WE ARE NOT STILL ABLE TO SUCCESSFULLY TREAT CANCER AND HIV?

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Nature of HIV and cancer phenomena. Problems in interpreting.

The HIV and cancer nature and the Life essence both lie in a common plane. So far, we don't understand the most crucial facts of the Life phenomenon: how did it appear on the Earth and in which way it is coded in chromosomes? Several hypothesis are available, and each of them at best represents just a piece of the reality. Here from the theoretical and biological difficulties in interpreting the HIC and cancer terms come and, therefore, mistakes emerge in treating respective diseases. The two morbiferous origins occupy the most vital part in any biological system, namely, its genetic apparatus, i.e. the body which contains organism's accumulated "self-knowledge". And this is a paradox: we seem to know good enough about chromosomes and DNA - oncogenes have already been found, the HIV genome has been studied, and it's clear how these informational structures function in chromosomes. The genetic code and ribosome operation principles also seem to have been investigated in detail. But by some reason it's not enough to develop universal methods for successful counteracting cancer and HIV development.

Half-truth is the worst lie. People get used to believe it, especially if this half-truth relates to the genetic coding "knowledge". In this field, everything is an impregnable bastion for critics, and everything is ruled by dogma. Even the key definition, the strategic scheme of genetic coding (DNA® RNA® protein), is called "the Central Dogma". Until recently, all attacks on this dogma seemed driftless and doomed to failure. And in vain, as it turned out. Accuracy and imprecision of HIV and cancer (and many other pathologies) research strategy depends on whether we orderly understand the genetic coding mechanism. The reverse transcriptase discovery smashed down the first breach in this dogma that automatically transformed into a hypothesis which is now described significantly more discreetly: DNAÛ RNA® protein. However, our ideas on protein biosynthesis are eroding, since each new model is just an approach to the truth, to the understanding of the genome language-image pluralism as a tool of coding the spatiotemporal structure of biosystems [32, 33].

What do we want to prove?

In this research we further explicate our ideas which are not aimed at final destruction of the so-called genetic code

"canonical" triplet model, but at the development and establishment of its exact position in the knowledge of the chromosome operation principles. Yes, it's possible to state that the triplet code is the truth. However, this truth is as correct as the statement that we could write a word using an alphabet. That's right. But if we try, based on only this knowledge, to go further and avouch that by means of this alphabet we can compile grammatically-correct sentences, this new statement won't be correct. Moreover, such a statement is incorrect in fact, because for the compilation of human beings' speech laws of nomology, logic and grammar have to be applied. As for genome, it's a very speech-like and logical structure, but its fundamental features are not the only way to express genome associative-semantic structures. Furthermore, we are inclined to admit V.V.Nalimov's ideas [43] leading us to the idea that a genome possesses quasi-conscious abilities. The logic we use and the models we developed are only an attempt to obtain higher-level knowledge of laws pertaining to genetic text structuring or to other genome vital structures, i.e. the knowledge which is now just aborning. A.G.Gurwitch [38], V.N.Beklemishev [29] and A.A.Lyubitchev [41], the Russian researchers, laid the foundation of the science late in the 1920s.

What could be supposed to develop and enrich the common-accepted genetic coding theory and how this innovations can assist in resolving the HIV and cancer issues, in particular? Let's assume, until getting a final proof, three statements which have already got definite theoretical and experimental confirmations [8, 32, 33, 37]:

1. DNA molecules, included in chromosomes, possess a substantially-wave duality which is similar to the dualism of elementary particles. In accordance with it, DNA codes an organism in two ways, both with assistance of DNA matter and by DNA sign wave functions, including the coding at its own laser radiation level [28].

1. Genetic apparatus is able to be illocal at the molecular level (holographic memory of a chromosome continuum) and at the same time quanto-illocal in compliance with Einstein, Podolsky and Rosen's effect [4]. The latter means that genome genetic and other regulatory wave information is recorded at the polarization level of its photons and is illocally (everywhere and in no time) transferred (plays out) throughout the entire space of a biosystem by polarization code parameter. This helps to set a quick-response information contact among billions of cells constituting an organism.
2. Genome on the whole and individual nucleus of cells can generate and recognize text-associative regulatory structures with the application of a background principle, holography and quantum non-locality.

What's the next step?

Let's assume that final proofs of the above-mentioned statements have been obtained. Then the problem of HIV and cancer raises in absolutely another intellectual dimension. Let's provide these ideas and facts with a theoretic-biological and medical explanation. For instance, what does the "DNA mater-wave dualism" mean and in which way it is linked with the chromosome numerous code functions which are dramatically differed from the known triplet genetic code? In some sense, genome operates like a complex multiwave laser with adjustable frequencies. It emits light DNA modulated by gene&sign by an amplitude, a phase, a frequency and a polarization. Moreover, genome is likely also a radio wave emitter converting a wide spectrum of coherent sign-polarized radio bands [37] (*P.P. Gariaev, G.G.Tertyshniy, Ye.A. Leonova, etc. Radio wave spectroscopy of local photons: exit to quanto-illocal bioinformational processes. Transducers and Systems (2000, ¹9, pp. 2-13*). Genome is also a mobile and changing multiplex quazi-hologram which is able to produce light and radio wave the gene-sign and other regulatory systems [37] upon its multi-wave auto-reading by its own photon radiation. These structures are the registers of electromagnetic marking schemes (calibration fields) of biosystems' space and time organization. And finally, genome is a quasi-text formation with elements of a quantum non-locality, which can without any time delay "read" itself in billions of its cells and use information, thereby received, as a life activity guidance and as a method of its structure organization [8, 37]. Many biologists and genetics, let alone doctors, are likely to consider these new ideas of the genome information measurement as extremely complicated. However, not all of them. These thoughts whose roots first raised in Russia in the 1920s have rapidly been taking pace over the last decade.

This clearly shows that, while it isn't too late, it's necessary to change the strategy of searching the HIV and cancer treating methods, since traditional approaches to resolving the issue increasingly resemble a wish to produce a good harvest, having planted an asphalt road. A strategy to appear has to be based on fundamental investigations of substantially-wave and quasi-speech attributes of a higher system genome. Let's stress once again that we consider a chromosome continuum as a sign laser & radio wave emitter [8, 33, 37], and direct experimental evidences allow to think so. For instance, to demonstrate laser abilities of genetic structures, we showed that DNA and chromatin in vitro could be pumped in as a laser-active medium for a consequent light laser generation [28].

If we know these vital characteristics of a genome, new specific issues arise: whether a sign character of

chromosome laser & radio wave radiation changes when a xenobiotic HIV genome is building-in in them? And, at the same time, what happens to the radiation "semantics" during a transposition of oncogenes or any other mobile polynucleotide sequences as well as during B« Z or other conformational transitions in DNA in vivo? Whether these changes are linked with an alteration of quasi- and holographic programs, i.e. whether new programs are created and old ones are varied, or whether these programs are erased, and so on? Does the radiation polarization parameter retain, in semiotic sense, its dynamic properties in the process of genome reorganization? Do all these changes influence ribosome operation? Further questions may arise. The answer to any of them can play a key role in interpreting the HIV and cancer nature.

Theoretical structures - more details

Or let's take another fundamental problem. Oncogene and HIV genomes, occupying certain positions in a 3D space of master cell chromosomes, do not produce themselves as pathogenic factors until a certain time. In this sense, the behavior of HIV in the infected man's organism is unpredictable. HIV latent period may vary from a week to 10 years. The certain mechanism of HIV-infection induction from the latent (sleeping) condition is thought to exist, but this mechanism is still misunderstood and, therefore, an opportunity of making the HIV viruses sleep in a human's organism for ever is been losing. Organism and cells simply "don't notice" them or even, as in the case of oncogenes, use them for their own benefit as a reproduction factor. Why an organism adequately (rightly) accept them until a certain time X, and why they are semantically reborn, causing a management catastrophe in cell, after the X-time has come? Following our logic, it's possible to think that both in the pathologic and normal state four factors are engaged, at least: genome "holography" and "linguistics", genome background (context) self-organization, and its quantum non-locality.

Biosystem evolution has produced their own genetic "texts" and a biocomputing genome as a quasi- intelligent "subject" which "reads and understands" these texts at its level. The fact that natural human texts (it doesn't matter what the language is) and genetic "texts" have similar mathematical & linguistic and entropy-statistical characteristics is extremely important for the genome elementary "intelligence" substantiation. This relates, in particular, to such a definition as a fractality of letters occurrence frequency density distribution (in genetic "texts", nucleotides execute function of letters) [21].

American researchers obtained another confirmation of the genome coding function linguistic interpretation [20]. Dealing with the "coding" and "non-coding" DNA-eukaryote sequences (in the frames of old concepts of a gene), they came to the conclusion which was similar with ours' and conflicted with the central dogma stating that sign functions are concentrated only in the protein-coding DNA sections. The researchers applied a statistical analysis method for studying natural and musical texts, known as Zipf-Mandelbrot's law, as well as the known Shennon's postulate of text information redundancy calculated as a text entropy (more information about text entropy and statistics of words distribution in texts is given in [1, 25, 27, 31]). As a result, they found out that DNA "non-coding" areas (space, intronic and others) had more in common with natural languages than the "coding" ones. Taking this for granted, the authors suppose that "non-coding" sequences of genetic molecules are a basis for one or more biological languages. Besides, the authors developed a statistical algorithm for searching DNA coding sequences; the algorithm they had developed demonstrated that protein-coding areas had significantly lower long-distance-acting correlations, as compared with areas separating these areas. The DNA-sequences distribution was so sophisticated that the methods the researchers applied stopped satisfactory working at the distance of over 10^3-10^2 of the base pairs. Zipf-Mandelbrot's distribution for "words" occurrence frequency, where the number of nucleotides ranged from 3 to 8, demonstrated that the natural language had more in common with the non-coding sequences, than with the coding ones. It's worth reminding that the authors therein considered the coding only just as a record of amino acid sequence information. And that was a paradox which made them state that DNA non-coding areas were not only a "junk", but the lingual structures designed for reaching some still unknown goals. Despite the discovery of a growing complexity of non-coding systems in the process of a biosystem evolution, the authors didn't understand the long-distance-acting correlations happening in these structures. They illustrated the process based on a family of genomes of the myosin heavy chain upon the evolutionary transition from lower taxons to higher taxons. The data presented in [20] are in full compliance with the ideas we had independently put forward [32, 33]; according to our point of view, DNA non-coding sequences, or appr. 95-98% of a genome, are a strategic informational content of chromosomes. The said context has a substantially-wave nature and, thereby, is multidimensional and functions as a holographic associative-image and semantic-semiotic program of the embryological origin, the semantic continuation and the logic end of any biosystem. Having intuitively understood that the old genetic coding model led to a dead-end, the authors [20] with a nostalgia said good-bye to the old and previously-valuable genetic code model, but didn't propose anything to replaced it.

Homonymous-synonymous ambiguity of genetic texts. What does an organism need them for?

Text homonymy and synonymy are the common fundamental semantic-semiotic properties of natural and genetic texts. These features provide chromosomes, natural texts and a speech with over-excessive and multivalent information and, thus, ensure some adaptive flexibility. Polysemy of the same genetic texts gets a monosemantic meaning owing to a variation of DNA sequences position in genome space through their transpositions and/or a transposition of their surroundings. This situation resembles the situation with natural texts and a speech, in which homonymous-synonymous ambiguities of a semantic field are eliminated by the context (a background, the background principle is described in [44]). Homonymies of coding doublets are easily found in the traditional genetic code triplet model. The meaning of these homonymies is still misunderstood and isn't estimated, with some exceptions [33, 35]. The unexplainable issue of information RNA (mRNA) homonymies of codons at once emerged upon the creation of the triplet model of amino acid coding in the process of protein biosynthesis. And immediately became a "time-delayed mine", since the correct explanation of a biological (informational) sense of these homonymies automatically leads to the necessity of significant rectification or complete revision of the triplet model. How codons homonymies are produced? A set of different amino acids is coded in mRNA codons by similar doublets; the third nucleotides in codons can relocate chaotically, they are wobbling and may become any of the four canonical ones. As a result, they don't correlate with the coding amino acids [3, 11]. That's why semantic ambiguity of ribosome's choice of anti-codons of transportation RNA (tRNA), carrying amino acids, appears. For instance, each synonymous codon of the standard code of higher biosystems (AGT and AGC) codes serine, while each synonymous AGA and AGG codon codes arginine. Since the third nucleotides of mRNA codons in combination with a sign doublet don't have exact amino acid correlates and despite the first two sign codon nucleotides are similar with one another, they at the same time code different amino acids, the ambiguity in selecting tRNA anti-codons is brought about. In other words, a ribosome with an equal probability may take serine or arginine tRNA; such an outcome can initiate synthesis of abnormal proteins. In fact, this mistake don't occur and the precision of the protein synthesis process is extremely high. These mistakes appear only in some metabolically abnormal situations (the presence of some antibiotics, a lack of amino acids, etc.). Usually a ribosome somehow correctly choose the tRNA anti-codons out of the homonymous doublets.

We think that the correct choice out of doublet anti-codons-homonyms is realized through a resonant-wave or context (associative, holographic) and/or the so-called "background" mechanisms. Amino acid code homonymity can be overcome in the way which takes place in natural languages - by the placement of a homonym (as a part) in a full system, i.e. into a completed phrase; the homonym decodes the context and attaches a unique meaning to it, thus establishing the unambiguity. That's why mRNA, being a kind of a "phrase" or a "sentence", should operate in the protein synthesis process as a functional coding integral system (illocaly) setting the sequence of amino acids at the level of tRNA aminoacylated associates which complementary interact with the entire mRMA molecule. Macrosteric disagreement between mRNA- and tRNA-continuums could be eliminated due to a conformational lability of macromolecules. The A-P sections of a ribosome are responsible for acceptation these associates, predecessors of protein, with a consequent enzymatic sewing of amino acids in a peptide chain. In this case, a context-oriented unambiguous choice and obviation of the doublet-anticodon homonymy will occur. Considering the above, it's possible to predict that the interaction of aminoacylated tRNAs with mRNAs has a collective phase character and is effected by the type of re-association ("annealing") of one-string DNA upon the temperature reduction after melting of a native polynucleotide. Do any experimental data, which can be interpreted in such a way, exist? Yes. A great deal of such information is available and collected in the analytical review [45]. Herein we just present some of the data. The correctness of terminating codons recognition by tRNA molecules is known to depend on their context surroundings (that's a confirmation of our theoretical models), in particular, on the existence of an uridane after the stop codon. For example, in Paper [9] the following information is presented. The insertion of a line consisted of nine rarely-used CUA-leucine codons in the position after the 13^{th} one in the compound of 313 codons of the tested mRNA results in active inhibition of their translation and doesn't notably influence on the translation of other CUA-codon-containing mRNA. Here, the translation context orientation is clearly seen. A strategic influence of the strictly-defined codon insertions in mRNA, located far away from the peptide bond formation point, on the inclusion (or non-inclusion) of certain amino acid in the composition of a protein, being synthesized. This is a remote influence, connected with the protein synthesis continuity (it's also an example of genetic apparatus' functions non-locality) when protein-synthesizing apparatus recognizes mRNA not only in parts (by nucleotides, locally), but in one piece (non-locally) as well. However, in the work being cited this key phenomenon is only stated and remains misunderstood for the researchers; and probably by this reason they don't even discuss it. The number of similar works is increasingly growing. In the work under discussion the authors refer to a half a dozen of analogous results in which interpretation in this way is rather difficult. This is obviously explained by the imperfection of the genetic code triplet model. The model also isn't correct due to the existence of unusually swollen anticodons. When they are involved in the protein synthesis, the number of base pairs in the ribosome A-site exceeds 3 [45]. This means that the dogmatic postulate of code tripletness in this case also fails. Results of the research of tRNA-tRNA interaction on a ribosome are presented in [45]; they completely confirm our hypothesis in which we consider an amino-acid-loaded tRNA associate (continuum) as a predecessor of a protein. In [45], an important idea, very close to our's, was put forward: the influence of the mRNA context on monosemantic

incorporation of amino acids into a peptide reflects some basic, still practically unstudied, laws of genetic information coding in the protein synthesis process. It's worth reminding that genetic information about protein synthesis occupies only some 1% of a chromosome total volume. The rest 99% of the whole contain programs of a significantly higher level.

Prions: the last blow to the molecular biology central dogma

As we can see, the previously-existed hypothesis on a genetic code and a sign operation of a protein-synthesizing apparatus were simplified. Prion phenomenon is likely to be the last quietus in favor of a final revision of the molecular biology central dogma. Prions are the low-molecular parasitic proteins (PrPsc) hitting brains of animals (cow madness) and human beings (Alzheimer's disease, Kreitsfeld-Jacob's syndrome, etc.). Virus-like strain-specificity is an unexplainable feature of prions. This strain-specificity is only attributable to microorganisms or viruses which have a genetic apparatus. At the same time, it's thought that prions don't have a genome, since all affords to find traces of DNA or RNA in them have always failed. An acute contradiction, which once again discredits the molecular biology central dogma, arises: prions don't have a genome, but genetic signs are present. Some scientists, not being able to explain this phenomenon and trying to "save" the central dogma, nevertheless suppose that DNA or RNA traces are hidden in prion molecule's wrinkles [10]. However, investigations, carried out in this field over decades and marked with the Nobel prize awarded to Stanley Prusiner in 1997, reliably demonstrated that prions neither had nucleic acids, nor a genome [23]. How to overcome this contrariety? If to admit that the central dogma does exist, it's impossible. Having rejected this dogma, we cam imagine the following prion biogenesis scenarios [34]. Herein, "prion virtual genome", i.e. a provisional genome mutually lent from master cells for some time, is a chief sign figure. To put it more exactly, this is a protein-synthesizing apparatus of master cells. Prions are likely to have retained the paleogenetic way as a way of their reproduction; in some cases this breeding method enables prions not to use genes, coding them in chromosomes, and to self-reproduce in another way, ignoring the central dogma of molecular biology and genetics statements. To synthesize prions, a cell has to address to their genes; it's rather a progressive, but, at the same time, organizationally and energetically difficult method. Prions can simplify the procedure. We suppose that NH-groups of peptide bonds PrPsc can enter into reaction with OH-groups of ribose remains of accepting CCA-sequences of respective tRNAs. In the course of hypothetical fermentative reaction, an emerging poly-tRNA-continuum, the collinear PrPsc, pairwisely in space draws together anticodons and forms a covalent and discrete "information RNA similarity" (iRNAs). This stage is practically a reverse process of the protein synthesis on a ribosome. The process is likely to take place on the ribosome's A- and P-sites. Then, the synthesis of RNA on iRNA passes. For this purpose, a respective RNA polymerase, which can work with an iRNA covalently-discrete matrix, is required. That's the mechanism of "mutual usage" of protein-synthesizing apparatus during the prion reproduction period. This impermanence creates an illusion that prions don't possess a genetic apparatus. In this process, prion peptide chains are used as matrixes on which poly-tRNA-continuum in pairs arranges on the ribosome's A-P sections, forming discrete polyanticodons. The latters, joining in pairs, either directly become a matrix for the RNA-dependent prion's mRNA synthesis, or (in the other case) polyanticodons through a specific slicing are cut off and then alloyed in a covalently-undisrupted mRNA matrix of prions. Thereafter, prion's mRNA polymerizes prions on a ribosome. That means that ribosome operates in the reverse direction, being a "prion-polyanticodon-dependent mRNA polymerase" in the process. And, therefore, violating the dogma, information is transferred from a protein to RNA. Thus, the scheme of the dogma completely changes: DNA® RNA® Protein. In this case, it isn't the dogma any longer, it's just a working model which needs further clarification, perfection and development. In accordance with this view on prion biogenesis, the prion stain-specificity is explained by peculiarities of reverse operation of ribosomes, temporary recruited during the synthesis of each prion strain. These peculiarities reflect a taxonomic position of prion-producing biosystems.

Now, back to the basic postulates of the genetic code model, still widely-accepted: genetic code is a triplet, unoverlapped, degenerated formation and doesn't have "commas", i.e. codons are not separated from each other. Information flows from DNA through RNA to a protein. And finally, code is universal. What's now left out of the initial postulates? Nothing, in general. Indeed, code is likely to be a multi-letter fractal and heteromultiplet structure coding both individual proteins and functionally-linked protein associates. It has overlaps formed due to a shift in ribosome's reading frames. It has commas, since heterocodons can be isolated from one another by sequences with another functions, including punctuation functions. The code is not universal: in 14 cases, it is differed from a standard code of higher-level biosystems. The mitochondrial, leavenous, microplasm, trematodian and other lower organisms' codes are included in these cases [5, 6].

And the last: a protein can be a matrix for RNA, as we can see from the prion example. How should we understand an actual genetic, or protein, to be more exact, code, taking into account all the above-mentioned contradictions and in line with our theory? It is possible to postulate qualitative, simplified, initial version of substantially-wave control over the amino acids lining-up order dictated by the associates of aminoacylated tRNA, predecessors of

proteins. Having admitted this assumption, it's easier to understand the operation of the protein code and consider it as a hierarchically-structured program of the substantially-wave biosystem organization. In this sense, the code is the first stage in a chromosome's plan of building a biosystem, since the genome language is multidimensional and pluralistic and is capable not only to set up the protein synthesis task. The basic statements of the initial model of substantially-wave sign processes in protein biosynthesis we propose are as follows:

1. Multicomponent ribonucleoproteid protein-synthesizing apparatus is a system to generate highly-organized sign radiation of acoustic-electromagnetic fields which strategically regulate its self-organization and the order of inclusion of amino acids in a polypeptide chain.

1. Aminoacylated tRNAs are associated in sequences, the predecessors of synthesizing proteins before the contact with the A-P site of a ribosome. The continuum of the tRNA pool anticodons is complimentary to the entire mRNA, excluding dislocations determined by the availability of non-canonical nucleotidic pairs.
2. Sequence of aminoacylated tRNA variation in associates, protein predecessors, is determined by sign collective resonance of all the participants involved in the amino acid sequence synthesis. In this process, pre-mRNA and mRNA, which functions as an integral continuum (macrocontext) of heteropolycodons variously-scaled by length, including an intronic fraction pre-mRNA, are the key wave matrixes. The main function of the wave matrixes is an associatively-context orientation of the aminoacylated tRNA sequence; orientation in a large degree, rather than F.Krick's "wobble-hypothesis" ignoring the rules of canonical pairing of nucleotides in the unidimensional space mRNA-tRNA. Laser-like radiations, emitting by the participants of this process and correcting the order of insertion of the amino acids remains into a peptide, also function on a ribosome in addition to and/or together with the resonance regulations of a mutual dislocation of the codon-anticodon continuums. A ribosome enzymatically-covalently "de jure" fixes the peptide bonds of amino acid sequences, selected "de facto" in a polyaminoacid-poly-tRNA-associate, the predecessor of a protein.
3. The resonance-wave "censorship" of the order of inclusion of amino acids in a peptide chain emends a potential semantic disorder in the creation of false protein "proposals" following from the homonymy of codon families, and ensures their correct "amino acid conceptualization" due to the context lift of the homonymy of multisided even doublets in codons. The same mechanism is engaged in a higher-ranked ambiguity when the number of codons is (n+1).
4. Genetic code degeneration is necessary for pre-mRNA-mRNA-dependent, contextly-oriented exact matching of aminoacylated tRNAs, determined by the nature of wave associative resonance interactions in a protein-synthesizing apparatus.
5. The mechanism of generating the correct sequences of aminoacylated tRNAs on the wave matrixes pre-mRNA-mRNA may be considered as a particular case of a partially complementary re-association of one-string DNA-DNA and RNA-DNA or, in general, as a self-building process known for ribosomes, chromosomes, membranes and other molecular- and super-molecular cellular structures.
6. Ribosome can facilitate RNA synthesis on a protein matrix.

Thus, the role the mRNA plays is many-sided and dualistic. This molecular, like DNA is a cornerstone in the evolution process and is marked by mutually-adding synergetic unity of material and wave gene information. An ambiguity of material (substantial) coding is set off by the precision of the wave one, which is likely to be realized through the mechanisms of collective resonance and laser-holographic (associative, contextual and background) effects in a cellular-tissue continuum. A jump to a more developed level of the wave regulation of the RNA®Protein translation is accompanied by a partial or complete refusal from the canonical laws of pairing of an adenine with an uracil (thymine) and of a guanine with a cytosine, attributable to the early (and more simple) evolutionary stages of the DNA replication and RNA transcription. Such a refusal is informationally necessary, unavoidable and energetically preferable at a higher biosystem level. It's worth stressing once again that the context associative-holographic mechanisms of operation of an organism's protein-synthesizing system are tightly linked with the so-called "background principle" [44] and also with a multivector and multisided logic of a sophisticated system management (Gerhard Thomas' kenogrammer) [26]. From this point of view, macrocontexts of pre-informational and contexts of informational RNA might be considered as a background which in this particular case is an "information noise source". This allows to significantly amplify a signal under which the correct choice (wave identification) of one in two homonymous aminoacylated tRNAs, with only of the two is to be build-in in a protein correct "phrase" and "word". This selection is only become possible after a ribosome managed to split a coherent component in the form of the repeats of the same "conceptualizations" (identifications) of one of the two similar doublets in codons. The following simplified example can explain the situation. Let's suppose that it's necessary to select one of the two words (analogues of codons with doublets-homonyms). The words are "a branch" and "a ranch". It's clear that the choice depends on the entire sentence, or on the context being here a background (noise) which helps to identify a signal, the correct word. If the sentence is "I saw a big branch on a tree", then the replacement of "a branch" with the word "a ranch" is equal to noise generation and to losing a signal. Pre-

informational RNA and introns are likely to play similar part; they are different levels of contexts which a live cell and its ribosome apparatus have to read and conceptualize to take a precise decision on tRNA anticodon selection in homonymy situation.

A family of various solitons (optical, acoustic, conformational, rotable-oscillating, etc.) excited in polynucleotide can become an apparatus for continual (non-local) “reading” of context RNA sequences on a whole. These solitons facilitate to gather semantic information on RNA contexts and then associatively regulate codon-anticodon sign interrelations. Biocomputing genomes of cells carry out semantic estimates. Soliton reading, scanning the RNA surface, is a method of polynucleotide continual reading. For instance, the solitons of running torque vibrations of nucleotides on a sugar-phosphate axis we physically and mathematically considered for one-string RNA-like DNA sections [30, 36]. These solitons respond to the nucleotide sequence alteration by the modulation of their dynamic behavior which acquires sign features and can probably be transmitted remotely, or over the distances significantly exceeding the hydrogen bond length. Without a remote (wave, continual) migration of a signal containing information about the whole system, i.e. about pre-mRNA-mRNA-sequences, it isn’t possible to realize associatively-context protein synthesis regulations. For this purpose, the wave capability of solitons (as well as of holographic memory) to deal both with separate parts and integral system as a whole, is required. This continuity or non-locality (what’s the same) ensures that the ribosome apparatus recognizes and correctly chooses an actual codon of the two available doublet-homonymous ones, the codon, pseudo-noised with a background (context).

How to use the nature of linguistic ambiguities of genetic texts in practice?

After all the above-mentioned discussions, here comes again the question of the linkage of the matters discussed with the HIV and cancer issues. Obviously, the linkage is direct. The HIV genome and oncogenes as well as other DNA structures, pseudogenes for instance, “are silent” (as factors of destruction), and this silence continues till a certain time. This key moment for initiation of a genome pathologic condition in cells, potentially inclined to abnormal reborn, is determined by transpositions of oncogenes an the HIV genome or by transpositions of their polynucleotide surrounding in the chromosomal space and time structure. In both cases, context surrounding of genomes and HIV genome changes. The latter is no longer homonymous, unrecognizable or acceptable as a normal one by a cell. Other signals aimed at HIV reproduction are turned on (“are read and conceptualized”). A cell under the new context recognizes oncogenes as factors having other (pathologic) command functions. The changed background (context) identifies and amplifies in the new polynucleotide situation potential signals and other meanings, which were hidden so far. The situation looks like that taking place in protein synthesis (choosing a correct codon out of the homonymic codons). Under this new context, cells are “confused in giving meanings” of DNA sequences and take-in wrong “decision” as correct; this results in the complete rebuilding of a metabolism and its re-adjustment to a “cancer way” - to reproduce HIV. Here, the dualistic situation occurs: the new decisions are wrong in relation to the organism, but are right pertaining to the HIV reproduction. That’s how pathogens identify themselves and uncover their real “targets”, keeping and multiplying themselves as allogenic particles through the destruction of a biosystem as a whole. The problem of the DNA sequences migration in chromosomes may be discussed more globally (oncogenes, HIV genome or any other transposons whose purposes are still unclear for us). Moving along a genome like over a context continuum, they obtain new and new senses and another semantics which depends on their location in a 3D space of interphase chromosomes. The same discussing logic is also true for “genetically-engineered” transgenesises of plants and animals. A growing number of artificial transgenetic organisms threatens with a global and rapid degeneration of all creatures living on the earth, because an uncontrolled automatic sign reconstruction of higher-ranked genetic codes, occurring after the introduction of foreign DNA molecules, isn’t taken into consideration. Practically uncontrolled intertaxonic transfer of foreign DNA-sequences, an avalanche-like semantic chaos in chromosomes and a metabolic chaos in all biosystems (including human beings) will be the result of these genetic-engineered manipulations. It’s becoming hard to slur over the first alarming signals.

The abstract enough theoretical structures of genetic material transpositions we propose are confirmed not only by the example of transgenetic biosystems, but also by R.B.Hesin’s fundamental work [47]. Euchromatic genes, moving to an intercalar heterochromatin, produce a positioning effect, i.e. they are inactivated in one somatic cells and continue to function in others. Oncogenic cellular sequences are able to build-in in retroviral structures which didn’t originally have their own oncogenes. As a result, relatively non-hazardous viruses sometimes become tumorigenic. For instance, the RaLV rat virus might transform, having included master’s determinants in the genome, into the RaSV sarcoma virus. Cellular oncogenes, like viral ones, acquire a transforming activity if the lengthy repeated viral end sequences (LTR) are alloyed to oncogenes’ 5’-ends. Under an appropriate surrounding, proviruses including HIV viruses (as we think) are converted into latent (“silent”) genetic elements. They can retain in a master’s genome without making any harm to it namely owing to the cellular DNA’s neighboring sequences repressing their activity. Taking into account this Hesin’s statement, it’s possible to imagine a reverse situation,

namely, the HIV genome activation in a surrounding of other DNA sequences when a cell in another DNA context already interprets HIV as a hostile semantic structure, but can do nothing to defend itself. However, as Mr. Hesin stresses, both peculiarities of the chromosomal DNA adjacent sections and operational principle which determine a provirus activity, are still a mystery. The mystery will remain unresolved, if not to apply new measurement criteria (semantically-vocal, wave or image measurements, i.e. the criteria we propose) to genome. In this aspect, an interesting comparison of chromosome semantic and holographic information appears. A higher biosystem genome have several levels of information non-locality, “smearing” and redundancy, with a chromosome continuum holographic memory being one of them. Information locality and unambiguity of genome’s mobile elements, the transposons, is contraposed to it; however, the multi-vector meanings of this information are developed dependent on a changing context of the transposon context surrounding; at the same time, transposons themselves are the triggers initiating the appearance, disappearance and repetition of the texts. A context “game” (combinatorial analysis) depends on current metabolic requirements of cells, tissues and an organism. The difference between a text and a context is conditional and depends on the domain of a part and an integer in a genome. The boundaries between the part and the integer are conditional and are likely have a mortho-functional character which depends on an organism’s quantum differentiation by a cell, a tissue, an organ and a biosystem levels. A more fine ranking - by functional and metabolic areas of a cell which are controlled by certain chromosome sections (up to protein-genetic and exon-intronic splitting) - is also exist. Each of these quanta is an integral system in relation to itself, and just a part if the splitting rank is higher. Isn’t here metabolic pathologies and herontologic manifestations are rooted when a biosystem stops identifying and differentiating many-sided patterns of a part and an integer? The HIV genome, like a transposon and like a conditional part, under some DNA context of master chromosomes might be invisible for a cell. That’s the way how molecular-semantic mimicry of pathogenic chromosome structures is produced. Each coding-noncoding homonymous (and synonymous as well) and any other DNA sequence can be considered as a potentially multi-meaning pseudo-noised signal (signals) or like an image (images) which have to be identified and understood on the background of other dynamic gene images. The genetic apparatus amplify each image signal and pick up the amplified signals out of the background (context, noise) not through the noise suppression procedure. On the contrary, a cell, a tissue and an organism use the background changing context as a means of extraction, amplification and understanding the meanings of each these available image signals. It’s also logic to discuss in the same way the role of 3’- and 5’ - flanking sequences of protein genes highlighting one or another meaning. If we realized that the proposed mechanism of the dynamic game of genetic text meanings could play an important role in HIV and cancer development and in an organism’s entire metabolic status on a whole and if we accepted an idea that the comparison of a genome with natural texts and images wasn’t just a poetic metaphor, then real opportunities for creation of a new biosystem management strategy, including management of viruses and oncogenes behavior, emerge.

Is it possible to apply a probabilistic approach for identification of individual, including pathogenic, meanings in a changing polysense continuum of a genome?

We have already mentioned some similarity between the Background Principle and Gerhard Thomas’ multi-vector logic (keno-grammar) and the prospects of these methodologies for the extraction and recognition of genetic or even metabolic vectors of multicellular organisms’ live functions. There’s another one direction in the natural languages theory, which, as we hope, is applicable to genetic linguistic. This direction was developed by V.V.Nalimov and is linked with a probabilistic approach to understanding a language [22, 43]. V.V.Nalimov considered that the semantic of each actual text (including a genetic one, as we think) could be described by its own distribution function (probability density), r (m). Text revision and evolution are linked with a spontaneous manifestation of the filter r (yl m), multiplicatively interacting with the initial function r (m), in a certain situation y. We consider an “y-change” in a genetic text as the natural transpositions of the DNA mobile elements, recombinations, the slicing and the alloying. The wrong (for a biosystem) transpositions of own (or foreign) DNA mobile elements, mutations and artificial transgenic manipulations are considered as “unnatural changes”. An introduction of viral genomes, the HIV genome for instance, into a biosystem’s chromosome material, relates to a “specific class of unnatural changes”. The interaction of the r (yl m) filter with the initial function r (m) is ruled by known Buys’ formula:

r (m l y) = kr (m)r (yl m),

where

r (m l y)	distribution function determining the semantic of a new text after the “y-changes”
k	normalization constant.

According to V.V.Nalimov, Buys' formula comes forward as a syllogism: based on the two statements - r (m) and r (m l y), a text with a new semantic r (m l y) comes to life. Let's assume that Buys-Nalimov's logic is applicable to genetic "texts". Then the "idea" of these "texts" taken as a whole is determined by 3 weight correlations which the r (m) function specifies. "Meanings", being a qualitative parameter in nature, obtain a new quantitative characteristic. With the help of the conditional distribution function r (m l y) V.V.Nalimov presents new, somewhat different from that used in Buys' statistics, interpretation. In his theory, r (m l y) shows the distribution density of a random value y under the given value m . Therefore, not y, but m can be considered as an argument of the r (m l y) function which plays a role of a filter. We think that the "y-changes" factor, initiating and exciting a new semantic situation, is a key element in this model. And namely this factor unpacks "understanding and re-understanding" of increasing number of new meanings as well as of holographic and other images in a variable semantic space of mobile DNAs in a multicellular organism's genome. Genome purporting continuum passes through the dynamic filters r (yl m) responding to it by dramatic "y-changes". Significantly, that V.V.Nalimov had been puzzled by the question what made reproduce the non-trivial r (yl m) filters, but didn't find an answer. Nevertheless, at the same time he put forward an idea about the role the environment played and about the variety of situations as a source and a reason of adequate filters formation. Here, V.V.Nalimov practically came up to the above-discussed Background Principle. After the unification and combination of Nalimov's model and the Background Principle statements it's logic to consider that the y-factor is nothing but a context (background) mechanism of switching on the r (yl m) filters. These filters pick up those semantic loading and meaning which are determined by an actual metabolic, including genetic, situation. For instance, the necessity for a cell to synthesize a huge amount of catalase at the moment, the process which is accompanied with a choice and expression of catalase gene from a gene multi-meaning continuum. Herein another, and may be the key mechanism of genome differential activation to produce different proteins, is seen. Therefore, the Background Principle and Buys-Nalimov's logic became linked by identical in nature definitions. G.Thomas' keno-grammar [26], which is largely based on context orientations in choosing priorities to manage complicated situations, is likely to adjoining the above-said ideas.

Now back to the "genetic engineering". Let's also remind of the "chromosomal engineering", when large blocks of a genome are used for production of useful hybrids. From the probabilistic approach to the mobile polysemantic chromosomal continuum, these "engineering" seem rather gloomy. Any manipulation here is an instant (as compared to the evolution pace) creation of new y-factors by people (and not by the evolution) and therefore, a mutation of the r (yl m) purporting filters, unhampered by any time (evolutionary) frames. That's the Earth's genetic fund forthcoming chaos.

Genetic apparatus paradoxiality

Genetic apparatus paradoxiality in the combination of two imaginably alternative properties - the information stability transferred from one generation to another, and a genome violatility [47]. Genome's mobility is provided by polynucleotide transpositions, soliton-like non-linear dynamics (electric acoustic), and conformative and halogen restructuring. These non-occasional (programming) movements of a chromosome continuum in live tissues are sophisticatedly distributed in a biosystem space and time. The said dynamics is a means of the wave management of re-dislocation of an organism's parts against each other. At the same time, it's a way of metabolic event sequences organization. These strong sign chromosomal non-linear dynamics, which is easily found even in vitro, is realized through its isomorphous image in an organism's space and time structure [32]. As a result, in a chromosomal continuum, as in a polysemantic and multiplex & holographic formation, permanent and variable semantic "game" of meanings goes. Some kind of "endogenic semiotic shows" of optically-acoustic regulatory (sign) images, which also have variable meanings, passes. One of these chromosome images was experimentally found in many laboratories and known as a phantom leaf effect (ref. to [32]). The phantom leaf effect theory is based and is developed on the holography principles [32, 37]. It's possible to say that the "game of meanings" is a function of a sign dynamics of interphase chromosomes. This is a prerequisite for storing and processing vast information volumes when a super-small volume of zygote mesomorphic chromosomes is able to operate a multi-vector and many-sided logic of development of extremely sophisticated biological systems. Herefrom comes an idea that a principally new strategy of approaches to the HIV and cancer treating presumes the understanding and the possibility of managing a multi-vector genome logic. If we master, applying genetic engineering methods, to purposefully (right in the target) introduce certain context DNA sequences to the 3' and 5' ends of oncogenes or HIV-genome, then it's worth expecting the inactivation of their pathologic origins. On the other side, if we know the principles of ribosome operation in a context orientation mode, then we can successfully fight with HIV in a ribosomal wave (laser, solitonic, polarization and radio wave) regulation zone. Ribosomes, synthesizing HIV proteins, must have thin wave vectors for management through context-background paths. Knowing them, it's possible to suppress viral protein synthesis by external artificial modified fields similar to those normal cells use.

Genetic apparatus non-locality levels. Preliminary experiments.

Now, let's talk about another genome operation phenomenon. We mean a supposed effect of quantum non-locality of chromosome sign conditions, which we more or less experimentally confirmed [8, 37]. The idea of quantum non-locality was proposed by Einstein, Podolsky and Rosen [4] (EPR-effect). This effect is good in line with the quantum physics explanations. In short, the sense of the EPR-effect is that elementary particles, two photons for instance, initially been in the so-called "entangled" state, retain the interbonds (this bond may be called "informational") by quantum parameters (for example, by polarization), even if these elementary particles are removed from one another at any distance. If the polarization of one of the particles has changed by any reason, for example, the photon passed through an optically-active layer and recorded the polarization modulations, then this photon disappears, but it manages to instantly (over a zero time) transfer the recorded polarization information to another photon. To be more correct, it's not a "transfer", it's a transition of one photon into another by means of a permissive teleportation mechanism. The first changed photon turns into the second one, independent of the distance between them. The second photon becomes a completed analogue of the first one. If this situation is in some a way reflected in the genetic apparatus, then we rocket to new higher orbits in understanding a metabolic process and the Life phenomenon as a whole. In strictly physical terms, the EPR phenomenon as a fact of photon teleportation was correctly confirmed only in 1997 [2].

Thereafter, other researchers soon obtained similar results, and not only based on photons. Multi-frequency physical fields are now teleported. Based on this data, it's possible to suppose that photon fields, emitted by chromosomes as sign fields, can be teleported within or even outside the organism's space. The same is true for wave photon fronts, which were read from the chromosome continuum similar to reading from a multiplex hologram. If photons are transformed into radio waves (the situation we found - ref. to [8, 33, 37]) through the EPR-mechanism, then this phenomenon is vital. In fact, the importance of quantum non-locality existence for a genome is hard to overestimate. We put forward and published this idea when we found with the help of the equipment we'd developed, probably, a more sophisticated variant of the EPR-effect. The said equipment includes a specially-designed laser which is capable to transform own photons into radio waves [46, 37, 8, 34]. The laser is featured with a unique light beam dynamic polarization which could in some a way simulate a dynamic polarization of chromosome laser radiations. It converts its photons (l =632.8 nm) into kHz-MHz-band radio waves upon the interaction of its beam with a matter and the introduction of probing photons back in the laser resonator. Under these conditions, we suppose, pairs of entangled photons aborning in a gaseous phase of the laser optic resonator are transformed during their splitting and interaction with any body, including the laser mirrors, into radio waves. Photons were found to be able to localize in fractal clusters of the laser metallized mirrors. If photons are probing an outer object, then the mirrors "store" its spectral characteristics. In such a way we have managed to record polarization & radio wave information of DNA preparations. This information carries morpho-genetic signals. This fact enabled us to develop a fundamentally new type of dynamic polarization laser-radio wave spectroscopy and to investigate quantum-illocal (teleportative) genetic processes.

We'd like to express some additional statements on the importance of a quantum teleportation of genetic & metabolic information for biology on a whole. Quantum non-locality of genetic (chromosomal) information as a method of manifestation of its wave total distribution (continuity) in the space of multicellular biosystems seems to be just a particular case. In biosystems, there are 6 non-locality levels, at least.

The first level is a constitutional (organism) level. Here, non-locality is produced in the ability of regeneration, planarium worms for instance possess. After cutting any part of worms' body is capable to reproduce an entire organism through regeneration. In other words, in this case there's no link point between the genetic information common pool and a part of a biosystem. The same is also applicable to vegetative breeding of plants.

The second level is a cellular level. It's possible to grow up an entire organism from each cell (not only from a zygote). Despite the difficulties, it's also possible for animal biosystems. Each cell is a potential continuum of an organism.

The third level is a cellular-nuclear level. Enucleation of nucleus from somatic and reproductive cells with a consequent introduction of other nucleus inside doesn't impede a normal organism development. Such kind of cloning has already been carried out at a higher biosystem level, on sheeps for instance. Each nuclei of a cell is also a potential continuum of a biosystem. There's no localization of genetic potencies at the level of individual cells.

The fourth level is a molecular level. Ribosome "reads" informational RNA either by individual codons, or on the whole, with the consideration of context, i.e. non-locally and continuously.

The fifth level is a chromosomal-holographic level. A genome possesses a holographic memory [37] which in nature is a typically-distributed (non-local) associative memory. At this and the next level non-locality obtains a new feature - a dualistic substantially-wave character, since electromagnetic and/or acoustic fields, bringing out geno-wave information outside chromosome matter, "read" holograms as a substance. A physical field (or fields), marking organism's prospective space (calibration), comes on scene. Brain crust's holographic memory, establishing mental, semantic and image spaces calibrating potential actions of higher biosystems, is likely to belong to this category. That's the way of realizing social and genetic processes.

The sixth level is a genome quantum non-locality. At the levels of up to 6^{th}, genetic information non-locality is realized in an organism's space. The 6^{th} level is of a special nature, since it acquires a new quality. It's manifested within the frames of one of the quantum non-locality forms, namely, in permissive form we postulate in the current paper. In this case, non-locality is realized both by biosystem space and by its own, shrinkable to zero, time. Geno-wave programs, instantly spreading in such a way, simultaneously operate in an organism "here and there" and therefore, the semantic construction "now and then" loses its meaning. And this is a strategic factor and a vital evolutionary achievement of multicellular biosystems. Billions of organism's cells have to instantly "know" a lot of information about each other. Without the "wave information instancy" phenomenon, a giant multicellular continuum of higher biosystems won't be able to completely coordinate a metabolic process and its physiological and other functions. The intercellular diffusion of signal substances and nerve processes are too inert for this purpose. Even if to assume, that sign electromagnetic fields are involved in an intercellular transfer process passing with a speed of light (this assumption is quite reasonable), it's not enough. A quantum non-locality mechanism, applicable to genetic apparatus and which can act as an instantly-distributed quantum (wave) object isomorphous with substantial chromosomes, is required. Using non-locality, genetic apparatus of higher biosystems creates an unparalleled phenomenon, when in certain periods of time the "here and there" and "now and then" structures operate within the biosystems' "closed" space and time as a continuity providing the organism with intrinsic super-coherence, information overredundance, a super-informativity and a linkage and, as a result, proper integrity (survival). The ability of lower organisms' (hydros, worms, amphibian, lizards, crustaceans) tissues and organs to regenerate (people have lost this ability in large) is a manifestation of this phenomenon. But, considering the biosystems wave self-organization principles we are developing, it can be re-activated. The world's first successful adaptation of donor tissues implanted to a blind man, which helped to return a sight to the patient, is a good example of regeneration. The ideology of this surgical operation and regeneration processes is described in [33-35].

At the same time, theoretical and experimental researches in this field are just emerging and need further physical and mathematical understanding and development.

Possible mechanism of recording information on laser mirrors

Now, let's return to some features of the phenomenon of a long-term recording of dynamic photon-polarization-radio wave information on laser mirrors. We think this is linked with the phenomenon of photon fields localization (compression) in the system of correlated dispersers of laser mirrors. Given that the disperser material possesses a low radiation absorption ability, the external light field is capable to retain in the system within a long time without the dissipation in other forms of energy. The reason of localization is connected with the interference of many times diffracted waves. An external electromagnetic signal (in our case, it's a laser beam modulated by polarization, for instance, by a DNA preparation) is localized ("recorded") in the system of non-uniform laser mirrors. Later, the signal can be "read" without a significant loss of information in the form of isomorphously (in relation to photons) polarized radio waves. Theoretical researches on a strain state of localized photons [12, 14-19, 24] say in favor of these thoughts. If this opinion is correct, then a chromosomal apparatus may also be considered as a fractal medium of localized photons accumulation, creating a coherent continuum with a quantum-illocally-distributed polarization radio wave genetic information. To some extent, this is in correspondence with our idea of genome quantum non-locality existence in one of its forms - ref. to [8, 34, 37]. It's possible that the apoptose phenomenon, which is likely to be involved in the regulation of multicellular creatures' life time, is connected with an abnormal compression of photons by a nuclei of a cell, which are accumulated to a maximal value and then destroy the nuclei. The background principle of gene operation (including anti-oncogenes) may be another supplemental apoptose regulation mechanism. For instance, an anti-oncogene coding the p53 protein could be controlled through the introduction of the DNA artificial flanking contexts from 3'-and 5'-ends of the p53 gene.

Analysis of experimental evidences of gene wave forms existence

We are unaware (with some exceptions, of course) of modern publications on wave genes theory and practice, available in the disclosed scientific journals. In the 1920-1940s, A.G.Gurvich, A.A.Lyubitchev and V.N.Beklemishev, who developed the first theoretical models, were the pioneers in this field; their ideas are described in detail in [32,

33]. In this paper, we are trying to produce more developed opinions of some possible synthesis mechanisms and functions of wave genetic structures, attributable to higher biosystems, as well as of the methods applicable for simulation of sign wave processes in chromosomes and model units simulating chromosome field functions and transferring wave genes. A publication and a patent, granted for the development of a device for the transfer of wave genes from a donor biosystem to an accepting one, are worth mentioning as an example of a rarely-appearing event. The said researches were carried out by Yu.V.Dzang Kangeng [39, 40]. Kangeng's device for a directed wave transmission of oncologic, including genetic, information to change hereditary characteristics of a biological accepting object is of a special interest. Unfortunately, there's no theoretical interpretation of the device operation principles. Kangeng's device has some common functional features with the equipment we developed and whose operation is based on similar principles. Kangeng's device includes space elements (forms) which enable to split the radiation of a high-frequency SHF electromagnetic field generator into two orthogonally-polarized beams which repeatedly, as in our installation (in our case, it's a laser beam transforming into radio waves), were passing through a donor biosystem and an accepting biosystems. Dzang Kangeng used a hexahedron, a cone, a sphere and a parabolic-reflector aerial as a kind of special forms. These forms provide a specific spinning (polarization) of the SHF field electromagnetic vectors. In our laser design, one of the mirrors used also had the form of a parabolic-reflector aerial directed to a resonator. During numerous repeated passes through an optically-active (an electromagnetic wave polarization rotating plane) hetero-mesomorphic donor biosystem, organism's tissues modulate the radiation (in our case, this is laser-radio wave radiation) by polarization, which is strengthen owing to repeated passes and is repeatedly and over a long time delivered to the accepting biosystem. In this process, the generator electromagnetic field, "stored" the donor biosystem gene-sign polarization modulations in its "memory", resonantly interacts with gene-sign polarizations polarization of the accepting biosystem electromagnetic fields. If the donor biosystem is at an early morphogenesis stage accompanied with an intensive fission of cells, it can't be excluded that the supposing polarization resonances are also of a holographic nature. Many times-amplified signal, carrying the wave information that was "read" from the donor biosystem chromosome continuum, passes through a substantially-wave structure of the accepting biosystem and makes it execute new polarization-gene-wave programs by means of the variation of their differential polarization structure. Change in the accepting biosystem polarization-gene-wave structure induced by the donor in the process of the field integration ("wave heterosis") leads to a restructuring of its morphologic (genetic and phenotypic) characteristics. Shear wave correlations of polarization angles during the donor-accepting mixture of physical waves, resulted in acquiring new morpho-genetic and biological properties from the accepting organism, are one of the most important quantum-electrodynamics events of the "wave hybridization" process. This fact allows Dzang Kangeng with the help of the wave method to transfer genetic information from ducks to hens, for instance. Hybrid chickens of hens have got typical features of a duck - a flat beak, an elongated neck, increased internal organs (a hard, a liver, a stomach, and a bowels). A weight of a one-year-old hen-duck hybrid is 70% higher, than a weight of hens grown up from irradiated eggs. The second generation of the hen-duck hybrids saved all changes, which were obtained in the first generation, even without further re-radiation. A wave transfer of peanuts' features to sunflower seeds resulted in the change of a form, taste and odor of a hybrid plant, which became similar to those of peanuts. Productivity grew by 1.8-fold; new features are transferred from one generation to another even without further re-radiation.

Let's highlight some common features of the experiments Dzang Kangeng and we independently carried out; they demonstrate the possibility of genetic information existence in a wave form. This similarity is in the polarization modulation of the radiation orthogonal beams with intensity re-distribution in primary orthogonal beams with a frequency secured in the radio wave spectrum we register, by a donor organism. The spinning polarization planes here act as gene-semiotic structures whose biological meanings are identified and coded by angular and intensity shifts by a frequency spectrum. Similarly-polarized waves are known to be able to interfere, while orthogonally-polarized waves do not interfere at all. Waves with a partially-coincided polarization produce, dependent on their polarization coincidence degree, a more or less contrast interference picture. In other words, an angle cosine of each vector in relation to their registration plane or to the wave interference plane is a crucial factor.

Biology, including genetics and embryology, has already come to a turning point in its development, which is similar to the period when physics first admitted an idea that the properties of waves and particles didn't contradict each other and even were compatible in quantum objects. A huge number of facts and scientific research outcomes available in modern molecular biology, genetics and embryology, can't be understood without such a definition as physical fields, for instance, or without the application of quantum electrodynamics principles. The idea of lingual attributes of higher biosystems' genome is a kind of humanitarian counterweight to an apparently excessive physical interpretation of Life functioning basic phenomena. Paces this idea is admitted by society are not high, and this idea faces furious resistance. Current situation is easy to explain: the issue of Life existence is too complicated. Nevertheless, time has come. If we are late with the understanding of wave gene-sign functions of biosystems including the human one, then such diseases as cancer and HIV we'll destroy our society. We'll lose an opportunity of a mighty jump in biotechnology and biocomputing. In the end, we'll also lose an opportunity to purposefully, rationally and positively influence sociogenetic and demographic processes. Following the above-described logic,

we are coming to the conclusion that human speech structures, which provide the major information influx for the mankind, possess fractally-scaled supergenetic properties. Evolution of the society is similar to organism's morphogenesis. Books, libraries, movies, computer memory and people's live speech in the end are the functional analogues of a cell chromosomal apparatus. The aim of these chromosomes is to control the creation of the society space (houses, roads, oil- and gas pipelines, telephony, the Internet) and to arrange relationships among people inside it. Chromosomal sign properties, which have a lot in common with organisms', have a substantionally-wave nature. For instance, a movie showing an ideal model of a social structure and people's relations within its frames is a substantional formation (video tapes). However, it uses a mentally-wave method to input information (light, sound, speech, idea, image). That's the method chromosomes apply. The latter produce marking and calibration fields to arrange organism's space and also control information & metabolic relations, using, in particular, quasi-speech methods (let's remind context orientations in the protein synthesis and functions of oncogenes and HIV). Therefore, people are worth carefully studying the operation principle of their own genetic apparatus and the "tricks" HIVs play to "mislead" our chromosomes. Such kind of a study is especially crucial today when Russia, and not only Russia, could face a demographic and social collapse within the next 5 to 10 years. We have declared the theoretical approach to describe the logic of sign speech-wave relationships between HIV genomes and a master cell as well as the oncogene behavior logic. However, it's not enough. We must get a set of key tools which would enable us to follow up at least the simplest wave command biocomputing functions of our chromosomes[1] and the reprogramming of our chromosomes by nucleotide sequences of HIVs and oncogenes. We have already developed this set of tools - it's a laser uniquely reflecting coherent polarization-laser-radio wave (PLRW) quantum-non-local sign processes in chromosomes. Physico-mathematical formalism characterizing the PLRW-quantum processes in such appliances is presented in our research[2]. PLRW-spectroscopy is the basis of wave information record to laser mirrors - the phenomenon we have discovered. We have also managed to record information from specially prepared mesomorphic DNA matrixes, to broadcast it in a waveform at a distance of 1 m and to introduce it in accepting biosystems. As an accepting biosystem, we took plant seeds. Using this phenomenon, we effected a "wave reparation" of a genome of radioactively-damaged old seeds of Athaliana gathered in the Chernobyl Nuclear Power Plant area in 1987, and initiated drastic changes in stem and tuber phenotype in the second generation of the Solanum tuberosum plant. These biological influences don't have the nature of mutations, they only have a sense meaning and are just another evidence that genetic information can exist in the form of electromagnetic field. Not less important that genetic information can be recorded, stored, read, transmitted and introduced in accepting biosystems. Here, two vital factors emerge. The first one is that the record of vast information volumes, including the genetic one, is an unparalleled event which confirms that it's possible to develop principally new carriers of the dynamic super-capacity analog memory (images, texts). This is rather important for future biocomputing. The second factor is that owing to the PLRW phenomenon we enter a huge area of genetico-metabolic wave sign processes. Numerous and unclear events of distant "recognition" of the pairs antigene $\leftrightarrow$ antibody and transmission RNA anticodon $\leftrightarrow$ information RNA codon, as well as complementary mutual recognitions of DNA single chains, self-construction of ribosomes, recognition sites of ferments, careful piloting and landing of transposons in the DNA and so on, are also embraced within the frames of these processes. Nothing of these phenomena can be explained by only Brownian movement and adjacent angstrom van der Waals, ion, hydrogen and electrostatic interactions. And finally, the most important thing for us in the context of the ideas we propose is a wave and sign behavior of viruses, HIV or influenza, for instance. Viruses can be considered as "orphaned" cells which retained minimum of chromosomal information required for a wave search of a site of landing on a master cell and exact place to cut-in own DNA as a transposon in the master cell's DNA with consequent possible precise re-transpositions. Wave "languages", which viruses use during the information contact with a cell's surface and its genome, are the most vulnerable parts of a virus. Viruses use these "languages" to enter semantic space of a cell and then to "mislead" the cell; after that, they undergo mimicry and are reprogrammed, reproduced and thus survive in the end. Cells are likely to be able to "mislead" viruses as well, creating a kind of "wave immunity". That's why certain balance of powers in the fight exists; the said balance can shift in favor of a virus - for instance, in favor of influenza virus if the temperature starts fluctuating. Cooling of a blood circulation in nose mucosa capillaries changes the temperature of liquid crystals in chromosome blood cells. At the same time, protective wave programs recorded on high topologies of chromosome mesomorphic phases can only be slightly distorted. As a result, the "cold temperature information breach" appears and is used by influenza virus to reproduce. As a response to this action, a compensatory reaction is evolving in the organism, i.e. the body temperature goes up to a sub-lethal level of 41° C. As we think, this reaction is designed to "submelt" mesomorphic phases of the virus nucleic acid and, therefore, to produce noise or completely erase virus wave programs which it needs to attack organism's wave semantic space and to kill the growing number of it's cells. Virus genome acoustic fields tightly linked with photon ones might act as wave bioprograms. Using method of correlative laser spectroscopy, we demonstrated drastic changes in acoustic performance of the DNA liquid crystals in vitro at temperatures of 40-41° C; the results obtained partially confirmed our suppositions. And that's only an example of wave sign processes in the relationship influenza virus $\leftrightarrow$ human organism. Similar sense relationships exist between HIV and man's cells, and the same issues raise - how to correctly find a site of landing on a cell's surface and precisely build-in the DNA (reverse transcriptasal copy of a viral RNA) as a mimicrying transposon into the master cell DNA. Thereafter, the task is to get accurately re-

transposed in a proper place of a chromosome and to detect and realize itself as a reproducing pathogen. Now we can initially list the bottlenecks of HIV wave programs and name countermeasures to eliminate the problems:

1. Searching and recognition of HIV on a landing site (by altering the radiation nature of a virus and/or sites of landing on a cell, it's necessary to distort the system of resonance-wave recognition mechanisms).
2. Searching and recognition of a viral DNA on the site of landing to the master cell's DNA (altering the radiation nature of a virus and/or sites of the landing on the cell's DNA, it's necessary to distort the system of resonance-wave recognition mechanisms).
3. Searching and mutual recognition of protein iRNA: HIV↔HIV RNA (wave distortion of this process).

Any violation of even small wave sign resonances in this triad will result in the loss of infection ability of HIV and other viruses, and the Nature has created an example. As it was already mentioned, it's an organism's temperature mode. In a way similar to the one found by the Nature it'll become possible to design a simple "wave" vaccine against HIV and other viruses and bacteria. Our goal is to study "alphabet" and "grammar" of wave "languages" of viruses' genome. And the foundation for this study has already been laid. A laser capable to "read" PLRW-wave genetico-metabolic information has been developed. However, the research in this field is rather difficult due to intrinsically natural inertia of the material understanding of genetic and metabolic information. Technical issues also exist. The laser we use generates only red photons, while the chromosomal apparatus of human beings and viruses uses a wide spectrum of coherent radiation ranged from 250 nm to 800 nm. Therefore, it's necessary to design lasers which function in a full span of the spectrum visible area. This aim is technically feasible, but significant investments are needed to achieve it. In our point of view, all attempts to produce a material vaccine or other drugs to fight against HIV or influenza virus will fail. Viruses continuously change its antigenic composition and thus bury all attempts of immunologists engaged in the vaccine development. Efforts to chemically block certain stages of virus morphogenesis are inefficient and only poison human organisms. Wave vaccine is a reality. This vaccine provides non-invasivity and environment friendliness, since it touches a narrow area of wave sign relations between a virus and a cell.

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