

Harmony of Living Nature, Symmetries of Genetic System and Matrix Genetics

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Accepted 29 August 2007

"The next important phase of scientific development must be directed towards understanding the functional expression of genes and the study of physiological systems under the control of these newly discovered nucleotide sequences."

Francis Collins

Director of the National Center for Human Genome Research at NIH

INTRODUCTION:

Recent progress in sequencing of genomes has resulted in a spectacular increase in the size of genomic databases. But what is it that these sequences tell us and what are the generalizations and rules that they are governed by? It seems that we understand too little about the genetic contexts to be able to "read" them correctly. Analytical, statistical, mathematical, and computational tools help in the process of decoding the secrets of biology. It is now apparent that opportunities to use molecular probes to explore complex biological systems will drive the next phase of advancement. As noted recently by Francis Collins, Director of the National Center for Human Genome Research at *National Institutes of Health (NIH)*, "The next important phase of scientific development must be directed towards understanding the functional expression of genes and the study of physiological systems under the control of these

newly discovered nucleotide sequences"

Molecular fundamentals of genetic code are mutual ones for all living organisms. Their structural peculiarities present a final result of a giant experiment by nature to create self-organizing and self-reproducing systems. Science has a challenge to understand a system organization of molecular genetic ensemble with its unique properties of reliability and productivity. Disclosing of key secrets of this organization means a big step in science about nature in a whole and a big step to create the most productive biotechnologies. Knowledge about this structural organization should become a part of mathematical natural science. In this reason it is essential what kind of methods is used from the very beginning to get such knowledge.

Investigation of symmetries of natural systems is one of the most effective methods of cognitions of the nature. Due to the efforts of many generations of scientists, modern science knows that deep knowledge about phenomenological relations of symmetry among separate parts of a complex natural system can tell much important things about evolution and

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mechanisms of this system. Modern physics and other natural sciences have a great number of successful applications of a symmetry method. The latter is considered, in addition, as one of the most ancient methods of theoretical investigation. Since ancient times theoretical doctrines about structures of the world worked for a symmetric classification of natural systems and for presentation of their knowledge in symmetrical schemes of square tables, symmetrically divided circular patterns, etc. Investigations of symmetries are the most relevant in that case when science does not know how to create a theory of a concrete natural system. Principles of symmetry got a new essential quality in modern science additionally. They became simultaneously as one of the bases of modern mathematical natural science. In our days, many physical theories, from the theory of relativity and from quantum mechanics, are created as theories of invariants of mathematical groups of transformations, in other words as theories of special kinds of symmetry.

Biological organisms belong to a category of very complex natural systems. Multiformality of organisms is very numerous. Their sorts differ from each other vastly by many aspects: by their sizes, appearances, kinds of motions, etc. But to the surprise of humanity, molecular genetics have discovered that from a molecular-genetic viewpoint all organisms are equivalent to each other by their basic genetic structures. Due to this revolutionary discovery, a great unification of all biological organisms took place in science, and the information-genetic line of investigations became one of the most perspective lines not only in biology but also in science on the whole. It is essential that a basic system of genetic coding has happened strikingly simple. Its simplicities and its orderliness throw down a challenge to specialists from many scientific fields, including specialists in a theory of symmetry and of anti-symmetry (He M. *et al.*, 2005).

It should be noted that fantastic successes of molecular genetics were defined in particular by a disclosure of phenomenological facts of symmetry in molecular constructions of genetic code and by skilful using of these facts in theoretical modeling. A bright example is a disclosure of a symmetrological fact, reflected in the famous rule by E. Chargaff, of an equality of quantities of nitrogenous bases in their appropriate pairs (adenine-thymine and cytosine-

guanine) in molecules of DNA in different organisms. This phenomenological rule was used skillfully in a theoretic modeling of a double spiral of DNA by F. Crick and J. Watson with using of additional symmetrological principles.

Molecular genetic code is a discrete encoding system, which operates according to the rules of quantum mechanics (from the viewpoint of classic physics, atoms and molecules can not exist at all). The very effective and traditional mathematical approach in the theory of coding and processing of signals and in quantum mechanics also is matrix analyses. A success of such approach permits not only to disclose structural secrets of genetic system but also to make a bridge between genetic system and named scientific fields, which have many useful notions and formalisms (cyclic principles, Hadamard matrices, spectral analyses of discrete signals, geometry of vector-signals, energy and power of signals, noise immunity and cyclic codes, etc.) (Ahmed *et al.*, 1975; Peterson 1972; Sklar 2001). This approach permits to construct new mathematical tools for investigation of genetic and other complex systems (He *et al.*, 2004; Petoukhov, 2001a; Petoukhov, 2001b; Petoukhov, 2001c; Waterman, 1989). These results are essential additionally from the viewpoint of modern tasks to create computers from DNA molecules and to understand genetic system as a quantum computer.

An application of matrix analyses in genetic field (“matrix genetics”) gives an opportunity the system analysis of natural parameters of molecular ensembles of a genetic code by means of a matrix representation of these ensembles, first of all, the nitrogenous bases and genetic multiplets. Mysterious sets of structures, realized by the nature in a hierarchic system of genetic codes, are confronted by a heuristic manner with families of mathematical matrices, which contain elements of these structures in symbolic and numerical forms. Matrix genetics has discovered (He, 2001; He, 2004; Petoukhov, 2001a; Petoukhov, 2001b; Petoukhov, 2001c; Petoukhov, 2003; Petoukhov, 2004; Petoukhov, 2005; Petoukhov, 2007):

- new phenomenological rules of evolution of genetic codes;
- existence of two branches of evolution within genetic code;

- hidden interrelations between the golden section and parameters of genetic multiplets;
- Hadamard matrices and matrices of a hyperbolic turn in genetic matrices;
- a cyclic principle in a structure of matrices of genetic code;
- materials for a chronocyclic conception, which connects structures of genetic system with chrono-medicine and a problem of internal clock of organisms;
- a relation between Pythagorean musical scale and an important class of quint genetic matrices which testifies into a favor of a molecular genetic base of a sense of musical harmony and of aesthetics of proportions. From a formal viewpoint, according to these results each genetic sequence has its own “intrinsic genetic music” (in particular, it is important for musical therapy and for searching of music with increased physiological effectiveness; it has permitted to propose a new musical scale of “the golden wurf”);
- parallels with famous symbolic tables of Ancient Chinese book “I Ching” which declares a cyclic principle in the nature and which is very important for all Oriental medicine (acupuncture, pulse diagnostics of Tibetan medicine, etc.);
- parallels with quantum computers;
- a new answer on the fundamental questions – “why 4 letter in genetic alphabet?” and “why 20 amino acids?”
- new mathematical tools of multidimensional numbers for genetic and other investigations;
- New structural connections between genetic code systems and physiology.

These results are important for bioinformatics, theoretical and mathematical biology in a whole.

References:

Ahmed N., Rao K.R. (1975) Orthogonal transforms for digital signal processing, Springer.

He M. (2001) Double helical sequences and doubly stochastic matrices. - *Symmetry in Genetic Information* (special double issue of the Journal “Symmetry: Culture and Science”, International Symmetry Foundation, Budapest), p.307-330.

He M. (2004) Genetic Code, Attributive Mappings and Stochastic Matrices, *Bulletin of Mathematical Biology* **66**: 965-973.

He M., Petoukhov S., Ricci P. (2004) Genetic Code, Hamming Distance and Stochastic Matrices. – *Bulletin of Mathematical Biology*, **66**:1405-1421.

He M., Narasimhan G., Petoukhov S. (2005) Foreword to “Advances in Bioinformatics and its Applications” (editors – M.He, G.Narasimhan, S.Petoukhov), Proceedings of the International Conference (Florida, USA, 16-19 December 2004), *Series in Mathematical Biology and Medicine*, **8**: V-VII.

Peterson W.W. (1972) Error-correcting codes, The MIT Press, Cambridge.

Petoukhov S.V. (2001) Genetic codes I: Binary sub-alphabets, bi-symmetric matrices and golden section. In: *Symmetry in Genetic Information*, (special double issue of the journal “Symmetry: Culture and Science”, International Symmetry Foundation, Budapest), 255-274

Petoukhov S.V. (2001) Genetic codes II: Numeric rules of degeneracy and a chronocyclic theory. In: *Symmetry in Genetic Information* (special double issue of the Journal “Symmetry: Culture and Science”, International Symmetry Foundation, Budapest) pp. 275-306

Petoukhov S.V. (2001) “The Bi-Periodic Table of Genetic Code and Number of Protons”, Moscow, (in Russian) <http://members.tripod.com/vismath/sg/petoukhov.htm>

Petoukhov S.V. (2003) The Bi-periodic Table and Attributive Conception of Genetic Code. Problem of Unification Bases of Biological Languages. In *Proc. Internat. Conf. on Mathematics and Engineering Techniques in Medicine and Biological Sciences METMBS-2003*, ed. by Valafar F. and Valafar H. (CSREA Press, Las Vegas, Nevada, USA) pp. 495-501.

Petoukhov S.V. (2003-2004) Attributive conception of genetic code, its bi-periodic tables and problem of unification bases of biological languages, *Symmetry: Culture & Science*, **14-15**, part 1, 281-307

Petoukhov S.V. (2005) The rules of degeneracy and segregations in genetic codes. The chronocyclic conception and parallels with Mendel’s law’s – In: “Advances in Bioinformatics and its Applications” (editors: M.He, G.Narasimhan, S.Petoukhov), *Series in Mathematical Biology and Medicine, World Scientific*, **8**, 512-532,.

Petoukhov S.V. (2005) Hadamard matrices and quint matrices in matrix presentations of molecular genetic systems, *Symmetry: Culture and Science*, **16**(3): 247-266.

Petoukhov (2007) S.V. Matrix genetics and bioinformatics: symmetries, noise immunity and multidimensional numbers. – Moscow, *ASM* (in Russian, in print).

Sklar B. (2001) Digital communications. Fundamentals and Applications, Prentice Hall PTR? New Jersey.

Waterman M.S., (1989) editor. Mathematical methods for DNA sequences, CRS Press Inc.