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Linguistic-Probabilistic and Quantum Understanding of Gene Operation

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Abstract

This paper introduces the hypothesis that during the biosynthesis of prion proteins, the ribosome works in the opposite direction and thus, it is a "prion-poly-anticodon-dependent mRNA polymerase". And accordingly, in violation of the Central Dogma, information flows from protein to RNA. This requires dogma formula to be re-written as follows: DNARNA Protein. The idea of contextual orientations of the ribosome on mRNA during protein biosynthesis is introduced. This ensures the selection of the correct amino acid or stop position due to the strategic role of the "wobbling" off the 3'-codon nucleotide in non-synonymous codons. This leads to the transition of the genetic code from purely a physico-chemical level of its operation to mental-textual one. This is a representation of the fact of one of the levels of non-locality (continuity) of the genome. There are six such levels of nonlocality. Level 1—Organizational. Here, non-locality is expressed with the ability to regenerate, for example, in planarians. Level 2—Cellular. From every cell, and not just from zygotes, you can grow a whole organism. Level 3—Cellular-nuclear. Enucleation of nuclei from somatic and germinal cells with the subsequent introduction of other nuclei into them does not prevent the development of a normal organism. Level 4—Molecular: the ribosome "reads" the informational RNA not only for individual codons, but for the whole RNA, taking into account the context, that is, non-locally, continually. Level 5—Chromosome-holographic. The genome has a holographic memory, and this is a typically distributed (non-local) associative memory. At this and subsequent levels, non-locality acquires a new quality, a dualistic, material-wave character, since holograms as a substance are "read" by electromagnetic and/or acoustic fields that carry genome-wave information beyond the substance of chromosomes. Level 6—Quantum non-locality of the genome. Up to level 6, the non-locality of genetic information is realized in the space of the organism. Level 6 has a special character and a new quality. It manifests itself in one of the forms of quantum non-locality, namely, permissive, postulated in

this work. In this case, the non-locality is realized both in the space of the biosystem and in its own, "compressible" to zero, time. Gene-wave programs that are instantly distributed in such ways, isomorphic to material ones, work in the body "here and there at the same time", therefore, the semantic construction "first and then" loses its meaning. And this is a strategic factor, an extraordinary achievement for multicellular biosystems. We have obtained theoretical and experimental results confirming our ideas.

Keywords

Ribosome, Genetic Code, Genome Non-Locality, Quantum Genome Operation

1. Difficulties in the Interpretation of Gene Functions

We still do not understand the basis of the phenomenon of Life. And most importantly—how it begins in our chromosomes, where we are recorded as texts and holograms. In this paper we will mainly cover the textual work of our chromosomes.

A half-truth is the worst lie. This half-truth is commonly believed, especially since it is a half-truth of "knowledge" about genetic coding. Everything here is an impregnable bastion for criticism, and everything is dogmatized. Even the basic concept, the strategic scheme of genetic coding (DNA→RNA→Protein) is called the "Central Dogma". Until recently, the attack on this dogma, seemed senseless, doomed for failure. However, as it turned out, the first fault in this dogma was found with the discovery of revertase, and then this dogma, turned into a "version", and now it sounds much more modest: DNA⇔RNA→Protein. But even with this modification, our ideas about protein biosynthesis remains subject to erosion, since it is just another approximation towards the truth, to understanding the linguistic-shaped pluralism of the genome as a means of encoding the spatial and temporal structure of biosystems [1] [2] [3].

2. What Do We Want to Prove?

In this study, we develop our ideas, the purpose of which, is not in the final destruction of the so-called "canonical" triplet model of the genetic code, but the development and establishment of its exact place in the system of knowledge about the principles of chromosomes. Yes, it can be said that the triplet code is the ultimate truth. But it is a truth similar to claiming that one can write any word using the alphabet. It's correct. But if we try to go further, having only this knowledge, and prove that with the help of the alphabet one can construct correct sentences, then, this is wrong, because the construction of human speech requires the laws of thinking, grammar and logic. And the genome is precisely speech-like and logical, although these fundamental features are not the only way to express its imaginative-semantic structures. Moreover, we tend to follow the ideas of V. V. Nalimov [4], which lead us to the idea that the genome is quasi-conscious. Our logic and models are an attempt to obtain higher-level know-

ledge about the laws of constructing genetic texts and other semiotic-linguistic structures of the genome, knowledge that is in the initial stage of development. The foundation of this knowledge was laid back in the 1920s by Russian researchers A. G. Gurvich [5], V. N. Beklemishev [6] and A. A. Lyubishchev [7].

What can be proposed for the development and amendment of the generally accepted theory of genetic coding? Before we reach the final proof, let's assume the below three provisions, which already have some theoretical and experimental evidence) are true: [1] [2] [3] [8] [9] [10].

1) DNA molecules in chromosomes have material-wave duality, akin to the dualism of elementary particles. In accordance with this, DNA encodes an organism in two ways—with the help of the DNA substance, and due to its *sign-oriented* wave functions, including at the level of its own laser radiation [11].

2) The genetic apparatus has the ability to be non-local at the molecular level (holographic memory of the chromosomal continuum) and quantum-non-local in accordance with the effect of Einstein, Podolsky, Rosen [12]. The latter means that the genetic and other regulatory wave information of the genome is recorded at the level of polarizations (spin states) of its photons and is transmitted non-locally (everywhere and in zero time) throughout the biosystem's space according to the code parameter of polarizations. This achieves inertialess informational contact between the body's billions of cells.

3) The genome as a whole and individual cell nuclei are quasi-conscious on different levels; both the genome and individual cell nuclei are capable of generating and recognizing textual-imaginative regulatory structures using holography and quantum non-locality.

3. What's Next?

Let's assume, we have received final proof of these provisions. Then, shall we look differently at material-wave dualism of DNA and how it is related to the numerous code functions of chromosomes that are significantly different from the known triplet genetic code? In a sense, the genome acts as a complex multi-wavelength laser with tunable frequencies. It emits light, which is *gene-linguistic* (*or gene-sign-oriented*)[1] modulated by DNA for its amplitude, phase, frequency and polarization. Moreover, the genome is also likely to be a raser. This raser converts coherent *sign-oriented* polarized photons into coherent isomorphically *sign-oriented* polarized broad-spectrum radio waves connected to photons teleportationally [3] [9] [10]. The genome is also a mobile, changing multiplex quasi-hologram, which, with its multi-wave automatic-reading by its own photon radiation, forms light-radio-wave *gene-linguistic* and other regulatory structures [9] [10]. Such structures are registries of biofield marking schemes

[1]Translator's note: This article refers to genome as *gene-linguistic* or *sign-oriented*, borrowing these words from Linguistics. According to Ferdinand de Saussure, language was a system of signs, in which each formed part of an interdependent whole. "Linguistic sign" has two parts:1) a signifier, the form; 2) something signified, what is referred to, the meaning. The author of this article implies that genes are linguistic and sign-oriented, they represent the forms that carry meanings and are able to construct the whole (texts).

(gauge fields) for constructing the space-time of biosystems. And finally, the genome is a quasi-textual formation, with elements of quantum non-locality, which can inertialessly "read" the billions of its own cells and use the information obtained as a guide to live and a way to organize its structure [8] [9] [10]. Perhaps, these ideas about new informational dimensions of the genome today are like "Tutnese (Double Dutch)" to many biologists and geneticists, and even more so to physicians today. However, fortunately, not to all of them. This kind of thinking, which originated in Russia in the 20's, has gained momentum with a sharp acceleration in the last decade. A new strategy for understanding the work of chromosomes should be based on fundamental studies of the material-wave and quasi-speech attributes of the genome of higher biosystems. We emphasize once again that we consider the chromosomal continuum as a linguistic *sign-oriented* laser-radio-wave radiator [3] [8] [9] [10]. And this has direct experimental evidence. For example, to prove the laser potency of genetic structures, we have shown that *in vitro* DNA and chromatin can be pumped as a laser-active medium with subsequent laser light generation [11].

This ensures the selection of the correct amino acid or stop position due to the strategic role of the "wobbling" of the 3'-nucleotide in non-synonymous codons. This leads to the transition of the genetic code from purely a physic-chemical level of its operation to mental-textual one—the Syhomy of genetic code. This is a representation of the fact of one of the levels of non-locality (continuity) of the genome and his speech-likeness [13]. This can be presented in the form of a genetic code Table 1 with a symmetric separation of the families of codons of synonyms

Table 1. The table of the genetic (protein) code.

	C		G		T(U)		A	
T(U)	TCT	Ser	TGT	Cys	TTT	Phe	TAT	Tyr
	TCC	Ser	TGC	Cys	TTC	Phe	TAC	Tyr
	TCA	Ser	TGA	Stop	TTA	Leu	TAA	Stop
	TCG	Ser	TGG	Trp	TTG	Leu	TAG	Stop
A	ACT	Thr	AGT	Ser	ATT	Ile	AAT	Asn
	ACC	Thr	AGC	Ser	ATC	Ile	AAC	Asn
	ACA	Thr	AGA	Arg	ATA	Ile	AAA	Lys
	ACG	Thr	AGG	Arg	ATG	Met	AAG	Lys
C	CCT	Pro	CGT	Arg	CTT	Leu	CAT	His
	CCC	Pro	CGC	Arg	CTC	Leu	CAC	His
	CCA	Pro	CGA	Arg	CTA	Leu	CAA	Gln
	CCG	Pro	CGG	Arg	CTG	Leu	CAG	Gln
G	GCT	Ala	GGT	Gly	GTT	Val	GAT	Asp
	GCC	Ala	GGC	Gly	GTC	Val	GAC	Asp
	GCA	Ala	GGA	Gly	GTA	Val	GAA	Glu
	GCG	Ala	GGG	Gly	GTG	Val	GAG	Glu

Red codons—Mixed codons or Syhoms (Synonyms + Homonyms); **Blue codons**—Synonyms.

and codons of hybrids of synonyms and homonyms (syhoms).

4. A Closer Look at Theoretical Constructions

The evolution of biosystems has created their own genetic "texts" and the genome-biocomputer as a quasi-conscious "subject". At his level, it "reads and understands" these texts. To substantiate this elementary "consciousness" of the genome, it is extremely important to recall that natural (and it does not matter what language it is) human texts and genetic "texts" have similar mathematical-linguistic and entropic-statistical characteristics. This applies, in particular, to the concept of fractality of the density distribution of the frequency of occurrence of letters (for genetic "texts" letters are nucleotides) [14].

There are data [15] (completely in line with our ideas) that were expressed earlier and independently [1] [2] [3], that "non-coding" DNA sequences, which is about 95% - 98% of the genome represent strategic informational content of chromosomes. This content is of material-wave nature and, therefore, it is multidimensional and actually acts as a holographic associative-imaginative and at the same time as a semantic-semiotic program of the embryological principle, a semantic continuation and a logical end of any biosystem. Intuitively understanding the hopelessness of the old model of genetic coding, the authors of [15] with nostalgic sadness say goodbye to the old and well-served model of the genetic code, but don't offer anything in return.

5. Homonymous-Synonymous Ambiguities of Genetic Texts. What Does the Body Need Them for?

The common fundamental semiotic-semantic property of natural and genetic texts is their synonymy and homonymy. This provides chromosomes, as well as natural texts and speech, with the excessive redundancy of information, its ambiguity (multiple meaning), and therefore, adaptive flexibility. The ambiguity of the same genetic texts becomes unambiguous due to the effect of changing position of DNA-sequences in the genome through their transpositions and /or the transpositions of their environment. And this is an analogue of situations in natural texts and speech, when the synonymous-homonymous ambiguities of parts of the semantic field are removed by the context (background principle [16]. In the traditional triplet model of the genetic code, homonymy of coding doublets is easily detected. The meaning of such homonyms has not yet been understood and appreciated, with some exceptions [3] [17]. The inexplicable homonymy of codons of informational RNA (mRNA) instantly arose with creation of a triplet model for the encryption of amino acids in the process of protein biosynthesis. And it immediately became a time bomb, since a correct explanation of the biological (informational) meaning of such homonyms automatically makes it necessary to substantially refine the triplet model, if not to say, to completely revise it.

How do codon homonyms reveal themselves? A number of different amino

acids are encoded by the same doublets as part of mRNA codons, and the third nucleotides in the codons can change randomly, they "wobble" and can be any of the 4 canonical ones. As a result, they do not correlate with the coded amino acids [18] [19]. This is the cause of semantic ambiguity in the anticodon choice made by the ribosome for aminoacyl-tRNA selection. For example, each of the synonymic codons of the standard code of higher biosystems AGT and AGC encodes serine, and each of the synonymic codons AGA and AGG encodes arginine. The third nucleotides of mRNA codons in combination with the *sign-oriented* doublet do not have exact amino acid correlates, and the first two *sign-oriented* codon nucleotides are the same but encode different amino acids, leading to ambiguity in the choice of tRNA anticodons. In other words, a ribosome with same probability can choose both serine and arginine tRNA, which can lead to the synthesis of abnormal proteins. In fact, such errors do not occur, the accuracy of protein biosynthesis is extremely high.

The errors occur only in some metabolically abnormal situations: the presence of some antibiotics, amino acid deficiency, etc. Normally, the ribosome somehow makes the right choice of tRNA anticodons from homonymous doublets. We believe that the correct choice of the anticodons-homonyms doublet is implemented by contextual mechanisms. The homonymity of the amino acid code can be overcome in the same way as it happens in natural languages by placing the homonym as a part into a whole, that is, into a complete phrase, the context of which is deciphered by the homonym assigning it a single meaning, resolving the ambiguity. Therefore, mRNA as a kind of "phrase" or "sentence" should work in protein synthesis as a functional coding whole (non-locally), defining the amino acid sequence at the level of associates of aminoacylated tRNAs that complementally interact with the entire mRNA molecule. Macrosteric discrepancies between the mRNA and tRNA continuums can be eliminated due to the conformational lability of macromolecules. 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 following the "elongation" of the native polynucleotide. Are there any experimental data that could be interpreted in such a way? There are many of them and they are summarized in one analytical study [20]. We'll introduce here some of them. It is known that the correctness of recognition of termination codons by tRNA molecules depends on their contextual environment (which proves our theoretical constructions): in particular, the presence of uridine behind the stop codon. So, this study [21] describes it as follows. Insertion of nine consecutive rarely used CUA-leucine codons after codon 13 as a part of 313 codon test mRNA, strongly inhibits its translation without an apparent effect on the translation of other mRNAs containing CUA codons. This clearly shows that translation has contextual orientation. Making clearly visible

the strategic influence of codon inserts in mRNA (strictly defined and remotely located from peptide bond formation) on the inclusion or non-inclusion of a specific amino acid in the composition of the synthesized protein. This distant influence, associated with the continuity of protein synthesis (this is also an example of the non-locality of genetic apparatus functions), when mRNA is perceived by a protein-synthesizing apparatus not only in parts (nucleotide-by-nucleotide, locally), but also as a whole (non-locally). However, in the cited study, this key phenomenon is simply stated, remaining incomprehensible to researchers and, apparently, therefore, is not even discussed. There are more and more of such works. The one that we mention here, for example, refers to half a dozen of similar results, where interpretation in this respect is also difficult. The reason for this, obviously, is the imperfection of the model of the triplet genetic code. The model is not accurate also because there are unusual swollen anticodons. When they are involved in protein synthesis, not three but more base pairs are involved in the ribosome A-site [20]. This means that the dogmatic postulate of the code tripletness is violated in this case too. The results of studies on the interaction of tRNA-tRNA on the ribosome are given in [20], and this also fully confirms our idea of an associate (continuum) loaded with tRNA amino acids as a precursor of protein. The study [20], proposed a significant idea (very close to our thinking) that the effect of mRNA context on the unambiguous inclusion of amino acids in a peptide represents some fundamental, and so far, poorly studied, principles of decoding of genetic information in the process of protein synthesis.

Recall, that genetic information of protein synthesis takes up only about 1% of the chromosome volume. 99% is employed by programs of significantly higher levels.

6. Prions are the Final Blow to the Central Dogma of Molecular Biology

As we see, the early ideas about the genetic code and the *sign-oriented* operation of the protein-synthesizing apparatus are simplified. Perhaps, the final argument in favor of the final revision of the central dogma of molecular biology is the phenomenon of prions. Prions are low molecular weight parasitic proteins (PrPsc) that infect the brain of animals (Mad Cow Disease) and humans (Alzheimer's disease, Creutzfeldt-Jakob syndrome and others). An inexplicable feature of prions is their virus-like strain-specificity. But strain-specificity is inherent only to microorganisms or viruses that have a genetic apparatus. At the same time, it is believed that the prion genome is absent, since all attempts to detect at least traces of DNA or RNA in prion composition ended in failure. A strong contradiction arises, which once again casts doubt on the central dogma of molecular biology: the prion has no genome but reveals clear genetic signs. Unable to explain this, "saving" the central dogma, they still assume that DNA or RNA residues are hiding in some folds of prion molecules [22]. However,

decades of prion research, which culminated in Stanley Prusiner being crowned with the 1997 Nobel Prize for research in this area, showed an absolutely exact absence of nucleic acids and, therefore, no genome in their composition [23].

How to overcome this contradiction? If you stick to the central dogma, it is impossible. Letting go of dogma, we can imagine the following scenario of prion biogenesis [24]. The main symbolic figure here is the "virtual prion genome", that is, the temporary genome, "borrowed" from the host cell. More precisely, it can be said that this is the protein-synthesizing apparatus of the host cell. Probably, prions as one of the breeding methods have retained a paleogenetic path, which in some cases allows them not to use genes encoding them in chromosomes, but to self-propagate in another way, ignoring the central dogma of molecular biology and genetics. For the cell, synthesizing a prion by means of addressing to their genes, is, albeit a progressive way, but is organizationally and energetically difficult. Prions can do better. We assume that the NH-groups of the PrPsc peptide bonds can react with the OH-groups of the ribose residues of the acceptor CCA sequences of corresponding tRNA. In the course of hypothetical enzymatic reactions, the emerging poly-tRNA-continuum, collinear to PrPsc, spatially pulls together anticodons in pairs, forming a covalently discrete *s*imilarity of *m*essenger RNA (*sm*RNA). This stage is almost the reverse to the protein synthesis on the ribosome. Probably, it occurs on the A- and P-sites of the ribosome. Then, RNA is synthesized into *sm*RNA. This requires the corresponding RNA polymerase, capable of working with the covalent-discrete matrix of *sm*RNA. This is what prion "borrowing" is about: the use of the host cell's protein-synthesizing apparatus for the time period of prion reproduction. Since this operation is limited in time, it creates an illusion of absence of genetic apparatus. At the same time, prion peptide chains serve as matrices on which the poly-tRNA-continuum is built in pairs on A- and P-ribosome sites, forming discrete poly-anticodons. The latter, bonding in pairs, either immediately serve as a matrix for RNA-dependent mRNA prion synthesis, or (in another case) poly-anticodons are cut out by specific splicing followed by ligation into a covalently continuous mRNA prion matrix. Next, prion's mRNA on the ribosome is polymerized by prions themselves. This means that the ribosome works in the opposite direction and thus, it is a "prion-poly-anticodon-dependent mRNA polymerase". And consequently, in violation of the Central Dogma, information flows from protein to RNA. This requires dogma formula to be re-written as follows: DNA⇔RNA⇔Protein. And it can no longer be called a dogma, but is a simple working formula, with which it is necessary to work, specifying and developing it. With such an outlook on prion biogenesis in mind, their strain-specificity is explained by the peculiarities of the reverse work of ribosomes, which are temporarily recruited during the synthesis of each of the prion strains. And these peculiarities are determined by the taxonomic position of prion-producing biosystems.

Let us return again to the generally accepted basic principles of the genetic

code model: it is triplet, non-overlapping, degenerate, has "no commas", *i.e.* codons are not separated from each other in any form. The flow of information goes from DNA to RNA and further to protein. And finally, the code is universal. What remains of these provisions? In fact, nothing. In fact, the code, apparently, is two-, three-, four-, …, ***n***-lettered as a fractal and heteromultiple formation, encoding not only individual proteins, but also functionally associated protein associates. It is overlapped by shifts in the ribosomes reading. It has commas, since heterocodons can be separated from each other by sequences with other functions, including punctuation functions. The code is not universal: in 31 cases it is different from the standard code of higher biosystems. All these cases refer to the mitochondrial, yeast, mycoplasmal, trematode and other codes of lower organisms [25] [26] and can be considered as a kind of dialect. But strategically, the Codes are close.

And the last: the protein is probably able to serve as a matrix for RNA, as we can see with the example of prions. How to interpret the real genetic (to be precise, protein) code, taking into account the above contradictions and the proposed logic of reasoning? It is possible to postulate a qualitative, simplified, primary version of the material-wave control of amino acid alignment, dictated by the associates of aminoacylated tRNA as protein precursors. Accepting this version, it is easier to understand the work of the protein code as one of the many hierarchical programs of the material-wave organization of a biosystem. In this sense, such a code is the first stage of chromosomal plans for the construction of a biosystem, since the language of the genome is multidimensional, pluralistic and not reduced to the task of protein synthesis. The main provisions of the proposed orientational model of material-wave *sign-oriented* processes during protein biosynthesis can be reduced to the following:

1) A multicomponent ribonucleoprotein protein-synthesizing apparatus is a system for generation of highly organized *sign-oriented* radiation of acoustic-electromagnetic fields that strategically regulate its self-organization and the order of incorporation of amino acids into a polypeptide chain.

2) Amino-acylated tRNAs associate in sequences are the "precursors of the synthesized proteins" before contact with the A - P region of the ribosome. Wherein, the continuum of anticodons of tRNA pools is complementary to the entire mRNA, except for dislocations, determined by the presence of non-canonical nucleotide pairs.

3) The order of alternation of aminoacylated tRNAs in protein precursor-associates is determined by the *sign-oriented* collective resonances of all participants in the synthesis of amino acid sequences. Here pre-mRNA and mRNA are the key wave matrices, they work as an integral continuum (macrocontext) of heteropolycodons of different length scales, including the intron fraction of pre-mRNA. The main function of the wave matrices is the associative-contextual orientation of the aminoacylated tRNA sequence. This orientation ignores the rules of canonical pairings of nucleotides in the one-dimensional mRNA-tRNA space to a greater extent than the "wobble hypothesis" of F. Crick. On the ribo-

some, in addition to and/or along with the resonant regulation of the relative position of the codon-anticodon continua, there are laser-like radiations of all participants of this process, correcting the order of incorporation of amino acid residues into the peptide. The ribosome enzymatically covalently fixes "*de jure*" peptide bonds of amino acid sequences, which are marked "*de facto*" in the polyamino-acid-poly-tRNA associate, as a precursor of the protein.

4) Resonant-wave "censorship" of the order of incorporation of amino acids into the peptide chain eliminates the potential semantic arbitrariness of creating erroneous protein "sentences", resulting from homonymy of codon families, and ensures their correct "amino acid understanding" by contextual removal of homonymy of ambiguous identical doublets in codons. The degeneracy of the genetic code is necessary for the pre-mRNA-mRNA-dependent context-oriented accurate selection of aminoacylated tRNA. The selection which is determined by the nature of the wave associative resonant interactions in protein-synthesizing apparatus.

5) One of the mechanisms of creating error-free sequences of aminoacylated tRNA on the pre-mRNA-mRNA wave matrices can be considered a special case of a partially complementary reassociation of single-stranded DNA-DNA and RNA-DNA or, more generally, as an act of self-assembly, known for ribosomes, chromosomes, membranes and other molecular-supramolecular structures of the cell.

6) A ribosome is able to work in the direction of RNA synthesis on a protein matrix.

Thus, the role of mRNA is *sign-oriented* multi-vector and dualistic. This molecule, like DNA, in evolution marks a nodal event—the complementary synergistic unity of material and wave genetic information. The ambiguity of material coding is removed by the precision of the wave coding, which is implemented, probably, by the mechanisms of collective resonances and laser-holographic (associative, contextual-background) effects in the cell-tissue continuum. A leap towards more advanced wave regulation of RNA-Protein translation is accompanied by partial or complete rejection of the rule of canonical pairing of adenine with uracil (thymine) and guanine with cytosine, which is characteristic of evolutionary earlier and simpler stages of DNA replication and RNA transcription. Such rejection is informationally necessary, inevitable and energetically preferable at the level of higher biosystems. We emphasize once again that contextual associative-holographic mechanisms of operation of the protein-synthesizing system of organisms are closely connected with the so-called "background principle" [15], and also, probably, with the multi-vector and ambiguous (polysemantic) logic of managing complex systems (Gerhard Thomas, kenogramatics). From this position, macrocontexts of pre-informational and contexts of informational RNA can be considered as a background, which in this situation and in this interpretation is a "noise source of information". This provides a sharp amplification of the signal, according to which the exact choice (wave recognition) of one of the two homonymous aminoacylated tRNAs takes place, one and only

one of which must enter the exact protein "phrase" or "word". This choice is possible after the selection of the coherent component in the form of echo of the same "comprehension" (discernment) by the ribosome of one of two identical doublets in codons. The situation can be explained with a simple example. For example, in the sentence, you must choose one of two words (analogs of codons with doublets-homonyms). Let's assume these words are "cat" and "cab". It is clear, that the word choice depends on the whole sentence, on the context, which acts as a background, allowing to highlight the signal—the missing word. If the sentence sounds "The cat would like to eat the mouse", then, replacing the word "cat" with "cab", would be equivalent to the introduction of noise and signal loss. Perhaps, the role of pre-informational RNA and introns is similar. They represent different levels of contexts that need to be somehow "read" and "comprehended" by the living cell and its ribosomal apparatus in order to make an accurate decision on the choice of the tRNA anticodon in a situation of homonymy. In this case, the ribosomal protein synthesizing system of the cell can be considered as a nanobiocomputer.

The apparatus for a continuous (non-local) "reading" of contextual RNA-sequences as a whole can be represented by a multi-faceted soliton family: optical, acoustic, conformational, rotational-oscillatory, and other solitons, excited in a polynucleotide. The functions of such solitons can act as methods of accumulating semantic information about RNA-contexts which is followed by semantic regulations of codon—anticodon *sign-oriented* interrelations. Wherein, semantic evaluation is carried out by the cells biocomputers—genomes. As a method for continual reading of polynucleotides, it is possible to imagine exactly the soliton method, scanning the RNA sequence. For example, solitons of running torsional oscillations of nucleotides on the sugar-phosphate axis, which we physically and mathematically examined for single-stranded RNA-like DNA segments [27] [28]. Such solitons react to changes in nucleotide sequences by modulating their dynamics, which acquire *sign-oriented* features, the dynamics that can probably be transmitted distantly, that is, at distances significantly exceeding the length of hydrogen bonds. Without distant (wave, continual) migration of a signal about the whole (*i.e.* about pre-mRNA-mRNA sequences), it is impossible to implement associative-contextual regulation of protein synthesis. For this purpose, some types of solitons need to exercise its wave nature/aspect (as well as their holographic memory) to be able to work not only with parts, but also with an extended polynucleotide whole. Such a continuity (or one and the same, non-locality) ensures ribosomal apparatus recognition and correct choice of a true codon from two doublet-homonymous codons, a codon, which is pseudo-suppressed by the background noise (context).

7. Practical Application of Linguistic Ambiguities of Genetic Texts

After all the above reasoning, the question arises: can our findings in any form help to solve the problems of HIV and cancer, which from the first sight seem to

be irrelevant to what we are talking about? The answer is: "yes", they are directly and immediately related to these problems. The genome of HIV and other retro viruses, as well as oncogenes, are "silent" (as destructive factors), as well as some other DNA structures are "silent", for example, pseudogenes. And this "silence" lasts up to a certain point. And this key point for the initiation of the pathological state of the genome of candidate cells for abnormal degeneration is determined by transpositions in the chromosomal space-time of oncogenes and the HIV genome, or by transpositions of their polynucleotide environment. In both situations, the oncogene and HIV genome context is changing. The latter, in this case, ceases to be homonymous, unrecognizable or perceived by the cell as the norm. Other signals, aimed at reproduction of HIV, are included ("read and understood") too. In the new context, oncogenes are perceived by the cell as factors with different (pathological) command functions. The changed background (context) reveals, amplifies in the new context-polynucleotide situation hitherto hidden potential signals, other meanings. The same thing happens as in the synthesis of proteins in the act of choosing from the homonymous codons the correct one. In this other context, cells are "deceived in the meanings" of DNA-sequences and take incorrect "decisions" for correct, which leads to a complete rearrangement of metabolism along the cancer path and in the direction of HIV reproduction. The relativity of the situation here is that these decisions are incorrect in relation to the organism, but correct in relation to the reproduction of HIV. In this way, pathogens identify themselves, revealing their true "goals", preserving and multiplying themselves as alien parts due to the destruction of the biosystem as a whole. We can consider the problem of migration of DNA-sequences in chromosomes more broadly, whether they are oncogenes, the HIV genome, or any other transposons that we cannot understand. Moving along the genome as a contextual continuum, they acquire more and more new meanings, different semantics, depending on their location in the 3-dimensional space of interphase chromosomes.

The same reasoning is valid with respect to the "genome-engineering" transgenesis of plants and animals. The growing sphere of artificial transgenic organisms threatens a global and rapid degeneration of all life on Earth because it does not take into account the uncontrolled automatic *sign-oriented* rearrangement of higher genocodes that occurs after the introduction of alien DNA molecules. The result of such "genome-engineering" manipulations will be an almost uncontrolled intertaxon transfer of alien DNA-sequences and an avalanche semantic chaos within chromosomes and metabolic chaos in all biosystems, including humans.

Fairly abstract theoretical constructions of the proposed by us meanings of transpositions of genetic material are confirmed not only by the example of transgenic biosystems, but also in the fundamental work of R. B. Khesin [29]. Euchromatic genes, moving to intercalary heterochromatin, show the effect of position: they are inactivated in some somatic cells, continuing to function in

others. Oncogenous sequences can be incorporated into retroviruses that initially do not have their own oncogenes. As a result, sometimes relatively harmless viruses become tumor-like. For example, the RaLV virus in rats can turn into a sarcomal RaSV virus, incorporating host determinants into its genome. Cellular oncogenes, like viral ones, acquire transforming activity if viral long-repetitive-terminal-repeats (LTR) are attached to their 5'-ends by ligation. In a certain environment, proviruses, including HIV (as we see it), turn into latent ("silent") genetic elements. They can be stored in the host genome without harm, thanks to repression of their activity by the neighboring sequences of cellular DNA. Bearing in mind this provision, cited by Khesin, it is also possible to assume the opposite—activation of the HIV genome, surrounded by other DNA sequences, when the cell interprets HIV in a different DNA context as a hostile semantic structure, but cannot oppose anything in its defense. However, as Khesin emphasizes, it remains a mystery what are the features of the neighboring chromosomal DNA regions and what determines the mechanism of provirus activity. This question will remain unanswered, if our understanding of the genome does not acquire other dimensions, in particular, semantic-speech, wave, imaginative, which is what we call for. In this aspect, it would be interesting to compare semantic and holographic information of chromosomes. The genome of higher biosystems has several levels of non-locality, "blurring", redundancy of information, one of the forms of which is the holographic memory of the chromosomal continuum. This is contrasted with the locality and unambiguity of information of mobile genome elements—transposons—but the multi-vector meanings of this information disclose themselves depending on the changing contextual environment of the transposons.

And the transposons themselves represent the initiating elements of the emerging, disappearing and repeating texts. A contextual "game" (combinatorics) depends on the metabolic needs of cells, tissues, the body at the moment. The difference between the text and the context is conditional and depends on the scope of the part and the whole in the genome. The boundaries of the part and the whole are conditional and are probably of a morpho-functional nature, depending on the quantization of the organism over the levels of the cell, tissue, organ and biosystem as a whole. There is a more subtle gradation—along the functional-metabolic regions of the cell, which are controlled by certain parts of the chromosomes, up to protein-gene and exon-intron splicing. Each of these discrete gradations is a whole with respect to itself, but it is a part, where the level of division is higher. Isn't this the origin of metabolic pathologies and gerontological manifestations when the biosystem ceases to distinguish and differentiate the multi-faceted patterns of the part and the whole? Here, the HIV genome (as a transposon and as a conditional part) in some DNA context of the host chromosomes may be invisible to the cell. This reveals one of the mechanisms of molecular-semantic mimicry of pathogenic chromosomal structures. Each coding-non-coding homonymous (and synonymous too) and any other DNA sequence can be viewed as a potentially multi-meaning (ambiguous) pseudo-sup-

ressed by noise signal(s) or as an image(s) that needs to be recognized and understood in the context of other dynamic genetic images.

The amplification of each of these signals-images, their isolation from background (context, noise) is achieved by the genetic apparatus not by suppressing the noise, but on the contrary, changing background-context serves as a means of isolating, amplification and "comprehension" by the cell, tissue and organism of the meanings of each of these potential signals-images. In similar fashion, it is logical to consider the role of the 3'- and 5'-flanking sequences of protein genes that highlight one or another of their *linguistic sign* (meaning). If we realize that the proposed mechanism for the dynamic game of meanings of genotexts can play a significant role in the development of HIV and cancer, in general, the whole metabolic status of the organism, and if we accept the idea that comparing the genome with natural texts and figures is, by no means, a poetic metaphor, then, there are real possibilities of creating new strategy for biosystem regulation, including regulation of behavior of viruses and oncogenes.

8. Does a Probabilistic Approach Allow Isolation of Individual (including Pathogenic) Meanings in a Changing Polysemantic Continuum of the Genome?

We have already noted some similarities between the Background Principle and the multi-vector logic (kenogrammatics) of Gerhard Thomas (see above) and possible perspectives of these methodologies for isolating and recognizing the genetic, or broader, metabolic vectors of the vital functions of multicellular organisms. There is a powerful direction in the theory of natural languages, applicable, as it seems to us, to genetic linguistics. This direction was developed by V.V. Nalimov and is associated with a probabilistic approach to understanding the language [4] [30]. Recall, that the genome is primarily a language (text). One of the natural texts, but specific. V. V. Nalimov believes that the semantics of each specific text (including genetic, as we believe) is given by its distribution function (the probability density)— $\rho(\mu)$. A text change, its evolution, is associated with a spontaneous appearance in some situation$y$of a filter $\rho(y/\mu)$ that multiplicatively interacts with the original function $\rho(\mu)$. For us, y is the change of the genetic text respresenting the natural transpositions of mobile DNA elements, recombinations, splicing, and ligation. Non-natural changes are "erroneous" (for a biosystem) transpositions of their own or foreign mobile elements of DNA, mutations and artificial transgenic manipulations of "genetic engineering". A special class of non-natural changes is the introduction of viral genomes into the chromosomal material of the biosystem, for example, the HIV genome. The interaction of the filter $\rho(y/\mu)$ with the original function $\rho(\mu)$ is given by the well-known Bayes formula:

$$\rho(\mu/y) = kp(\mu)\rho(y/\mu),$$

where

$\rho(\mu/y)$ is the distribution function determining the semantics of the new

text after its

y —changes;

k —the normalization constant.

The Bayes formula, according to V. V. Nalimov, acts as a syllogism: two premises— $\rho(\mu)$ and $\rho(y/\mu)$, are necessarily followed by the text with the new semantics $\rho(\mu/y)$.

We shall assume that the idea of Bayes-Nalimov is applicable to genetic "texts". Then, the "meaning" of these "texts", taken as a whole, turns out to be given by the weight ratios determined by the function $\rho(\mu)$. "Meanings", being qualitative in nature, acquire a quantitative characteristic. Such a conditional distribution function $\rho(\mu/y)$ is interpreted by V. V. Nalimov slightly differently from the generally accepted in Bayes's statistics. According to him, $\rho(y/\mu)$ -is the density distribution of a random variable y at a given value μ. Thus, the argument of a function $\rho(y/\mu)$ that performs the role of a filter can be considered not μ but y.

The key moment in this model is probably the initiation, exciting a new semantic situation change factor y. It is thisthat unpacks "understanding and re-understanding" of all new meanings, as well as holographic and other images, in the changeable semantic space of mobile DNA of the genome of multicellular organisms. The semantic continuum of the genome passes through dynamic filters $\rho(y/\mu)$ that meet the sharpchanges of y. It is significant that V. V. Nalimov wondered what influences the ability to generate non-trivial filters $\rho(y/\mu)$ and did not find the answer. But then he expresses the idea of the role of the environment, the role of the diversity of situations as the origin, the reason for the formation of adequate filters. Here, V. V. Nalimov actually ended up with the Background Principle, discussed above. After bringingthe model of V. V. Nalimov and the Background Principle together, it is logical to assume that factor$y$ is nothing but an extended-contextual (background) mechanism for triggering filters $\rho(y/\mu)$. These filters highlight exactly the semantic load and meaning, which are determined by a specific metabolic, including genetic ("contextual") situation. For example, the need for the cell to synthesize at the moment a large amount of catalase, which entails the selection and expression of the catalase gene from the multi-meaning gene continuum. This reveals another, and perhaps the key, mechanism for the differential activation of the genome for the production of certain proteins.Thus, the Background Principle and the Bayes-Nalimov idea turned out to be connected, in essence, with identical concepts. Probably, Gerhard Thomas kenogramatics [31] (see above) can be added here too, since it is largely relying on contextual orientations in the selection of priorities for managing complex systems.

Let us again return to "genetic engineering" and alsorecall "chromosome engineering," when they operate with large genome blocks, trying to create useful hybrids. From the standpoint of a probabilistic approach to mobile polysemantic chromosome continuum, such "engineering" looks rather gloomy. Any manipulation here is an instant (compared to the pace of evolution) creation by us (and not

evolution) of new factors y, therefore, unauthorized by the time (evolutionary) frameworks of the mutation of semantic filters $\rho(y/\mu)$. This is the coming chaos of the gene pool of the Earth, if we understand the functions of the genome in the old way.

9. The Paradox of the Genetic Apparatus

The paradox of the genetic apparatus is that it combines seemingly mutually exclusive properties—informational stability, passed down from generation to generation with the inconstancy of the genome [29]. The genome is mobile due to polynucleotide transpositions, nonlinear dynamics (electro-acoustics) of soliton type, conformational rearrangements and holographic rearrangements. These non-random (programmatic) movements of the chromosomal continuum in living tissues are complexly distributed in the space-time of the biosystem. These dynamics are one of the methods of wave control of the distribution of parts of the body relative to each other. This is also the way to organize a sequence of metabolic events, that is, biological time, which is fractal. Such powerful *sign-oriented* chromosomal nonlinear dynamics, easily detectable even *in vitro*, is realized through its isomorphic representation in the space-time structure of the organism [1] [2]. As a result, in the chromosomal continuum, as a polysemantic and multiplex-holographic formation, there is a constant and changeable semantic "game of meanings". There is a kind of "endogenous semiotic demonstration" of optico-acoustic regulatory (*sign-oriented*) images, which also have variable meanings. One of the types of such chromosome images was experimentally found in many laboratories as a phantom leaf effect (for more details, see [1] [2].

The theory of this effect was developed on the principles of holography [1] [2] [9] [10]. It can be said that the "game of meanings" is a function of *sign-oriented* dynamics of interphase chromosomes. This is a necessary condition for the storage and processing of extremely large amounts of information, when the ultra-low volume of the liquid crystal chromosomes of the zygote is able to operate with the multi-vector, multi-meaning logic of the development of an extra-complicated biological system. Hence, the clear idea that a fundamentally new strategy for the development of methods for treating HIV and cancer lies in understanding and control of the the multi-vector genome logic. If we learn to apply correct genetic engineering methods, we can efficiently introduce certain DNA-sequences connected to oncogenes or HIV genome from the 3 "and 5" ends, then, we should expect inactivation of their pathological natures. On the other hand, if we know the laws of ribosomes operation in the contextual orientation mode, then, we can fight HIV in the zone of the ribosomal wave (laser, soliton, polarization-radio wave) controls. Ribosomes, synthesizing HIV proteins, must have subtle wave vectors of control via context-background paths. Knowing them, it is possible to suppress the synthesis of viral proteins by external artificially modified fields, similar to those used by the cells themselves in normal conditions.

10. Levels of Non-Locality of the Genetic Apparatus. Preliminary Experiments

Let's talk about another phenomenon of genome operation. This is a hypothetical, and to some extent justified by us experimentally, effect of quantum non-locality of *sign-oriented* states of chromosomes [8] [9] [10]. The idea of quantum non-locality was expressed by Einstein, Podolsky, and Rosen (EPR effect) [12]. It is flawless in terms of the formalism of quantum physics. Briefly, the essence of EPR is that elementary particles, for example, two photons, originally located in the so-called entangled state, when separated from each other at any distance, keep the connection (this can be described as informational) by quantum parameters, for example, polarization. If the polarization of one of them for some reason has changed, for example, the photon passed through some optically active layer and recorded polarization modulations, then, this photon disappears, but instantly (in zero time) transmits the recorded polarization information to another photon. It would be more accurate to say that there is no "transmission", but there is a transition of one photon into another using the mechanism of permissive teleportation. The transformation of the first modified photon into the second occurs, regardless of the distance between them. The second photon becomes a complete analog of the first. If this somehow works in the genetic apparatus, then, we open completely different horizons of understanding metabolism, and the phenomenon of Life in general. In purely physical terms, the EPR phenomenon was correctly confirmed only in 1997 as a fact of photon teleportation [32].

Similar results were soon obtained by other researchers, and not only on photons. They already teleported multi-frequency physical fields. Based on these data, it can be assumed that the photon fields emitted by the chromosomes as linguistic *sign-oriented* can be teleported in the space of the organism or even beyond its limits. The same applies to photon wave fronts, read from the chromosomal continuum as from a multiplex hologram. If the photons are converted into radio waves, which we have discovered [3] [8] [9] [10], and this happens in the chromosomes by the EPR mechanism, then, the significance of this phenomenon is fundamental. Indeed, the importance of the reality of quantum non-locality for the genome is difficult to overestimate. This idea was expressed and published by us after we discovered, apparently, a more complex version of the EPR effect using the equipment we developed. It includes a special type of laser that can translate its own photons into radio waves [8] [9] [10] [24] [33]. This laser is characterized by the ability for a unique dynamic polarization of the beam, perhaps remotely simulating the dynamic polarization of the laser radiation of chromosomes. It converts its photons (λ = 632.8nm) into radio waves from a kilo to megahertz range during beam interaction with matter and injection of the probe photons back into the laser resonator. We believe that under such conditions, pairs of entangled photons (produced in the gas phase of the laser optical resonator) during their separation and interaction with any matter,

including laser mirrors, turn into radio waves. It was found that photons are able to localize in fractal clusters of the metallized laser mirrors. When photons probe any external object, then their spectral characteristics are "remembered" by mirrors. So we managed to record polarization-radiowave information of DNA preparations. Such information carries morphogenetic signals. This gave us the opportunity to develop a fundamentally new type of dynamic polarization laser-radiowave spectroscopy and investigate quantum non-local (probably, teleportational) genetic processes.

Let us additionally introduce some considerations about the significance of quantum teleportation of genetic-metabolic information for biology as a whole. It seems that the quantum non-locality of genetic (chromosomal) information, as a manifestation of its wave total distribution (continuity) in the space of multicellular biosystems, is a special case. In biosystems, at least there are six levels of non-locality.

Level 1—Organizational. Here, non-locality is expressed in ability to regenerate, for example, in planarians. After cutting such worms, any part of their body gives the whole organism during regeneration. In other words, in this case there is no linkage of the total pool of genetic information to some part of the biosystem. The same applies to vegetative propagation of plants.

Level 2—Cellular. From every cell, and not just from zygotes, you can grow a whole organism. For animal biosystems, this is difficult, but possible. Each cell is a potential continuum of the organism.

Level 3—Cellular-nuclear. Enucleation of nuclei from somatic and germinal cells with the subsequent introduction of other nuclei into them does not prevent the development of a normal organism. Cloning of this kind is already carried out on higher biosystems, for example, on sheep. Each cell nucleus is also a potential continuum of a biosystem. There is no localization of genetic potencies on any individual cell.

Level 4—Molecular: the ribosome "reads" the informational RNA not only for individual codons, but for the whole RNA, taking into account the context, that is, non-locally, continually.

Level 5—Chromosome-holographic. The genome has a holographic memory [9] [10], and this is a typically distributed (non-local) associative memory. At this and subsequent levels, non-locality acquires a new quality, a dualistic, material-wave character, since holograms as a substance are "read" by electromagnetic and/or acoustic fields that carry genome-wave information beyond the substance of chromosomes. A physical field or fields, such as a gauge field, marking the future space of an organism, appear on the scene. This also includes, apparently, the holographic memory of the cerebral cortex, which determines mental, semantic and imaginative spaces, calibrating the potential actions of higher biosystems. This is where socio-genetic processes are realized.

Level 6—Quantum non-locality of the genome. Up to level 6, the non-locality of genetic information is realized in the space of the organism. Level 6 has a special character and a new quality. It manifests itself in one of the forms of quan-

tum non-locality, namely, permissive, postulated in this work. In this case, the non-locality is realized both in the space of the biosystem and in its own, "compressible" to zero, time. Gene-wave programs that are instantly distributed in such ways, isomorphic to material ones, work in the body "here and there at the same time", therefore, the semantic construction "first and then" loses its meaning. And this is a strategic factor, an extraordinary achievement for multicellular biosystems. Billions of cells must "know" about each other, if not about everything, then a lot, and moreover, instantly. Without the phenomenon of "wave information instantaneousness," the giant multicellular continuum of higher biosystems is unable to fully co-ordinate metabolism, its physiological and other functions.

Intercellular diffusion of signaling substances and nerve processes are too inert for this. Even if we assume that *sign-oriented* electromagnetic fields with light speeds are involved in the intercellular transmission, which is sufficiently justified, even then, this is not enough. The mechanism of quantum non-locality is necessary, and it is applicable to the genetic apparatus, which can act as an instantly distributed quantum (wave) object, isomorphic to material chromosomes. Using non-locality, the genetic apparatus of higher biosystems create an amazing phenomenon: when in the moments of "collapsed" space-time,"here and there", "first and then", the biosystem works as a continuity, providing supercoherence, information over-redundancy, overinformation, connectedness and, as a result, integrity (survival). A manifestation of this, for example, is the ability to regenerate organs and tissues in lower organisms (hydra, worms, amphibians, lizards, crustaceans), an ability that has been largely lost by humans. But, given the principles of wave self-organization of biosystems that we are developing, it can be activated. An illustration of this is the world's first successful engraftment of donor tissue implanted to a blind person with restoration of vision. The ideology of such a surgical operation and regenerative processes was based on research [3]-[17].

In recent years, have obtained theoretical and experimental results confirming our ideas. We have expanded the theoretical model of the linguistic nature of genetic information by introducing the concept of "delegating" the function of other Code letters to the 3'-nucleotides of non-synonymous codons. We introduced the concept of SYHOMY—the phenomenon of functional hybridization of synonymous and homonymous codons, which explains the leap of the genetic coding of proteins to the level of real textual (mental) structures [29] [34]-[47]. But this is a topic for a separate article.

Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

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