with frequencies from 2ω to 0, according to mechanisms of photons localization - delocalization. Wherein,

obviously, the quantum nonlocal (teleportation) polarization connection is preserved across the whole spectrum of frequencies, including radio waves. Using such a laser as a reading-transmitting photon-radio-wave system, imitating similar wave biocomputer linguistic nonlocal processes of intercellular communication, facilitated the distant wave transmission of directive genetic-metabolic information from donor's biosystems to recipient's biosystems (the so-called addressed transmission). In light of this fact, it seems important to propose more advanced formalism of bio- linguistic photon-polarization-holographic processes in the chromosome apparatus of higher biosystems, especially since we know that radio-wave equivalents of these processes have pronounced morphogenetic potencies.

Let's record a vector diffraction Kirchhoff's integral in paraxial approximation, which describes a wave field, for instance a photon field, formed by a non-stationary fragment of a biosystem. These coherent photon fields may radiate from the liquid crystal continuum of a chromosome (LCCC) *in vivo*. This type of radiation may be expressed by the following equation:

$$E_{ob}(x,y,z,\omega,t) \approx \frac{i}{2\pi c} \iint\limits_{S_0 T_0} \frac{\omega}{r} E_{ob}(x_0,y_0,z_0,t_0) exp\omega \left[(t-t_0) - \frac{1}{c}\right] dt_0 dS_0 \qquad (1)$$

where $\boldsymbol{c}$ — speed of light; $\boldsymbol{\omega}$ — frequency; x_0, y_0, z_0, t_0 and x, y, z, t – space-time coordinates of a LCCC's point and an observation point, respectively; $\boldsymbol{r}$ -distance between these points; $\boldsymbol{S_0, T_0}$ - time-space interval, occupied by LCCC; $\boldsymbol{dS=dx_0, dy_0}$.

In equation (1) $\boldsymbol{E_{ob}\ (x_0,\ y_0,\ z_0,\ t_0)}$ represents the distribution of field amplitude of LCCC. This field is present for every polarization mode which are orthogonal and are independent until a turn occurs in their planes from their initial positions of vectors of median frequency waves of $\boldsymbol{\omega_0}$ (which are polarized mono-frequency waves, slightly shifted by frequency in relation to one another), propagating along $\boldsymbol{z}$ axis with Jones vector. Remember, chromosomes are characterized by high optical activity, expressed by optical spin dispersion and spherical dichroism that is a

prerequisite for this formalism.

$$E_0 = E_{0x} exp - \frac{i\omega_0 z}{c}\begin{pmatrix}1\\ \iota\varepsilon\end{pmatrix}, \quad 0 \le \varepsilon = \frac{E_{0y}}{E_{0x}} \le 1 \tag{2}$$

Field $\boldsymbol{E_0}$ passes via non-stationary fragment of LCCC with Jones matrix.

$$M_{ob}(x_0, y_0, z_0, t_0) = \begin{pmatrix} m_{11}(x_0, y_0, z_0, t_0) & m_{12}(x_0, y_0, z_0, t_0) \\ m_{21}(x_0, y_0, z_0, t_0) & m_{22}(x_0, y_0, z_0, t_0) \end{pmatrix}$$

For simplification, we will consider that non-stationary LCCC is not a function of the frequency of translucent light.

Both polarization modes of coherent light are depolarized by the gene-linguistic non-stationary nature of LCCC (discussed above) and are partially elliptically polarized. At the same time, they may interfere with formation of speckle patterns, and their total intensity is transferred from one mode to another by means of an earlier postulated way [Prangishvili, Gariaev et al., 2000(a)]. This in turn, leads to modulation of radio waves, formed from chromosomal photons by the mechanism of their delocalization [Prangishvili, Gariaev et al., 2000(b)].

Immediately behind the object, modified Johns' vector of orthogonally polarized passed waves may be represented in a form of partially coherent orthogonal components of elliptical polarization:

$$E_{ob}(x_0, y_0, z_0, t_0) = [E_{Ax} M_{ob}(x_0, y_0, z_0, t_0)\begin{pmatrix}1\\ i\varepsilon\end{pmatrix} E_{By} M_{ob}(x_0, y_0, z_0, t_0)\begin{pmatrix}i\varepsilon\\ 1\end{pmatrix}] exp i\omega t_0 \tag{3}$$

where $\varepsilon = {}^{E_{Ay}}\!/_{E_{Ax}} = {}^{E_{Bx}}\!/_{E_{By}}$; $0 \le \varepsilon \le 1$; $\oplus$ - a sign of non-coherent sum of amplitudes, which is introduced for partially polarized light; $\boldsymbol{E_A}$ – complex amplitude of one basis component; $\boldsymbol{E_B}$ – complex amplitude of another basis component, orthogonal to the previous one and non-coherent.

In a biosystem in the composition of LCCC (with only one

polarization component) as a hypothetical we use a carrying wave, which passed, for instance, through an infinitely narrow time shutter lock, possessing $\boldsymbol{\delta}$ - like characteristic of time transmission. Such a shutter lock completely depolarizes the initially polarized wave. The resulting wave, passed behind the shutter lock, is characterized by a continuous spectrum in the whole range with evenly distributed spectral density, and the modified vector of the carrying wave has a form of orthogonal basis of elliptical polarization:

$$E_{0\text{п}} = \left[E_{0x} expi\varphi \begin{pmatrix} 1 \\ \iota\varepsilon \end{pmatrix} E_{0x} expi\left(\phi - \frac{\pi}{2}\right)\begin{pmatrix} \iota\varepsilon \\ 1 \end{pmatrix}\right] expi\omega\left(t - \frac{1}{c}z\right) \qquad (4)$$

where $\varepsilon^{E_{0y}}\!/_{E_{0x}}$, E_{0x}, E_{0y} - amplitudes; $\boldsymbol{\phi}$, $\boldsymbol{\varphi}$ – initial phases of two mutually non-coherent components.

For our case, where sometimes both polarization components are employed, the above assumption about the infinitely narrow time shutter lock is not necessary, and the sum of the field in the plane of the polarized hologram takes the following form:

$$E_\Sigma(x, y, z, t) = E_{ip} + E_{ob} \qquad (5)$$

$$E_\Sigma(x, y, t, z) = \{E_{0x} expi\varphi\ expi\omega\left(t - \frac{1}{c}z\right) + \frac{i}{2\pi c}\iint\limits_{S_0 T_0} \frac{\omega}{r}$$

$$E_{Ax} M_{ob}(x_0, y_0, z_0, t_0) expi\omega\left[(t - t_0) - \frac{1}{c}r\right] dS_0 dt_0\}\begin{pmatrix} 1 \\ \iota\varepsilon \end{pmatrix}$$

$$\{E_{0x} expi\left(\phi - \frac{\pi}{2}\right) expi\omega\left(t - \frac{1}{c}z\right) + \frac{i}{2\pi c}\iint\limits_{S_0 T_0} \frac{\omega}{r} E_{By}$$

$$\cdot M_{ob}(x_0, y_0, z_0, t_0)\ expi\omega\left[(t - t_0) - \frac{1}{c}r\right] dS_{0_0} dt_0\}\begin{pmatrix} \iota\varepsilon \\ 1 \end{pmatrix}$$

The real part of equation (5) represents the tension of the electrical vector of the aggregate wave

$$Re(E_\Sigma) = p cos\omega t + g\ sin\omega t \qquad (6)$$

Parameters of the ellipse $\boldsymbol{p}$ and $\boldsymbol{g}$ are defined via ellipse components of polarization of each basis $\boldsymbol{A}$ and $\boldsymbol{B}$,

$$p = Re(E_\Sigma)_A \oplus \mathrm{Re}(E_\Sigma)_B = p_A \oplus p_B \qquad (7)$$
$$g = Im(E_\Sigma)_A \oplus Re(E_\Sigma)_B = p_A \oplus g_B$$

Endogenous biological registration of the aggregate wave field (5) pertaining to LCCC as a basic element of the DNA-wave biocomputer, implies the presence of a polarization-sensitive medium in organisms, which is spectrally non-selective across the whole range of active frequencies (like non-stationary fragments of a biological object, for instance LCCC).

The polarization characteristics of the inducing light in the light-sensitive registering medium of LCCC allow photo-anisotropy and photo-gyrotropy. To describe the vector photo-response of polarized-sensitive media in the papers functions of isotropic $\boldsymbol{s}$, anisotropic $\boldsymbol{v}_L$ and gyrotropic $\boldsymbol{v}_G$ reactions are introduced, which are constant for all frequencies of active radiation. Using Johns' matrices and rules of their formation for cases of partially polarized inducing radiation, for the resulting Johns' matrix we get:

$$M = exp(-2i\chi dn_0) \cdot \begin{pmatrix} M_{11} & M_{12} \\ M_{21} & M_{22} \end{pmatrix}, \qquad (8)$$

where

$$M_{11,22} = 1 - \frac{i\chi d}{2n_0}[s(I_1 + I_2)_A + s(I_1 + I_2)_B \pm v_L cos20_A \cdot$$
$$\cdot (I_1 - I_2)_A \pm v_L cos20_{B\cdot}(I_1 - I_2)_B]$$
$$M_{12,21} = -\frac{i\chi d}{2n_0}[v_L sin20_{A..}(I_1 - I_2)_A + v_L sin20_B \cdot$$
$$\cdot (I_1 - I_2)_B \mp iv_g(I_\pm - I_\mp)_A \mp iv_g(I_\pm - I_\mp)_B]$$

In (8) $\chi = {}^{2\pi}/_{\lambda}$, λ is the length of the initial translucent endogenous wave (for instance, photonic radiation of chromosomes *in vivo*); d– thickness of registering LCCC; $\boldsymbol{n}_0$ – complex coefficient

of diffraction of LCCC in its original, non-irradiated state; $(I_1 + I_2)_A$ and $s(I_1 + I_2)_B$– first Stokes' parameter; $(I_1 - I_2)_A$ and $s(I_1 - I_2)_B$– second Stokes' parameter; $(I_\pm - I_\pm)_A$ and $(I_\pm - I_\pm)_B$ – fourth Stokes' parameter for $\boldsymbol{A}$ and $\boldsymbol{B}$ components; $\boldsymbol{\theta}_A$ and $\boldsymbol{\theta}_B$ – orientational angles of the large ellipse's polarization axis for $\boldsymbol{A}$- and $\boldsymbol{B}$- components, respectively measured counter-clockwise in relation to $\boldsymbol{x}$ axis.

Expressing in (8) Stokes' parameters via $\boldsymbol{p}_A$, $\boldsymbol{p}_B$, $\boldsymbol{g}_A$, $\boldsymbol{g}_B$, for holograms' matrix represented as a sum of the three matrices, in the whole range of active frequencies we will get:

$$M = M_0 + M_{-1} + M_{+1}, \tag{9}$$

where $\boldsymbol{M}_0$ – matrix describing non-diffracted beams;

$$M_0 \approx exp(-2i\chi dn_0)\left[1 - \frac{i\chi ds}{n_0}(1+\varepsilon^2)E_{0x}^2\right]\begin{pmatrix}1 & 0\\ 0 & 1\end{pmatrix}; \tag{10}$$

$\boldsymbol{M}_{-1}$ – matrix describing virtual image;

$$M_{-1} \approx \frac{\chi d}{4\pi c n_0} exp(2i\chi dn_0)\begin{pmatrix}(M_{-1})_{11} & (M_{-1})_{12}\\ (M_{-1})_{21} & (M_{-1})_{22}\end{pmatrix} \tag{11}$$

with matrix elements

$$(M_{-1})_{11,22} = \iiint\limits_{S_0T_0\Omega} \frac{\omega}{r}\{E_{Ax}[(s \pm v_L)(m_{11} + i\varepsilon m_{12}) - i\varepsilon(s \mp v_L)(m_{21} + i\varepsilon m_{22})]E_{0x}exp - i\varphi + E_{By}$$
$$\times [(s \mp v_L)(m_{22} + i\varepsilon m_{21}) - i\varepsilon(s \pm v_L)(m_{12} + i\varepsilon m_{11})]E_{0x}exp - i\left(\phi - \frac{\pi}{2}\right)\}$$
$$expi\frac{\omega}{c}zexp - i\omega\left(t_0 + \frac{1}{c}r\right)d\omega dt_0 dS_0,$$

$$(M_{-1})_{12,21} = \iiint\limits_{S_0T_0\Omega} \frac{\omega}{r}\{E_{Ax}[(v_L \pm v_G)(m_{21} + i\varepsilon m_{22}) - i\varepsilon(v_L \mp v_G)(m_{11} + i\varepsilon m_{12})]$$
$$\times E_{0x}exp - i\varphi + E_{By}[(v_L \mp v_G)(m_{12} + i\varepsilon m_{11}) - i\varepsilon(v_L \pm v_G)(m_{22} + i\varepsilon m_{21})]$$
$$\times E_{0x}exp - i\left(\phi - \frac{\pi}{2}\right)\}expi\frac{\omega}{c}\zeta exp - i\omega\left(t_0 + \frac{1}{c}r\right)d\omega dt_0 dS_0;$$

$\boldsymbol{M}_{+1}$ – matrix describing real image

$$M_{+1} \approx -\frac{\chi^d}{4\pi c n_0}\exp(2i\chi d n_0)\begin{pmatrix}(M_{+1})_{11} & (M_{+1})_{12}\\ (M_{+1})_{21} & (M_{+1})_{22}\end{pmatrix} \quad (12)$$

with matrix elements

$$(M_{+1})11,22 = \iiint\limits_{S_0T_0\Omega}\frac{\omega}{r}\{E^*_{Ax}[(s \pm v_L)(m^*_{11} - i\varepsilon m^*_{12}) + i\varepsilon(s \mp v_L)(m^*_{21} - i\varepsilon m^*_{22})]E_{0x}expi\varphi + E^*_{By}$$

$$\times [(s \mp v_L)(m^*_{22} - i\varepsilon m^*_{21}) + i\varepsilon(s \pm v_L)(i\varepsilon m^*_{11})]$$

$$\times E_{0x}\exp i\left(\phi - \frac{\pi}{2}\right)\}\exp - i\frac{\omega}{r}z\exp i\omega\left(t_0 + \frac{1}{c}r\right)d\omega dt_0 dS_0,$$

$$(M_{+1})_{11,22} = \iiint\limits_{S_{00}T_0\Omega}\frac{\omega}{r}\{E^*_{Ax}[(v_L \pm v_G)(m^*_{21} - i\varepsilon m^*_{22}) +$$

$$i\varepsilon(v_L \pm v_G)(m^*_{11} - i\varepsilon m^*_{12})]E_{0x}\exp i\varphi + E^*_{By}[(v_L \pm v_G)(m^*_{12} - i\varepsilon m^*_{11}) + i\varepsilon(v_L \mp v_G)(m^*_{22} - i\varepsilon m^*_{21})]$$

$$\times E_{0x}\exp i\left(\phi - \frac{\pi}{2}\right)\}\exp - i\frac{\omega}{c}z\exp i\omega\left(t_0 + \frac{1}{c}r\right)d\omega dt_0 dS_0.$$

Here $\boldsymbol{m}_{ij} \equiv \boldsymbol{m}_{ij}(\boldsymbol{x}_0, \boldsymbol{y}_0, \boldsymbol{z}_0, \boldsymbol{t}_0)$ – elements, depending on coordinates and time of the 2D matrix of non-stationary LCCC fragment. Under the condition of rationality in biological objects, interrelation between functions of media reaction may be the following:

$$s = v_L \qquad v_L = -v_G, \quad (13)$$

and expressions (11) and (12) can be simplified. In publication it is noted, that conditions in (13) are met with a high precision for a very large class of polarized-sensitive media.

Provided that conditions in (13) are met, $\boldsymbol{M}_{-1}$ and $\boldsymbol{M}_{+1}$ matrices take the following form:

$$M_{-1} \approx \frac{\chi d v_L}{2\pi c n_0}\exp(-2i\chi d n_0)\iiint\limits_{S_0T_0\Omega}\frac{\omega}{r}M_{ob}P\exp - i\omega\left[t_0 + \frac{1}{c}(r - z)\right]d\omega dt_0 dS_0, \quad (14)$$

$$M_{+1} \approx \frac{\chi d v_L}{2\pi c n_0}\exp(-2i\chi d n_0)\iint_{S_0T_0\Omega}\frac{\omega}{r}P^*M^*_{ob}\exp i\omega\left[t_0 + \frac{1}{c}(r - z)\right]d\omega dt_0 dS_0, \quad (15)$$

In (14) and (15) LCCC matrix $\boldsymbol{M}_{ob}$ is marked, and $\boldsymbol{P}$ represents the following matrix

$$P = \begin{pmatrix}\alpha + \varepsilon^2 b & -i\varepsilon(a - b)\\ i\varepsilon(a - b) & \varepsilon^2 a + b\end{pmatrix},$$

where

$$a = E_{Ax}E_{0x}exp - i\varphi$$

$$b = E_{By}E_{0x}\exp - i(\emptyset - \frac{\pi}{2});$$

$\boldsymbol{P}^*$ $\boldsymbol{M}_{ob}{}^*$ – Hermitian adjoint matrices.

Under condition of endogenous illumination of the received hologram by reconstructing non-polarized waves with complex amplitudes

$$E'_{0x}expi\varphi', E'_{0y}expi\emptyset' \left(\varepsilon' = {E'_{0y}}\Big/{E'_{0x}}\right)$$

endogenous or exogenous in relation to the biosystem, and frequency $\boldsymbol{\omega}$'

$$E_{rec} = \left[E'_{0x}expi\varphi' \begin{pmatrix} 1 \\ i\varepsilon' \end{pmatrix} \oplus E'_{0x}expi\left(\emptyset' - \frac{\pi}{2}\right)\begin{pmatrix} i\varepsilon' \\ 1 \end{pmatrix}\right] expi\omega'\left(t' - \frac{1}{c}z\right) \qquad (16)$$

the wave passed through the biological hologram is formed as follows:

$$E(x', y', z', t') = \frac{i}{2\pi c}\int_s \frac{\omega'}{r'} M E_{rec}\ exp - i\frac{\omega'}{c}r'dS \qquad (17)$$

where $\boldsymbol{S}$ – fragment size of LCCC's hologram; $\boldsymbol{r'}$– distance between the point on the hologram surface and observation point.

Then, successively substituting in (17) expressions for matrices (10), (14) and (15), let's define null, virtual and real images, formed by the hologram. And only now determine, what endogenous or/and exogenous wave is necessary for the organism to utilize as to reconstruct the required fragment of the wave image in a virtual form. To achieve this, it is necessary to determine their own vectors and corresponding to them values of $\boldsymbol{P}$ matrix. It turns out that with a precision of up to a constant multiplier, the vectors of $\boldsymbol{P}$ matrix are in essence $\begin{pmatrix} \mathbf{1} \\ \boldsymbol{i\varepsilon} \end{pmatrix}$ and $\begin{pmatrix} \boldsymbol{i\varepsilon} \\ \mathbf{1} \end{pmatrix}$ with their respective values $(\mathbf{1} + \boldsymbol{\varepsilon^2})\boldsymbol{a}$ and $(\mathbf{1} + \boldsymbol{\varepsilon^2})\boldsymbol{b}$.

It follows that reconstruction should be performed by a wave identical to the one used during recording by the carrying wave. As apparently, in biosystems at LCCC level recording and reconstruction happens either simultaneously or in accordance with the last condition, then the reconstructed virtual image depiction corresponds to the real one and is not subject to any distortions. The latter is of principle importance for preservation of the wave image-vectors of morphogenesis, despite of the biosystem's mobility in general as well as its LCCC in particular. Nonetheless, the non-stationary nature of images will appear, though over long time periods during organism aging and its pathological states, for instance in the case of carcinogenesis.

For a wave passed without diffraction, the null image has the following form:

$$E_0 \approx \exp(-2idn_0X)\left[1-\frac{idsX}{n_0}(1+\varepsilon^2)E_{0x}^2\right][E_{0x}expi\varphi\begin{pmatrix}1\\ i\varepsilon\end{pmatrix} \oplus E_{0x}expi\left(\emptyset-\frac{\pi}{2}\right)\begin{pmatrix}i\varepsilon\\ 1\end{pmatrix}]\ expi\omega(t'-\frac{1}{c}z'), \tag{18}$$

where the virtual and real images are presented as:

$$E_{-1}(x',y',z',t') \approx \frac{idv_L\chi}{(2\pi c)^2 n_0}\exp(-2idn_0\chi)E_{0x}^2(1+\varepsilon^2) \tag{19}$$

$$\int_S\int_{S_0}\int_{T_0}\int_\Omega \frac{\omega^2}{r'r}\left[E_{Ax}M_{ob}(x_0,y_0,z_0,t_0)\begin{pmatrix}1\\ i\varepsilon\end{pmatrix}\oplus E_{by}M_{ob}(x_0,y_0,z_0,t_0)\begin{pmatrix}i\varepsilon\\ 1\end{pmatrix}\right]\times$$

$$\times \exp i\omega\left[(t'-t_0)-\frac{1}{c}(r'+r)\right]d\omega dt_0 dS_0 dS,$$

$$E_{+1}(x',y',z',t') \approx -\frac{idv_L\chi}{(2\pi c)^2 n_0}\exp(-2idn_0\chi)E_{0x}^2\int_S\int_{S_0}\int_{T_0}\int_\Omega \frac{\omega^2}{r'r}[P_A^*M_{ob}^*(X_0,y_0,z_0,t_0)\begin{pmatrix}1\\ i\varepsilon\end{pmatrix}\oplus P_B^* \tag{20}$$

$$\times M_{ob}^*(X_0,y_0,z_0,t_0)\begin{pmatrix}i\varepsilon\\ 1\end{pmatrix}]\exp i\omega\left[(t'+t_0)-\frac{1}{c}(r'-r+2z)\right]d\omega dt_0 dS_0 dS,$$

where

$$P_A^* = \exp i\varphi P^*,$$

$$P_B^* = \exp i\left(\phi-\frac{\pi}{2}\right)P^*$$

Integrals, pertaining to (19) and (20), are solved in a linear approximation for distances $\boldsymbol{r}$ and $\boldsymbol{r}'$ and for infinitely large areas of integration S, S_0, T_0, Ω. Integrals S and Ω have a character of spatial and time $\boldsymbol{\delta}$-function respectively. The final expressions lead to the following equations for the formed space-time polarized hologram. For the formed virtual image under condition of $z' = z_0$ from (19) we have:

$$E_{-1}(x', y', z', t') \approx -\frac{2\pi i\chi dv_L}{n_0}\exp(-2i\chi dn_0)E_{0x}^2(1+\varepsilon^2)[E_{Ax}M_{ob}(x', y', z', t') \times \begin{pmatrix}1\\ i\varepsilon\end{pmatrix} \oplus E_{by}M_{ob}(x', y', z', t')\begin{pmatrix}i\varepsilon\\ 1\end{pmatrix}]. \quad (21)$$

An analysis of the last equation shows that - with precision up to the multiplier - it depicts complete reconstruction of space-time structure as well as polarization characteristics of the field of its non-stationary object wave for example, via LCCC. It is convenient for the biosystem to use this structure-image to organize itself in time and space, as this structure-image fully preserves the original calibrating scale without any distortions imposed by the dynamic nature of the biosystem and reproduces it in adequate dimensions for a developing or an adult organism. Reconstructed wave gradients of scanned polarization holograms direct four-dimensional organization of metabolic flows and morphogenetic movements of cells and tissues during embryogenesis as well as partial regeneration of biosystems in case of damage.

Applying equation (20) for the real image where $z' = 2z - z_0$ we have:

$$E_{+1}(x', y', z', t') \approx -\frac{2\pi i\chi v_L}{n_0}\exp(-2i\chi dn_0)E_{0x}^2[P_A^*M_{ob}^*(x', y', z', \frac{2z}{c} - t') \times \begin{pmatrix}1\\ i\varepsilon\end{pmatrix} P_B^*M_{ob}^*\left(x', y', z', \frac{2z}{c} - t'\right)\begin{pmatrix}i\varepsilon\\ 1\end{pmatrix}] \quad (22)$$

From equation (22) it follows that the image with pseudoscopic spatial structure of the objective fragment of the LCCC field is formed in a distance of $z' = 2z - z_0$, symmetrically to the virtual image (19) in relation to the hologram. Wherein, the circulation of its time profile is delayed. The delay is caused by the light passing the distance of $2z = z' + z_0$, which is equal to the distance from the point of observation to the point on the surface of the real image, with conversion of polarization state, determined by P_A^* and P_B^* types of matrices.

By polarized-holographic bio-management we imply endogenous or intentional (artificial) modification of a recipient's cellular structure and conditions as a result of directive holographic effects from a donor's side. In our case, a holographic signal, modulated by healthy cells of the donor, is transmitted and recorded onto recipient's diseased cells in the form of a hologram. Then, the process of management occurs as follows. In the beginning, the holographic image of donor's healthy cells is scanned from the recipient's modified cells by means of a regenerative wave. It is reconstructed as a terahertz wave diapason in a form of 3D image, encompassing every recipient's cell together with its content.

Mainly, there are two forms of regenerative wave sources. The first form is endogenous. In this instance the processes occur due to innate reserves, i.e. "internal" irradiation from the neighbouring cells. The second form is exogenous reconstruction, when the sources of irradiation are external. Both forms of sources "operate" in the recipient's cells and act simultaneously and continuously, regenerating and complementing the same image of donor's healthy cells over and over again. Growth and regeneration of recipient's diseased cells occur along the gradients of intensity of the reconstructed donor's cell image, using it as a "blueprint". Recipients' cells here play the role of a photographic film, on which a hologram of the healthy donor's cells is recorded. Processes of growth and regeneration, occurring similar to processes of photo-tropism, take some time. As a result, the recipient's "diseased" cells are partially converted to healthy and partially destroyed. Then, the

waste products are excreted from the recipient organism.

Thus, in the process of replacement of the recipient's "diseased" cells with healthy ones (analogous to those of donor's), polarized-holographic-management takes place, which is in effect "germination" of biomass of the recipient's diseased cells into the offered dynamic holographic form of healthy donor's cells. Hence, during this management process, the form and dynamic state of recipient's cells is gradually modified under the managing signal – "directive", obtained from the donor.

Needless to say, such a "directive" is much more complex than one in simple management systems. It sets spatial distribution of the terahertz signal, the gradients of which guide the growth and formation of live cells in the recipient. Therefore, the processes of growth and formation of recipient's cells occur in line with bio-chemical laws, which control their vital functions, and the "directive" signal programs the growth of the structure of the young healthy cells as well as programs the modulation of intracellular processes.

To give a more comprehensive description of the mechanism of internal operation of the holographic circular-polarized informational-laser transformation in live organisms, it is necessary to understand the basics of polarized-dynamic theory of holography and information exchange between live healthy donor-cells and all other cells, included in organs and tissues of the diseased organism. To provide these details, we refer to the studies of Denisyuk [Denisyuk, 1974], who developed the basics for registration and reconstruction of holographic construction of images of the material structures. We managed to prove experimentally, that besides image registration and reconstruction, there is a possibility for intracellular transformation of recipient's biological structures according to the scheme of reconstructed donor's image, that is recorded on the holographic structures of the recipient.

Transmission of modulated information from donor to recipient occurs by means of rectilinearly propagating longitudinal mutually interfering waves, carrying multilevel modulating

information. For short-distance transmission, we can use the notion of cellular nucleuses being – "optical-polarizers". For long-distance transmission, we can use the notion of the "quasi-lens" (see the previous chapter).

Let's look at the description of this process, proposed for the registration of color holograms without use of lasers [Alexandrov, 1998]. Adapting it to a biosystem, we will list the necessary conditions for realizing the non-coherent polarized-holographic management method. It is worth noting, that microscopic polarisers, i.e. cells' nucleuses, as well as optically active protein substances, which rotate the polarization plane of radiations passing through them, were discovered long ago during microscopic studies of such systems. These processes have been known to researchers for a long time [Bischof, 1995], however, until now this observed phenomenon was neither explained nor utilized.

Suppose that the light falls on the first intracellular polarizer and then passes through an optically active medium, for example, through a biological protein, at an angle of $\boldsymbol{\theta_1}$ from an arbitrary point of the biological donor-object. After passing through the second cellular polaroid, the light falls on the registering biological medium of the recipient.

After passing through the first polaroid, the wave amplitude can be written in the form $\boldsymbol{E_1 = A_1(\sin\beta_1 i + \cos\beta_1 j)}$, where $\boldsymbol{A_1 = A_1'\cos\varphi}$, $\boldsymbol{\varphi}$ - the phase of the wave; $\boldsymbol{A_1'}$- real amplitude of the light wave after passing through the polarizer ***P1;*** $\boldsymbol{\beta_1}$ - angle that determines the position of the first polarizer in the selected system of coordinates. Then, the light passes through optically active medium (protein) and its polarization plane rotates to an angle $\boldsymbol{\alpha}$, which is dependent on the refraction angle $\boldsymbol{\theta_2}$ at a fixed thickness $\boldsymbol{d}$ of optically active protein:

$$\alpha = \frac{bd}{\cos\theta_2} \qquad (3)$$

where $\boldsymbol{b}$ - the constant of polarization vector rotation. From this formula, it can be seen that rotation of the polarization vector does

not depend on the wavelength of the scanning wave (the formula does not include the wavelength $\boldsymbol{\lambda}$), but depends only on the degree of rotation activity of medium $\boldsymbol{b}$, its thickness $\boldsymbol{d}$ and its refraction angle $\boldsymbol{\theta_2}$.

In view of introduced indicators, the amplitude of the light wave takes the form:

$$\boldsymbol{E_2 = A_2[\sin(\alpha + \beta_1)i + (\alpha + \beta_1)j]}$$

where $\boldsymbol{A_2 = A_1\tau_1}$ - transmission coefficient.

After passing through the second biological polarizer, scalar wave amplitude in the plane of polarization has the form:

$$E = A_3[\sin(\alpha + \beta_1)\sin\beta_2 + \cos(\alpha + \beta_1)\cos\beta_2] = A_3\cos(\alpha + \beta_1 - \beta_2),$$

where $\boldsymbol{A_3 = A_2\tau_2, \tau_2}$ - transmission coefficient, $\boldsymbol{\beta_2}$ - angle that determines the position of the second polarizer in the selected system of coordinates.

Then, the light intensity is equal to

$$I = I_0 T\cos^2(\alpha + \beta_1 - \beta_2), \qquad (4)$$

where the $\boldsymbol{T}$ - transmission coefficient for the intensity, $\boldsymbol{I_0}$ - intensity of light, scattered by a point, located on the scanned biological donor-object.

Substituting (3) into (4) we obtain:

$$I = I_0 T\cos^2\left(\frac{bd}{\cos\theta_2} + \beta_1 - \beta_2\right). \qquad (5)$$

Analyzing the resulting equation (5), it can be noted that the law of the intensity distribution of the polarization fringes in this formula is similar to the well-known law of intensity distribution of the interference fringes in Gabor's zone plate patterns, i.e. it is an axial hologram of the object's point. Furthermore, the intensity value depends on the angle $\boldsymbol{\theta_2}$, and at $\boldsymbol{\theta_2 = const}$, and $\boldsymbol{I = const,}$ the very light intensity distribution should be in the form of alternating dark and light polarization rings with alternating period.

If we take into account that $\boldsymbol{\theta_2}$ depends on value of diffraction coefficient of the optically active medium (in our case cellular protein), we can write the value of $\boldsymbol{\cos\theta_2}$:

$$\cos\theta_2 = \frac{1}{n}\sqrt{n^2 - \sin^2\theta_1}. \tag{6}$$

Considering the above (4) let's rewrite (5) as follows:

$$I = I_0\cos^2\left(\frac{bdn}{\sqrt{n^2 - \sin^2\theta_1}} + \beta_1 - \beta_2\right).$$

Disregarding refraction, that is when $\boldsymbol{\theta_2=\theta_1}$, we get an equation for $\boldsymbol{\cos\theta_2}$:

$$\cos\theta_2 = \frac{L}{\sqrt{L^2 + r_2}}, \tag{7}$$

where $\boldsymbol{L}$ - the distance from the point of biological object (donor) to the hologram recording plane (recipient), and $\boldsymbol{r}$ - distance from the axial line, passing through the center of the hologram registrar to the target point hit by the beam, emanating from the biological donor-object.

Let's assume that the polarization elements are arranged in parallel, i.e., $\boldsymbol{\beta 1 = \beta 2}$. Then, substituting (6) into (4) we obtain:

$$I = I_0 T\cos^2\left(\frac{bd}{L}\sqrt{L^2 + r^2}\right). \tag{8}$$

The last expression shows that the law of distribution of light intensity in the recipient registration plane is a function that depends on the position of holographed point, located inside or on the surface of a biological recipient-object.

When the beam falls normally on the first polaroid $\boldsymbol{(\theta_1 = 0)}$ and the maximum intensity value is observed, the rotation angle of the second polaroid $\boldsymbol{\beta_2}$ must follow the equation $\alpha_0 - \pi m_0 = \beta_2 - \beta_1$. Here $\boldsymbol{\alpha_0 = bd}$ - angle of rotation of the light polarization when

normally falling beam passes through an optically active cellular protein. $\boldsymbol{m_0}$ - the number of rotations of the polarization plane by 180^0 when a normally falling beam passes through an optically active protein of recipient's cell. Wherein, the distribution of the intensity of light originating from a donor in the registration plane of the hologram, where the recipient is located, will take the form $I = I_0 t\, cos^2(\alpha - \alpha_0)$, where using the formula's (4) and (7), we obtain:

$$I = I_0 T\, cos^2\left[\frac{bd}{L}\left(\sqrt{L^2 + r^2} - L\right)\right]. \quad (9)$$

Inside the circle of radius $\boldsymbol{r}$ are located $\boldsymbol{N}$ light (or dark) rings, determined by the formula $N = \frac{bd}{\pi L}\left(\sqrt{L^2 + r^2} - L\right)$. Hence the $\boldsymbol{N}$th ring radius can be determined by the formula:

$$r = L\sqrt{\frac{\pi N}{bd}\left(\frac{\pi N}{bd} + 2\right)}.$$

For comparison let's introduce the intensity distribution in a conventional coherent axial hologram of the point, resulting from interference of the objective spherical wave and carrying plane wave:

$$I_1 = 4I_0 cos^2\left[\frac{k_0}{2}\left(\sqrt{L^2 + r^2} - L\right)\right], \quad (10)$$

where $k_0 = {}^{2\pi}/_{\lambda}$.

Comparing expressions (10) and (9), it can be noted that cosine arguments differ by the scale multiplier, proportional to ${}^{d}/_{L}$, characterizing contribution of the optically active medium into an aggregate light path.

In a Cartesian coordinate system, the intensity distribution for the hologram point (8) can be written as:

$$I(x', y', z') = I_0(x, y, z)T\ cos^2\left[\frac{bd}{z' - z}\sqrt{(x' - x)^2 + (y' - y) + (z' - z)^2}\right], \quad (11)$$

where $T = T(x' - x, y' - y, z' - z)$.

Superposition of distributions represents the hologram of the donor's location (11), and the intensity distribution in the recipient's hologram has the following form:

$$I_\Sigma(x', y', z') = \int_v I_0(x, y, z)T\ cos^2\left[\frac{bd}{z' - z}\sqrt{(x' - x)^2 + (y' - y) + (z' - z)^2}\right] dxdydz, \quad (12)$$

From here, we can write the impulse characteristic (or holographic point spread function) as follows:

$$h(x, y, z) = T(x, y, z)cos^2\left(\frac{bd}{z}\sqrt{x^2 + y^2 + z^2}\right). \quad (13)$$

Holographic transmission function can be determined on the basis of Fourier transformation of equation (13). Remember, the wavelength of the scanning signal is not included in this formula, therefore, this wave can be selected from the wide range of waves: light, electromagnetic and acoustic waves. The created hologram contains complete information about spatial coordinate characteristics of holographed donor-objects or about spatial distribution of all donor's points relative to the registering planes of recipient's holograms.

Thus, the resulting solution of the task, generally speaking, is common to a traditional approach. At the same time, the proposed method is fundamentally different from other known interferential methods and has certain advantages.

Firstly, instead of a wavelength $\boldsymbol{\lambda}$ with its monochromatic and coherent nature, we use dispersion rotational capacity of optically active medium $\boldsymbol{b}$ and spatial locally-distributed polarizing filtration. The above is suffice to record the polarisation-dynamic hologram of the donor, when donor cell movements are present under conditions of recipient's non-coherent broadband spectrum irradiation.

Secondly, this method allows the discovery of the causes for vibrational stability during registration and reconstruction of holograms without laser light sources inside the biosystems in the terahertz wave range. Its efficacy is determined by the value of polarization-optical rotation ability ***b*** and thickness of the optically active medium layer ***d.*** It is known that rotation ability of certain liquid crystals reaches 40,000 degrees/mm, which when used in holographic information-laser transducer is sufficient for polarization-holographic transmission of information, and hence, for holographic management of structures and processes in biosystems.

Experimental works on wave interaction in living systems actively started in 1980s. In the beginning these were the works on intercellular interactions [Kirkin, 1981; Molchanov, 1985], followed by works on interaction of living organisms [Burlakov et al., 1999]. These works were successfully continued by A.B. Budagovsky et al. [Budagovsky, 1990; Budagovsky, Evseeva, 1995; Budagovsky et al, 1997; Budagovsky et al, 2001]. Eventually, it was demonstrated that there is a communicational information exchange of non-chemical (wave coherent) origin. Such kinds of metabolic processes, occurring with participation of bio-regulatory signals and without molecular and ion information carriers were called "Remote Intercellular Interaction" (RII) [Budagovsky, 2004]. However, it seemed impossible that weak electromagnetic cellular signals could produce management directives under conditions of strong background electromagnetic interference signals of natural and artificial origin. Nonetheless, it turned out that during coherent reception, when light and other non-coherent electromagnetic noise is averaged, it is nulled; at the same time weak coherent and deterministic signals may accumulate [Tertyshniy et al., 1997, 1998, 2000].

In recent years, these works were developed further in the Institute of Management Problems. In particular, it was proposed to apply polarization-dynamic holography, which allows the generation of low-motion polarization rings. A sensory-quasi-lens was created to be able to transmit undistorted images of every

donor's point to the remote recipient's zone. On this basis, a holographic apparatus was designed for experimental testing of holographic management possibilities.

2. Quantum teleportation of genetic-metabolic information in the permissive version [Prangishvili, Gariaev, Maksimenko et al., 2000(б);]

The above given biological experiments on a remote "transfer" of morphogenetic, or more accurately, genetic-metabolic information, from a donor to recipient may be interpreted from views of nonlocalized contacts in accordance with mechanisms of quantum teleportation in the permissive variant. The laser apparatus, practically – a quantum biocomputer (mentioned above), besides its unique capability of wave "transfer" of morphogenetic information, also performs a conversion of red coherent photons into radio waves of a broad spectrum. These very waves are the candidates for the primary acts of scanning and "transfer". What takes place during laser beam scanning of bio-samples or of some other substances, is in fact a special type of biologically active spectroscopy. We proposed a tentative explanation of this phenomenon [Gariaev, Tertyshniy, Gotovsky, 1997], which is the primary substantiation of a new type of spectroscopy – "polarization laser-radio-wave spectroscopy (PLRS)" [Prangishvili, Gariaev at al., 2000 (b)]. Such spectroscopy is designed to examine unknown spin-fluctuating quantum-molecular characteristics of biosystems, bio-tissues, solid, liquid and gas substances, as well as plasma states. The type of PLRS described here, is active in a narrow optical range – red light, however, there are plans for modifications for operation in the UV to IR range.

This present version of the apparatus – a He-Ne laser (λ=632.8nm) with two orthogonal, linked in their intensity, optical modes, which are mobile and depend on the scanned object, as well as are connected in a way that total sum of their intensities remains constant despite of the scanned preparation. When at least one of the modes interacts with a substance - reflected or scattered radiation from which returns to the optical resonator - redistribution of intensity of these optical modes occurs according

to the law of polarization change; the resulting intensity corresponds to a new state after beam's interaction with dynamic micro-polarizers, which are located on the cross-section of the illuminated area of the examined sample. Dynamics of the micro-polarizers is determined by internal dynamics of the examined object (metabolism, acoustics of chromosomes and DNA *in vivo-in vitro*, crystal grids oscillations and so on). One laser mode, in the mode of modulated photon return to the resonator, can become (during the process of interaction with the substance) the cause of modulated broadband radio wave emission by our apparatus, where these broadband radio waves are correlating with modulations in optical modes of laser emission. These modulations depend on rotational oscillations of micro-structural components (for example, of LCC chromosomes' domains *in vivo-in vitro*) of the examined substances and their optical activity. Frequency interval of radio waves, generated during conversion from photons, in accordance with a theoretical model (see below), is in the range from $2\boldsymbol{\omega}$ to 0. The maximum frequency of such irradiation is about 1 MHz. The radio wave signal, after detection, undergoes digital signal processing with a special software on a computer. The output Fourier spectrum of radio-emission is registered, which characterizes polarization-dynamic properties and the spectral memory of examined substances (interacting with one of the laser beams). At the same time, the second light beam returns to the laser resonator for creation of resonant interaction with the atomic oscillators of the gas mixture. The reason for photons conversion into radio waves, as we believe, is inelastic scattering and localization of light of the main laser mode upon the system of non-homogeneity of the mirrors within the laser resonator. The localisation mechanism (localization in inelastic scattering channel) is described below. In particular, we believe that in the resonator there is also an *elastic* scattering of localized light. The radio wave emission, generated by the laser, is able to "read information", for example, from DNA samples or organs and tissues. The "reading" mechanism resembles the mechanism of common induced radiation. An option of "closing and opening" the

laser's resonator allows to localize or "record" on itself the "spectrums" of various examined objects. Radio wave radiation scans and re-transmits such spectrums. This is when we discovered an effect of spectral memory: during a certain macroscopic length of time, radio wave spectrums of objects are reproduced, these objects reflect the laser beam back into the resonator and are later removed from the exposition zone. That's how DNA spectrums were registered and their high biological activity revealed, this activity is possibly related to wave "transfer" of genetic-metabolic information. [Gariaev, Leonova, 2003]. It seems that quantum nonlocality of genetic (chromosome) information, manifested as its total distribution (continuality) inside multi-cell biosystems, is a special case. In reality, there are at least six levels of nonlocality in biosystems.

1st level – organism level. Nonlocality here is expressed in ability for regeneration, for example, in Planaria worms. After cutting these worms, any part of their body regenerates the whole organism. In other words, in this case there is no attachment of the generic pool of genetic information to any particular part of these worms. The same applies to vegetative reproduction in plants.

2nd level – cellular. A whole organism can be grown from any cell (not just from the zygote). It is more difficult, however, possible for living biosystems. Every cell is a potential continuum of the organism.

3rd level - cellular-nucleotide. Enucleation of nucleuses from somatic and gamete cells with subsequent injection of other nucleuses does not hinder normal development of an organism. Cloning of this kind is currently performed on higher-level biosystems, for example, on sheep. Every cellular nucleus is also a potential continuum of a biosystem. There is no localization of genetic potencies on any certain types of cells. Gamete cells perform the same role but with a haploid set of chromosomes: in a zygote they combine into a diploid set (as it happens in somatic cells).

4th level – molecular. Ribosomes "read" informational RNA not only

codon-by-codon, but they "read" the whole RNA contextually, that means nonlocally, continually.

5th level - chromosomic-holographic. The genome has a holographic memory [Gariaev et al., 1991; Gariaev, 1994], and this memory is typically distributed (nonlocal) associative memory. At this and subsequent levels, nonlocality obtains a new quality, a dualistic material-wave nature, since holograms (similar to matter) are "read" by electromagnetic or/and acoustic fields, which carry out gene-wave information beyond the material substance of chromosomes. Here, we deal with a physical field or fields, as calibration formations, which mark the future space-time of an organism. It appears that holographic memory of the cortex pertains to these fields as well, as it sets mental, rational and imaginary spaces, which calibrate potential actions of higher biosystems in a society as a super-organism. This is the highest level of socio-genetic processes.

6th level - quantum nonlocality of genome. Up to this level, nonlocality of genetic information is manifested in a space of an organism and also in a society. This level has a special character and a new quality. It is expressed in one of the forms of quantum nonlocality, namely – permissive, postulated in this paper. In this, case nonlocality is instantly realized across *the space* of the biosystem as much as its *time is* "compressed" to zero. Isomorphic to material gene-wave programs, instantly distributed in the described manner, operate within the organism "here and there simultaneously", therefore, it is meaningless to use semantic structure of "now and then". This is a strategic factor, an incredibly vital evolutionary achievement for multi-cellular biosystems. Billions of cells of the organism ought to "know" everything or at least a lot about one another, and moreover, know instantly. Without the phenomena of "wave informational instantaneity", the gigantic multi-cellular continuum of the highest biosystems is not able to holistically coordinate the metabolism of its own physiological and other functions. Intercellular diffusion of signalling substances and nervous processes are overly slow and inert for these purposes. Even if we assume that linguistic

electromagnetic fields with light speeds (which is sufficiently substantiated) take part in intercellular exchange, this is not fast enough. The mechanism of quantum nonlocality is necessary. And this mechanism can be applied to the genetic apparatus, which may act as an instantly distributed quantum (wave) object, isomorphic to material chromosomes. Using nonlocality, the genetic apparatus of the highest biosystems creates an amazing phenomenon: in certain moments in the "compressed" space-time of the biosystem, "here and there", "now and then" are working as a continuity, which provides organisms with super-coherence, informational super-abundance, connectedness and as a result, integrity (survival). This manifests in the ability of inferior organisms (hydra, worms, amphibians, lizards, Crustaceans), to regenerate their organs and tissues, the ability which has largely been lost by humans. However, this may be activated on the basis of the principles of wave self-organization processes, that we advance and develop in this book and in our experiments. The first-ever successful grafting of implanted donor's tissues in a blind human with recovery of vision is a great illustration of these phenomena [Muldashev, 2000]. Our models of morphogenesis and holographic memory of the genome were the ideological foundation for these surgeries and regenerative processes. The key component of this surgery was application of a donor's retina as a hologram and intercellular substance (alloplant) as a system for additional coordination of post-embryonic eye morphogenesis, which in fact had been predicted by us earlier [Gariaev, 1994].

Nevertheless, theoretical-experimental studies in this area are still in an initial stage and require further development from the physics-mathematical perspective. That's why we will present a formalised model of photonic-radio-wave processes, generated during our apparatus laser beam interaction with substances. These processes can be tentatively seen as a foundation for PLRS and as a version of quantum informational events in chromosomes.

The theories of light localisation in dispersed spatially correlated systems set the foundation for our logic. Since 1985, after the studies of Albada [Albada, 1985], the phenomenon of light

localization has received wide acknowledgement. Today this is one of the most dynamically developing fields in physics, closely related to such problems as quantum teleportation, new methods of recording and reading information and so on.

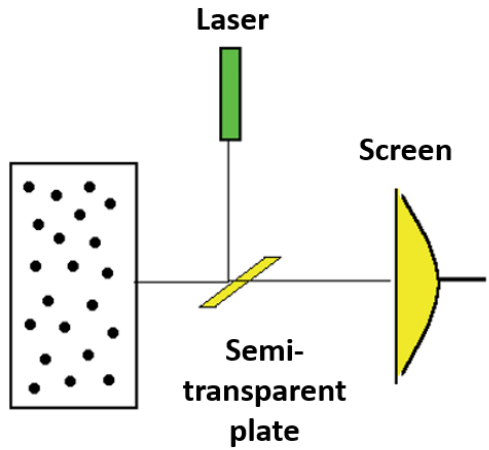


Fig 5. Scheme of experiment for observation of weak localization of light

Albada [Albada, 1985] studied reflection of light from semitransparent material, filled with minute particles of latex, suspended in water, under conditions when the wavelength of the incident photons equals to the average distance between the particles. Against the background of Fresnel reflections in a strictly reverse direction, one could observe a very narrow peak of scattered light intensity (Fig. 5). The signal was twice the strength than its background. To explain the effect, it is suffice to look at a pair of particles, which happen to be in the photon's trajectory. Part of the photon trajectory, namely, the trajectory of the photon where it is reflected strictly backwards, is an infinitely narrow loop, located between this pair of particles. Let's assume that a photon can traverse this loop in two ways – clockwise and counter-clockwise. These two options are shown in Fig. 6a. These ways are undiscernible.

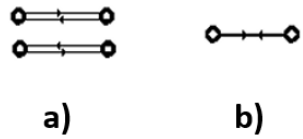


Fig 6. **a)** Two ways of photon passing the loop on its trajectory under condition of weak localization; **b)** photon spread between two particles

In these cases, quantum mechanics prescribes to calculate the probability of a photon $\boldsymbol{P}$-turn as follows. Each of the processes is matched with an amplitude of probability $\boldsymbol{a}$ and a probability of a turn $\boldsymbol{P = |a + a|^2 = 4|a|^2}$ (we took into account that both amplitudes under the modulus sign have the same phases – this is the specifics of movement along the loop [14]). If we had a hypothetical possibility to distinguish between these methods, the rotation probability would be calculated completely differently and would be half the size: $\boldsymbol{P = |a|^2 + |a|^2 = 2|a|^2}$. This is the formal cause for the peak in backwards direction. However, the appearance of the peak in the backwards direction is not accompanied by a corresponding decrease of light diffusion in any particular direction. How such case could be possible given the law of conservation of energy? Where did the additional photons come from? Why aren't they observed when the light is reflected from a continuous hemi-space? And at last, why did we decide that there are two ways of possible photon movement between two particles? If the trajectory of the photon between these particles is a one-dimensional straight line, then how can we talk about two different ways of its traversing? The photon's turn between the two lenses is a clearly defined procedure shown in Fig. 6b.

Well, we would really like to see two ways for a photon to traverse this infinitely narrow loop between the two particles. This can be achieved, if we assume that the topological dimension of the photon trajectory under the condition of weak localization is $\boldsymbol{d<1}$. Only under this condition we can place within a one-dimensional line (Fig. 6b) two different "lines" - a topological object, looking like a loop, i.e., characterized by two different ways of its traversing.

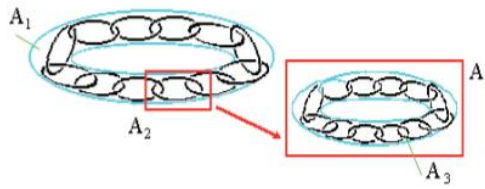


Fig 7. Antoine's necklace

There is an elegant mathematical formula, which, on one hand, is similar to what in physics is called a line or a trajectory, and on the other hand, its topological measurement ***d*** is indeed smaller than 1. Moreover, ***d=0***. We speak of the so-called Antoine's necklace [Boltyanskii, Efremovich, 1982]. This object as no other is suitable for describing the process of continuous regeneration of multi-scale loops in a photon's trajectory.

Antoine's zero-dimensional set (Antoine's necklace) has the following construction. At the first stage, the starting "thick" locked loop ***A1*** is considered. At the second stage – ***A1*** is substituted by a chain of smaller links of ***A2***, located inside of ***A1***. Then, each link of ***A2*** is replaced by the chain of even smaller links $A3 \subset A2$ and so on. If we continue this process, we get a sequence of $A1 \supset A2 \supset A3 \ldots$ (see Fig .7). Intersection of these multiple sets represents Antoine's zero-dimensional compactum A^*. The described structure is the simplest version of Antoine's necklace.

Despite of the fact that Antoine's necklace is zero-dimensional, it does retain certain properties of a common one-dimensional line. If from a common one-dimensional set A_0, for example, one can easily remove the ring "threaded through" from a limited set of points, without crossing A_0 anywhere. The same cannot be done with a zero-dimensional A^* set.

Let's assume that the photon's trajectory under conditions of strong and weak localization is an Antoine's set with topological dimension of ***d=0***. This leads us to the interesting conclusions. If the photon moves along Antoine's trajectory, then, it is rather difficult to leave this set. It experiences problems moving into the

real world with ***d=1,2,3***, similar to, a person locked in a room without windows and doors. There is a possible physical interpretation of the mechanism of light retention in the system, the interpretation determined by the unusual topology of Antoine's trajectories. Substituting a real 3D photon with a zero-dimensional object, leads to the singular energy distribution along the trajectory of Antoine's photon. Such a trajectory manifests a peculiar "mechanical stiffness". Intertwined "stiff" links of Antoine's set resist any attempt of release. This is why the photon is retained near the pair, or to be precise, it is retained near itself.

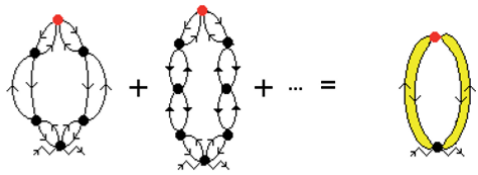


Fig 8. Antoine's rings photon's trajectory

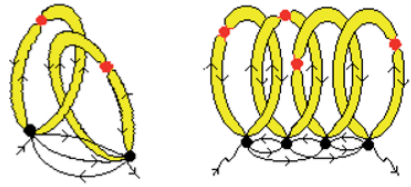


Fig 9. Intertwining of Antoine's rings

Is it possible for the Antoine's photon to regain "freedom" and exit into the "real world"? This narrow peak directed backwards (when light is scattered by the dispersing system under condition of weak localization) is in fact, nothing else but initiated by light emission of Antoine's photons.

Analysis of a number of theories of excitation for a photon propagator in a system of particles shows that there are trajectories isomorphic to Antoine's set. These trajectories, looking like a loop composed of two parts (similar to the rings of the handcuffs), are presented in Fig. 8. Two semi-rings (they are not necessarily identical) interlock at the top particle. The total sum of such loops is indicated in the figure as a colored ring. During their motion, these rings may intertwine (see Fig. 9). In turn, every propagator

line (the intertwined rings are made of these lines) also represents a set of intertwined rings of the smaller scale (Fig. 10). And this is replicated infinitely.

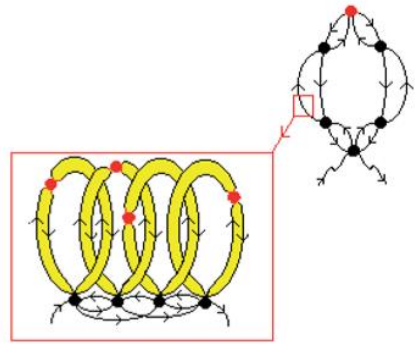


Fig 10. The structure of the propagator line of Antoine's rings

A very strong renormalizing or reduction of the wavelength of the photon entering the system is a necessary condition for localization. As already known, in systems with high values of dielectric penetrability, the photon wavelength $\boldsymbol{\lambda_{int}}$ becomes much smaller than the wavelength of the incident photon $\boldsymbol{\lambda}$. Wherein, the frequency of the photon $\boldsymbol{\omega}$ does not change - changes the effective speed of the photon $\boldsymbol{v}$ according to the equation $\boldsymbol{\omega = 2\pi v/\lambda_{int}}$. We are interested in the case, when $\boldsymbol{\lambda_{int} \to 0}$, otherwise, the photon does not "fit" in the diminishingly small links of Antoine's set, wherein, the effective speed of a photon becomes zero.

A fractal cluster, consisting of slowly absorbing particles-monomers represents an object, where strong renormalizing of the radiation's wavelength is possible. Heterogenic systems which are scale-invariant, are called fractal systems. Any small fragment of the system, when magnified, reproduces spatial structure of the whole system. Fractal Cluster (FC) is an agglomerate of a micro size, comprised of nanometer hard particles, held together by Van der Waals forces. FC are created either as a result of highly unbalanced condensation of vapor from hard substances and subsequent aggregation of nanometer particles-monomers, or at the initial stages of crystallization process from solutions or fusions.

Scale invariance of a cluster determines relatively slow diminishing of paired correlations in the location of its particles. Pair correlation function is: $g(r) \sim r^{D-3} \exp(-r/L_c)$

where $\boldsymbol{D}$ - the fractal dimension of the cluster, $\boldsymbol{L_c}$- typical size of the correlation block. Fractal dimension determines the number particles-monomers of cluster $\boldsymbol{N}$, located within the imaginary sphere of $\boldsymbol{r}$ radius : $\boldsymbol{N \sim r^D}$. The value of $\boldsymbol{D < 3}$ (not necessarily an integer) is the specifics of the fractal cluster. In common densely packed particles, paired correlations diminish considerably faster, disappearing according to exponential law at certain distances of about few particles' radiuses long. FC scale invariance is visually displayed in its loose structure. The density of particles in a fractal cluster volume $\boldsymbol{r^3}$ is not constant but proportionate to $1/r^{3-D}$.

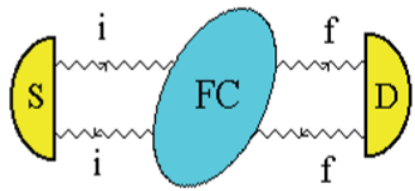


Fig 11. Photon "retention" between the source and the detector whilst elastic scattering on FC

Renormalizing is caused by remote correlations in the location of FC particles, visually expressed in coherence of the cluster and presence of a large number of empty spaces inside the cluster. It can be explained in the following way. Let photon, incident onto a cluster with wavelength of about $\boldsymbol{\lambda}$-range of a typical cluster $\boldsymbol{L}$ to be captured by some relatively large FC cavity (resonant cavity). This capturing leads to the increase of the effective dielectric penetrability of the cluster $\overline{\varepsilon}$ ($\overline{\varepsilon}$ increases near any electromagnetic resonance [Boren, Hoffman, 1986]). Increase in $\overline{\varepsilon}$ value, in turn, initiates photon's wavelength reduction because $\boldsymbol{\lambda_{int} = \frac{\lambda}{\sqrt{\overline{\varepsilon}}}}$. Photon with renormalized wavelength $\boldsymbol{\lambda_{int}}$ finds another

cavity of a smaller size. This new capturing stimulates increase of $\bar{\varepsilon}$ value again and new reduction of λ_{int} and so on. Eventually, all FC cavities could be filled with renormalized photons, including those with a wavelength $\lambda^{int} \rightarrow 0$.

The physics of light localization in fractal systems and the calculation scheme are described below. In between the source and the detector of the radiation, there is always a photon, which is circling in a locked loop (Fig. 11). Intertwined stiff Antoine's rings on the photon's path retain the photon there (Fig. 12). The rings are formed as the result of numerous photon renormalizations in FC particles-monomers. Then, we calculate the interaction amplitude of a virtual photon pair, photons located inside the area, marked as FC (fractal cluster) in Fig. 12. One of them corresponds to the upper "edge" and the second – to the lower. Typical processes causing this amplitude can be seen in Fig. 12 (when ignoring the undulatory lines of real photons). Interaction amplitude can be found by solving the relevant Bethe-Salpeter equation. One can show that the virtual part of this amplitude describes photon "retention" and localization in the system.

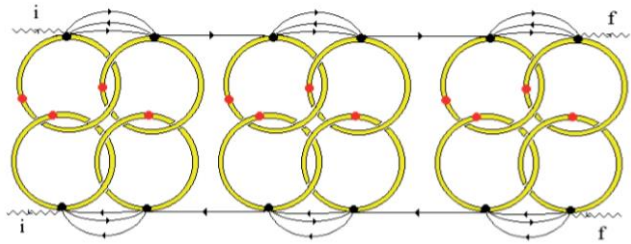


Fig 12. Physical explanation of photon "retention"

The resulting calculation leads to the following expression for the differential cross-section of the elastic light scattering by the cluster [Maksimenko, 1999]:

$$\frac{d\sigma}{dn_f} = \frac{1+2\left(e_i e_f\right)^2}{60} N^{\frac{3-2D}{D}\frac{N}{2}} |\varepsilon - 1|^2 \frac{\omega^4 R^6}{c^4} \left[-\frac{1}{\beta}\frac{d}{d\beta}\delta(\beta) + i\frac{4t_0^3}{(3-D)N^2}\frac{\sin\beta\, t_0}{\beta\, t_0} \right] \quad (1)$$

where $\beta = 2\frac{\omega L_c}{c}\sin\frac{0}{2}, \theta$ - dissipation angle,
$\boldsymbol{\delta(x)}$- Dirac delta-function,
$\boldsymbol{c}$– light speed in vacuum,
$\boldsymbol{e}$– single polarization vectors of the incident ***(i)*** and scattered ***(f)*** quanta,
$\boldsymbol{\omega}$ – frequency of the incident light,
$\boldsymbol{n_f}$ **–** singular vector in scattered photon direction,
$\boldsymbol{N >> 1}$ – a number of particles in a correlation block,
$\boldsymbol{\varepsilon}$ – dielectric permeability of the particles substance and
$\boldsymbol{R}$ – radius of particle-monomer.

Parameter $\boldsymbol{t_0}$ has a weak dependancy on $\boldsymbol{D}$**.** Virtual part of the cross-section describes "absorbtion", determined by localization. When $\boldsymbol{D < 3/2}$, this cross-section is very large.

When $\boldsymbol{\Theta \neq 0}$, differential cross-section of scattering becomes purely virtual. This means, that when $\boldsymbol{\Theta \neq 0}$ there is no scattered by cluster light beam at all! Any photon, scattered "sidewase" is captured by the cluster and starts fluctuating along corresponding $\vec{n}_f$.

The singularity of forward scattering is another surprising factor of expression (1) for $d\sigma/d\vec{n}_f$. Taking into account the connection

$$J_{n_f} = I\frac{d\sigma}{d\vec{n}_f}$$

between the beam of scattered in direction $\vec{\boldsymbol{n}}_{\boldsymbol{f}}$ of radiation $\boldsymbol{J_{n_f}}$and the density of the incident light radiation $\boldsymbol{I}$, one can see that singularity in the cross-section means that there is a possibility for an ultimate "current" of photons in the system, even at the zero density of the beam of incident radiation. Singularity $d\sigma/d\vec{n}_f$ in forward direction describes forced light radiation from the cluster.

This is a typical “laser” effect.

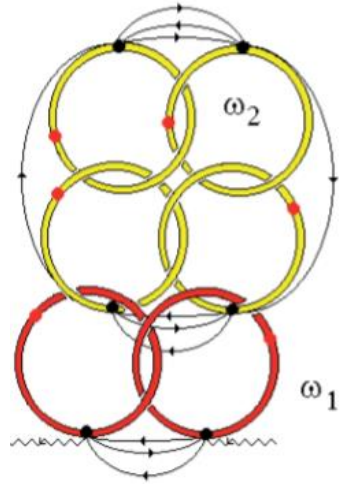


Fig 13. Physical cause of the induced light emission, localized in a cluster

Coherency of the induced radiation is provided for “zero-dimensionality” of localized Antoine’s photons, the ability to concentrate large in quantity on a small scale. The physical cause of coherent release of these photons is simple and illustrative. Any photon, scattered “sidewise” is captured by the cluster and begins to oscillate in it along the direction of scattering without a right to exit the cluster. Antoine’s rings, intertwined with corresponding rings of the localized photon, are formed on its trajectory. This very intertwinement “retain” such photon in a cluster. Most of the rings belong to the photon scattering at zero angle – virtual part $d\sigma/d\vec{n}_f$ has its maximum value when $\boldsymbol{\theta} = \mathbf{0}$ (see equation (1)). And at the same time, only such a photon has a chance to break through from the cluster, which is described by the real part of the cross-section. This photon, hooked up by its rings with corresponding rings of the localized photons, pulls them outside (Fig. 13). This is how, by means of Antoine’s rings, it is possible to understand the nature of the induced light radiation.

We anticipate that such kind of effects, in particular – localization of light, take place in the system of correlated mirrors of apparatus described here. Here, the localization is possible

between any two out of the entire pool of omnifarious combinations of mirror.

The spectrum of excitations in any system is largely determined by its boundaries or surface. A common example of such excitations are plasmon-polaritons on metal surfaces or surface plasmons in small metal particles. Is it possible “to read” spectrums (specific to these kind of excitations) and to record them on some data storage unit for the purpose of long-term storage and subsequent reading? We are going to discuss perspectives and problems of such studies.

As is known, when a photon is reflected from a flat surface, its polarization state does not change – this is forbidden by isotropy of the task in relation to rotations in the surface’s plane. It would seem that during light reflection from a flat plate with two walls, the situation would not change. However, it is not so, if we consider localization of light between the boundaries of the plates. Such effects can be observed whilst light scattering is in a strictly backwards direction in even and consistent ensembles of the smallest particles [Maksimenko et al. 1992] This relates to the possibility of a scattered backwards photon “to pull out” another photon localized in a system. In this case, polarization of the reflected light can change. The reason for a scattered backwards photon to “pull out” a localized photon, as we know it, is not related to the photon-photon interaction (which can be disregarded in this example) but is related to intertwinement of Antoine’s rings of both scattered and localized photons.

This effect, combined with rotational-oscillating and polarizational characteristics of the scanned objects, can be used for effective extraction from the object of (localized in it) its own excitations or its “spectrum”. Let’s review a scheme given in Fig. 14.

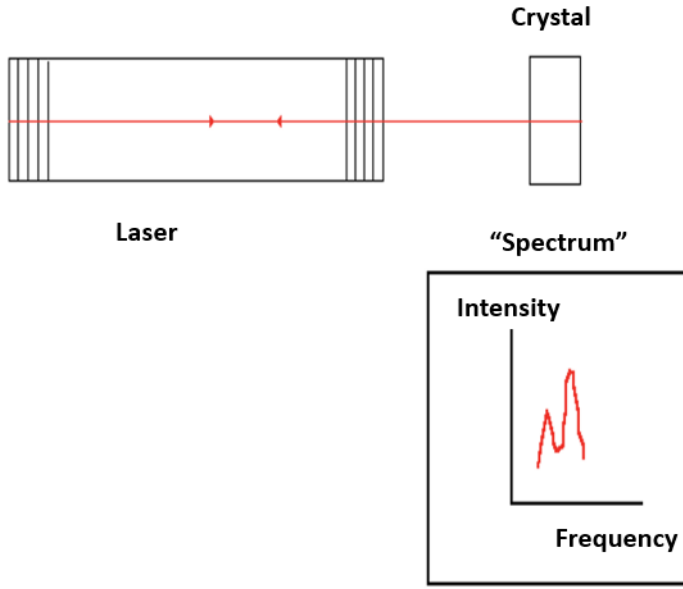


Fig 14. Scheme of the typical experiment of recording Polarized-Radio-Wave-Spectrum of scanned objects, e.g. crystalized minerals.

The picture shows the laser, referred to earlier, and crystal, which spectrum we intend to “pull out”. The standard laser construction had undergone one addition modification. The semi-transparent plate (positioned at a Brewster's angle in relation to the laser’s axis) has been removed from the laser. This semi-transparent plate was designated to filter parasitic light from other sources than the main polarization. This was done in order to allow the light (that was reflected from the crystal and has changed its polarization as a result of “pulling-out” localized photons from the crystal) to re-enter into the resonator and then repeat its route multiple times. We expect the effectiveness of “pulling out” of localized photons (which are recording information about the object) to be high enough for experimental observation. Later, these delocalized photons can localize again but this time in the system of laser mirrors. After this, we remove the crystal, but the “spectrum” of its excitations, localized in the laser, as we expect, would be active for a while. The system would reproduce spectral memory about the object – the object that by this time has already

been removed from the exposition zone. The role of crystal can be utilized by any system where field localization is possible. For example, by biological objects, namely, genetic structures which have a fractal liquid crystal packaging. Perhaps, these were the types of spectral memory effects that we observed in our experiments (Fig. 15)

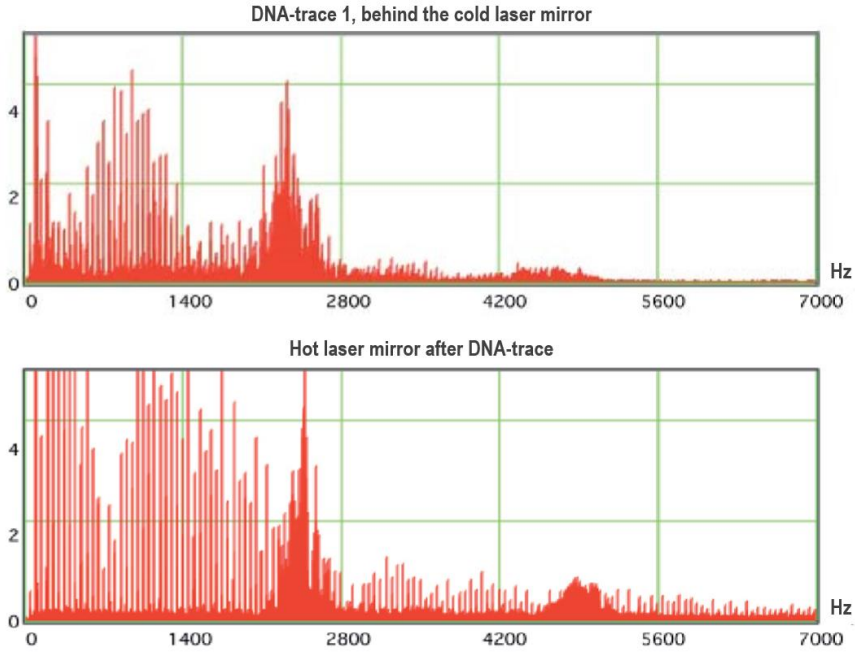


Fig 15. Polarized Laser-Radio-Wave Spectrums (PLRS) of a highly polymeric DNA preparation from calf's thymus gland (upper spectrum), and its spectral "trace" on laser mirrors (lower spectrum) after preparation removal from the laser scanning zone. DNA sodium salt was dissolved in distilled water at a concentration of 1 mg/ml, then, the drop was placed on a glass slide and covered by the another glass slide, forming a "sandwich". This was exposed to the laser beam in the "return beam" mode (passed through the "sandwich") back to the resonator, as described in Fig. 14. Control spectrum of clear glass slides (clear "sandwich" without preparation) within the same frequency range did not produce peaks typical for DNA inside the "sandwich".

We'd like to emphasize that we speak about the possibility of "reading" with a laser radiation of a fixed frequency ω_0, the whole spectrum of the object – a wide range of frequencies. The fact is that a laser photon with ω_0 frequency has "no preference" for which localized photon "to pull-out" from the object: with the

same $\boldsymbol{\omega_0}$ frequency or with another frequency, if there is any.

An absolutely unexpected application of the light localization idea can be found in the problem of quantum teleportation – instant message "transmission" across randomly large distances. This promising area of research, starting with the works of [Bennet et al, 1993; Bouwmeester et al., 1997], attracts more and more attention from biologists. Let's briefly review the basic provisions of the "classical" theory of quantum teleportation.

As is well known, any wave function of a pair of photons (photon 2 and photon 3), where each photon has two polarization states (horizontal $|\leftrightarrow\rangle$ and vertical $\langle\updownarrow|$ polarizations) can be considered to be from four basic conditions (the so-called Bell's conditions) which form the complete orthonormalized system of functions [22]

$$|\Phi^+\rangle = \left(|\updownarrow\rangle_2|\updownarrow\rangle_3 + |\leftrightarrow\rangle_2|\leftrightarrow\rangle_3\right)/\sqrt{2}$$

$$|\Phi^-\rangle = \left(|\updownarrow\rangle_2|\updownarrow\rangle_3 - |\leftrightarrow\rangle_2|\leftrightarrow\rangle_3\right)/\sqrt{2}$$

$$|\Psi^+\rangle = \left(|\updownarrow\rangle_2|\leftrightarrow\rangle_3 + |\leftrightarrow\rangle_2|\updownarrow\rangle_3\right)/\sqrt{2}$$

$$|\Psi^-\rangle = \left(|\updownarrow\rangle_2|\leftrightarrow\rangle_3 - |\leftrightarrow\rangle_2|\updownarrow\rangle_3\right)/\sqrt{2} \qquad (2)$$

Condition $|\Psi^-\rangle$ (later it will be of the more interest to us than the rest) has an interesting property: upon detection of a photon with a specific polarization, the polarization of another photon turns out to be the opposite.

The possibility to experimentally distinguish one Bell's condition from another is provided by their different symmetries. Out of four conditions (2), the first three are boson conditions (their wave function does not change the sign, when particles 2 and 3 are interchanged). The last condition $|\Psi^-\rangle$ is a fermion condition (when particles 2 and 3 are interchanged, the sign of the wave function changes). This peculiarity of condition $|\Psi^-\rangle$ allows this state to stand out in a number of experiments well described in literature, experiments, which implement the interference of two specially

prepared light beams [Bouwmeester et al., 1997].

Taking the chance to work further with condition $|\Psi^-\rangle$, we can use the following almost classical experimental scheme [Bennet et al, 1993.; Bouwmeester et al, 1997.; Kadomtsev BB, 1999]. There are two players in the game: Alice and Bob, and a source of a photon pair, described by condition $|\Psi^-\rangle$. Alice's task is to transfer photon 1 (that she has) to Bob, located anywhere away from her. However, Alice does not use the usual classical method, and proceeds as follows. Alice and Bob simultaneously receive a pair of photons 2 and 3, described by the condition $|\Psi^-\rangle_{23}$. Alice receives photon 2, and Bob - photon 3. Alice "mixes" photon 1 and 2. Herein, in one case out of four, she is able to observe the condition

$$|\Psi^-\rangle_{12} = \left(|\updownarrow\rangle_1|\leftrightarrow\rangle_2 - |\leftrightarrow\rangle_2|\updownarrow\rangle_1\right)/\sqrt{2}\,.$$

Soon as she discovers this condition, photon 3 immediately goes into the initial state of photon 1. This happens for the following reason. Alice's observation of conditions $|\Psi^-\rangle_{12}$ means that under a certain condition of photon 1, photon 2 will have the opposite polarization state. Since photons 2 and 3 are also in a condition $|\Psi^-\rangle_{23}$, photon 3 will be in a condition which is orthogonal to condition of photon 2, i.e. in the condition of photon 1. Thus, the photon 1 teleportation happens from Alice to Bob, regardless of the distance between them. Teleportation occurs instantaneously.

The fact is that during this type of teleportation, the polarizational state of teleported photon 1 is not known to Alice, as photon 1 "mixes" with photon 2, resulting in the state $|\Psi^-\rangle_{12}$.

The described teleportation procedure is flawless from the point of view of quantum mechanics formalism. Nevertheless, the physical meaning of these basic Bell's conditions is still unclear, and there is still no clarity in the resolution of Einstein-Podolski-Rosen's paradox (remember, that these conditions were in the first place introduced to describe this EPR-paradox) [Einstein, Podolsky, Rosen, 1935]. How can one understand that when measuring polarization ↔ of one of the photons, which is for example in a condition $|\Psi^-\rangle$, the polarization of another photon instantaneously

becomes ↕, despite of the long distances between them, and knowing that any kind of information about the condition of the second photon can be received by us after a certain time period?

Photon pairs, described by conditions (2) or by their linear combinations, are usually called EPR-photon pairs or entangled photons. Until we fully comprehend the physical cause for these instant correlations in photons properties, we will not understand the physics of teleportation, regardless of the immaculacy of all logical derivations.

Surprising, as it may seem, the problems of the EPR-paradox and teleportation can be approached differently – from the position of the existance of localized light. One version of the EPR-paradox is further described below. Let's consider, for example, s-scattering of a photon by spherical particle, that is, the scattered wave is spherically isotopic (see Fig. 16). Let the scattered photon approach a detector at the point A (Alice). This act of registration allows us to conclude, that at the very same moment this scattered photon reaches a detector at point B (Bob), which is located at any distance from point A. Wherein, any information from B to A can be transmitted only after a certain period of time. If we exclude the possibility of signal propagation at superluminal speed, this case may be explained in the following way. What if the registration act of light's arrival at point A is not related to the scattered photon, but related to a localized "long" photon, after it was knocked out from the AB "channel"? We "capture" its "left end". Then, there is nothing strange about the fact that simultaneously, at point B, registration occurs of its "right end". There is no superlumenal signal propagation, as there is no propagation of a signal at all. A "long" localized photon is "pulled out" from a cavity by means of interlocking of stiff Antoine's rings of localized and scattered photons. This interlocking is similar to what was outlined above, the interlocking in a fractal cluster.

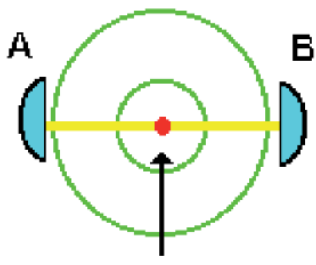


Fig 16. Experimental scheme for scanning, recording and storing information

Now, let's assume that there is

no photon scattering on a particle. Yet, there is a “cavity” between Alice and Bob, filled with a photon, localized in it. Alice sends her photon into this cavity. This photon captures a localized photon according to the described above mechanism and presents it to Bob. Thereby, as a result of Alice’s actions, Bob instantaneously receives some information (yet, nobody knows what kind of information, since many properties of localized photons are not known).

As we can see, in this case, for instantaneous signal “transmission” instead of EPR-correlated photon pairs, it is sufficient to have only one localized photon (however, if one wishes, it may be seen as a pair of interacting virtual photons – a photon of the upper edge and a photon of the lower edge of Fig. 1 and 2). Moreover, in [Bouwmeester et al., 1997], an EPR-pair teleported to Bob the unknown photon from Alice. In our case, Alice’s photon, after affecting the “left end” of the unknown to anyone localized photon, presents its “right end” to Bob. These are the similarities and the differences of the two mechanisms of teleportation.

Does this teleportation contradict the foundations of special relativity, postulating that speed of information transmission cannot exceed the speed of light? Obviously, no. In Bennet-type teleportation [Bennet et al., 1993; Bouwmeester et al., 1997], a signal unknown to anyone is instantly transmitted. Within the framework of our model, there is nothing transmitted at all. Bob receives what is already located next to him, yet, is not accessible to him until certain time. The information already pre-exists. Alice instantly “allows” Bob to take it. Therefore, this modification of quantum teleportation (nonlocality) we call “permissive” (from the word “permission”). It is noted that such nonlocality seemingly spreads further, since in our case, the photons (modulated by the object) instantly or nonlocally convert into radio waves, storing “photonic polarization information”. It is also possible that in our experiments, the photons scanning the object and interfering incident photons, record the object’s dynamic polarizational hologram (for example DNA), and tranform it into a bioactive radiowave (isomorphic to photonic) hologram.

Let's look at a possible cause of radio wave generation by a polarized laser-radio-wave spectrometer (PLRS). Here we will talk about a new mechanism of inelastic light scattering in electronic systems – in this case in the system of metallic layers of mirror coatings of the laser resonator, which is the main element of the spectrometer. This mechanism is different from traditional combinatory photon scattering. As opposed to a discrete set of Stokes and anti-Stokes peaks, the spectrum of the given inelastic dissipated light is continual and occupies the whole range of frequencies from $0\omega_i$ to $2\omega_i$, where ω_i – the frequency of the incident photon. The physics of the considered inelastic scattering is very simple. We will state its main regulatities based on an example of inelastic scattering with excitation of volumetric and surface plasmons in a small metallic particle. Electromagnetic modes of the finest metallic particles are called surface plasmons. They are bound with the oscillations of particle's electron conductivity, interacting via coulomb potential. These modes manifest themselves as distinct resonances in the spectra of elastic light scattering and light absorption by small metallic particles. The frequencies of the surface plasmons, depending on concentration of electrons of conductivity inside the particles, belong to the border of visible UV light and is determined by the following formulae:

$$\omega_l = \omega_0 \sqrt{\frac{l}{2l+1}},$$

where $l = 1,2,3 \ldots$, and $\boldsymbol{\omega_0}$ – classical plasma frequency of free electronic gas;

$$\boldsymbol{\omega_0} = \sqrt{\frac{4\pi n_0 e^2}{m}},$$

where n_0 - density of conductivity electrons in metal, $\boldsymbol{e}$ and $\boldsymbol{m}$ – electron's charge and mass.

Excitation, where $l = 1$, is called a dipolar surface plasmon, and excitation with frequency $\boldsymbol{\omega_0}$ is called volumetric plasmon. Such kinds of oscillations exist in thin metal films, which are usually

used for modeling mirror coatings, like the ones used in the considered laser. Here they are called plasmon-polariton modes, their properties are different, but at this stage we are interested only in the physics of the phenomenon.

The classical mechanism of inelastic light scattering by a particle is the following. A photon flying towards a particle with the energy $\hbar\boldsymbol{\omega_i}$ excites within this particle a fluctuation of electronic density, discharging some of its energy $\hbar\boldsymbol{\omega}$. The energy of the efferent photon is $\hbar\boldsymbol{\omega_f} = \hbar\boldsymbol{\omega_i} - \hbar\boldsymbol{\omega}$. This process is symbolically depicted in Fig. 17. The shaded corner depicts the fluctuation of electronic density $\boldsymbol{\delta\rho}$, which is a superposition of a large number of electron-vacant pairs, excited by photons. The cross-section of the process is especially large, if a photon manages to "swing" dipole surface and volumetric plasmons. For a particle with a much smaller size than the wavelength of an approaching photon, the differential section of inelastic scattering is [Lushnikov et al., 1982]:

$$\frac{d^2\sigma}{dn_f} = \frac{1}{3\pi} r_0 \lambda_0 \frac{\omega_0^2 R^3}{c^3(\omega_i - \omega_f)^2} \frac{\omega_f}{\omega_i}\left(\omega_i^2 + \omega_f^2 - 2\omega_i\omega_f \cos\Theta\right) \times,$$

$$\times \left[\omega_0 \int \sigma(\omega_i - \omega_f - \omega_0) d\omega_f + \omega_1 \int \sigma(\omega_i - \omega_f - \omega_1) d\omega_f\right] \qquad (1)$$

where $\boldsymbol{n_f}$ – single vector directed towards the scattered quantum,
θ - scattering angle,
$\boldsymbol{R}$ – radius of a separate particple in a pair,
$\boldsymbol{r_0}$ and $\boldsymbol{\lambda_0}$ – classical electon radius and Compton's wavelength of the electon, respectively.

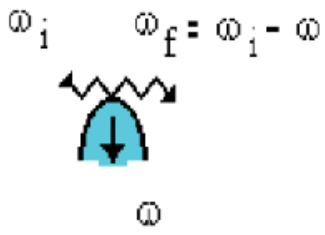


Fig 17. Classical scheme of inelastic dissipation of photons

If the energy, discharged by the photon, is enough for excitation of plasmoms $\boldsymbol{\omega_i - \omega_f > \omega_0}$, then

$$\frac{d\sigma}{dn_f} = \frac{r_0\lambda_0}{6\pi}\left(\frac{R}{c}\right)\left\{\frac{(\omega_i-\omega_0)}{\omega_i}\frac{\omega_0^2}{\omega_0}\left[\omega_i^2+(\omega_i+\omega_0)^2-2\omega_i(\omega_i-\omega_0)\cos\Theta\right]+\right.$$
$$\left.+\frac{(\omega_i-\omega_1)}{\omega_i}\frac{\omega_0^2}{\omega_1}\cdot\left[\omega_i^2+(\omega_i-\omega_1)^2-2\omega_i(\omega_i-\omega_1)\cos\Theta\right]\right\} \quad (2)$$

As we can see from the analysis of expression (1), only a discrete discharge of photon energy is possible, one that corresponds to the excitation of a volumetric and dipole surface plasmon. This is reflected by the presence of the Dirac delta-functions in the corresponding expression. The cross-section of the process is smaller than the cross-section of elastic light scattering by the particle by $\boldsymbol{r_0\lambda_0\lambda / R^3}$ times.

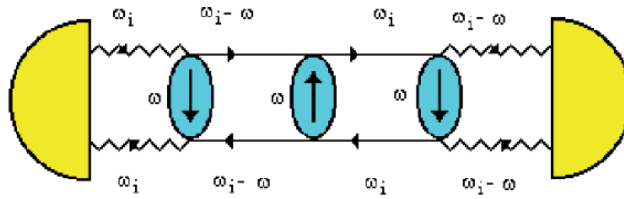


Fig 18. Proposed mechanism of inelastic scattering of photons

The mechanism we have proposed is principally different. Let's assume that between the source of the radiation and the detector there is a photon, which is constantly "circulating" in a closed loop, repeatedly exchanging fluctuations of electronic density with itself; these fluctuations are excited in a system of diffusers, located between the source and the detector. The shaded loops describe propagation of electronic density fluctuation in the system of diffusers – these are the so called "driving polarized density-density operators" or, simply are correlators of the electronic density. Wavy lines represent the wave functions of real photons, horizontal lines represent photon propagators. For example, the upper top of a randomly odd-numbered loop describes generation of an electronic density fluctuation by a photon with $\boldsymbol{\omega_i}$ energy due to photon's energy reduction by $\boldsymbol{\omega}$; the lower top of a randomly odd-numbered loop describes the shut down of electronic

density fluctuation due to photon, receiving back its energy $\boldsymbol{\omega}$. There can be any number of such loops along a photons trajectory. Our photon exchanges its energy with itself an infinite number of times in the process of inelastic scattering. This results in a specific exchange interaction of the photon with itself, similar to a common metabolic-exchange interaction in quantum chemistry. This very interaction retains the photon in the "cavity" between the source and the detector, substantiating our assumption about possibility of on first sight such strange, photon "circulation" between the source and the detector.

The differential cross-section of the given process looks like:

$$\frac{d\sigma}{dn_f} = \frac{1}{4}\frac{r_0\lambda_0}{6\pi}\left(e_i e_f\right)^2\left(\frac{R}{c}\right)^3\left\{\frac{(\omega_i-\omega)}{\omega_i}\frac{\omega_0^2}{\omega_0}\left[\omega_i^2+(\omega_i-\omega)^2-2\omega_i(\omega_i-\omega)\cos\Theta\right]+\right.$$

$$\left.+\frac{(\omega_i-\omega)}{\omega_i}\frac{\omega_0^2}{\omega_1}\cdot\left[\omega_i^2+(\omega_i-\omega)^2-2\omega_i(\omega_i-\omega)\cos\Theta\right]\right\} \qquad (3)$$

where $\boldsymbol{e_i}$ and $\boldsymbol{e_f}$ – the unit polarization vectors and $\boldsymbol{\omega}$ – discharged frequency.

In between expressions (2) and (3), despite of their superficial resemblance, there is a fundamental difference. Within the framework of the classical mechanism, only a discrete discharge of the incident photon's energy is possible, corresponding to the excitation of the volume (with the frequency $\boldsymbol{\omega_0}$) and dipole surface plasmon (with the frequency $\boldsymbol{\omega_1}$) in particles. Any other energy discharge is prohibited by the $\boldsymbol{\delta}$-functions present in equation (1). In regard to the proposed mechanism, the red shift of the incident photon frequency can be any within the range. If $\boldsymbol{\omega \cong \omega_i}$, the result of the process is the experimentally observed generation of radio waves.

Along with a "red" shift, a "blue" shift of photon frequency is possible... Thus, the spectrum of inelastic scattered light (with account of localization) should occupy the entire frequency range from $\boldsymbol{0}$ to $\boldsymbol{2\omega_i}$. These kinds of effects are actually observed in experiments involving gigantic combinatory light scattering by molecules, adsorbed on the surface of the finest metal particles – it

is called the "gigantic white background", and it still remains a mystery.

The processes (Fig. 17), where $\boldsymbol{\omega} \cong \boldsymbol{\omega_i}$, qualitatively explain the increased background of the radio emission of the given laser. Quantitative calculation, of course, requires consideration of the system's specifics.

Additional theoretical approaches here, possibly, lie in the effects of the so-called "weak influences" [Chukova, 2002]. Apparently, regenerative and cytoprotective effects in our experiments have an endoergic character: even weakly absorbed (by biological preparations) energy of coherent red polarized laser radiation contributes to growth of Helmholtz free energy, accumulated in chemical bonds of biological-preparation's metabolites, which leads to significant biological effects. When atoms of informational macromolecules (DNA, RNA, proteins), interact with the laser beam, they acquire not only the energy of light quanta, but also the light quanta momentum of motion quantity. This creates an inverse population of nuclear Zeeman levels, i.e chemical polarization of nucleuses. The output of quantum polarization, namely, the number of excess nuclear spins at the upper Zeeman level per each absorbed quantum of light can be 30%. An inversely populated protonic-spin system can release quanta with the energy of 6.5×10^{-26} Jouls, which correspond to frequencies of about 100Mhz [Buchachenko, 1979].

In advancing the aforementioned, one can think that when bio-preparations are scanned by the laser beam, there are combinatory frequencies, occupying the blue and UV range. Moreover, as we previously suggested in the relevant model of localized light, there is transformation of frequencies in the range from 2 omega to zero. [Prangishvili, Gariaev et al, 2000 (b)]. Besides that, broadband radio irradiation of the gas discharge in the laser takes place when bio-preparations are scanned. Taking this into account, we believe that in our experiments, donor biological preparations are scanned ("read" by the laser) in multiple-frequencies. The biochemical metabolites of the biolocial

preparations interacting with dynamically polarized red light of the scanning laser (and the wide spectrum of additional radiation), can generate electromagnetic radio frequency oscillations. In this case, the preparations of pancreas and spleen "assume" the role of peculiar organ-molecular-radiostations, where all types of molecules have their own characteristic frequencies, which may be reinforced due to stochastic resonances. On the other hand, in treated diseased animals, certain types of pancreatic molecules, affected by alloxan, and/or stem cells in their blood can resonantly absorb such radiation, which carry an informational component for initiation of biochemical reactions leading to regeneration of pancreas tissues, and initiation of protective anti-alloxan processes. This does not exclude the significant role of the previously discussed mechanisms, related to teleportational and holographic properties of donor's bio-preparations. Considering well known provisions of chemistry and physics, *http://www.chem.msu.su/rus/publ/Buchachenko/buch5.html,* which dictate the quantum scenario for the given genetic-bio-chemical events. In the ensemble of molecules-products with an inversed population in Zeeman's reservoir, energy is accumulated. This energy may dissipate through heat (via spin-grid magnetic relaxation), or it can be converted into stimulated radiation at Zeeman's nuclear frequency. In this case, the reaction does, in fact, become a radio frequency emitter, quantum generator with chemical pumping (similar to chemical lasers). This new phenomenon – radiation of the chemical reaction - was predicted theoretically and then later discovered experimentally. This phenomenon occurs when Zeeman's reservoir energy exceeds the generation threshold; then, the motion of the nuclear spins spontaneously become coherent, and such a coherent system of nucleuses becomes a quantum generator, radiating within the microwave range. Yet, this is only one aspect of chemical radio-physics. A chemical reaction may not only be the generator but also the receiver of microwave radiation. Reception at the chemical level follows principles of spin chemistry: resonant microwave radiation stimulates triplet-singlet conversion of radical pairs (or pairs of

other spin carriers) and changes the output of chemical products. Thus, magnetic-spin effects make biochemical reactions receivers of microwave radiation. Moreover, such reception can be performed selectively. If the microwave pumping involves all radical pairs (biochemical substrata), then, the total result ultimately leads to a change of the output of reaction products at resonant frequencies. This effect is called *reaction yield detected magnetic resonance* (RYDMR). If the "pumping" is selective and involves only radical pairs with magnetic nucleuses, it creates the phenomenon – *radio induced magnetic isotopic effect* (RIMIE). And, finally, if the microwave "pumping" is also selective in respect to nucleuses' spin orientation (i.e. involves ensembles of radical pairs with chosen orientation of the nucleuses' spins) then, it brings *stimulated polarization of the nucleuses* (SPN). This is related to the so-called spin catalysis. It is notable for reagent's spin conversion, induced by a paramagnetic particle - spin catalyzer. Conversion occurs as a result of metabolic interaction of a catalyst (ferment) with reagents. Spin catalysis accelerates recombination of radicals, wax-isomerization of compounds with double bonds (by a factor of seven to eight), recombination of spin-polarized atoms and so on. It is possible that spin catalysis is involved into the bio-chemical processes of the discussed pancreas's regeneration and in the cyto-protective effect. Manipulation with electronic and nuclear spin, lies in the basis of spin chemistry and chemical radio-physics. When such manipulations are performed by the chemical reaction itself, magnetic-spin effects appear, including generation of microwaves, then the reaction becomes a molecular radiostation. When manipulation of spin occurs under the influence of microwaves, secondary magnetic effects are generated. They serve as indicators of microwave reception. Spin chemistry and chemical radiophysics are closely related, however, they have their individual goals. Spin chemistry investigates new principles of chemical reaction management (including management with microwaves), whereas chemical radiophysics has a significant practical bio-medical aspect.

The existance of molecular–tissue "radiostations" raises a

principle question about the cause of a highly permeable ability of modulated broadband electromagnetic radiation (MBER). Recall, one group of the rats in our experiment were placed in an isolated concrete laboratory basement and, nonetheless, the effect of MBER on the animals was authentically and reliably recorded. If the biologically (morphogenetically) active part of MBER occupies the microwave range of Zeeman's reservoir, then, this region of MBER spectrum would have been filtered by the concrete walls of the laboratory basement, where the rats were placed at the time of wave irradiation. Yet, the rats received the radiation. But how? A possible explanation could be that the electrons of Zeeman's levels energies of all metabolites, including genetic structures, whilst being placed into potential "energy hole", experience a super fine Lamb shift of those levels by about 1000Mhz. This shift is possible due to the existence of longitudinal photons of atomic nucleuses, generating its longitudinal (electrostatic) field which dipolarly excites vacuum, and moving orbital atomic electrons interact with this excitation. In turn, these electrons have their own electrostatic field, composed of similar longitudinal photons. Thus, the atomic system of electrons (alternating in time) induces around itself a composite alternating longitudinal electric field. This field, in the form of a longitudinal electric wave (LEW), moves instantly and infinitely in the entire surrounding environment. Umov-Poynting vector of this wave equals zero, i.e. a given atomic system does not emit any impulse-energy. However, there are vortexes of Maxwell's longitudinal electric field, described by the material part of biquaternions [Berezin et al, 2003]. These biquaternions are able to transfer information, which has a numerical energy equivalent of Shannon and Brillouin. Produced in such a way LEW, having abnormally (incredibly) high permeability properties, pass almost without attenuation through various obstacles (metal screens, ferromagnetics, dielectrics, concrete and so on). Cellular nucleuses and their main component – DNA – excite solitons [Smelov, 2001] of related electron waves and solitons of hypersonic oscillation of liquid crystal chromosomic structures, i.e. electron-vibron oscillations [Bersuker, 1976] or electron-nucleus wave oscillations

of DNA's double helix. The electron-vibron waves retransmit (scatter) the received LEW back into the ether and can be received by other biosystems, similar to the biosystem, affected by the primary (LEW) wave of excitation.

Due to the high Q-factor ~10^{14} of all electron-vibron oscillation systems, they have high sensitivity, estimated by fractions of Planck's quanta of energy for one element of a coherent oscillating chain, which, for example, may be a DNA spiral or cellular membrane. In open states of a DNA spiral, initiated by thermal motion in a live cell, electron-vibron oscillations exist in a form of solitonic (helicoids, spiral, vortical) motions of atoms in the strand. These are the so-called Salerno-Maslov solitons, and they are capable of reading information from the "text" of DNA-RNA sequences. Radiation of such "informational" solitons is generated by electron-vibron oscillations of DNA and RNA. Notably, information, scanned from genetic molecules, can be transmitted to other cells (and beyond biosystems) in a relay mode according to the mechanism of scattering with LEW's frequency fluctuations, radiated into the area of radio- and acoustic-frequences. Wherein, informational radio-emission of electron-vibron oscillations in the form of LEW at certain frequencies, in principle, can direct biochemical processes. And the oposite is true too: biochemical reactions in preparations, scanned by polarized laser radiation, can generate electromagnetic radiofrequency oscillations.

Due to the probable linguistic wave genetic content of vortical solitonic states, initiated on DNA and RNA molecules *in vivo*, let's consider these processes in more detail.

MATHEMATICAL MODELING OF SOLITONS ON DNA[13]

Mario Salerno was first to start computer experimention with solitons on DNA, not only as formal mathematical structures, he also tried to relate their behavior within a single-dimensional space of poly-nucleotides with their bio-genetic, or to be precise, epi-genetic functions. At the same time he advanced the first soliton theory of DNA proposed by Englander et al. This model and its further detailed variations including ours (see below) is introduced in terms of mechanical systems as a chain of oscillators (DNA bases), connected by elastic non-linear sugar-phosphate bonds. Following Salerno, our main focus was on existing already known DNA sequences and their influence on soliton behaviour. In the first stage we have replicated Salerno's experiments, yet on significantly longer DNA fragments. Indeed, kink-type soliton excitations are sensitive to the site of their initiation; and their motion along one of DNA strands (when they are "open" - dsDNA is denatured as a result of temperature fluctuations) is accompanied by a specific modulation of kinks' trajectories in time and single-dimensional space of polynucleotides. Such solitons represent structures emitting electromagnetic and acoustic fields; their inner oscillating structure is capable of reflecting and re-transmitting texts and other linguistic structures of DNA into intracellular and extracellular space, at least at the level of large blocks of sequences. Below is an example of the kink's behaviour on a fragment of a single stranded DNA of 1020 nucleotides long from bird sarcoma virus:

(5′-start) GGC CTA TGT GGA GAG GAT GAA CTA CGT GCA CCG AGA CCT GCG GGC GGC CAA CAT CCT GGT GGG GGA GAA CCT GGT GTG CAA GGT GGC TGA CTT TGG GCT GGC ACG CCT

[13] [Blagodatskikh, Gariaev et al., 1996; Gariaev, 1997]

CAT CGA GGA CAA CGA GTA CAC AGC ACG GCA AGG TGC AAG
TTC CCC ATC AAG TGG AGA GCC CCC GAG GCA GCC CTC TAT
GGC CGG TTC ACC ATC AAG TCG GAT GTC TGG TCC TTC GGC
ATC CTG CTG ACT GAG CTG ACC ACC AAG GGC CGG GTG CCA
TAC CCA GGG ATG GGC AAC GGG GAG GTG CTG GAC CGG GTG
GAG AGG GGC TAC CGC ATG CCC TGC CCG CCC GAG TGC CCC
GAG TCG CTG CAT GAC CTT ATG TGC CAG TGC TGG CGG AGG
GAC CCT GGA GGA GCG GCC CAC TTT TCG AGC TAC CTG CAG
GCC CAG CTG CTC CCT GCT TGT GTG TTG GAG GTC GCT GAG
TAG TGC GCG AGT AAA ATT TAA GCT ACA ACA AGG CAA GGC
TTG ACC GAC AAT TGC ATG AAG AAT CTG CTT AGG GTT AGG
CGT TTT GCG CTG CTT CGC GAT GTA CGGGCC AGA TAT ACG
CGT ATC TGA GGG GAC TAG GGT GTG TTT AGG CGA AAA GCG
GGG CTT CGG TTG TAC GCG GTT AGG AGT CCC CTC AGG ATA
TAG TAG TTT CGC TTT TGC ATA GGG AGG GGG AAA TGT AGT
CTT ATG CAA TAC TCT TGT AGT CTT GCA ACA TGG TAA CGA
TGA GTT AGC AAC ATA CCT TAC AAG GAG AGA AAA AGC ACC
GTG CAT GCC GAT TGG TGG AAG TAA GGT GTA CGA TCG TGC
CTT ATT AGG AAG GCA ACA GAC CGG GTC TGA CAT GGA TTG
GAC GAA CCA CTG AAT TCC GCA TCG CAG AGA TAT TGT ATT
TAA GTG CCT AGC TCG ATA CAA TAA ACG CCA TTT GAC CAT
TCA CCA CAT TGG TGT GCA CCT GGG TTG ATG GCT GGA CCG
TCG ATT CCC TAA CGA TTG CGA ACA CCT GAA TGA AGC AGA
AGG CTT CATT <= 1020 (3′-ending)

C-region of DNA (1 =>1020 nucleotides) on 3′-end of bird sarcoma virus contains several "semantically" defined segments such as the polypeptide-coding segment (between 558 and 675 nucleotides); PolA (936) - 3′-end of virus RNA, polyadenylation site; 916 nucleotide - 5′-end of virus RNA ("capping site"); Red-segment - (917-936) – short end replica of the virus genome; Pro – possible component transcription observation (between 870-900); palindrome – "pin" (870 - 912)[14] .

In Fig. 1 and 2 the kinks appear in the form of "mountain ranges" rather than as steps, as a derivative of Sine-Gordon equation function. Here the horizontal axis describes the DNA sequence, and the vertical axis describes the soliton amplitude. And

[14] Hesin R.B. "The Volatility of the Genome". Moscow, 1984, p.248

the third axis, pointed towards the reader, describes time. One can see how the change of soliton's initiation location on certain poly-nucleotide sequences significantly alters the single wave dynamics (in the form of its rotational-oscillating motions along the DNA sequence).

The examined molecule region is rich with functionally (semantically) biologically significant segments, and we reasonably expect these segments to alter, modulate, that is to introduce "textual" information into single chain DNA or RNA. This information will be realized in the oscillation spectrum of the solitonic wave along the polynucleotide chain. Such a spectrum will mirror nucleotide sequences and, by doing so, will perform the role of a genetic information message carrier. Such modulation of soliton oscillation structure is clearly observed in the presented graphs. It is plausible to believe that the spectral composition of soliton oscillation frequencies appears to be a mechanism for conversion of textual structures of DNA and RNA into waveform and a means for transmitting genetic and other messages in a single-dimentional space alongside poly-nucleotide chains, and (or) in the three-dimensional genome of a separate cell and/or of the tissue continuum of the biosystem.

This is how the computer model of soliton dynamic works. Englender was the first to apply mathematical modeling to solitons, that was later developed by Salerno. Salerno formally described rotational oscillations of DNA molecule nucleotides in order to explain experimental data from hydrogen-tritium exchange in DNA. In accordance with Engleder's model, "open states" ("melting" of DNA double-helix in short segments, enriched by AT-couples) in the form of localized dislocations can appear and propagate within DNA strand.

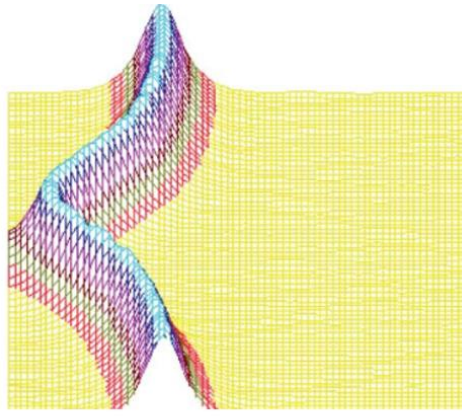


Fig 1. Effects of nucleotide DNA dynamics by a conforming perturbation on a soliton wave. Nucleotide sequence – bird sarcoma virus (first 600 pairs) Epicenter of the perturbation – 400th nucleotide.

y – soliton amplitude; ***x*** – polynucleotide length (quantity); ***z*** – time.

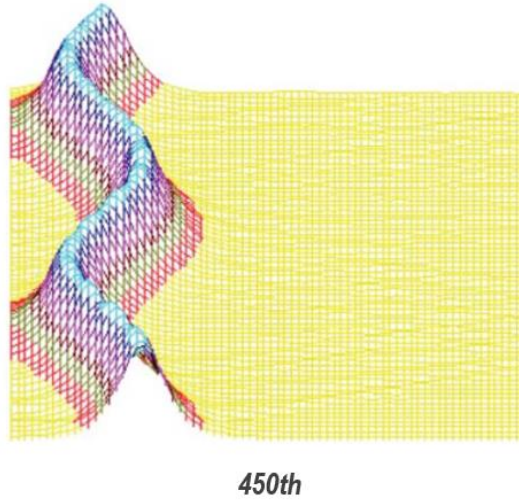


Fig 2. Effects of nucleotide DNA dynamics by a conforming perturbation on a soliton wave. Nucleotide sequence – bird sarcoma virus (first 600 pairs) Epicenter of the perturbation – 450th nucleotide.

Mario Salerno, continuing the works of Englender in a simplified version, discovered an influence of nucleotide sequence on non-linear solitonic dynamics of rotational oscillations of nucleotides within single-stranded DNA segments, which form such "open state" regions. Later, Yakushevich, Fedyanin and Homma et al. reviewed various generalizations of Englender's model, evaluating the specifics of DNA structure, considering the breakage of hydrogen bonds during base pair opening, pairedness of DNA strands and other degrees of freedom, different from rotational. However, the above-mentioned works hardly said anything about the causes of base pair opening in DNA. We propose a possible mechanism for this process in DNA, which is an alternative to Englender's hypothesis that thermal noise is the reason for base pair opening. We think that base pair opening in DNA happens with a change in the period of the DNA spiral (to a large extent this idea belongs to Maslov M.Yu.). In our model, DNA nucleotides are viewed as oscillators, suspended on a weightless non-extendable pivot: sugar-phosphate bonds between neighbouring nucleotides in a strand are modeled by linear springs; spiralisation along the strand is not taken into account; hydrogen bonds between complementary bases are modeled by "gravitational" potential. The Hamiltonian operator, in accordance to M. Salerno, looks as follows:

$$H = \sum_{i=1}^{N} \frac{1}{2}\{I_i(\varphi_i^2 + \theta_i^2) + K_i(\phi_{i+1} - \phi_i)^2 + \overline{K}_i(\theta_{i+1} - \theta_i)^2\} + \lambda_i\beta[1 - \cos(\phi_i - \theta_i)], \quad (1)$$

where: θi,φi nucleotides' rotational angles in different strands, $K_i, \overline{K}_i$ constants of elasticity along strands, $\boldsymbol{N}$ — number of pairs in a strand, $\boldsymbol{I_i}$ — inertia moment of the bases, $\boldsymbol{\beta}$ — elasticity constant of the hydrogen bonds bentween complementary bases.

Coefficient $\boldsymbol{\lambda_i}$ in equation (1) is determined according to the rule: $\boldsymbol{\lambda_i = 2}$ in case of pairs AT and TA, $\boldsymbol{\lambda_i = 3}$ in case of pairs GC and CG; $\boldsymbol{\beta = 2 \times 10^{-3}}$ parameter, determined by Fedyanin and

Yakushevich[15] and obtained on the basis of sine-Gordon equation and experimental data. Later on for the sake of model simplification, it is considered that $K_i = \overline{K}_i = K,\ I_i = I$.

Motion equation for the difference $\varphi_i = \phi_i - \theta_i$, derived from (1), according to M. Salerno, can be presented as:

$$\ddot{\varphi}_i = \varphi_{i-1} - 2\varphi_i + \varphi_{i+1} - \lambda_i \beta \sin(\varphi_i). \qquad (2)$$

where substitution was made $t \to \sqrt{\frac{I}{K}}\, t$.

In case of $\boldsymbol{\lambda_i = \lambda = 1}$, in the system (2) it is possible to go to the finite differential sine-Gordon equation:

$$\varphi_{tt} = \varphi_{xx} - \sin\varphi, \qquad (3)$$

"continuous analog" of the system (2). This equation has solitonic solutions, namely, single-solitonic solutions, or kink, corresponding to dislocation in the DNA strand.

The main assumption of the Englender-Salerno models is that interaction between complementary bases is described by the potential $V(\varphi) = 1 - \cos(\varphi)$ (4), where hydrogen bond breakage is not taken into account.

In our work we look at the following potential:

$$\bar{V}_C(\varphi) = \begin{cases} 1 - \cos\varphi, & \cos\varphi > \cos C \\ 1 - \cos C, & \cos\varphi \le \cos C \end{cases}.$$

Besides that, the viscosity of the water medium is taken into account (the viscosity of water is $\boldsymbol{\gamma \sim 1}$).

We also look at the factors, leading to DNA spiralization; wherein they are considered to be external forces, determined by the potential

[15] Fedyanin I.A., Yakushevich L.V.// Stud. Biophys. 1984.V.103.P.171

$$\bar{V}_C^L(\varphi_i, i) = \begin{cases} 1 - \cos\big(\varphi_i + L \cdot (i-1)\big), & \cos\varphi > \cos C \\ 1 - \cos\big(C + L \cdot (i-1)\big) & \cos\varphi \le \cos C \end{cases},$$

$$L = \frac{2 \cdot \pi}{D},$$

where $\boldsymbol{D}$ — spiral's period.

Equations (2) with the potential $\bar{V}_C^L(\varphi_i, i)$ with consideration of viscocity take the following form:

$$\ddot{\varphi}_i = \varphi_{i-1} - 2\varphi_i + \varphi_{i+1} - \frac{\partial \bar{V}_C^L}{\partial \varphi}(\varphi_i, i). \qquad (5)$$

It is known that DNA spiral period changes according to humidity. In particular, for a crystalline DNA $\boldsymbol{D_0 = 10}$ in, but in a water medium $\boldsymbol{D_1}$ varies from 10.3 to 10.6. This is the very factor causing the phenomenon of spiralization. When the spiral period in DNA is changed (with fixed and locked ends), the result is tension, related to a lack or excess of spiral turns (necessary for its relaxed state). If $\boldsymbol{D_{Dry} - D_{Water} = 0.5}$, then, during transition from dry to moist conditions for a strand of 300 base pairs long, an excess occurs of $\boldsymbol{250 \cdot D_{Dry}^{-1} - D_{Water}^{-1} \approx 1.2}$.

Based on results of numerical modelling, given below, it is assumed that the change in the spiral period can lead not only to superspiralization, but also to local divergence of both complementary DNA strands. Furthermore, during superspiralization, the tension in the strand is not released completely, that is why local divergence possibly may take place simultaneously with superspiralisation.

The system (5) is numerically integrated in the interval $\boldsymbol{T} \in [\boldsymbol{0.2000}]$ with the increments of $\boldsymbol{\Delta T = 0.1}$. The initial conditions were the following:

$$\varphi_i(0) = \varphi_i^D(0), \quad \dot{\varphi}_i(0) = \varphi_i^D(0), \quad D = D_1,$$

Spiral period in the system (5) is $\boldsymbol{D = D_1}$, the length of *poly*(A)-strand is 300 base pairs. That is, the parameters of the spiral period in the initial conditions and in the system (5) are different. Thus, the DNA transfer from a crystalline state to a moist state

(close to the *in vivo* state) was modeled.

The boundary conditions are the follows (we call them "quasi-cyclic"):

$$\varphi_0 = \varphi_N - T,\ \ \varphi_{N+1} = \varphi_1 - T,\ \ T = \varphi_N = \varphi_1.$$

A distunguishing factor of this model is that during the transition from a state with a spiral period of 10 base pairs to a state with a spiral period of 10.5 base pairs, almost the whole strand is denatured ("melted"). The result given below describe the process of renaturing of such a strand, with the appearence of dislocations.

The following parameters varied in these experiments:

1) the dissipation $\boldsymbol{\gamma = 0.1 \ldots 1}$,

2) the ratio of the elasticity parameters $\boldsymbol{\beta / K = 0{,}1 \ldots 0.5}$,

3) the angle of hydrogen bonds breaking $\boldsymbol{C = \varphi_{cut} = 10^0 \ldots 20^0}$.

Fig. 3 and 4 present the results of numerical integration of system (5). They show not the function itself $\boldsymbol{\varphi(x,t)}$, but the difference $\boldsymbol{\varphi(x,t) - \varphi^{D1}(x)}$, as the area of the function change $\boldsymbol{\varphi(x,t)}$ (approximately from 0 to 160) is too large compared to the characteristic changes in the system (approximately from 0 to 9). The horizontal part of the graphs correspond to non-dislocated/undenatured DNA segment (double strand) with a spiral period $\boldsymbol{D_1}$. The inclined part of the graphs in Fig. 3 (a), 4 (a) corresponds to dislocation.

Based on this model, we can assume that

1) the ability to form dislocations in this model is strongly dependent on $\boldsymbol{\varphi_{cut}}$. When $\boldsymbol{\varphi_{cut} = 20^o}$ dislocation took place in all cases.

2) the ability to form dislocation also depends strongly on the parameter $\boldsymbol{\beta/K}$. In all cases, when parameter $\boldsymbol{\beta/K}$ is large ($\boldsymbol{\beta/K = 0.5}$), in Fig. 1(a) and 2(a), dislocation took place. Comparison of Fig. 3(a) and 4(g) also provides evidence for this.

As additional calculations show, the influence of $\boldsymbol{\gamma}$ on effect is less pronounced. Dislocation is formed or not formed regardless

of the γ value ($\gamma = 1$ or $\gamma = 0.1$). For larger values of γ, the dislocation occurs slower than for smaller values.

3) Figures 3(a), 4(c, d), show that the dislocation has a kink-like form.

The dislocation width depends on the parameters β/K (the greater β/K, the smaller the dislocation width) and φ_{cut} (the greater φ_{cut}, the smaller the dislocation width).

Further developing the models of soliton excitations in DNA (together with Maslov et al.), we applied conditions, where DNA strands are modeled by a set of rovibronic oscillators, suspended on a weightless non-extendable pivot; for simplicity of spiralization, strands are not taken into account, and rovibronic degrees of freedom of one of the strands are considered "frozen".

In this case, the Hamiltonian operator for the "active" strand is as follows:

$$\begin{aligned} H &= H_0 + H_1 + H_2 \\ H_0 &= \frac{1}{2}\sum_{i=1}^{N} I\varphi_i^2, \\ H_1 &= \frac{1}{2}\sum_{i=1}^{N} K\left(1-\cos\Delta\varphi_i^2\right), \\ H_2 &= \sum_{i=1}^{N} \lambda_i\ \beta[1-\cos\varphi_i] \end{aligned} \qquad (1)$$

where: N - the number of base pairs in the strand; H_0 – Hamiltonian, describing own monomers' oscillations (φ_i - rotation angles of nucleotides in the strand, I – inertia moment of the bases); H_1 – Hamiltonian, characterizing non-linear-periodic bond between the oscillators (K - constant of strand elasticity, $\Delta\varphi_i = \varphi_{i+1} - \varphi_i$), H_2 – Hamiltonian.

For small $\boldsymbol{\Delta\varphi_i}$ Hamiltonian $H_1 = \frac{1}{2}\sum K\Delta\varphi_{i,}^2$ which coincides with the corresponding part of the general Hamiltonian, used earlier (see above). In this case the equations of motion for $\boldsymbol{\varphi_i}$, derived from (1) have the form:

$$\varphi_i = \varphi_{i-1} - 2\varphi_i + \varphi_{i+1} - \lambda_i\beta\sin(\varphi_i) \qquad (2)$$

where there was a replacement of $t' \to \sqrt{\frac{1}{K}}t$.

If $\boldsymbol{\lambda_i} = \boldsymbol{\lambda}$ in the system (2), we can go to a finite differential of sine-Gordon equation:

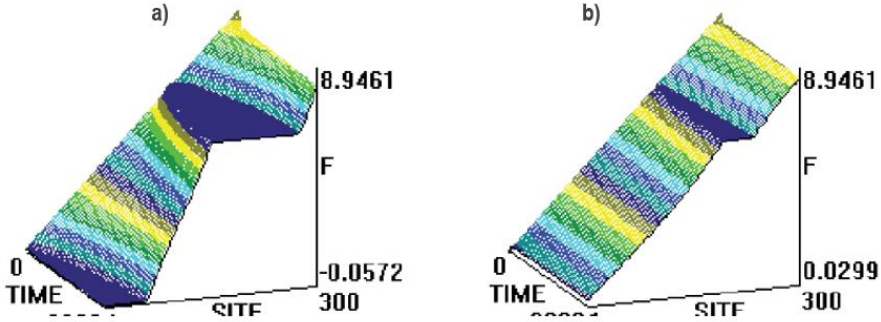
$$\varphi_{tt} = \varphi_{xx} - \sin\varphi, \qquad (3)$$

"continuous analog" of the system (2). This equation has soliton solutions, namely, single-soliton-solution, or kink, which describes the dynamics of the dislocations distribution in the strand.

In accordance with (1), a system of nonlinear equations of motion is written as follows:

$$\ddot{\varphi}_i = \sin(\varphi_{i-1} - \varphi_i) + \sin(\varphi_{i+1} - \varphi_i) - \lambda_i\frac{\beta}{K}\sin(\varphi_i) \qquad (4)$$

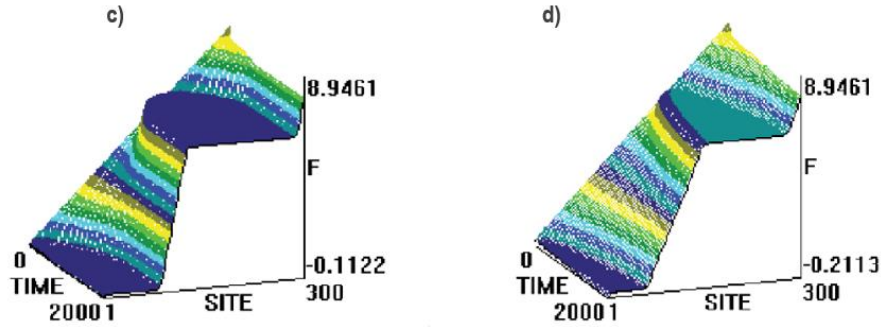
As you can see, systems (2) and (4) are significantly different. Note, however, that executed numerical modeling of dynamics for the systems (2) and (4) showed the following: if we choose a single-soliton solution of its "continuous analog" (3) - kink (see above) as initial conditions for numerical integration (2), there will be critical similarities in the solution types.



a) γ=1, β/K=0.5, φ_{cut}=10^0
a)***x0=200***

b) γ=1, β/K=0.1, φ_{cut}=10^0
b)***x0=250***

Fig 3.



c) γ=1, β/K=0.5, φ_{cut}=20^0
c) ***x0=300***

d) γ=1, β/K=0.1, φ_{cut}=20^0
d) ***x0=350***

Fig 4. Describes the nonlinear relationship between "active" and "frozen» ($\boldsymbol{\varphi_i = 0}$) DNA strands ($\boldsymbol{\beta}$ – elasticity constant of hydrogen bonds between complementary bases, $\boldsymbol{\lambda_i}$ coefficients in equation (1) are determined in accordance with the rule: $\boldsymbol{\lambda_i = 2}$ in the case of AT and TA pairs, $\boldsymbol{\lambda_i = 3}$ in the case of GC and CG pairs; $\boldsymbol{\beta = 2 \times 10^{-3}}$ - the parameter obtained earlier (see above) and determined on the basis of sine-Gordon equation.

However, when the initial conditions are given in the following form:

$$\varphi(x,0) = \varphi^0(x) = \begin{cases} 0 & A(x-x_0) < 0 \\ A(x-x_0) & 0 \le A(x-x_0) \le 2\pi, \\ 2\pi & A(x-x_0) > 2\pi \end{cases}$$

$$\dot{\varphi}(x,0) = \dot{\varphi}^0(x) = \begin{cases} 0 & A(x-x_0) < 0 \\ 1 & 0 \le A(x-x_0) \le 2\pi, \\ 0 & A(x-x_0) > 2\pi \end{cases} \quad (5)$$

where $\boldsymbol{\varphi^0(x)}$ – "step" function with a $\boldsymbol{2\pi}$ step height and the angle of the inclination of the shoulder $\boldsymbol{A}$, the difference in the dynamics of given systems was revealed (compare Figures 1, 2, and 3.).

More precisely, systems (2) and (4) were numerically integrated by the Runge-Kutta method of order 4 with initial conditions, specified in the form (7), in the interval $\boldsymbol{T \in [0,750]}$ with an increment of $\boldsymbol{\Delta T = 0.1}$. The border conditions - "quasi-cyclic":

$$\varphi_0 = \varphi_N - T, \quad \varphi_{N+1} = \varphi_1 - T, \quad T = \varphi_N = \varphi_1.$$

$\boldsymbol{\lambda_i} = 2$ (poly-A-sequence). The system parameter $\boldsymbol{\beta/K = 0.1}$. The parameter $\boldsymbol{A}$ (angle of the inclination of the shoulder of the function $\boldsymbol{\varphi^0(x)}$) was varied.

Numerical integration of the system (2) showed that two solitary waves are formed, moving from right to left along the strand with a constant velocity. The first wave has a quasi-kink form, and the second wave has a quasi-briser form, wherein, the velocity of the first wave exceeds the one of the second. Both waves, due to "quasi-cyclic" border conditions, after arriving to the left end, appear in the right end without any changes in their form. A quasi-kink wave, traversing along the chains of pendulums, changes the coordinate of each pendulum to a certain angle (the pendulum makes a full cycle). Therefore, traversing through the closed-loop chain of pendulums $\boldsymbol{K}$ times, it changes the coordinate of each pendulum by the angle $\boldsymbol{K \times 2\pi}$. This explains the "shoulder-like" form of the graphs. Fig 2. shows the integration results for system (4) under the same conditions. The figure shows that the same two solitary waves are formed – quasi-kink and quasi-briser. Yet, the principal distinction from the previous case is that in the very

beginning the quasi-kink wave moves with a negative acceleration, so that as a result its velocity turns out to be slower than the velocity of the quasi-briser. Note, that these experiments were conducted on homogeneous *poly*-A-sequence; so the change of the quasi-kink velocity cannot be explained by the influence of non-homogeneous nature of the strand. This effect is explained by non-linear interaction between its monomers.

Fig. 3 illustrates the results of integration for the system (4) with similar conditions, except that ***A=2***. In this case, only a quasi-kink wave is realized and its negative accelation in the beginning eventually makes it move in the direction opposite to initial. With implementation of the system (2) under similar conditions also only a quasi-kink wave is formed. And its velocity does not change in comparison with the case shown in Fig 1.

Importantly, under appropriate conditions in a system of DNA or RNA type, over excited rovibronic states may take place. In quantum language this would be similar to a re-population of highly located quantum levels compared to the base levels (realization of population inversion). In this case, an attractive idea may come to mind, an idea that the invention of a bio-solitonic laser (BSL) on DNA molecules[16] may be possible.

However, in the theory of biopolymer dynamics, it is well known that conformational motions are realized according to the mechanism of limited diffusion, due to the strong influence of dissipative forces from the micro-environment. For this reason, the solution to the problem for the creation of a bio-solitonic laser (on DNA) looks quite problematic. At least, for the proof of the idea it is necessary to fulfil the conditions $\tau \approx \frac{\Delta x}{v} < \tau_{diss}$, where Δx and v - soliton width and velocity respectively, τ_{diss}- dissipation time. If $\Delta x = 5\text{A}$ and $v = 10^5 cm/s$ (the velocity of sound), we get $\tau_{diss} > 5 \times 10^{13} \boldsymbol{s}$. Note that the characteristic time of the dissipation due

[16] Note also the idea of J.N. Zhivlyuk, associated with the creation of lasers based on the phase transitions of bio-macromolecules (personal correspondence).

to water hydrodynamic forces is $\tau_{diss} = 10^{12} \div 10^{10}\boldsymbol{s}$ and attenuation time, determined by the processes within the molecule itself is $\tau_{diss} = 10^{11} \div 10^{9}\boldsymbol{s}$ (see, for example, Shaitan K.V. Biophysics. Moscow, 1994. V .39. P.949 Chernavsky et al. 1986. № 287. P. 21.).

There is also another complication, related to self-concordance between biosolitons and electromagnetic wave reradiation. Let us remember that mathematical modeling in this case was conducted on monotonous *poly*-A-DNA and therefore, it was unclear whether heterogenic natural DNA sequence has any influence on the dynamics of solitonic excitation in a molecule. To test this, as earlier, a DNA C-region from the 3′-end of bird sarcoma virus was used as a testing ground for soliton initiation at various segments of the polymer. This time the function derivative was calculated to better illustrate the motion of solitons.

Similar to Fig. 1-3, Fig. 5-7 distinctly shows significant modifications in solitons' behavior when altering parameter **A**. This is especially evident in Fig. 7, where the solitonic wave travels, similar to the one in Fig. 5-6, at first to the left and then sharply turns to the right. This has a certain biological significance. Soliton as a potential DNA "reader" must "review" prolonged contextual zones, rather than get stuck, fluctuating sinusoidally on the same "words" - locuses of DNA and RNA.

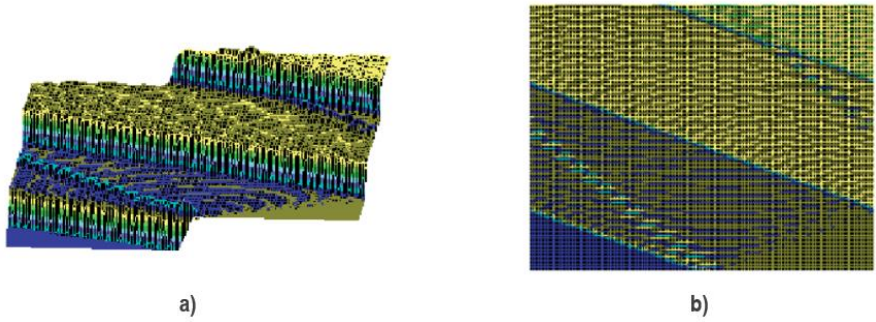


Fig 5. Results of numerical modelling of excitation propagation dynamics in DNA based on system (2) where parameter ***A=1.*** a) Side view b) Above view.

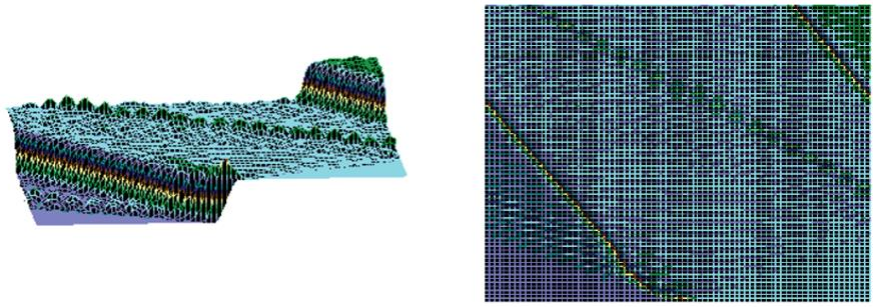


Fig 6. Results of a numerical modelling of excitation propagation dynamics in DNA based on system (4) where parameter ***A=1.*** a) Side view b) Above view.

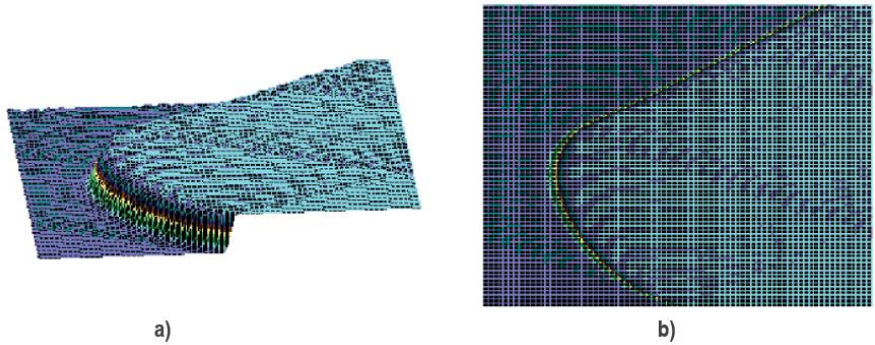


Fig 7. Results of numerical modelling of excitation propagation dynamics in a DNA based on system (4) where parameter ***A=2.*** a) Side view b) Above view.

Considering non-linearity of co-valent bonds in the sugar-phosphate DNA backbone, then, we observe additional features of solitons' behavior (Fig. 8-10): the shift of a solitonic wave initiation area within the birds sarcoma virus DNA-fragment between the 200th and 500th nucleotide, then, these are additional rotational waves of oscillations, propogating in both directions from the main excitation wave. Bouncing back from the fixed DNA ends (*in vivo* nucleosomes act as fixators), they return to the central excitation and further modulate it. Such additional waves play a role of "informants" about nucleotide composition and bases' sequence in the scanned segment of DNA or RNA, and this information can be "memorized" on the level of return of the Ferni-Pasta-Ulam

Problem and be used by the chromosomal biocomputer for making appropriate “decisions”.

A substantial feature, DNA “scanning” by solitons is especially well seen in Fig. 8-10. This is the presence of additional (besides the main one) trajectories of solitons with rich modulation. Such additional modulated solitons’ trajectories (with a kink and briser structure) can bear additional subtle nuances of distribution of wave genetic information along the DNA and RNA strands.

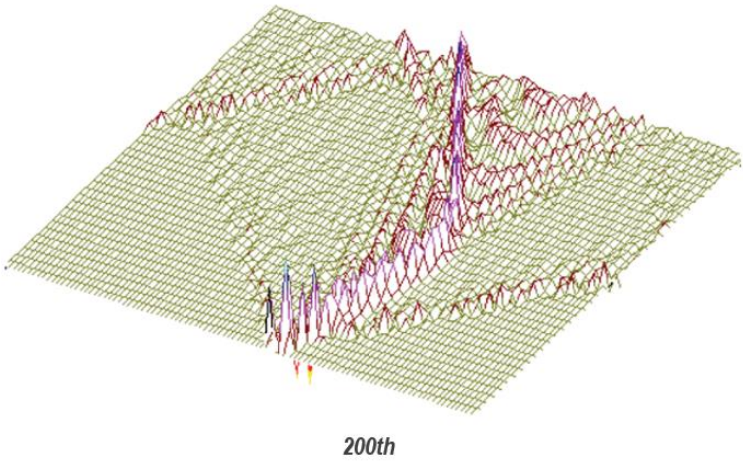


Fig. 8 DNA solitonic excitation, taking into account non-linearity of covalent bonds in the sugar-phosphate DNA backbone. Nucleotide sequence – bird sarcoma virus (first 600 base pairs). Excitation center – 200th nucleotide.

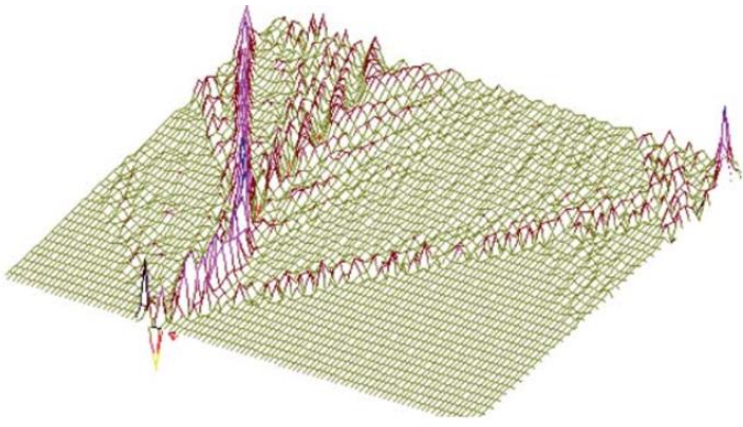


Fig. 9 Same as in Fig.8, but excitation center – 400th nucleotide

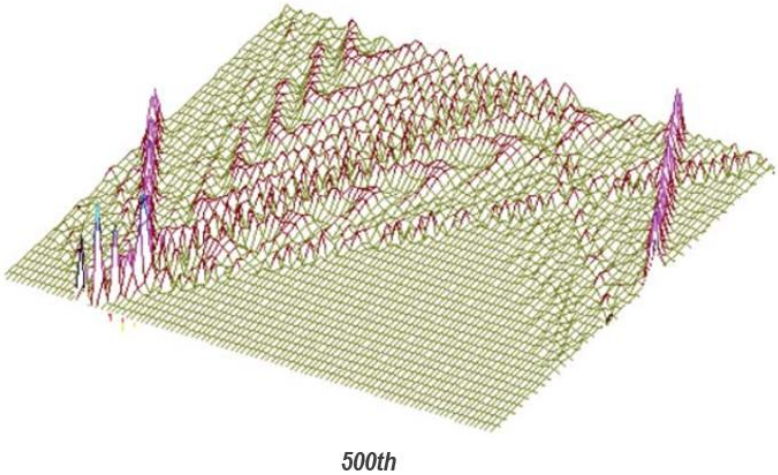


Fig. 9 Same as in Fig. 8,9, but excitation center – 500th nucleotide

ANTENNA MODEL

Earlier, we have noted [Gariaev, Maslov et all, 1996 (a); Gariaev, Maslov et all., 1996 (b)], that proteins are the main molecules (if not the primary molecules), which perceive external electromagnetic fields as regulatory fields. This is especially true for metalloproteins. Functioning of some biological macro-molecules (namely, ferments) is largely determined by processes, taking place in the active centres, surrounded by biopolymer strands with a linguistic topology. Taking such a view on informational bio-macro molecule structure, it is natural to assume that their interaction with physical fields, external in relation to the biosystem and internal (organismic) radiations, leads to excitation of dipolar-active oscillations of monomers, forming the given biopolymer strands, and the latter in turn induce oscillation in the active centre. In other words, such system will work as a kind of antenna. These excited oscillations may lead to bio-macro-molecule transformation into other conforming (topological, linguistic) state.

This concept is valid for a whole set of functionally vitally important bio-macro-molecules, for example, chlorophyll, haemoglobin, myoglobin and so on. These macromolecules have in common two structural features:

1) there is an ion in their geometrical centre (in the case of chlorophyll – magnesium, in the case of haemoglobin – iron);

2) four pyrrole rings (pseudo flat structure) are symmetrically placed near the ion.

Other types of polymers, valid for the antenna model, could be represented by relatively simple cycles, such as valinomycin (potassium ions' carrier) and complex supramolecular chromosome structures, DNA of which contains highly organized associates of such metals as magnesium, calcium, nickel, cobalt, copper, iron, zinc and others. Wherein, their role is not clear and mainly reduced by researchers to neutralization of OH-groups of polynucleotide phosphoric acid remnants. It seems to us that metals functions in

DNA and RNA are substantially broader and are realized in accordance with linguistic and/or energy interaction with physical fields, endogenous and exogenous in relation to the biological-system. The same is valid for proteins without a porphyrin centre, which still in a specific way bind metals. For example, these could be site-specific proteins with "zinc-fingers" type of domain, which participate in gene regulation are often are far away from those directing proteins. Metal atoms of DNA and proteins can resonantly interact via electromagnetic channels within the framework of this antenna model. Let us define the concept of antenna model.

External energy (in particular, related to resonant interaction of high-frequency electromagnetic radiation with proteins) reaches the periphery, that is onto the ensemble of sub-units (not necessarily identical in structure). As the result of active "conversation", predetermined by bio-chemical bonds between the peripheral acceptors (which have received encoded energy) and the associate-centre (in this case, the ion of heme-containing proteins' metal), the latter receives the energy (information) and this initiates a biological action. The degree of bio-macro-molecules reactive ability depends, to a large extent, on the level of excitation of the central sub-units. Let's look at the potential mechanisms of physical fields wave interactions with the active centres of informational bio-macro-molecules within the framework of proposed antenna model.

As an example of the simplest model for illustration of the antenna effect, let's consider a 2-dimentional closed (cyclic) monomeric strand. In the centre of this cyclic strand, there is an active centre, related to the monomers of the strand by dipole-dipole interaction.

Let's mark the coordinate shifts of monomers as $\boldsymbol{x_1}, \dots, \boldsymbol{x_{N'}}$, and the shift of the active centre as $\boldsymbol{y}$. For the potential function we have:

$$U(x_1,\dots,x_N,y)=\sum_k\left[\omega_x^2x_k^2+\frac{\xi_x}{3}x_k^3\right]+\omega_y^2y^2+\frac{\xi_y}{3}y^3+$$
$$+\sum_k\frac{\omega_{xx}^2}{2}[(x_k-x_{k-1})^2+(x_k-x_{k+1})^2]+$$
$$+\sum_k\frac{\xi_{xx}}{3}[(x_k-x_{k-1})^3+(x_k-x_{k+1})^3]+\cdots \quad (1)$$

The first two terms in (1) correspond to the oscillations of monomers (the second term takes into account the anharmonicity); the last two terms are responsible for communication between the monomers, remaining members are responsible for interaction between the monomers and the active centre.

The equation of motion can be written as:

$$\ddot{x}_k+2\lambda\dot{x}_k=\frac{\partial U}{\partial x_k}+f(t),\qquad \ddot{y}+2\lambda y=\frac{\partial U}{\partial y}, \quad (2)$$

where $f(t)=f_0\cos\omega t$ external monochromatic force, acting only on monomers, $\boldsymbol{\lambda}$ - coefficient of attenuation, introduced phenomenologically (for the sake of simplicity, considered to be the same for monomers and for the active center).

With regard to (1), the system of equations (2) takes the form:

$$\ddot{x}_k+\lambda\dot{x}_k=-\omega_x^2x_k-\xi_xx_k^2-\omega_{xx}^2(x_{k-1}-2x_k+x_{k+1})+$$
$$+\omega_{xy}^2(y-x_k)+\xi_{xy}(y-x_k)^2+f(t), \quad (3)$$
$$\ddot{y}+\lambda\dot{y}=-\omega_y^2y-\xi_yy^2-\omega_{xy}^2\sum_{k=1}^{N}(y-x_k)+\xi_{xy}\sum_{k=1}^{N}(y-x_k)^2,$$
$$x_k+\lambda x_k+\left(\omega_x^2+\omega_{xy}^2\right)x_k-\omega_{xy}^2y=$$
$$=-\omega_{xx}^2(x_{k-1}-2x_k+x_{k+1})+\omega_{xy}^2x_k+\xi_{xy}(y-x_k)^2+f(t),$$
$$y+\lambda y+\left(\omega_y^2+\omega_{xy}^2N\right)y-\omega_{xy}^2\sum_{k=1}^{N}x_k=\xi_yy^2$$
$$-\xi_{xy}\sum_{k=1}^{N}(y-x_k)^2. \quad (4)$$

Let's introduce the common coordinate for the ensemble of monomers:

$$x = \sum_{k=1}^{N} x_k \tag{5}$$

Then, the system of equations (4) in the linear approximation takes the form:

$$\begin{gathered} \ddot{x}_k + \lambda \dot{x}_k + \omega_1^2 x_k - \omega_0^2 y \\ = -\Omega_0^2 (x_{k-1} - 2x_k + x_{k+1}) + \xi_x x_k^2 + f(t), \\ \ddot{y} + \lambda \dot{y} + \omega_2^2 y - \omega_0^2 x = 0, \end{gathered} \tag{6}$$

where:
$\omega_1^2 = \omega_x^2 + \omega_{xy}^2$,
$\omega_2^2 = \omega_y^2 + N\omega_{xy}^2$,
$\omega_0^2 = \omega_{xy}^2$,
$\Omega_0^2 = \omega_{xx}^2$,
$\boldsymbol{N}$ – is the number of monomers.

Taking into account (5), we have

$$x + \lambda x + \omega_1^2 x - N\omega_0^2 y = Nf(t), \tag{7.1}$$

$$y + \lambda y + \omega_2^2 y - \omega_0^2 x = 0. \tag{7.2}$$

From (7.2) follows

$$x = \frac{1}{\omega_0^2}(y + \lambda y + \omega_2^2 y) = 0. \tag{8}$$

Substitution of (8) into (7.1) gives

$$y^{(4)} + 2\lambda y^3 + (\omega_1^2 + \omega_2^2 + \lambda) y^{(2)} + \lambda(\omega_1^2 + \omega_2^2) y^{(1)} + (\omega_1^2 \omega_2^2 + N\omega_0^4) y = N\omega_0^4 f(t). \tag{9}$$

The corresponding characteristic equation has the form (after substituting $\boldsymbol{y = e^{kt}}$ into the homogeneous equation):

$$(k^2 + \lambda k + \omega_1^2)(k^2 + \lambda k + \omega_2^2) = N\omega_0^4 \tag{10}$$

Denoting $z_k = k^2 + \lambda k$, we get

$$z^2 + (\omega_1^2 + \omega_2^2)z + \omega_1^2\omega_2^2 - N\omega_0^4 = 0,$$

so that

$$z_{1,2} = -\frac{1}{2}(\omega_1^2 + \omega_2^2) \pm \sqrt{(\omega_1^2 + \omega_2^2)^2 + \omega_1^2\omega_2^2 - N}\omega_0^4. \qquad (11)$$

In the future, we assume these statements to be validated:

$$\omega_1^2 < \frac{\omega_1^2\omega_2^2}{\sqrt{N}}, \qquad \sqrt{\omega_1^2 + \omega_2^2}. \qquad (12)$$

The first condition corresponds to the case of weak interaction between monomers and the active center, the second corresponds to the small attenuation of monomer oscillators.

For our values we have

$$k_{1,2} = -\frac{\lambda}{2} \pm \sqrt{\Omega_1^2 - \frac{\lambda^2}{4}}, \qquad k_{3,4} = -\frac{\lambda}{2} \pm \sqrt{\Omega_1^2 - \frac{\lambda^2}{4}}, \qquad (13)$$

where collective frequences are introduced:

$$\Omega_1 = \left\{\frac{1}{2}(\omega_1^2 + \omega_2^2)^2 + \left[\frac{1}{4}(\omega_1^2 - \omega_2^2)^2 + N\omega_0^4\right]^{1/2}\right\}^{1/2},$$

$$\Omega_2 = \left\{\frac{1}{2}(\omega_1^2 + \omega_2^2)^2 - \left[\frac{1}{4}(\omega_1^2 - \omega_2^2)^2 + N\omega_0^4\right]^{1/2}\right\}^{1/2}. \qquad (14)$$

We are interested in the forced oscillations (the external force $f_0\cos\omega t$):

$$y = A\cos\omega t + B\sin\omega t. \qquad (15)$$

Substitution of (15) into (9) and equating corresponding coefficients, where $\cos\omega t$ and $\sin\omega t$, lead to the system of algebraic equations:

$$\begin{cases} A(\omega^2 + \alpha_2\omega^2 + \alpha_0) - B(2\lambda\omega^3 + \alpha_1\omega) = F_0 \\ A(2\lambda\omega^3 + \alpha_1\omega) - B(\omega^4 + \alpha_2\omega^2 + \alpha_0) = 0 \end{cases},$$

where:

$\alpha_0 = \omega_1^2\omega_2^2 + N\omega_0^4$,

$\alpha_1 = \lambda(\omega_1^2+\omega_2^2)$,
$F_0 = N\omega_0^2 f_0$.

As a result we get

$$y = \frac{F_0}{\sqrt{p^2+q^2}}\cos(\omega t + \varphi),$$
$$p = (\omega^2 - \omega_1^2)(\omega^2 - \omega_2^2) + \lambda^2\omega^2 + N\omega_0^4,$$
$$q = \lambda\omega(2\omega - \omega_1^2 - \omega_2^2),$$

where $\tan\varphi = \frac{q}{p}$.

After simple but cumbersome transformations for the forced oscillations of the active center, we get:

$$y = \frac{N\omega_0^2 f_0\cos(\omega t+\varphi)}{\sqrt{(\omega^2-\Omega_1^2)(\omega^2-\Omega_2^2)+\omega^2\lambda^2\left[\omega^2\lambda^2+(\omega^2-\Omega_1^2)^2+(\omega^2-\Omega_2^2)^2\right]}}. \quad (16)$$

From (16) we see that the highest amplitude of the forced oscillations of the active center is achieved under condition of a collective resonance: of either $\boldsymbol{\omega = \Omega_1}$, or $\boldsymbol{\omega = \Omega_2}$.

In any of these cases, for the forced fluctuations amplitude we have:

$$y = \frac{N\omega_0^2 f_0}{\omega\lambda\sqrt{\omega^2\lambda^2+\left(\Omega_1^{2^2}-\Omega_2^2\right)}}. \quad (17)$$

From (17) it follows that the greatest effect of the resonant swing of the active center is achieved under condition of a greater number of “antenna” peripheral subunits, under the condition of a higher value of the coefficient describing the intercation of the active center with monomers, and under condition of the lowest coefficient of attenuation and the smallest disbalance of collective modes.

It is also easy to identify the "choreography" (the dynamics of forced oscillations) of the individual monomer units. In accordance with (6), the equation for $\boldsymbol{k}^{th}$ monomer can be written as:

$$\ddot{x}_k + 2\lambda\dot{x}_k + \omega_0^2 x_k = \Omega_0^2(x_{k-1} - 2x_k + x_{k+1}) + \omega_0^2 y + f(t). \quad (18)$$

Introducing the collective coordinates

$$z_m = \sqrt{\frac{2}{N+1}} \sum_{k-1}^{N} \frac{\sin mk\pi}{N+1} x_k , \qquad m = 1, \dots N$$

and applying the method from linear algebra, for the forced oscillations of monomers we obtain:

$$x_k = \sqrt{\frac{2}{N+1}} \sum_{m-1}^{N} \frac{\sin mk\pi}{\sqrt{(\omega^2 - v_m^2)^2 + \lambda^2 \omega^2}} [f_0 \cos(\omega t + \delta_{m1}) + y_0 \cos(\omega t + \delta_{m2})]. \qquad (19)$$

where

$v_m^2 = \omega_0^2 + \Omega_0^2 \sin^2 \frac{m\pi}{2N+1}$,

$m = 1, \dots N$,

$$s_m = \sqrt{\frac{2}{N+1}} \cdot \frac{\sin \frac{\pi}{2} m \cdot \sin \frac{\pi}{2} \frac{N}{N+1}}{\sin \frac{\pi}{2} \frac{m}{N+1}}$$

y_0- is determined from (16).

Thus, within the framework of antenna model, the maximum effect of an external monochromatic field $f(t) = f_0 \cos \omega t$ is realized under the condition of collective resonance:

$$\Omega_1 = \omega, \quad \Omega_2 = \omega .$$

Repeating the arguments of section 2, we can make the following conclusions:

1) When the the external signal amplitude modulation is realised, there are additional possibilities for resonant influence on bio-macro-molecules at the frequencies:

$$\Omega_{1,2} = \begin{cases} \omega, \\ \omega + \Omega, \\ \omega - \Omega. \end{cases}$$

2) Consideration of non-linearity during quadratic relation for a monochromatic signal introduces an additional resonance at the second harmonic $\boldsymbol{\Omega_{1,2} = 2\omega}$.

3) Consideration of non-linearity during the amplitude modulation determines a number of resonant possibilities:

$$\Omega_{1,2} = \begin{cases} \omega, \\ 2\omega, \\ 2\omega \pm \Omega, \\ 2(\omega \pm \Omega). \end{cases}$$

Thus, when the resonant electromagnetic field affects the bio-macro-molecules with the active centre (containing metal atoms), collective wave effects play a significant role. In this case, the properties of the very radiation predetermine wide possibilities for regulatory effects on bio-macro-molecule dynamics in general, and, hence, regulatory effects on biological processes, in which they are involved, thus, directly or indirectly realizing directing and (or) disorganizing signals.

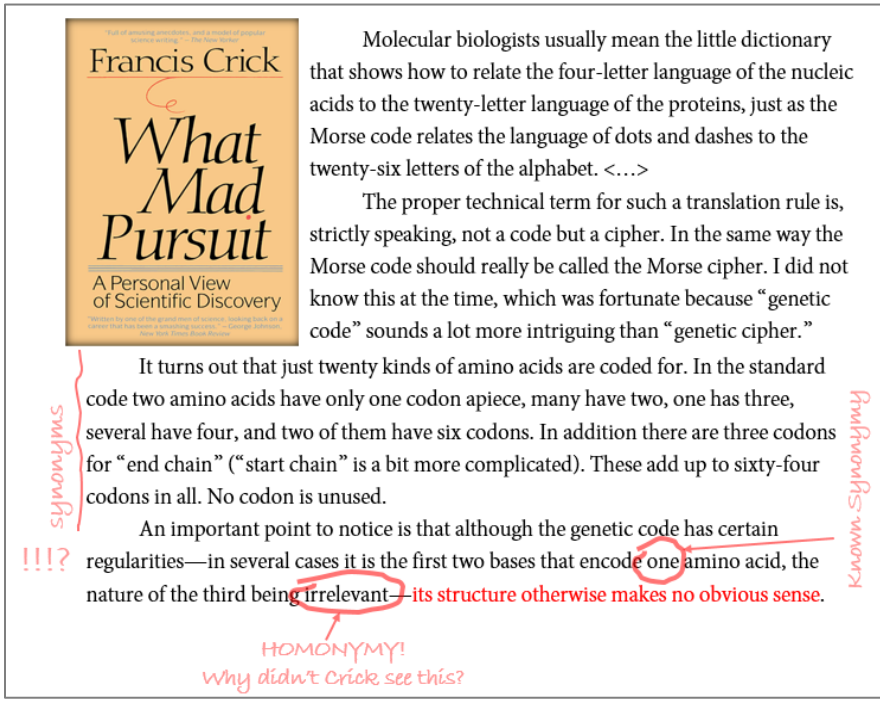
THE WAY FORWARD

Analysing the present state of genetics, I appeal mainly to logic and common sense, operating with well-known scientific data with F. Crick's triplet model of the protein code at the core. This model contains a strategic gap, in a form of a purely logical hole the size of Mont Blanc. And surprisingly, this Mont Blanc seems to be unseen. At the same time everyone admits that the code contains codon synonyms, which are subject to Lagerkvist's "two out of three" method.

I postulate a very simple and logically correct idea that the triplet protein code, in addition to synonyms, contains homonyms. Lagerkvist's method, based on F. Crick's experiments and Wobble Hypothesis states: anticodons 'read' codons by the first two nucleotides, the third nucleotide oscillates, wobbles, is random, i.e., represents a "steric crutch." This method is valid for synonyms, and this was quite clear without Lagerkvist. But will Lagerkvist's method be valid for non-synonyms (homonyms, according to my theory)? Will this rule of "anticodon – codon reading" apply to homonyms? F. Crick had nothing to say in this regard. Lagerkvist, the author of the "two out of three" method, also has nothing to say. Nothing is found in the scientific literature either.

Not long before his death, in his book, F. Crick confessed that he actually did not understand his own model: *"although the genetic code has certain regularities—in several cases it is the first two bases that encode one amino acid, the nature of the third being irrelevant—its structure otherwise makes no obvious sense."* What are these cases when it does not have any sense? I am sure that F. Crick ran into amino acid-stop ambiguity codon-homonyms. F. Crick probably saw this and realized that such ambiguity reveals a significant, fundamental deficiency in his model. But what did this mean to F. Crick personally? It meant and means that using the canonical table of the code suggested by him, all organisms, including Humans, will ingloriously die at the moment of selection

of amino acids and stop positions when ribosomes meet codons-homonyms. What did F. Crick do, realizing all this? Nothing. And why would you do anything? All went well. The proteins (seemingly disregarding the homonyms of the template-RNA) are successfully synthesized *in vitro* and *in vivo*, and the Noble Prize had already been received. What else may you wish for? However, there was a problem of a personal nature - scientific conscience. Only before his death F. Crick voiced a thought about the un-deciphered aspect of "*no obvious sense*" in the code [F. Crick "What Mad Pursuit?" A Personal View of Scientific Discovery ISBN 10: 0465091385, ISBN 13: 9780465091386, 1990].



In short, the problem was actually ignored; nobody wanted to be more saintly than the Pope of Rome (Crick). Lagerkvist in the Proceedings of the National Academy of Sciences tried to state something reasonable and came up with the "Two out of Three" method, already obvious to all [Ulf Lagerkvist, Proc. Nati. Acad. Sci. USA Vol. 75, No. 4, pp. 1759-1762, April 1978, Biochemistry, ""Two out of three": An alternative method for codon reading". (codon-

anticodon recognition/translational fidelity/wobbling/organization of the genetic code)]. By doing so, he patched the obvious (homonymous) contradiction and obscured the problem, stating the knowingly unacceptable: these homonyms are rare (when in fact, they are 50% of the code!), so there is no big deal… A cancerous tumor of misunderstanding was anointed with iodine…

Let's admit, the ignorance of homonym problem turned out to be very costly. The first warning signals were the questionable safety of transgenic foods and the mass deaths of honeybees in transgenic crops in the United States.

Acknowledging this, we have to admit that the Genetics and Molecular Biology which do not consider the real linguistic, mental component (with codon-homonyms as a vector), such Genetics and Molecular Biology is in fact nothing more than a colossus with feet of clay (weak in the knees). However, there have been, and there are minds capable of fundamental and thorough analysis of the protein code without shading. Deceased Yu. B. Rumer, came close to the problem of homonyms in his last work [B.G. Konopelchenko and Yu.B. Rumer. The wobble hypothesis and the sequence of nucleotides\\reprint 75-26\The Institute of Nuclear Physics, Novosibirsk, 1975] and suggested interpretations of Crick's Wobble Hypothesis on 'codon-anticodon' recognition. His interpretation essentially introduced the concept of the probability character of codon recognition. V.I. shCherbak, close to this field of mathematical genetics, also demonstrated that the genome uses the language of mathematics. In other words, the genome has quasi-intellect. This fundamental idea is very much disliked by orthodox materialists, and some of them went to all means and lengths, going far beyond the scope of scientific ethics and science, to present counterarguments.

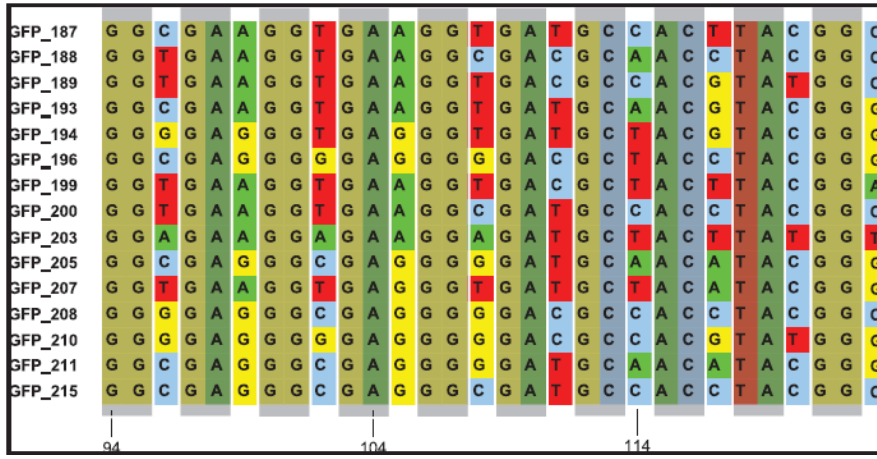
But all this is just the prelude. The main show is still ahead. We have reviewed the synthesis of proteins and found that we don't clearly understand, we miss the mental, the main operating component of the genome. This component in itself has a wave quantum foundation. That is the main point. After 80 years of

stagnation in this field, since the pioneering research of Gurwitsch, Lubishchev and Beklemisheva, now we evidence a clear and powerful breakthrough, driven by the works of Jiang Kan Jen, Mosolov, Budagovsky, Kaznacheev-Mihailova-Trofimov, Burlakov-Burlakova-Golichenko-Voeikov-Belousov, the brilliant work of Daniel Fels in PLoS ONE. And finally, our works, based not on bare empiricism, but on physics-mathematics and theoretical-genetic analysis, which laid the foundation for the creation of a pilot model for a quantum biocomputer - a model of the genetic apparatus functioning on the wave level. This quantum biocomputer allowed us at a higher level, with more competence and complexity, confirm earlier known facts about the distant transmission of working wave genetic information.

Yet, there is still some dissatisfaction in regards to the triplet genetic protein code model. Suggested by us amendments to this model about the functions of codon-homonyms have a purely logical character. Can our righteousness be proven experimentally? Can we prove that codon-homonyms represent a linguistic vector, which in its own fashion consciously direct the biosynthesis of proteins? This is of fundamental importance, but not easily done. I assume, that it is possible.

Let's consider an article "Coding-Sequence Determinants of Gene Expression in Escherichia coli" by the authors Grzegorz Kudla, Andrew W. Murray, David Tollervey and Joshua B. Plotkin [www.sciencemag.org SCIENCE VOL 324 10 APRIL 2009]. This is a well-written high-standard article, but it contains a fundamental mistake that is very significant. The authors used a library of modified (mutant) genes of the so-called green fluorescent protein (GFP). They introduced these mutant genes into *E. coli* and using fluorescence, analyzed GFP synthesis. The key data and, at the same time, the main demonstration of their errors, are presented in the table below.

(Fig. 1B) An example of alignment, demonstrating the variety of sequences amongst 15 synthetic GFP genes. Long columns represent the first two nucleotides (doublets) in codons, which did not mutate. These are the doublets of GG, GA, GC, AC, TA families. Shorter columns represent the third (wobbling) nucleotides in codons, which randomly mutated.



The authors present the aligned sequences of 15 synthesized GFP genes, erroneously believing that for the third nucleotide mutations they only used codons-synonyms. A simple reference to the canonical-table of the genetic code is enough to prove this.

The authors write that they worked only with synonymous (syn-codons), introducing mutations to the third codon nucleotides in GFP genes. Naturally, they expected that all proteins synthesized by *E. coli* with these genes should be identical. To quote the authors: “We synthesized a library of green fluorescent protein (GFP) genes that varied randomly in their codon usage, but encoded the same amino acid sequence. By placing these constructs in identical regulatory contexts and measuring their expression, we isolated the effects of synonymous variation on gene expression”.

The Table of the Genetic (Protein) code.
Red codons – Homonyms, **Blue codons** - Synonyms

	C	G	T(U)	A
T(U)	TCT Ser TCC Ser TCA Ser TCG Ser	TGT Cys TGC Cys TGA Stop TGG Trp	TTT Phe TTC Phe TTA Leu TTG Leu	TAT Tyr TAC Tyr TAA Stop TAG Stop
A	ACT Thr ACC Thr ACA Thr ACG Thr	AGT Ser AGC Ser AGA Arg AGG Arg	ATT Ile ATC Ile ATA Ile ATG Met	AAT Asn AAC Asn AAA Lys AAG Lys
C	CCT Pro CCC Pro CCA Pro CCG Pro	CGT Arg CGC Arg CGA Arg CGG Arg	CTT Leu CTC Leu CTA Leu CTG Leu	CAT His CAC His CAA Gln CAG Gln
G	GCT Ala GCC Ala GCA Ala GCG Ala	GGT Gly GGC Gly GGA Gly GGG Gly	GTT Val GTC Val GTA Val GTG Val	GAT Asp GAC Asp GAA Glu GAG Glu

It will be true, indeed, if you use a replacement for the third nucleotide in syn-codons. And that is confirmed by the authors in their protocols. In that particular case, it was possible to say that they obtained the "same amino acid sequence" in the synthesized GFPs. But in fact, the authors used for their manipulations not only syn-codons, but also homonymous codons (See Fig. 1B). And here comes another author's oversight, an inexcusable one. There was no control of peptide sequences of synthesized proteins. Instead, the authors looked only at the fluorescence of the synthesized proteins. And this fluorescence varied significantly. Why was it variable? The authors believe that fluorescence variations of produced GFP could be explained by changes in their primary and secondary structures. They have not verified this fact either. The authors side-tracked, showing what was already previously known - a strong correlation between the type of the secondary structure of

mRNA and fluorescence. This provided them with a simple mechanistic explanation that substantial folding of mRNA, encoding GFP proteins, impedes the translation initiation, and therefore, impedes GFP synthesis. This is trivial and this is not the main point. The main point is that the authors introduced mutations for the third position, including into the codon-homonyms, erroneously considering them to be synonyms. Paradoxically, this error provokes the idea to check codon-homonyms role in protein synthesis. Following the hypothesis about the semantic (or in reality, mRNA- textual) orientations of the cells genome, then, these manipulations with mutagenesis were changing the texts (contexts) of at least some of the mRNA pool of the obtained GFP genes library. And consequently, due to different contexts, the meaning (semantics) of the codons-homonyms were also different compared to the original genes. If this is truly the case, it is logical to expect the substitution of amino acids (at least in the part of the synthesized GFP) compared to the control, when, let me remind you, in reality the authors didn't perform any (control). Substitutions of amino acids in synthesized, allegedly silent mutant GFP, could have gone two ways.

1st (canonical). As for example in the homonymous TT family, TTG → TTT substitution in homonym leads to Leu → Phe substitution, or in any other homonymous codon families - AT, TA, CA, AA, GA, TG, AG, if substitution is done for the third nucleotide.

2nd (contextual, hypothetical). When the substitution for the third nucleotide in some codon-homonyms changes the contextual landscape of remaining intact codon-homonyms and, consequently, they can no longer remain obscure and undefined, they get their exact meanings. In this case, tRNA interprets codon-homonyms according to the context of the entire mRNA. This allows for an unambiguous selection of a particular amino acid or a stop. It is this path proves the codon-homonym-semantic (mental) vector of protein synthesizing system of the cell and its entire genome.

Analysis of Fig. 1B, proposed by authors, suggests that they,

contrary to their assertion, worked not only with syn-codons, but also with homonymous codons. DNA sequences in obtained 15 mutant genes (from 94 to 123 nucleotide) contain six syn-codons and four homonymous codons. The last ones belong to GA and TA families. GA is responsible for the selection of Asp and Glu, TA is responsible for the selection of Tyr and Stop (depending on the context, modified by mutant codon-homonyms). The mutants were obtained by the authors in the following synonymous families - GG, GC, AC. And this is only for 15 synthetic genes (out of 154 in total).

However, we should be careful, thinking that working only with homonym-mutant genes in the third nucleotide will necessarily lead to success. We do not know the required length of the genetic text and the required proportion of homonyms and synonyms for some codon-homonyms to produce different code meanings. A lot of experimental work is required with many different genes. Linguistic Genetics, as a component of Wave Genetics, is in its infancy.

Let's summarize the proposed methodology for the codon-homonyms' role verification.

The initial canonical statement - "amino acids and stops are coded only by the first two bases of (two out of three) codons, the third base is not involved in the coding and may be any of the four" - is evident from the table of the standard code. 'Any' means that in all codon families, the third nucleotide position is monotonous and the same - T,C,A,G. And this contrasts with the unique combinatorics of the bases of the first two positions in all codons.

Formulation of the problem

Ribosome selection of the synonymous codons (amino acids and stops) is simple and redundant (isoacceptor tRNA's). In case of homonymous (ambiguous) codons, the ribosome (or rather the protein synthesizing apparatus and the entire cell) faces the task of selecting one of two different amino acids, as well as the task of

selecting an amino acid or stop. How are these fundamental tasks resolved *in vivo*?

Hypothesis

In homonymous situations (when ribosomes meet non-synonymous codons with weak, according to Yu. B. Rumer, two-sign roots - meaningful doublets of bases), the selection is based on the facts that:

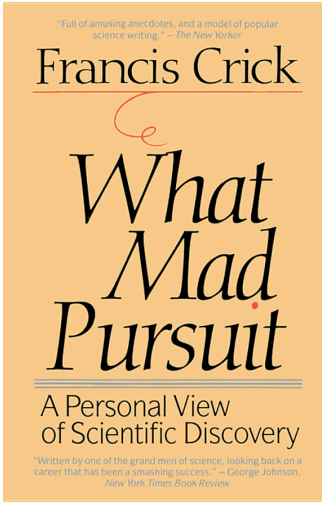
a) the genetic apparatus and the entire cell represent a biocomputer, capable of elementary acts of consciousness-intelligence,
b) capable of reading and comprehending mRNA as a real (non-metaphorical) linguistic structure, namely, as a text (context),
c) capable of making a decision on the selection of amino acids (stops) on the basis of a simple comprehension of the meaning and purpose of the mRNA (protein) in the organization of biochemistry and other higher functions, including quasi-consciousness.

Example of experimental proof of the hypothesis

GFP gene consists of 240 codons. The authors of the aforementioned article randomly introduced silent-mutations for the third base position in synonymous codons of 154 genes, with no change to the first and the second base positions. Notably, the synthesized structures were placed in identical regulatory contexts and the expression of such modified genes was determined in *E. coli* cells. As expected, these genes did not cause any changes in the structure and fluorescence of GFP, expressed in *E. coli*. Though these genes affected the yield of GFP; the yield of proteins was also affected by variations of the secondary mRNA structure, caused by substitution of bases. Remember, that the code meaning of synonymous codons in each family does not depend on the type of the third (3') base. The same rule should apply to the families of

homonymous codons, though it is not declared anywhere. In this case, automatically, there comes the problem of ambiguous selection of amino acids and stops by the ribosome. In this situation, it seems logical to introduce a mutation for the third position of bases for some homonymic codons. The "two out of three" reading method of homonymic codons by anticodons must be valid (See The Table of The Code), but this contradicts the ambiguity of the code assignments of their coding doublets (the first two codon bases). That is why, the other part of homonymous codons must change the code's meaning, depending on the modified context and mRNA meaning (due to mutations in the third base). For this reason, one can expect a change in the primary structure of expressed by *E. coli* GFP, which will not be identical to the original GFP, not only in structure but also in functionality, as well as in fluorescence.

It should be noted that the quantitative aspect of these kinds of experiments is unknown, namely, what should be the ratio of synonymous and homonymous codons within mRNA. You can only be confident that the number of codon-homonyms should be more than one. If there is one homonym or a small number of homonyms, then, their unambiguous reading probably will be determined by the secondary mRNA structure.



In his memoires in the book "What A Mad Pursuit", F. Crick says in a nutshell: "An important point to notice is that although the genetic code has certain regularities—in several cases it is the first two bases that encode one amino acid, the nature of the third being irrelevant—its structure otherwise makes no obvious sense." The key point of this phrase is that, if we do not accept the idea of wobbling for the 3rd nucleotide in the code model, then, the model completely loses its sense.

The biggest question is, what are the *'several cases'* that Crick had in mind? He doesn't give any answer, neither does Lagerkvist, neither does anyone else. Ulf Lagerkvist though tried to classify the codon families but made it in a strange fashion [Lagerkvist, 1978]. He divided them into 2 groups:

1) "Strong mixed codon interactions": 5 synonyms and 2 non-synonyms (homonyms);
2) "Weak mixed codon interactions": 2 synonyms and 5 homonyms.

What are the strengths and weaknesses of these groups? Why both groups contain mixed codons, e.g. why they contain both synonyms and homonyms? The author does not provide any clarifications to these questions. And the main reason for this, is that neither F. Crick, nor anyone after him, tried to understand the functions of non-synonymous codons, e.g. homonyms, to my definition. This has remained their blind spot.

U. Lagerkvist was the first who tried to exacerbate the problem by pointing at the dangerous ambiguity of non-synonyms,

with dangerous errors in protein synthesis, but limited himself to the incorrect statement about the alleged rare occurrence of codons – non-synonyms. The problem here is that F. Crick, neither in his Wobble Hypothesis nor anywhere else, answers the key question: does the wobbling of the third nucleotide occur in all codons or only in synonymous ones? And this state of uncertainty is still there nowadays, causing confusion in understanding the true motives of the triplet protein code operation. I believe that now it is time to say that wobbling of the third nucleotide is inherent to all 64 codons, or indeed, it will lead us to a dead end.

Yet, there is one more uncertainty in understanding the code function. How are amino acids (and stops) selected in non-synonymous codons? The key vector here is the context orientations of ribosomes on mRNA. It's easy to notice but it hasn't been noticed so far that under the condition of the 3rd nucleotide wobbling in *all* codons, for example, the family of coding doublets AG encodes SIMULTANEOUSLY Ser and Arg. Wherein, they are synonymous pairwise and they redundantly encode only Ser and only Arg. Here the choice is simple: there are isoacceptor tRNAs. But triplets AGT and AGC (Ser) HOMONIMOUSLY oppose the AGA and AGG (Arg) triplets within the AG family. Hence, these TWO pairs can code both, Ser and Arg. And here it is NECESSARY to make a CHOICE - either Ser, or Arg – the same one tRNA cannot accommodate the two different amino acids. The selection becomes possible due to contextual orientations of the ribosome on mRNA. Such inner synonymous-homonymous duality of codons-homonyms (with additional paired synonyms) is fundamental. The biological function of such dualism (within the families of homonymous codons) perhaps, is to ensure even higher flexibility of the code in combining synonymy and homonymy.

You may argue, saying that my proof of the double synonymous-homonymous degeneracy of the genetic code is not direct enough or, basically, is indirect. My argument is based on pure logic. The direct argumentation will be to verify the existence of total collinearity of the codons and amino acids, on a representative sample of a few large proteins and their mRNA's.

Such careful and tedious work has not been performed yet, apart from the single and poorly convincing case of sickle-cell anemia. If the concept of synonym-homonym degeneracy of the protein code is true, it is possible to predict that the same homonymous codons, depending on the context of different mRNA's, will encode different amino acids and stop positions within different proteins or within the same large protein. This work must be done, and it is surprising that this exhaustive analysis has not been done yet. The current situation of genetics and molecular biology's relationship with the protein code can be described as follows: we counted on a high sprint performance of an athlete who has lost one leg and has an artificial (prosthetic) limb instead.

What about modern understanding of the role of mRNA context? Did anyone provide an accurate description of how mRNA contexts define the meaning (semantics) to codons during their transcoding (the fact about transcoding that has been well-known before and that we referred to in our analysis in this book)? There is an answer in a recent review published in "Nature Reviews Genetics". This paper analyses many strange codon-functioning situations, including their transcoding [Pavel V. Baranov, John F. Atkins and Martina M. Yordanova. Augmented genetic decoding: global, local and temporal alterations of decoding processes and codon meaning. NATURE REVIEWS | GENETICS VOLUME 16 | SEPTEMBER 2015 | pp. 517-529]. This is what the authors write about context-dependent codon transcoding (what we find very relevant and critical to our research): "The meaning of a codon can be changed in the context of a specific mRNA or at a specific location within the mRNA. To distinguish it from codon reassignment, this phenomenon is often termed codon redefinition and is considered to be a class of recoding events. Naturally, because codon redefinition takes place in the context of a single or a subset of mRNAs, these mRNAs should have specific properties or sequence elements that distinguish them from other mRNAs".

What are these mysterious "specific properties or sequence elements" of mRNA, responsible for codon transcoding? There is no answer to the authors yet. But the answer is here and it is very

simple. The protein synthesizing system and the entire genome are capable of thinking and have quasi-intelligence, since this is the required attribute that makes it possible for the protein-synthesizing system to define the meaning of codons-homonyms based on mRNA context. Grasping the meaning of mRNA allows the understanding of the semantics of codons-homonyms. The authors of this article are absolutely right, and we stand in solidarity with them, that Crick's concept of the "frozen accident" of the protein code begins "to melt" under the pressure of new facts and ideas. That's what they say in this regard: "Crick's 'frozen accident' hypothesis for the origin of the genetic code, according to which the genetic code is not only universal but also unchangeable and un-evolvable. Ironically, the time of the hypothesis formulation also marked the beginning of a series of experimental observations of various exceptions from what are known as the standard rules of the genetic decoding, leading to a 'melting' in perceptions of the universality of the genetic code".

So, what is the third wobbling nucleotide in the codon about? It is not only the steric "crutch" that provides greater strength of the codon-anticodon pair, it is also the "switch sign" for tRNA codon reading from synonymy mode to homonymy mode and back. And this takes protein coding into endless semantic realms and opens the endless prospects for control of biosystem metabolism, though, under one "little" condition: we have to understand the language, the meaning and the grammar of the protein genes.

The presence of 3rd nucleotide wobbling in both codon types (synonymous and homonymous) provides protein genetic code with semantic coding sustainable abundance. This is an evolutionary universal wisdom of the code.

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