

Non-coding DNA-sequences in the light of the theory "EVOLUTION of NUCLEIC BIOENERGY SYSTEMS"

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Abstract

It is presented on the basis of fundamental laws of the evolution of energy systems in nature a hypothesis of the origin of "junk DNA". The noncoding DNA sequences originated according to her on the base of a combination of genetic variability and selection of these mutations in the evolution process of the "nucleic bioenergy systems".

Keywords: Genome; "Nucleic Bioenergy Systems"; Mutation; "Junk DNA"

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Introduction

It was determined after completion of the project to decipher the human genome in 2003 that the protein-coding sequences make up only about 1.2% of the genome. The remainder of the genome is noncoding DNA [6].

The project "Encyclopedia of DNA Elements" (Encode) performed since 2003 in order to identify all functional elements in the human genome, including the biological significance of the "junk DNA". It has shown in the publications of this project in 2012, that 80% of the genome has a biochemical function [3]. But the understanding of the functions of all genes and their regulation remains far incomplete.

It is based on the law of multiple changes (n-multiplicity-law) of quantum energy, emanating from the general theory "Evolution of energy systems and following causal relationships in the process of the evolution of nature", which we do not consider here at the moment, because she is extensive, **a concept suggested**, that the "junk DNA" are a remainder of noncoding, repetitive DNA sequences, which produced during the genesis of life. That is, the emergence of "noncoding DNA" was caused through the evolution process of the "nucleic bioenergy systems".

Non-coding DNA as the result of evolution of the nucleic bioenergy systems

The evolution of bioenergy systems is a natural process of development of living nature, which flows a long time and includes certain stages.

Thus arose as a result of "primary photosynthesis" the "carbohydrate Bioenergy Systems".

The next stage of the evolution of bioenergy systems were "protein bioenergy systems", which prototype are existing at present the special class of infectious agents, called as prions.

On the basis of the "protein bioenergy systems" arose "nucleic bioenergy systems".

The primary bioenergy system (1) in the series of the "nucleic bioenergy systems" was RNA-bioenergy system. It had only one single gene. This gene is responsible for translation of one protein, which was necessary for the construction of the shell of this primary bioenergy system. A prototype of the RNA-bioenergy system is at the moment existing RNA viruses, secondary bioenergy systems (2). RNA virus genome contains at least three structural genes: gag gene encodes the capsid protein, pol gene - reverse transcriptase, env gene - shell glycoprotein.

A methylated RNA (instead of uracil - thymine) was after deoxygenation of the ribose in a certain time of evolution the development of bioenergy systems on earth a base of the formation from RNA-energy systems for the DNA energy system [10].

The following bioenergy systems were in the evolution of the series from "nucleic bioenergy systems" according to the RNA bioenergy systems the DNA "virus" - bioenergy systems. Virus genome contains 3 to 150 genes.

The next level of evolution of bioenergy systems - single cell bioenergy systems, from whose genome contains up to 5 000 genes, further different types of multi cellular organisms, up to homo sapiens, human genome consists of 20 000 - 25 000 genes.

If, outgoing from an evolution-dialectic view of life development on earth, the ontogenesis repeats the phylogenesis (**biogenetic law**), the cell organization of energy systems has information in the DNA-code about evolutionary previous energy systems whose prototypes, e.g., nowadays existing RNA- and DNA-viruses, are the following ones: this is evolutionary primary RNA-, virus "-energy system, followed by the DNA-, virus "-energy system and, in the end, the cell energy system etc..

Therefore the presence of the genes of retroviruses is in the single cell bioenergy systems, in multi cellular organisms, up to homo sapiens regularity. It is currently established, that the genes of retroviruses represent about 1% of the human genome [4]. They have the important meaning in different physiological processes, such as for example the formation of the placenta [4].

We consider for the explanation of the being of noncoding DNA sequences from our general theory „of the evolution of energy systems and the causal-following connections in the evolution process of nature" **the law of multiple change of the quantum energy** (n-multiplicity-law) in the evolution rows of all kinds of the energy systems:

$$n = k \cdot \frac{m \cdot (m + 1)}{2}$$

n - quantity of the multiple quanta of the energy in the searching energy system,

m - quantity of the sequential numbering of the searching energy system in the given, searching row of the energy systems, certain energy kind,

k - quantity of the quanta of the energy in the first energy system of the given, searching row of certain energy systems [10].

On the basis of this law (n-multiplicity law) propose a theoretical model of the organization of the DNA code "nucleic bioenergy system", e.g., cell with the differentiation of the 2nd degree, as shown on figure "CD".

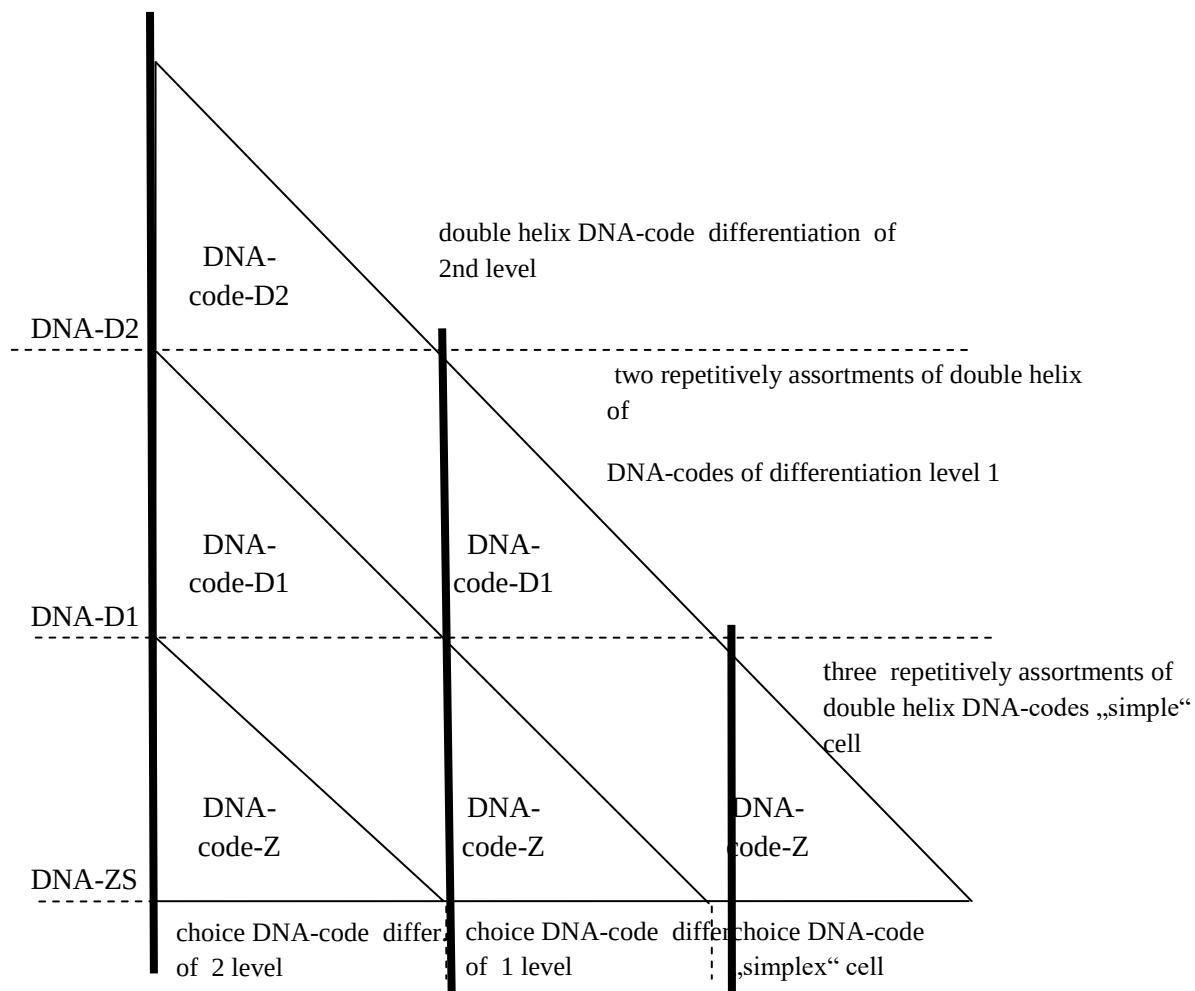
On this pattern the charting of the full DNA-code (full program of genetic information) is portrayed of the cell with the differentiation of the 2-nd level. There the so-called exons and introns can be seen well. The structural organisation of celloncogens (c- src) was suggested by J. Bishop in 1982 [7]. After his theoretical model, the celloncogen was anyhow „caught" by the retro virus. The introns seclude themselves (elimination) and the summarised exons insertieren to themselves (insertion) to the virus gene, complete v- src genome. It was cleared up that the cell oncogene associated later historically with the retro virus genome. After my theory, a cell energy system has the program of genetic information which is encoded in DNA, about the evolutionary leading energy systems whose existing prototypes nowadays are RNA and DNA viruses. So the occurrence of the virus genome in the DNA of the cell on account of my theory of the evolution of energy systems is legitimacy.

The theoretical model of the DNA- code, which is shown on figure "CD", makes clear also the evolution-dialectic spiral of the development of the bioenergy systems. With tricking this pattern (figure "CD") around 90 ° clockwise one can clearly see the evolution spiral of the cell energy systems: the base of the cell energy system evolution is the „simple“ cell (**DNA-code – Z**); the following bend of the evolution spiral is the cell with differentiation of 1 level (**DNA-code – Z // DNA-code – Z + DNA-code – D1**); afterwards the cell with differentiation of the 2nd levels (**DNA-code – Z // DNA-code – Z + DNA-code – D1 // DNA-code – Z + DNA-code –D1 + DNA-code –D2**) etc.. Everything shown on top mentioned on figure „CD“.

Full DNA-code in case of existence of the cell in level:

- „simple“ cell (**DNA-code – Z**)
- differentiation of 1st level (**DNA-code – Z + DNA-code – D1**)
- differentiation of 2nd level (**DNA-code – Z + DNA-code – D1 + DNA-code –D2**)

Figure “CD”



Sum DNA-code of the cell with differentiation of 2nd level

This charting of bioenergy system evolution which based on dialectic basic laws (the law of negation of negation, turning quantity into quality) is, in my opinion, the theoretical reason of the repetitive DNA-sequences, so-called satellite –DNA [5].

The combination of genetic variability and selection plays an important role in the processes of biological evolution, in the origin of new, more advanced forms of the organization of living matter.

We consider these processes on the proposed theoretical model of the cell with the differentiation of the 2nd degree, as

shown on figure "CD". The material for the evolution of “nucleic bioenergy systems” serves the heritable changes - the accidental production of alternative options.

The result of the accumulation by the mutations in the DNA of the simple cell (**DNA-code - Z**) and the selection of the genetic changes in the evolutionary process, the “nucleic bioenergy systems” **is an abrupt increase of the information codes of the DNA - "phenomenon of the quantization (quantum) of genetic energy in the bioenergy systems "**, which occurs in the process of division this bioenergy system.

Thus forms from the simple cell (**DNA- code - Z**) the "nucleic bioenergy system" the next stage of evolution - the cell with the differentiation of the 1. degree (**DNA- code -Z // DNA-code - Z + DNA- code -D1**).

Similarly forms in the course of evolution from the cell with the differentiation of the 1st degree (**DNA -code -Z // DNA-code -Z + DNA- Code-D1**) the "nucleic bioenergy system" the subsequent level of evolution - the cell with the differentiation of the 2nd degree (**DNA- code-Z // DNA-code - Z + DNA-code -D1 / DNA-code - Z + DNA-code -D1 + DNA-code - D2**), etc. - the evolution spiral of the "nucleic bioenergy system". That the new genes appear in the depths of "old" genes. Proof of this is the similarity in the DNA sequences of different organisms. According to the opinion of Jacob, „evolution does not create new structures de novo, it restructures old structures“ [9].

The degree of differentiation of the cell - the functional level of the cell genome is determined by the „selected cell“, more exactly said by the full of DNA Code of the differentiation - or Z, or D1, or D2 (figure "CD") which are in the structure of the genetic information of cell nucleus - in the chromosomes. And the choice of the „selected cell“, the program of the genetic information is regulated by the methylation process of the cytosine bases of DNA. That is, the cell differentiation process regulated by epigenetic processes - methylation of the pyrimidine bases of DNA during cell division, to be more precise, during its completion - in the "phase of determination of cell differentiation" [11].

The nature of these epigenetic processes is the bioenergetics of the cell - 3 energy-rich compounds of the molecule adenosintri-phosphat are necessary for the formation of 1 molecule S-adenosylmethionin [8].

The human body has about 220 different types of cells, the size of the genome is over more than 3 billion nucleotide base pairs and on the basis of the law of multiple change (n-multiplicity-law) of the quantum energy consists of - $n = 1 \cdot \frac{220 \cdot (220+1)}{2} = 24310$ genes.

There are no "Junk DNA" in the human genome in light of the theory of evolution of the "nucleic bioenergy systems" (see theoretical model – figure "CD").

Evolution caused stages of differentiation - structurally repetitive levels of the function of DNA- code of the

human genome, that arisen in the course of evolution of the "nucleic bioenergy systems" (see figure "CD"), **explain the essence of the so-called noncoding, repetitive DNA sequences in the human genome**. These repeated components of DNA (satellite DNA) guarantee for stability of the genetic material of "nucleic bioenergy systems". The noncoding DNA sequences are often similar among many kinds, even also with evolutionary very much distant organisms. This is also a confirmation for theory of evolution of the "nucleic bioenergy systems".

At this theoretical model of the evolution of "nucleic bioenergy systems", how shown on figure "CD", can clearly see the **"high repetitive" DNA segments (DNA-Code – Z)** and the **"middle-repetitive" DNA sequences (DNA-Sode-D1)**.

Than evolutionarily older the DNA sequences are in this "nucleic bioenergy system", **the more give these repetitive DNA sequences in the Genom** (s. figure „CD“):

(DNA-Code-Z) are **3 repetitions** and **(DNA-Code-D1)** are **only 2 repetitions**.

On the basis of the law of multiple change (n-multiplicity-law) of the quantum energy can determine, calculate the quantity of genes in all kinds of "nucleic bioenergy system", which arose as a result of evolution: RNA- viruses, DNA- viruses, the cell energy systems, multicellular organisms, up to homo sapiens.

The confirmation of the authenticity, the evidence for the law of the multiple change of the quantum energy (n-multiplicity-law) in the evolution process of the "nucleic bioenergy systems" is

that, that due to the **formula of this law** $[n = k \cdot \frac{m \cdot (m+1)}{2}]$;

there **k = 1** gene, because RNA- bioenergy system **(1)** - the base of evolution "nucleic bioenergy systems had 1 – gene.] **the calculation** of the quantity of genes **(n)** in these bioenergy systems coincides similar data obtained at decoding their genomes, for example:

- RNA virus **(m-2)** contains 3 gene and based on the law of multiple change of the quantum energy also - $n = 1 \cdot \frac{2 \cdot (2+1)}{2} = 3$ genes.

- E. coli contains about 95 species of proteins of the primary structure (**m-95**), its genome consists of 4288 genes [2] and based on the formula of this law obtain –
$$n = 1 \cdot \frac{95 \cdot (95 + 1)}{2} = 4560 \text{ - genes.}$$
- Drosophila has approx. 165 cell types with different differentiation degree
- accordingly the similar number of proteins of the primary structure (**m-165**), Genome contains 13,600 genes [1], and from the law of multiple change of the quantum energy obtains - $n = 1 \cdot \frac{165 \cdot (165 + 1)}{2} = 13695 \text{ genes.}$

- The human body has about 220 different types of cells (**m-220**) and the human genome contains 20 000 – 25 000 genes.
On the basis of the n-multiplicity-law its genome is from - $n = 1 \cdot \frac{220 \cdot (220 + 1)}{2} = 24310 \text{ genes.}$

The primary evaluation of the human genome was more than 100 thousand genes. Then the analysis of the human genome revealed initially 40 thousand genes, later up to 30 thousand genes. After completion of the Human Genome Project in 2003 in the human genome are from 20 to 25 thousand genes. Based on our theory “Evolution of the nucleic bioenergy systems” Homo sapiens genome consists of 24.310 genes.

Table of comparison of the quantity of genes in the bioenergy systems obtained at decoding their genomes and under the calculation due to the formula from law of multiple change of the quantum energy

Bioenergy systems:	The quantity of genes obtained at decoding their genomes	The quantity of genes obtained due to the n-multiplicity-law
RNA virus	- 3	- 3
E.coli	- 4 288	- 4 560
Drosophila	- 13 600	- 13 695
homo sapiens	- 20 000 - 25 000	- 24 310

The main attention was focused in the theoretical research of the nature of noncoding DNA to the structural genes, which encode enzymes, structural proteins. Other regulatory DNA sequences: promoters, operators, terminators, etc. secondary, in essence, as well as in understanding of the theoretical interpretation of noncoding DNA.

Conclusion

The noncoding, repetitive DNA sequences in the human genome are because of the general theory "Of the evolution of energy systems and the causal-following connections in the evolution process of nature" **an objective consequence of the evolution of "nucleic bioenergy systems".**

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