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GENETIC CODES II: NUMERIC RULES OF DEGENERACY AND A CHRONOCYCLIC THEORY

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INTRODUCTION

This article continues the theme of the author's previous paper in this issue on symmetrological investigations of genetic codes. It is devoted to phenomenological rules of numbers of degeneracy of those 17 genetic codes, which modern biology knows. They demonstrate the existence of numeric evolutionary invariant in a form of two opposite (Yin and Yang) categories of numbers of degeneracy, which divide a set of 20 amino acids into appropriate subsets of 8 and of 12 amino acids. These rules were discovered by the author in a course of investigation of symmetries in genetic codes from the viewpoint of the chronocyclic theory of evolution of genetic codes, which was put forward by him in application to genetic codes and to genetic languages on the whole. This chronocyclic theory opens a new way to explore heuristic parallels between genetic code and chronobiology, including chronocyclic conceptions of Ancient Oriental medicine.

A set of basic structures of genetic codes, which is the same for all biological organisms, consists of nitrogenous bases, 64 triplets and 20 amino acids. A universal set of 64 triplets is formed by a universal set of nitrogenous bases. But at the biological level, where 64 triplets code 20 amino acids, modern science discovered the existence of many evolutionary variants of genetic codes, that is a genetic code has no universal meaning at this level at all. These genetic codes differ through their specifics of degeneracy (or by concrete relations between 20 amino acids and 64 triplets). More precisely, several amino acids are coded by a different number of triplets in different genetic codes. Modern science does not know why such numeric phenomenology is realized in nature and why just these numeric relations are observed in genetic codes.

A set of evolutionary variants of degeneracy of genetic codes reflects peculiarities of bio-evolutionary process at the very basic level of living nature. This set of variants seems to be the source of the very important information about essence of biological organisms or about life on the whole. It should be mentioned that one could try to understand peculiarities of genetic codes from the very different initial positions. The history of science has known many attempts to discover numeric secrets of degeneracy of genetic code from morphological, symmetrical and several other initial viewpoints. For example, it is well known so-called “rhombic” model of degeneracy of genetic code by the famous physicist G. Gamov. He analyzed morphological specifics of a molecule of DNA to explain on the basis of its peculiarities, why quantity of coded amino acids is equal to 20. For such aim, one can analyze peculiarities of atomic composition of elements of genetic code also, for example, quantities of protons in nitrogenous bases and amino acids. Or one can use abstract group-theoretic methods to connect numeric characteristics of degeneracy of genetic codes with different mathematical groups of symmetries by analogy with group-theoretical approaches of physics of elementary particles.

It is very surprising for the author, that he could not find attempts to explain degeneracy of genetic codes from a chronocyclic (or biorhythmic) viewpoint in scientific literature. It seems that widespread knowledge about the importance of chronocyclic processes in biological organisms has never been used in science early to solve the problem of degeneracy and other structural peculiarities of genetic codes. If the gentle reader of this article knows published facts about using biorhythmic or chronocyclic conceptions to explain degeneracy of genetic codes, the author will be very grateful to them for any information about such publications. It is possible, that the absence of chronocyclic conception about the numeric peculiarities of this degeneracy until this moment is conditioned by the following circumstance: the field of molecular genetics was developed by molecular biochemists mainly, for which investigations of morphology of biochemical molecules are more simple and more habitual than investigations of factors of time in cyclic processes of complex bio-molecular ensembles in vivo.

Initial prerequisites for a chronocyclic theory of genetic codes. The statement that biological organisms exist in accordance with cyclic processes of environment and with their own cyclic physiological processes is one of the most classical statements of biology and medicine from ancient times. Literature sources have many brilliant words about the great importance of biorhythms for organisms. For example, the famous Russian physiologist A. Bogomolets wrote about "universal rhythmic movement in biology": "The world exists in rhythms, cosmic processes follow the law of rhythmic movement … The day replaces night, the time of activity replaces the dream ... The vital processes work in an organism rhythmically … A heart works rhythmically, and lungs breathe rhythmically, and processes of feeding of an organism are worked rhythmically, and nervous system follows the law of a rhythm, creating a rhythm of mental life" (Vogralik and Vogralik 1978, p. 11).

Modern science knows many astonishing facts also about cyclic processes in proteins, the structures of which are coded genetically. For example, it is a well-known fact that proteins in biological organisms are re-built (re-created) by systematic cyclic processes. It means that a set of physicochemical factors inside biological organisms disintegrates proteins into amino acids permanently and then it re-builds them from amino acids again in a cyclic manner. A half-life period (a duration of renovation of half of a set of molecules) for proteins of human organisms is approximately equal to 80 days in most cases; for proteins of the liver and blood plasma – 10 days; for the mucilaginous cover of bowels – 3-4 days; for insulin – 6-9 minutes. Such permanent rebuilding of proteins provides a permanent cyclic renovation of human organisms. These known facts are described in biological encyclopedias already (for example, see Encyclopedia of biology, 1998, v. 2, p. 19).

According to the famous concepts of Ancient Oriental medicine about the cyclic nature of biological processes, "each organ has more or less a definite time interval for its culmination (its own time interval), when its activity is maximal, … each organ has a maximum sensitiveness to pathogenic and medicinal influences just in this special time interval" (Vogralik and Vogralik 1978, p. 11). This phenomenological knowledge about the chronocyclic essence of biological organisms was used and tested during several thousand years by generations of oriental doctors, which were specially selected from many candidates in accordance with the criteria of their talents and of their brains. Many effective methods were constructed on the basis of this knowledge. One of them is the pulse diagnostics of Tibetan medicine. This pulse diagnostics was a universal method of diagnostics for an experienced doctor, who could determine not only many kinds of diseases, but report sometimes about physiological past and future of his patient. It is known that a doctor traditionally examines the state of 12 main organs during a session of pulse diagnostics (Pulse diagnostics of Tibetan medicine, 1988, p. 7). This method testifies additionally, that chronocyclic processes (pulse processes, etc.) in biological organisms carry astonishingly complete information about organism on the whole.

From the ancient times, medicine connects chronocyclic processes of biological organisms with chronocycles of the surrounding world, first of all, with the solar cycles of the changing of days and nights. It was found that the duration of such solar cycles could be divided comfortably for many practical tasks into 24 equal parts ("hours" by their modern name). For example, this division was comfortable in connection with the periodical activity of human organs. Ancient Oriental doctors divided 24 hours into 12 equal parts with a two-hour duration for each part. Each part was considered traditionally as a time interval of culmination activity of one of 12 main physiological organs. The other 11 main organs work in this time interval as well, but without their culmination activity. This division of 24 hours into 12 equal parts is used intensively in recipes of acupuncture, in methods of pulse-diagnostics and in other branches of Oriental medicine (see, for example Vogralik and Vogralik 1978). It is very interesting that many of these branches of Oriental medicine, including acupuncture and pulse-diagnostics, recommend time intervals of application of their recipes and methods in accordance with a table of 64 hexagrams and other symbolic structures of "The Book of Changes" (see, for example Falev 1991). In these applications, the table of 64 hexagrams (which is connected with the bi-periodic table of 64 genetic triplets (Petoukhov 1999, 2001) has an interpretation and meanings in terms of chronocycles.

It should be marked that a set of biological organisms consists of two main categories of organisms: autotrophic and heterotrophic organisms. Autotrophic organisms obtain carbon, which is needed to build their bodies, from CO_2 of the surrounding world only by means of their mechanisms of photosynthesis, based on the use of solar energy. But the sun shines from morning till night only. Intervals of cyclic activity of autotrophic mechanisms of photosynthesis are dependent on solar cycles "day-night", of course. It is well known that "autotrophic organisms with their photosynthesis mechanisms play a decisive role in nature because they generate a main mass of organic material in the biosphere… The existence of all other organisms and the course of biogeochemical cycles (! – S. P.) are determined by activities of autotrophic organisms" (Biological Encyclopedic Dictionary, 1989, p. 9). It seems to be obvious that the solar cycle with its form "day-night" is the most important for autotrophic organisms. This solar 24-hour cycle can be considered as a main cycle of the outer world for biological objects. Is it possible that structural evolution of genetic codes was realized without a connection with chronocycles of the whole organism and of the outer world and, in particular, without a connection with this solar 24-hour cycle?

Due to described reasons, genetic codes of autotrophic organisms are the most interesting and significant for the investigation of possible connection between genetic structures and the solar 24-hour cycle. Heterotrophic organisms are less interesting for this task. They obtain carbon for their bodies not from CO_2 and photosynthesis , but from exogenous organic materials. And heterotrophic organisms can be adapted to secondary chronocycles of those biological organisms, from which they obtain their

organic food. So, in our subsequent investigations of genetic codes, we will differentiate cases of autotrophic and heterotrophic organisms attentively.

But how can one search a trace of chronocyclic processes, and, first of all, a trace of solar 24-hour cycle in structures of genetic codes? Is it possible, for example, to interpret separate groups of amino acids (or groups of triplets) as special "organs", which have their culmination time intervals of their cyclic activity in 24-hour solar cycle by analogy with time intervals of culmination activity of organs from the above-mentioned conception of Oriental medicine? Of course, the cyclic activity of such genetic "organs" is coordinated with (or consists of) cyclic activity of all collective of physicochemical factors, which provides their work, including a necessary activation of amino acids. It is well known that "the necessary condition of proteins synthesis, which is expressed by polymerization of amino acids at all, is the existence of non-free, but so called activated (! – S. P.) amino acids in the system, which amino acids have their own resource of energy. Activation of free amino acids is realized by means of specific ferments" (Berezov and Korovkin 1990, p. 409).

Numbers of degenerations of genetic codes. Each amino acid is coded in a concrete genetic code by a certain number of triplets. This number of its triplets will be named as number of degeneracy of this amino acid in this genetic code. For example, amino acid Thr is coded in the vertebrate mitochondria code by four triplets ACC, ACA, ACU, ACG. In other words, its number of degeneracy in this genetic code is equal to 4. In another genetic code, this amino acid can have another number of degeneracy, for example, this number can be equal to 8. Different genetic codes have different sets of numbers of degeneracy.

Modern science knows 17 genetic codes, which are realized in different kinds of organisms or of their subsystems (first of all, in mitochondria, which play a role of factories of energy in biological cells). Known phenomenological data about numbers of degenerations and about other characteristics of 17 genetic codes were taken by the author from the website of the authoritative National Center for Biotechnology Information (NCBI, Bethesda, USA): http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/ /wprintgc.cgi . This website under the title "Genetic Codes" is devoted to all known genetic codes. It was prepared by A. Elzanowski and J. Ostell and it was updated by them on October 5, 2000. These genetic codes are represented below in thematic tables, constructed by the author.

Numeric rules of evolutionary invariance of genetic codes relative to two categories of numbers of degeneracy. Table 1 demonstrates 17 genetic codes with their numbers of degeneracy. Each amino acid is written in the left column, where an individual number of degeneracy of this amino acid is shown in brackets for each genetic code. Numbers of degeneracy, which are observed in genetic codes, are equal to numbers from 1 to 8. For example, the first genetic code in this Table has 12 amino acids, which number of

degeneracy is equal to 2 (Asn, Asp, Cys, Gln, Glu, His, Ile, Lys, Met, Phe, Trp, Tyr), 6 amino acids, which number of degeneracy is equal to 4 (Ala, Arg, Gly, Pro, Thr,Val), and 2 amino acids, which number of degeneracy is equal 6 (Leu, Ser).

One can see from Table 1 that the distribution of numbers of degeneracy of amino acids in a set of 17 genetic codes is very chaotic or non-regular on the whole. But a series of all numbers of degeneracy can be divided into two regular categories: a sub-series of numbers of degeneracy from 1 to 3 (a first category) and a sub-series of numbers of degeneracy from 4 to 8 (a second category). Each from these categories has a permanent quantity (12 and 8) of corresponding amino acids for all genetic codes practically. In other words, the set of 20 amino acids is divided into two subsets with 12 and 8 amino acids in accordance with their two categories of degeneracy as a rule. This regularity and subsequent regularities, which were discovered by the author in a course of analysis of genetic codes from the viewpoint of chronocyclic conception, can be described in the form of phenomenological numeric rules, the first of which is the following.

Genetic code and its numbers of degeneracy for each amino acid (in brackets)	Distribution of numbers of degeneracy from 1 to 8 among 20 AA								ΣAA with ND from 1 to 3	ΣAA with ND from 4 to 8
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**		
1) **The Vertebrate Mitochondrial Code:** Ala(4), Arg(4), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(2), Leu(6), Lys(2), Met(2), Phe(2), Pro(4), Ser(6), Thr(4), Trp(2), Tyr(2), Val(4), [Stop(4)]		12		6		2			**12**	**8**
2) **The Standard Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(6), Lys(2), Met(1), Phe(2), Pro(4), Ser(6), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(3)]	2	9	1	5		3			**12**	**8**
НЕТ КОДА 3 !!!										

4) **The Invertebrate Mitochondrial Code:** Ala(4), Arg(4), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(2), Leu(6), Lys(2), Met(2), Phe(2), Pro(4), Ser(8), Thr(4), Trp(2), Tyr(2), Val(4), [Stop(2)]		12		6		1		1	**12**	**8**
5) **The Echinoderm Mitochondrial Code:** Ala(4), Arg(4), Asn(3), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(6), Lys(1), Met(1), Phe(2), Pro(4), Ser(8), Thr(4), Trp(2), Tyr(2), Val(4), [Stop(2)]	2	8	2	6		1		1	**12**	**8**
6) **The Euplotid Nuclear Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(3), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(6), Lys(2), Met(1), Phe(2), Pro(4), Ser(6), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(2)]	2	8	2	5		3			**12**	**8**
7) **The Bacterial and Plant Plastid Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(6), Lys(2), Met(1), Phe(2), Pro(4), Ser(6), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(3)]	2	9	1	5		3			**12**	**8**
8) **The Ascidian Mitochondrial Code:** Ala(4), Arg(4), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(6), His(2), Ile(2), Leu(6), Lys(2), Met(2), Phe(2), Pro(4), Ser(6), Thr(4), Trp(2), Tyr(2), Val(4), [Stop(2)]		12		5		3			**12**	**8**

9) **The Flatworm Mitochondrial Code:** Ala(4), Arg(4), Asn(3), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(6), Lys(1), Met(1), Phe(2), Pro(4), Ser(8), Thr(4), Trp(2), Tyr(3), Val(4), [Stop(1)]	2	7	3	6		1		1	**12**	**8**
10) **Blepharisma Nuclear Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(3), Glu(2), Gly(4), His(2), Ile(3), Leu(6), Lys(2), Met(1), Phe(2), Pro(4), Ser(6), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(2)]	2	8	2	5		3			**12**	**8**
11) **Chlorophycean Mitochondrial Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(7), Lys(2), Met(1), Phe(2), Pro(4), Ser(6), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(2)]	2	9	1	5		2	1		**12**	**8**
12) **Trematode Mitochondrial Code:** Ala(4), Arg(4), Asn(3), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(2), Leu(6), Lys(1), Met(2), Phe(2), Pro(4), Ser(8), Thr(4), Trp(2), Tyr(2), Val(4), [Stop(2)]	1	10	1	6		1		1	**12**	**8**
13) **Scenedesmus obliquus mitochondrial Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(7), Lys(2), Met(1), Phe(2), Pro(4), Ser(5), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(3)]	2	9	1	5	1	1	1		**12**	**8**

14) **Thraustochytrium Mitochondrial Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(5), Lys(2), Met(1), Phe(2), Pro(4), Ser(6), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(4)]	2	9	1	5	1	2			**12**	**8**
15) **The Alternative Yeast Nuclear Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(3), Leu(5), Lys(2), Met(1), Phe(2), Pro(4), Ser(7), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(3)]	2	9	1	5	1	1	1		**12**	**8**
16) **The Yeast Mitochondrial Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(2), Glu(2), Gly(4), His(2), Ile(2), Leu(2), Lys(2), Met(2), Phe(2), Pro(4), Ser(6), Thr(8), Trp(2), Tyr(2), Val(4), [Stop(2)]		13		5		1		1	**13**	**7**
17) **The Ciliate, Dasycladacean and Hexamita Nuclear Code:** Ala(4), Arg(6), Asn(2), Asp(2), Cys(2), Gln(4), Glu(2), Gly(4), His(2), Ile(3), Leu(6), Lys(2), Met(1), Phe(2), Pro(4), Ser(6), Thr(4), Trp(1), Tyr(2), Val(4), [Stop(1)]	2	8	1	6		3			**11**	**9**

Table 1: 17 genetic codes and distributions of their numbers of degeneracy (ND) among 20 amino acids (AA). „Stop" means stop-codons. A set of observed numbers of degeneracy of amino acids in genetic codes consists of numbers from 1 to 8. The two right columns show quantities of amino acids, which have numbers of degeneracy from 1 to 3 (the first category of amino acids with low degeneracy) and which have numbers of degeneracy from 4 to 8 (the second category of amino acids with high degeneracy). Bold frames mark two categories of numbers of degenerations.

Rule № 1. In genetic codes, the set of 20 amino acids consists of two subsets; the first subset consists of 12 amino acids with their numbers of degeneracy from 1 to 3, and the second subset consists of 8 amino acids with their numbers of degeneracy from 4 to 8.

The first category can be named as the category of amino acids with low degeneracy, and the second category can be named as the category of amino acids with high degeneracy. As far as the author can judge, this rule is held true in nature without any exceptions for genetic codes of autotrophic organisms (it was emphasized above that a case of autotrophic organisms is the most important for chronocyclic theory because of "a course of biogeochemical cycles are determined by activities of autotrophic organisms"). This fact of perfect realization of the rule № 1 for autotrophic organisms testifies additionally in favour of a connection between numeric peculiarities of genetic codes and chronocycles.

Rule № 1 has small exceptions in two cases of heterotrophic organisms in a form of numeric shifting from the regular ratio "12 and 8" to the nearest integers ratios: "Yeast Mitochondrial Code" has the ratio "13 and 7" for these two categories of amino acids, and "Ciliate, Dasycladacean and Hexamita Nuclear Code" has the ratio "11 and 9" (see Table 1, the codes №s 16 and 17). These non-standard ratios encircle the canonical ratio "12 and 8" from the contrary sides of numeric axis. These non-standard ratios demonstrate additionally the main role of the canonical ratio "12 and 8" as that centre, around which minimal numeric fluctuations are realized.

If one likes Oriental terminology, these two categories of amino acids can be named as Yang- and Yin-categories. For those readers, who are interested in Oriental medicine and in Ancient Oriental culture, it could be mentioned that there is a special meaning to the numeric pair "12 and 8", which is one of the distinquished pairs there: "8 and 12 are a standard measure of alternative separations of space-time in Chinese chronotopograms … The symbol of the Earth – a square – is characterized by number 8, and the symbol of heaven – a circle - is characterized by number 12" (Kobzev 1994, p. 39, 40).

A discussion of rule № 1. Considered numbers 12 and 8 are the greatest divisors of the number 24 from the solar 24-hour cycle. And number 24 is the nearest mutual divisible integer for numbers 8 and 12. One of the possible ways of analyzing this aspect of degeneracy of genetic codes is analogy with Oriental medicine, where solar 24-hour cycle is divided into 12 parts with a 2-hour duration of each part and where each part is interpreted as a time interval of culmination activity of the appropriate organ from a set of 12 main organs. From such a model viewpoint, 12 amino acids of the first category of degeneracy can be interpreted conditionally as a certain interrelated ensemble of "organs", which divides a 24-hour cycle into a sequence of 12 equal parts with a 2-hour duration of each part. And each part corresponds to a time interval of culmination activity of one of these amino acids (together with all team of physicochemical factors, which serves this amino acid). The idea of chronocyclic culmination activities of

considered amino acids (with their teams of servicing) is placed here in a parallel with the phenomenological knowledge of Oriental medicine, which was tested during a few thousand years in a practical manner, about the chronocyclic culmination activities of physiological macro-systems. It is essential, that one can try to examine experimentally the existence of cyclic culmination activity of each amino acid together with its team of physicochemical servicing. In our opinion, this experimental task of investigation of chronocyclic activities of amino acids in vivo is very important for the development of the chronocyclic theory and for the understanding of the genetic coding system.

Another group with 8 amino acids can be interpreted in such a model also (together with their teams of servicing) as a certain interrelated ensemble of "organs", which divides a solar 24-hour cycle into a sequence of 8 equal parts with a 3-hour duration of each part.

Of course, one can illustrate these divisions schematically in the form of a circle with 12 (or 8) parts and vertexes, where the symbols of amino acids from two considered categories are disposed in different variants for each genetic code. Figure 1 and 2 show such circles for sequences of 8 vowel and 12 consonant amino acids in the case of the Vertebrate Mitochondrial Code.

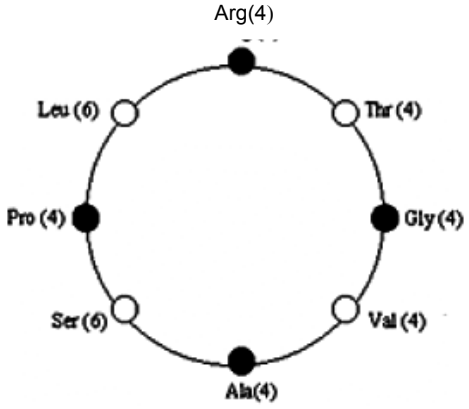

Figure 1: The large circle of a set of 8 vowel amino acids (or the category of 8 amino acids with a high degeneracy) for the case of the Vertebrate Mitochondrial Code. The number in brackets means the number of degeneracy of the appropriate amino acids in this genetic code. According to rule № 8, this set has a subset of 4 complementary amino acids (Ala-Arg and Gly-Pro), which are symbolized by black small circles, and it has also a subset of 4 non-complementary amino acids (Leu, Ser, Thr, Val), which are symbolized by small white circles.

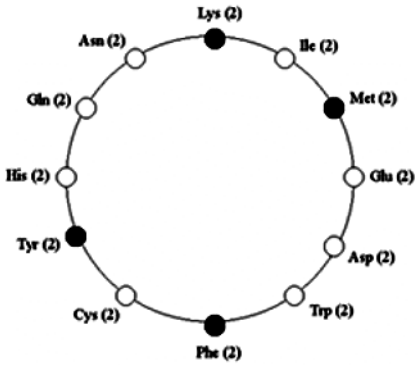

Figure 2: The large circle of a set of 12 consonant amino acids (or the category of 12 amino acids with a low degeneracy) for the case of the Vertebrate Mitochondrial Code. The number in brackets means the number of degeneracy of the appropriate amino acids in this genetic code. According to rule № 8, this set has a subset of 4 complementary amino acids (Lys-Phe and Met-Tyr), which are symbolized by black small circles, and it has also a subset of 8 non-complementary amino acids, which are symbolized by small white circles.

Figures 1 and 2 demonstrate simultaneously an interrelation between two categories of degeneracy of amino acids and two categories of complementation of amino acids, which are described in rule № 8 below. The author has constructed many variants (more that 100 variants for a special scientific collection) of such circular representation of two categories of amino acids, which are valuable for better understanding of structures of genetic codes. The bi-periodic table of triplets, which was shown in the previous author's article in this issue, is useful for the ordering of amino acids in such circular representations.

About "consonant" and "vowel" amino acids. In the described modelling approach, each amino acid (with its team of serves) receives a new theoretical parameter, connected with chronocyclic processes: the duration of its time interval of culmination activity. More precisely, 12 amino acids of the first category of low degeneracy receive a relatively shorter duration (2 hours). 8 amino acids of the second category of high degeneracy receive a relatively greater duration (3 hours). It permits to introduce comfortable and heuristic terminology from linguistics for two considered categories of amino acids.

According to the opinions of many authors, a set of 20 amino acids is a genetic alphabet for proteins, which exists along with genetic alphabet of 4 nitrogenous bases at a higher level of genetic hierarchy. An analogy between genetic code and linguistics has been widely used in science for a long time by many authors (see a brief review in (Petoukhov 2001, 2003a, 2003c). But alphabets of linguistic languages always consist of consonant letters and vowel letters, which differ phonetically in terms of their time

durations and relative quantities in each alphabet (the quantity of consonant letters is greater than the quantity of vowel letters). The alphabet of 20 amino acids with two categories of amino acids, which differ in terms of their time durations in the described modelling approach, has a new obvious parallel with alphabets of human languages relative to their two categories of consonant letters and of vowel letters. Due to this parallel, one can name 12 considered amino acids with a shorter time duration (2 hours) as consonant amino acids, and 8 other amino acids with a relative greater duration (3 hours) as vowel amino acids. The quantity of consonant amino acids is greater than the quantity of vowel amino acids in concordance with the relative quantities of consonant letters and of vowel letters in linguistic alphabets.

Let us continuie the description of the new phenomenological rules of genetic codes. An investigation of distribution of the two categories of amino acids from genetic codes in both – left and right – halves of the bi-periodic octet table of genetic codes reveals additional regularity (see Table 3 in our previous article as an example). This regularity is reflected in the following rule № 2, which completes rule № 1.

Genetic code	The left Tabular half		The right tabular half		Σ kinds of ND	Stop-codons and their tabular numeration numbers
	ΣAA with ND from 1 to 3	ΣAA with ND from 4 to 8	ΣAA with ND from 1 to 3	ΣAA with ND from 4 to 8		
1) The Vertebrate Mitochondrial Code	**6**	**4**	**6**	**4**	12	20(UAG) 28(UAA) 32(AGG) 40(AGA)
2) The Standard Code	**6**	**4**	**6**	**4**	16	12(UGA) 20(UAG) 28(UAA)
3) The Mold, Protozoan, and Coelenterate Mitochondrial	**6**	**4**	**6**	**4**	16	20(UAG) 28(UAA)
4) The Invertebrate Mitochondrial Code	**6**	**4**	**6**	**4**	20	20(UAG) 28(UAA)
5) The Echinoderm Mitochondrial Code	**6**	**4**	**6**	**4**	24	20(UAG) 28(UAA)

6) The Euplotid Nuclear Code	**6**	**4**	**6**	**4**	16	20(UAG) 28(UAA)
7) The Bacterial and Plant Plastid Code	**6**	**4**	**6**	**4**	16	12(UGA) 20(UAG) 28(UAA)
8) The Ascidian Mitochondrial Code	**6**	**4**	**6**	**4**	12	20(UAG) 28(UAA)
9) The Flatworm Mitochondrial Code	**6**	**4**	**6**	**4**	24	20(UAG)
10) Blepharisma Nuclear Code	**6**	**4**	**6**	**4**	16	12(UGA) 28(UAA)
11) Chlorophycean Mitochondrial Code	**6**	**4**	**6**	**4**	23	28(UAA) 12(UGA)
12) Trematode Mitochondrial Code	**6**	**4**	**6**	**4**	24	28(UAA) 20(UAG)
13) Scenedesmus obliquus Mitochondrial Code	**6**	**4**	**6**	**4**	28	30(U**C**A) 28(UAA) 12(UGA)
14) Thraustochytrium Mitochondrial Code	**6**	**4**	**6**	**4**	21	28(UAA) 20(UAG) 14(U**U**A) 12(UGA)
15) The Alternative Yeast Nuclear Code	**6**	**4**	**6**	**4**	28	12(UGA) 20(UAG) 28(UAA)
16) The Yeast Mitochondrial Code	**7**	**3**	**6**	**4**	20	20(UAG) 28(UAA)
17) The Ciliate, Dasycladacean and Hexamita Nuclear Code	**5**	**5**	**6**	**4**	12	12(UGA)

Table 2: The 17 genetic codes and distributions of amino acids (AA), which belong to the two categories of numbers of degeneracy (ND), in the bi-periodic table of triplets. For example, the column with the heading "ΣAA with ND from 1 to 3" shows the quantities of amino acids, which have number of degeneracy from 1 to 3, for each genetic code in the appropriate half of the bi-periodic table. Sums of all kinds of numbers of degeneracy, which are presented in each genetic code, are demonstrated in the column with the heading "Σ kinds of ND" (see rule № 5 below). Stop-codons with their numeration numbers from this bi-periodic table are shown in the right column as well. (Explanation in text).

Rule № 2. In genetic codes, half of each subset of amino acids, described in rule № 1 (that is a subset of 12 consonant amino acids and a subset of 8 vowel amino acids), is disposed in the left half of the bi-periodic table of genetic triplets, and the second half of each such subset is disposed in the right half of this table. In other words, both the left and the right halves of this table contain 6 consonant amino acids and 4 vowel amino acids.

There should be noted the following specifics of tabular calculation of amino acids for this rule. Amino acid Ser, which has its triplets in both halves of the bi-periodic octet table, is enlisted in the left tabular half, where a quantity of its triplets is always greater. Amino acid Thr is listed in the right tabular half, where its triplets are disposed entirely in 16 genetic codes, though seventeenth genetic code from Table 1 (Yeast Mitochondrial Code) contains triplets, which code this amino acid, in both tabular halves equally. Since the left half and the right half of this bi-periodic table are differentiated by reciprocal interchanging of purines and pyrimidines in all positions of all 64 triplets, it is obvious that rule № 2 demonstrates a symmetrical role of purines and pyrimidines in the structure of the considered subsets of 12 and 8 amino acids. Rule № 2, like rule № 1, has minimal exceptions for the same two cases of genetic codes of heterotrophic organisms, but for the left half of the bi-periodic table of triplets only. More precisely, these exceptions have a form of a shifting from the regular ratio “6 and 4” in the left tabular half to nearest integers ratios: “Yeast Mitochondrial Code” has the ratio “7 and 3” for two considered categories of amino acids, and “Ciliate, Dasycladacean and Hexamita Nuclear Code” has the ratio “5 and 5” (see Table 2, the codes №s 16 and 17). These non-standard ratios encircle the canonical ratio “6 and 4” from the contrary sides of numeric axis. So these non-standard ratios demonstrate additionally the main role of the canonical ratio “6 and 4” as that centre, around which minimal numeric fluctuations are realized in the left half of the bi-periodic table of triplets. Rule № 2 is held true for the right half of the bi-periodic table without exceptions for all genetic codes.

Let us go to the next rule. Some triplets code different amino acids in different genetic codes. For example, the triplet AUA codes amino acid Met in the Vertebrate Mitochondrial Code (the code № 1 in Table 1) and this triplet codes amino acid Ile in the Standard code (№ 2 in Table 1). Let us write out all such changing of meaning of triplets for amino acids, when we compare code № 1 from Table 1 to all other genetic codes. Since only two categories of amino acids without stop-codons are considered, this list will not have those cases, when a stop-codon of this code № 1 begins to code an amino acid in another genetic code or when an ordinary triplet of code № 1 obtain a new meaning as a stop-codon in another genetic code. This list is the following: AUA

(Met - Ile), CUU (Leu - Thr), CUC (Leu - Thr), CUA (Leu - Thr), CUG (Leu - Thr), AAA (Lys - Asn), UGA (Trp - Cys), CUG (Leu – Ser). The meaning of the triplet of code № 1 is shown in the first place in brackets and the meaning of the same triplet in another code is shown in the second place. It is easy to check on the basis of Table 1, that the following rule exists, where the term "ordinary triplet' means that it is not a stop-codon.

Rule № 3. When the meaning of an ordinary triplet in one genetic code, where it codes a consonant (vowel) amino acid, is changed by its new ordinary meaning in another genetic code, this new meaning corresponds to the amino acid from the same category of numbers of degeneracy (or corresponds to consonant (vowel) amino acid conformably).

Let us prolong our investigation. The initial hypothesis of our chronocyclic conception supposed a connection between numbers of degeneracy of amino acids and the solar 24-hour cycle. Number 24 has the following divisors, which are not equal to 24: 1, 2, 3, 4, 6, 8, 12. Numbers 1, 2, 3, 4, 6, 8 from this series of divisors are represented in all genetic codes as main dominating numbers of degeneracy. It is quite seldom, that additional numbers 5 and 7 are realized as numbers of degeneracy in genetic codes (see Table 1). Really, four genetic codes from 17 genetic codes have one amino acid only, which is coded by 5 or 7 triplets (codes №s 11, 13-15: Chlorophycean Mitochondrial Code, Scenedesmus obliquus mitochondrial Code, Thraustochytrium Mitochondrial Code, Alternative Yeast Nuclear Code). The following rule takes place from these facts, which is one indirect confirmation of the chronocyclic theory.

Rule № 4. Numbers of degeneracy for amino acids in genetic codes are divisors of a number 24 as a rule.

Prediction: on the basis of this rule, the author predicts a future detection of a genetic code with number 12 as number of degeneracy for an amino acid there, because number 12 is a divisor of number 24 as well.

The probability of the predicted realization of number 12 as number of degeneration in genetic codes is reduced by the following circumstances. The category of vowel amino acids, to which amino acid with number 12 of its degeneracy belonged, should have 7 vowel amino acids elsewhere according to rule № 1. Even if these 7 amino acids would have minimal number 4 of degeneracy from this category, they should be coded by 28 (=7x4) triplets. In conjunction with the predicted amino acid with number 12 of its degeneracy, this category of amino acids occupies 40 triplets. Then another category of

12 consonant amino acids in conjunction with stop-codons will have 24 triplets only. And only one or two triplets could code each consonant amino acid in a such genetic code practically.

Let us address materials for the next rule. A sum of numbers of degeneracy has different values in different genetic codes. For example, code № 1 from Table 1 has numbers 2, 4, 6 as numbers of degeneracy of amino acids, and the sum of these numbers is equal to 12 (= 2+4+6). The sum of all numbers of degeneracy, which are presented in a concrete genetic code, will be named as a cumulative number of degeneracy of this code. A set of such cumulative numbers of degeneracy from different genetic codes form a regular numeric series: 12, 16, 20, 24, 28 (see Table 2, second column from the right). This series represents an arithmetic progression with difference 4. All numbers of this series have their mutual divisor 4. Values from this series are presented in 15 from 17 genetic codes and each of them is repeated in a few codes. The other two genetic codes (№ 11 - Chlorophycean Mitochondrial Code, № 14 - Thraustochytrium Mitochondrial Code) have such values of their cumulative numbers of degeneracy, which are equal to 23 and 21 correspondingly. These values do not meet in other codes and can be considered as small fluctuations from the following rule.

Rule № 5. Cumulative numbers of degeneracy of genetic codes, which are repeated in different genetic codes, have their mutual divisor 4, and they form the fragment of a series of arithmetic progression with difference 4: 12, 16, 20, 24 and 28.

Essential and nonessential amino acids of human organism in two categories of degeneracy. Biological organisms are differentiated by their possibility of synthesis of amino acids and of nitrogen-containing compounds, which they can use for biosynthesis of proteins. For example, higher plants can synthesize all amino acids, which are necessary for synthesis of proteins, by using ammonia or nitrates as a source of nitrogen. Higher vertebrates do not synthesize all necessary amino acids. Human organisms (and, for example, the organism of white rats) synthesize only 10 from 20 amino acids, which are coded genetically and which are called nonessential amino acids. The other 10 amino acids are not synthesized in the human organism, so they were named essential amino acids in a composition of its food (see, for example Berezov and Korovkin 1990, p. 323). A list of 10 nonessential amino acids of human organisms contains Ala, Asn, Asp, Cys, Gln, Glu, Gly, Pro, Ser, Tyr. The list of essential amino acids contains Arg, His, Ile, Leu, Lys, Met, Phe, Thr, Trp, Val.

Why just these dichotomic equal sets of essential and nonessential amino acids are realized for the human organism? It is one of the questions, which are too difficult for

modern science. To solve this problem, many scientific materials should be studied in future, including symmetrological peculiarities of genetic codes.

The author marked early that these subsets of essential and nonessential amino acids are disposed in a dichotomic manner equally – in 5 representatives – between the left and the right halves of the bi-periodic table of triplets (Petoukhov 2001, p. 120). But how are these essential and nonessential amino acids of the human organism distributed between the two considered categories of degeneracy of amino acids in different genetic codes, first of all, in the standard code and in the vertebrate mitochondrial code (the codes №s 1 and 2 in Table 1)? Are dichotomic regularities realized there by nature as well?

Analysis of the considered 17 genetic codes reveals a new regularity (see Table 3), which holds true for both subsets of essential and nonessential amino acids of the human organism. This regularity is reflected in the following rule.

Rule № 7. A distribution of a considered set of 10 essential (nonessential) amino acids in two categories of numbers of degeneracy of amino acids consists of two subsets: a subset of 6 amino acids with low degeneracy and a subset of 4 amino acids with high degeneracy (in other words: two subsets with 6 consonant amino acids and 4 vowel amino acids). The left half and the right half of the bi-periodic octet table equally consist of half quantities of these subsets: 3 consonant essential (nonessential) amino acids and 2 essential (nonessential) vowel amino acids.

Genetic code	Distribution of nonessential AA in two categories of degeneracy of AA (data from the both halves of BT: left+right)		Distribution of essential AA in two categories of degeneracy of AA (data from the both halves of BT: left+right)	
	Σ AA with ND from 1 to 3	Σ AA with ND from 4 to 8	Σ AA with ND from 1 to 3	Σ AA with ND from 4 to 8
1) The Vertebrate Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
2) The Standard Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
3) The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma /Spiroplasma Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**

4) The Invertebrate Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
5) The Echinoderm Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
6) The Euplotid Nuclear Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
7) The Bacterial and Plant Plastid Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
8) The Ascidian Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
9) The Flatworm Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
10) Blepharisma Nuclear Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
11) Chlorophycean Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
12) Trematode Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
13) Scenedesmus obliquus mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
14) Thraustochytrium Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
15) The Alternative Yeast Nuclear Code	**6 (3+3)**	**4 (2+2)**	**6 (3+3)**	**4 (2+2)**
16) The Yeast Mitochondrial Code	**6 (3+3)**	**4 (2+2)**	**7 (4+3)**	**3 (1+2)**
17)The Ciliate, Dasycladacean and Hexamita Nuclear Code	**5 (2+3)**	**5 (3+2)**	**6 (3+3)**	**4 (2+2)**

Table 3: Genetic codes and the numeric distribution of subsets of the 10 essential and 10 nonessential amino acids (AA) of the human organism in the two categories of numbers of degeneracy (ND) of amino acids in different codes. Their numeric distribution in two halves (the right and the left) of the bi-periodic table (BT) of triplets (see Table 3 in the previous paper in this issue) is also shown in brackets.

The author succeeded in finding the following minimal exceptions from this rule № 7. A set of essential amino acids has a small exception in a heterotrophic case of "the Yeast Mitochondrial Code", which contains 7 consonant essential amino acids and 3 vowel essential amino acids (instead of a canonical ratio 6 and 4 correspondingly). In this case, the left half of the bi-periodic table of this genetic code has an exception only because this half consists of 4 consonant amino acids and 1 vowel amino acids (instead of a canonical ratio 3 and 2 correspondingly). The right tabular half has no exception from the rule (see Table 3).

A set of 10 nonessential amino acids has a small exception from the rule № 7 in another heterotrophic case of «the Ciliate, Dasycladacean and Hexamita Nuclear Code» (a set of Ciliata is a set of heterotrophic organisms, just as a set of yeast). In this code, the mentioned set consists of 5 consonant and 5 vowel nonessential amino acids. Only the left half of the bi-periodic table of this genetic code has a minimal exception again because it contains 2 consonant and 3 vowel nonessential amino acids (instead of a canonical ratio 3 and 2 correspondingly).

From the viewpoint of chronocyclic theory, rule № 7 testifies indirectly that both categories of essential and nonessential amino acids are based on chronocyclic processes also because they are interlaced with the categories of numbers of degeneracy of amino acids so naturally.

Why is the quantity of amino acids, which are coded genetically, equal to 20? The author connects the answer to this fundamental question with a phenomenon, described above, of a decomposition of a set of 20 amino acids in two subsets of 12 and 8 amino acids by binary-opposite criteria of small and large numbers of degeneracy (that is, with a decomposition of this set into subsets of consonant and vowel amino acids). In our opinion, a future answer is based on a chronocyclic theory and, most probably, on the existence of two fundamental kinds of chronocyclic processes, which are connected with the solar 24-hour cycle. Observed ratio 12:8 in the subsets of consonant and vowel amino acids play an important role, in particular, in connection with its equality to the ratio 3:2 and with the following circumstance: number 24 (from the solar 24-hour cycle) has numbers 8 and 12 as its greatest divisors, and the results of such divisions of number 24 by 8 and by 12 are equal to 3 and 2. Besides all, $(12 \times 3 - 8 \times 2) = 20$, that can be represented as the value of the determinant of a proper matrix. The ratio 3:2 has happened among elements in different parts of genetic codes many times (Petoukhov 2001). The author hopes to publish more detailed analysis of this theme later in connection with golden genetic matrices (Petoukhov 2003c, 2003e).

About the division of the set of 20 amino acids into subsets with 8 and 12 amino acids by specific quantities of protons in their molecules. The division of the set of 20 amino acids into two categories with 8 and 12 amino acids is realized not only by specifics of the numbers of their degeneracy, but also by specifics of the number of protons in their molecules (Petoukhov 2001). More precisely, 12 amino acids have such quantities of protons in their molecules which are divisible by 8. They are called eightfold amino acids (Table 4). And 8 other amino acids have such quantities of protons in their molecules, which are not divisible by 8. They are called non-eightfold amino acids.

The series of quantities of protons in the category of 12 eightfold amino acids contains 8 values only, which are divisible by 8 and which give a complete series of residues of such divisions without a gap: 5, 6, 7, 8, 9, 10, 11, 12. The greatest number of protons in this category of amino acids is equal to 8x12=96.

Table 5 demonstrates how these two kinds of divisions of a set of 20 amino acids - into the categories of low and high degeneracy and into the categories of eightfold and non-eightfold amino acids – are interlaced. The four parts of this table contains the following quantities of amino acids: 6, 6, 6 and 2.

	Amino acids
12 eightfold AA with a quantity of protons, which is divisible by 8	Gly (40=8x5), Ala (48=8x6), Ser (56=8x7), Val (64=8x8), Thr (64=8x8), Cys (64=8x8), Leu (72=8x9), Ile (72=8x9), Lys (80=8x10), Met (80=8x10), Phe (88=8x11), Tyr (96=8x12).
8 non-eightfold AA with a quantity of protons, which is not divisible by 8	Pro (62), Asn(70), Asp (70), Gln (78), Glu (78), His (82), Arg (94), Trp (108)

Table 4: The division of the set of 20 amino acids (AA) into two subsets in accordance with the quantities of protons in their molecules. The first subset contains 12 amino acids with such quantities of protons which are divisible by 8. The second subset contains 8 amino acids with such quantities of protons which are not divisible by 8. A quantity of protons for each amino acid is shown in brackets after its brief name.

	Vowel AA (with numbers of degeneracy from 4 to 8)	Consonant AA (with numbers of degeneracy from 1 to 3)
Eightfold AA	Cys, Ile, Met, Lys, Phe, Tyr	Gly, Ala, Ser, Val, Thr, Leu
Non-eightfold AA	Arg, Pro	Asn, Asp, Gln, Glu, His, Trp

Table 5: The distribution of the set of 20 amino acids (AA) in two kinds of binary-oppositional categories: the two categories of numbers of degeneracy (consonant and vowel amino acids) and the two categories of eightfold of quantities of protons.

About the division of the set of 20 amino acids into two subsets with 8 and 12 amino acids by a criterion of pairs of complementary amino acids. The division of the set of 20 amino acids into two categories with 8 and 12 amino acids is realized also by specifics of relations among their triplets. More precisely, some pairs of amino acids have such correspondence between sets of their codons, that codons, which code the first amino acid of the pair, are anti-codons of those codons, which code the second amino acid of this pair. It is known that such pairs of amino acids are named as pairs of complementary amino acids, according to G. Gladyshev (Karasev 2003, p. 36). For

example, the amino acid Pro (which is coded in different genetic codes by a set of triplets CCC, CCA, CCU, CCG) and the amino acid Gly (which is coded by a set of anti-triplets GGG, GGU, GGA, GGC) form a pair of complementary amino acids. In special cases, two complementary amino acids can have unequal quantities of their coding triplets in some genetic codes, but a triplet's set of one amino acid should be as a set of anti-codons relative to a set of triplets of a second amino acid of the pair. An example of such unequal case in the Standard code is a pair of complementary amino acids Arg (which is coded by six triplets CGU, CGC, CGA, CGG, AGA, AGG) and Ala (which is coded by four triplets GCA, GCG, GCU, GCC, all of which are anti-codons relative to corresponding triplets of Arg). Some amino acids have no complementary amino acids and they are named as non-complementary amino acids.

The author revealed that different genetic codes have 8 complementary amino acids and 12 non-complementary amino acids as a rule. The distribution of complementary and non-complementary amino acids between the two categories of consonant and vowel amino acids has a regular manner, described in the following rule and illustrated by Figure 1 and 2.

Rule № 8. In genetic codes, a set of 20 amino acids consists of two subsets with 8 complementary amino acids and with 12 non-complementary amino acids. The first subset of 8 complementary amino acids is distributed equally (at a ratio of 1:1) between the two categories of vowel and consonant amino acids: 4 complementary amino acids (Gly-Pro, Ala-Arg) belong to the category of 8 vowel amino acids, and the other 4 complementary amino acids (Lys-Phe, Met-Tyr) belong to the category of 12 consonant amino acids. The second subset of 12 non-complementary acids is distributed proportionally (with a ratio 1:2) between the two categories of vowel and consonant amino acids: 4 non-complementary amino acids (Leu, Ser, Thr, Val) belong to the category of 8 vowel amino acids, and the other 8 non-complementary amino acids (Asn, Asp, Cys, Gln, Glu, His, Ile, Trp) belong to the category of 12 consonant amino acids.

This rule has many analogies with rule № 1. As far as the author can judge, this rule is held true in nature without any exceptions to genetic codes of autotrophic organisms. The fact of perfect realization of rules №s 1 and 8 for autotrophic organisms testifies additionally in favour of a connection between numeric peculiarities of genetic codes and chronocycles. Just as rule № 1, rule № 8 has minimal exceptions in the same two cases of heterotrophic organisms, more precisely in the cases of the genetic codes №s 16 and 17 from Table 1. In these both codes, these exceptions relate to the category of 12 non-complementary amino acids only, where a canonical numeric ratio is "4 vowel amino acids and 8 consonant amino acids" according to rule № 8. These exceptions are

realized in a form of numeric shifting from this regular ratio "4 and 8" to the nearest integers relation: code № 16 (Yeast Mitochondrial Code) has the corresponding ratio "3 and 9", and code № 17 (Ciliate, Dasycladacean and Hexamita Nuclear Code) has a ratio of "5 and 7". These non-standard ratios encircle the canonical ratio "4 and 8" from the contrary sides of numeric axis. These non-standard ratios demonstrate additionally the main role of the canonical ratio "4 and 8" here as that centre, around which minimal numeric fluctuations are realized. rule № 8 holds true for the category of 8 complementary amino acids without exceptions in all genetic codes.

About the meaning of the second position in triplets for coding of consonant and of vowel amino acids. The following rules №s 9 and 10 represent some results of analyzing the distribution of nitrogenous bases C, A, G, U in first, second and third positions in those two subsets of triplets, which code consonant and vowel amino acids in considered genetic codes (in other words, amino acids from the categories of low and of high degeneracy).

Rule № 9. In genetic codes, triplets with nitrogenous base C in their second position code vowel amino acids only (in other words, amino acids with numbers of degeneracy from 4 and more).

This rule holds true for all 17 genetic codes without exceptions.

Rule № 10. In genetic codes, triplets with a nitrogenous base A in their second position code consonant amino acids only (in other words, amino acids with numbers of degeneracy from 3 and less).

This rule has single exceptions in 3 from 17 genetic codes. All single exceptions are connected with a change of meaning of the triplet UAG and they are realized in ~~the~~ codes № 11 (Chlorophycean…), № 13 (Scenedesmus…) and № 17 (Ciliate…) from Table 1.

A list of such rules will be studied in future publications.

The periodical tables of biological elements of genetic codes. Described facts of division of a set of 20 amino acids by a few ways into different pairs of subsets with 8 and 12 amino acids correspondingly can be used to construct appropriate periodic tables of 20 amino acids for these cases. More precisely, the author proposes an individual periodic table with sizes [4x5] for each case, where 20 amino acids are disposed in periodic manner from the viewpoint of the appropriate attribute of amino acids.

For example, Table 6 is one of the possible variants of a periodic table of a set of 20 amino acids from the viewpoint of the a two categories of degeneracy of amino acids (or of two categories of vowel and consonant amino acids). Each column contains amino acids of the same category that provides an appropriate periodic property for this table. Tables 7 and 8 represent possible variants of periodic tables for two other cases of division of a set of 20 amino acids into subsets with 8 and 12 amino acids. One can construct periodic tables for each subset with 8 and 12 amino acids separately also.

Vowel AA	Vowel AA	Consonant AA	Consonant AA	Consonant AA
Gly	Ala	Cys	Ile	Lys
Pro	Arg	Asn	Trp	Phe
Ser	Val	Gln	His	Met
Leu	Thr	Glu	Asp	Tyr

Table 6: A periodic table of 20 amino acids (AA) according to their two categories of vowel and consonant ones.

	Complem. AA	Complem. AA	Noncompl. AA	Noncompl. AA	Noncompl. AA
G	Gly	Ala	Val	Asp	Glu
C	Pro	Arg	Leu	His	Gln
A	Lys	Met	Thr	Ile	Asn
U	Phe	Tyr	Ser	Cys	Trp

Table 7. A periodic table of 20 amino acids (AA) according to their two categories of complementary (complem.) and non-complementary (noncompl.) amino acids.

Non-eightfold AA	Non-eightfold AA	Eightfold AA	Eightfold AA	Eightfold AA
Pro	His	Gly	Ala	Ser
Asn	Asp	Val	Thr	Cys
Gln	Glu	Leu	Ile	Lys
Arg	Trp	Met	Phe	Tyr

Table 8: A periodic table of 20 amino acids (AA) according to their two categories of eightfold or non-eightfold of their quantities of protons.

In the author's opinion, sets, which have two binary-oppositional non-equal subsets with proportional ratios 3:2, 6:4, 9:6, 12:8, 15:10, 18:12, 21:14, etc., should be searched in the field of bioinformatics systematically as probable variants of structural organizing biological alphabets, including alphabets of linguistic languages. For example, the Cyrillic alphabet with its subsets of vowel and consonant letters can be characterized by this manner approximately.

About stiop-codons. Regularity, concerning stop-codons, is described below additionally. Comparative analysis of genetic codes in aspects of disposition and of natural numerations of stop-codons in the bi-periodic table of triplets permits to formulate the following property, materials for which are presented in the right column of Table 2. There is neccessary to explain the term "a circle of triplets of the bi-periodic table of triplets" preliminarily. Such circle is a circumference, which carries 64 equidistant points, a sequence of which is confronted in one-one manner with an enumerated sequence of 64 triplets from the bi-periodic table of triplets (see Table 3 in our previous article in this isssue). In other words, this enumerated sequence of 64 triplets is disposed along such circle in the described way.

The property of symmetrical disposition of stop-codons: in genetic codes, stop-codons, which have purines (A or G) in their second position, are disposed by a mirror-symmetrical way on a circle of genetic triplets of the bi-periodic table of triplets relative one of its diameter.

It should be emphasized, that all 64 genetic triplets get their natural numerations and natural ordering in the bi-periodic table of triplets that, in particular, permits to analyze the positional relationship of enumerated stop-codons in different genetic codes. It is obvious that this regularity has a non-trivial character for those genetic codes only, which have more than two stop-codons. This regularity resembles those regularities, which were recently discovered in poetry by L. Porter (2003).

One can note that all stop-codons in all genetic codes have purines (A or G) in their second position practically (Table 2). Only 2 from 17 genetic codes have a single stop-codon, which has pyrimidines in its second position (Table 2, the codes №s 13 and 14). The disposition of these abnormal triplets on the circle of triplets relative to other stop-codons of their codes has an asymmetric character. Because of this peculiarity, these single triplets are not represented in the regularity, which was formulated.

Additional remarks on the chronocyclic theory in biology. It should be summarized at the end of this article, that the following facts and associations, first of all, have given an initial impulse for the described chronocyclic investigation of genetic codes:

1. Symmetrical disposition of amino acids in the bi-periodic octet matrix $P^{(3)}$ (see Table 3 in our previous article in this issue). It was essential for the author that the genetic matrix $P^{(3)}$ had a formal connection with the famous table of 64 hexagrams of Ancient Chinese "The Book of Changes", which was used in chronocyclic conceptions of Oriental medicine and which was utilized for several thousand years as a base for chronocyclic recipes in acupuncture, pulse-diagnostics, etc.

2. Structures of all physiological systems, which have a chronocyclic character of their work, should be coordinated with structural peculiarities of genetic coding system to provide an evolutionary possibility of their re-creations in next generations.

3. Alphabets of all human languages have two categories of their letters, which are differentiated by their phonetic durations: the categories of consonant letters and of vowel letters. But a famous conception exists in linguistics for many years, that all human languages are based on the most ancient - genetic - language and that they are a prolongation of a genetic language (see a brief review in Petoukhov 2001, 2003a, 2003c). From this viewpoint, analogues of two linguistic categories of consonant letters and vowel letters should be searched in a universal protein's alphabet, which consists of 20 amino acids.

The chronocyclic theory of genetic codes considers molecular-genetic processes as chronocycles, included in a mutual chorus of chronocycles of the nature. It has been known for a long time, that processes of synthesis of proteins have a cyclic character. From an ordinary viewpoint, structures of genetic code are destined to code amino acids and proteins. From the new viewpoint of the chronocyclic theory, it is likely that these genetic structures are coding time parameters of cyclic processes of amino acids and of protein's synthesis simultaneously. Moreover, one can think that genetic structures are coding, first of all, these chronocycles exactly, due to which a coding of amino acids (and of proteins) is realized in a secondary manner. In other words, DNA and RNA are carriers of information not only about primary composition of proteins, but about time temps of chronocyclic organization of amino acids and of proteins too. From this position, those biorhythms which are observed at very different physiological levels so widely, should be derived not from peculiarities of final ensembles of proteins, but from peculiarities of pre-protein's genetic structures, which carry chronocyclic information in a long train of biological generations. It is very likely that universal nitrogenous bases of genetic codes have one more hidden attribute – chronocyclic (time) attribute. For example, complementary nitrogenous bases can be characterized by equal typical time of a process of their junction during the formation of DNA (and of their separation during the splitting of DNA). Two pairs of complementary bases with their 3 and 2 hydrogen bonds can have the appropriate ratio 3:2 of their typical times. Appropriate bi-periodic tables, which include a factor of time, can be written for mono- and polyplets of genetic systems.

The described phenomenological rules of №s 1-10 can be useful to understand the key meaning of chronocycles for the whole organism in all its manifestations. The chronocyclic approach to the evolution of genetic codes is capable of producing new important materials about biological evolution and about the significance of coordination of biological chronocycles with solar chronocycles, lunar cycles, etc. The chronocyclic theory also opens a new way to exploring heuristic parallels between genetic codes and chronobiology, including the chronocyclic conceptions of Ancient Oriental medicine. By the way, G. Stent, who is a famous specialist in the field of molecular genetics, wrote a book entitled *The Coming of the Golden Age* in 1969, in which he put forward a hypothesis about a possible connection between a set of 64 genetic triplets and a table of 64 hexagrams from the Ancient Chinese *The Book of Changes*. As far as we know, it was the first publication on this theme, and so G.Stent should be considered as a pioneer in this field of analyzing of parallels between modern molecular genetics and mysterious knowledge of Ancient civilizations. Our brief review of publications in this field by different authors was published in the book (Petoukhov 2001, pp. 195-201).

As was mentioned above, proteins in biological organisms are re-built (re-created) by systematic cyclic processes. It means that a set of physicochemical factors inside biological organisms disintegrates proteins into amino acids permanently and then re-builds them from amino acids again in a cyclic manner. But such cyclic forms of life of proteins in organisms are generally not considered in literature in genetic codes. Such literature focuses all attention on the assembling of proteins from a sequence of amino acids which is coded genetically. But it is very probable that genetic structures are coding not only the first half of cycle of protein's life, but the whole cycle with its second half (disintegration half) also. One can think that a future theory of genetic systems will include a theoretic consideration of these cyclic phenomena of protein's life in connection with other chronocycles of the nature.

The author will publish further results of continued analyses of evolutionary invariance of genetic codes later. It is obvious, that several of the described rules can be reformulated in a form of rules of prohibition. These rules can be used for predictions of peculiarities of genetic codes, which can be discovered in future. The author tries to develop a physico-mathematical apparatus of this theory, in particular, in connection with density matrices of quantum-statistical mechanics and with Hermitian complex matrices.

Due to the chronocyclic theory of genetic codes, the conception of existence of "vowel" and "consonant" amino acids appeared, which determined a new class of parallels between linguistic alphabets and the genetic alphabet of 20 amino acids. If we continue this line of thoughts, we collide with the common question about the probable existence of two binary-opposite categories of durations of physiological processes on very different levels and branches of biological evolution (with their conditional names: "vowel" and "consonant" categories).

Human speech and writing are constructed on the basis of alternating change of vowel and consonant elements, and chained sequence of proteins is based on alternating changes of vowel and consonant amino acids. It is probable that numerous number of physiological processes is constructed in a similar chained pattern with alternating changes of their vowel and consonant elements, which are realized there by nature. In this context about binary-opposite categories of physiological sub-processes, vowel element is a representative from a category of more prolonged sub-processes, and consonant element is a representative from a category of shorter sub-processes. For example, the human cardio cycle lasts 1 second approximately at rest. This cycle consists of a more prolonged activity phase and a shorter repose phase. The ratio of duration of these phases is 6:4. These two phases of cardio cycles can be correlated with two categories of durations (vowel and consonant). It should be noted that this 6:4 = 12:8 = 3:2 ratio is met permanently in ratios of vowel and of consonant amino acids in genetic codes (see the rules formulated above).

From an informational viewpoint, all physiological processes in an organism can be represented as information messages to interchange by information among different subsystems of organisms (or all physiological processes have their information components additionally). In our opinion, this information interchanging is realized in more or less uniform languages, which are coordinated with genetic languages, and their alphabets have vowel and consonant elements also. Due to this reason, one should investigate all physiological processes to find representatives from two binary-opposite categories of durations (vowel and consonant) there by analogy with linguistic alphabets.

Our hypothesis about physiological processes as chains of representatives from two binary-opposite categories of sub-processes should be examined in human creative productions also, first of all, in musical compositions. Can musical compositions, which have physiological effectiveness, for example, stimulate the growth of plants, be represented as regularity chains of representatives from two binary-opposite categories

of durations? This and many other questions from the field of chronocyclic theory are a theme for future investigations.

By the way, computer informatics does not use such alphabetic symbols ordinary, which are differed by their time durations. The reason is, that a trigger technology provides equal times for trigger transitions into "on" or "off" states. So, computer informatics and human languages have important differences in this aspect, which is connected with deep physiological mechanisms of human speech and of biological informatics on a whole.

Relative frequency of presence of consonant (vowel) letters in linguistic texts is a traditional theme of investigations in linguistics. In a similar way, there should be an investigation into the relative frequency of the presence of consonant (vowel) amino acids in proteins systematically. As a first step, the author investigated the relative quantities of these two categories of amino acids in the simplest gene of insulin. Initial data about this gene, which has alpha- and beta chains, were taken from the book (Inge-Vechtomov 1983, pp. 321-323):

- *alpha-chain:* Gly→Ile→Val→Glu→Gln→Cys→Cys→Thr→Ser→Ile→Cys→Ser→ →Leu→Tyr→Gln→Leu→Glu→Asn→Tyr→Cys→Asn;

- *beta-chain:* Phe→Val→Asn→Gln→His→Leu→Cys→Gly→Ser→His→Leu→Val→ Glu→Ala→Leu→Tyr→Leu→Val→Cys→Gly→Glu→Arg→Gly→Phe→Phe→Tyr→ →Thr→Pro→Lys→Thr.

The results are as follows. In this gene, the alpha-chain with its 21 amino acids has a ratio between consonant and vowel amino acids, which is equal to 14:7 = 2:1 correspondingly. The beta-chain with its 30 amino acids has a ratio between consonant and vowel amino acids, which is equal to 15:15 = 1:1 correspondingly. Such proportional ratios seem to be very interesting to prolong the program's investigations.

The author has no information about genetic codes other than the 17 genetic codes, which were analyzed in this article. Just before sending this article to the journal for publishing, he wrote a special letter to the National Center for Biotechnology Information (Bethesda, USA) about possible knowledge of additional variants of genetic codes there. And he received an answer from "NCBI Help desk", that a content of the site www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi "is the most up-to-date of what we have". The data of this site have been used in our article basically.

It seems that our chronocyclic theory of numbers of degeneracy of amino acids can be connected with the famous Eigen's theory of hypercycles and of molecular self-organization. In particular, the Eigen's theory considers the self-organization of chemical reactions, when a cyclic organization of reactions of one level has become an element of a cycle of a higher level. According to Eigen, hypercycles are arising, which determine the reproduction of subsequent proteins. These hypercycles play the role of a self-reproducing system of chemical reactions. One can think about a possibility of an application of Eigen's theory to explain the phenomenological numeric rules of degeneracy of genetic codes, described in our article.

In our opinion, a chronocyclic theory of genetic codes has an essentially wider base, connected not only with chemical reactions, but also with physical factors. For example, the idea of biosolitons has an important meaning in our theory (Petoukhov 1999). Biosolitons are connected with solitonic kinds of self-organizing of energy in non-linear biological systems. It is well known, that physical solitons exist in different non-linear systems without their definition by chemical composition or by chemical reactions in general case. They can exist without chemical reactions at all. Many kinds of solitons have a pulsate (chronocyclic) character and they can be direct participants of chronocyclic phenomena in biological and non-biological systems. As far as we can judge, chronocycles in biological substance exist even in those cases when there are not those transformations of one kind of molecules into molecules of another kind, which can be connected with these chronocycles directly. So, we are interested at this stage of development of our chronocyclic theory, first of all, in chronorhythms (in peculiarities of time) of physiological processes, but not in cyclic transformations of biochemical matter in a closed circle: matter A is transformed into matter B, which is transformed into matter C, etc. till the producing of the initial matter A after an appropriate number of transformations. In our opinion, the Eigen's theory about self-organizing properties of ensembles of chemical molecules and of chemical reactions should be considered as important, but not the single part of a future chronocyclic theory of biological systems, which includes the chronocyclic theory of genetic codes. But now, in the very beginning of development of chronocyclic theory of degeneracy of genetic codes, the molecular theory of Eigen can be used as a central basis for theoretical understanding of phenomenological rules of degeneracy, which are described in this article. It should also be mentioned that the author does not know publications with a serious analyses of a possible correspondence between the Eigen's theory and numeric peculiarities of degeneracy of genetic codes, though one from many possible variants of 3D-table of genetic code was published in Eigen's book (Eigen and Schuster 1979, Figure 64).

In our opinion, experimental researches of chronocyclic peculiarities of genetic code system are one of the most interesting ones now to examine the chronocyclic theory and to get new invaluable facts in this field.

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