The Cipher of the Genetic Code

Miloje M. Rakočević

Department of Chemistry, Faculty of Science, University of Niš, Serbia
(E-mail: mirkovmile@mts.rs; mirkovmiloje@gmail.com; www.rakocevcode.rs)

Abstract. In the paper is presented a new approach to understanding of the genetic code. In order to overcome the key paradox (and Darwinian selection problem) that the highly complex amino acid Phe is encoded by the simplest codons (UUY), and the simplest Gly encoded by the most complex codons (GGN); as well as the paradox of the duplication of some amino acids in the encoding process (Leu, Ser, Arg), we proposed an extension of the notion (and concept) of genetic code. For a better (and lighter) understanding of genetic coding, we proposed a hypothesis after that (under the conditions of allowed metaphoricity and modeling in biology) genetic code has to be understood, analogously to understanding in cryptology, as the unity of the three entities: the code, the cipher of the code and the key of the cipher. In this hierarchy the term (and notion) "genetic code" remains what has been from the beginning: a connection between four-letter alphabet (four Py-Pu nucleotides, in form of codons) and a twenty-letter alphabet (twenty amino acids); the cipher is a specific chemical complementarity in chemical properties of molecules in the form: similarity in dissimilarity versus dissimilarity in similarity ("Sim in Diss vs Diss in Sim") and the key of cipher: the complementarity on the binary tree of the genetic code in the form: 0-15, 1-14, 2-13, ..., 6-9, 7-8. Just only with this understanding, it appears a possibility for an additional understanding that within the two main Genetic Code Tables (of the nucleotide doublets and nucleotide Triplets) exists a sophisticated nuancing and balancing in the properties of th constituents of GC, including the balance of the number of molecules, atoms, and nucleons.

Keywords. Genetic code; cipher of the code; the key of the cipher; protein amino acids; canonical amino acids; particles number balance.

1. INTRODUCTION

From the time when the genetic code (GC) began to be considered practically deciphered (Crick, 1966; Rumer 1966), up to the present day, on the scientific scene is a paradigm according to which, in the interpretation of genetic code, the terms (and notions) "cipher" and "code" are synonyms. The word, however, must be about that thing, that in the interpretation of the genetic code, the terms "code", "cipher" and "key of the cipher" must be distinguished, analogously as it does in cryptology and cryptography. Just this position will be the backbone of this paper.

A little hint of such an idea, the idea of mediating by the "something" in the coding process, we had already have in the seventies of the last century. It was that T. Jukes has rebelled against the almost plebiscite attitude of the genetic code researchers that it exists

a direct affinity between the codons and amino acids (AAs), and set out the hypothesis that it will be rather a kind of mediation, at least a mediation of specific adapters:

"Various authors have advanced schemes for the origin of the genetic code based on proposals for direct affinity between amino acids and nucleotide bases or groups of bases. Such affinities are deemed to have played a part in the origin of life on the lifeless 'primitive soup'…. The present genetic code, however, and presumably its immediate antecedents, involve the intervention of adapter molecules ... which combine enzymatically with amino acids, rather than direct affinity between amino acids and nucleic acid molecules" (Jukes, 1973).

True to the will, there were also other authors who suggested that it might be mediation in the affinity of codon and amino acids, even from the very beginning of understanding of genetic code. Thus, F. Crick (1966, 1968) could not understood (nor accepted) that in most cases similar codons (trinucleotide aggregations) encode similar AAs, and in three cases (Leu, Ser, Arg) similar and non-similar, start with the hypothesis, that, if coding does not hold affinity, i.e. stereochemical conditions, then encoding within the genetic code must be "mediated" by "pure chance".

At the same time Y. Rumer (1966) suggests that encoding by dinucleotide aggregations is mediated by "grammatical" formalism (the relation between words and the root of the word), semantics (one-meaning and multy-meaning codon families) and by semiology, i.e. semiotics (the classification of nucleotide doublets[1] after the number of their hydrogen bonds which apear here as "signifiant" and "signifié" (signifier and signified) at the same time, that is as their unity (De Saussure, 1985, p. 99). [In further examples for grammatical, semantic and semiological analogies, we will not cite the signs of the allegations, since these relationships in the science of genetic code are generally known.]

Almost twenty years after the afore mentioned works by F. Crick and Y. Rumer in 1966, R. Swanson (1984) found that the coding in genetic code is mediated by Gray code based on the binary numbering system. Starting from R. Swanson's conclusion that "Gray code binary symbols [represent] the numbers 0-63", we have shown that the Gray code model as well as the Genetic Code Table (GCT) can be developed into binary tree with a codons display at exactly 0–63 positions (Rakočević, 1988a,b; 1998a).[2]

Ten years later, after the R. Swanson's work, V. Shcherbak showed that genetic coding is mediated by Pythagorean triples within specific patterns of the number of

[1] Nucleotides are the basic building blocks of DNA and RNA; the deoxynucleotides and ribonucleotides, respectively. As the monomers the nucleotides consist from the organic bases, the derivatives of Pyrimidine and Purine (Py-Pu) plus sugar (ribose or deoxyribose) and phosphate. For a general dessignation, we use for the nucleotides the abbreviated signifiers: Y for pyrimidine, R for purine and N for all four types of nucleotides.

[2] The Genetic code six-bit binary tree represents, *per se*, the Boolean space, i.e. the Boolean cube B^n (n= 0, 1, 2, ..., 5, 6) (Rakočević, 1994, 1997a). From the chemical point of view, the cases for n = 2, 3, 4 are particularly important, where the latter case (n=4) represents a display of 16 nucleotide doublets.

nucleons in canonical AAs, such patterns that they themselves "represent analogies with quantum physics" (Shcherbak, 1994).

Now, in this paper, it will be shown that this mediation is far wider. According to our hypothesis, the asignement of codons to amino acids is mediated by a specific *cipher* (and its key), based on a specific chemism in correspondence with the binary-code tree.

[**Nota bene**: "Before discussing these problems ..., we must address a preliminary one. We must face the *ontological problem* of the reality of the organic codes: are they real codes? Do they actually exist in living systems? It is a fact that the genetic code has been universally accepted into Modern Biology, but let us not be naive about this: what has been accepted is the *name* of the genetic code, not its *ontological reality*. More precisely, the genetic code has been accepted under the assumption that its rules were determined by chemistry and do not have the *arbitrariness* that is essential in any real code. The theoretical premise of this assumption is the belief that there cannot be arbitrary rules in Nature, and this inevitably implies that the genetic code is a metaphorical entity, not a real code. This idea has a long history and let us not forget that for many decades it has been the dominant view in molecular biology" (Marcello Barbieri, 2018, p. 2).][3]

2. A POSSIBLE SCENARIO OF SELECTION OF CONSTITUENTS

2.1. The "Aufbau principle" of the genetic code

With the revelation of the GCT, in both forms as the Table of the nucleotide triplets (Crick, 1966) and the Table of nucleotide doublets (Rumer, 1966) (Comment 1), it has become an obvious scenario by which the chemical constituents of the genetic code are generated; both builders, of nucleic acids, as well as of protein amino acids (Figures 1 and 2).

Comment 1. Both mentioned Tables (as Table 1.1 and Table 2.1, respectively) are given here, in a customized processing. Table 1.1 is a generalized GCT of nucleotide triplets in the sense that the triplets are reduced to doublets, according to the corresponding permutation of Py-Pu bases (Section 3.1), their positions in the Table of doublets (Table 1.2), as well as on the binary-coded tree (Rakočević, 1998, Figure 1).

The first thing that is directly visible is the fact that all constituents (molecules) of genetic code are built from the first few simplest elements (non-metals) at the beginning of the Periodic System of Chemical Elements (PSE). From the first four elements (H, C, N, O), pyrimidine (Py) and purine (Pu), that is their genetic code derivatives, were constructed; also the 18 AAs. [These four elements are in immediate neighborhood, three in continuity (C, N, O), at the beginning of the 4^{th}**,** 5^{th} and 6^{th} groups, respectively, and H

[3] "The very first **model** of the genetic code was the *Stereochemical Theory*, an idea proposed by George Gamow in 1954 ... The second **canonical model** was the *Coevolution Theory* proposed by Wong (1975, 1981), according to which the genetic code coevolved with the biochemical pathways that introduced new amino acids in protein synthesis" (Barbieri, 2018, p. 2) (The bolding: MMR).

at the beginning of the 7^{th} group, as the diagonal neighbor of oxygen.] To complete the nucleotide molecules, and to build two more AAs, which have sulfur, the Darwin's selection sieve must expand its openings in order to select phosphorus (as the vertical neighborhood of nitrogen) and sulfur (as the vertical neighborhood of oxygen) from the next period of PSE.

From these facts it can be concluded that the structure of chemical constituents of genetic code, in part directly, and partly indirectly, corresponds to the "Aufbau principle" of PSE.

2.2. The starting molecules and derivatives

In Figure 1, we can see three "start" precursor molecules: benzene (I), methane (III) and cyclopropane (IV), the simplest hydrocarbons from the corresponding groups – arenes (the most stable hydrocarbons), alkanes and cycloalkanes, respectively. The potential candidates for builders are themselves, or their derivatives.[4] By looking at the ten formulas in Figure 1, we find that aromatic hydrocarbons provide precursors for all four Py-Pu bases and all four aromatic AAs – the simplest aromatics, from the most stable six-membered and five-membered groups. On the other hand, observing the structure of the methane molecule (III), we note that here (in the act of selection), besides the principle of similarity, the principle of self-similarity applies: methane structure pattern is not only the pattern included into the "head" (amino acid functional group) of each of 20 AAs, than also in the body of all 16 AAs of the alanine stereochemical type. [Beside that the methan structural pattern (through the CH_2 group, located between the head and the "body", i.e. side chain of AA) makes the basis of the alanine stereochemical type, the glycine type possess also the same pattern.][5]

2.2.1. Derivative of derivative

Through the structure of alanine, the simplest amino acid of the alanine stereochemical type, all four aromatic AAs are included in a set of 16 AAs of alanine type. Phenylalanine, as its name suggests, is an alanine derivative by replacing a hydrogen atom in the side chain of alanine, in the CH_3 group, with a benzene phenyl group. By this act appears the situation which is also readable as so that phenylalanine is formed as a derivative of derivative: in the benzene derivative toluene (II in Fig. 1), one hydrogen atom is replaced by an amino acid functional group. All together, the self-similarity of amino acid molecules in them-selves is realized.[6]

---

[4] The details about the precursors of AAs can be seen in (Rakočević, 1998b).

[5] About four stereochemical types of AAs one can see in (Popov, 1989; Rakočević & Jokić, 1996).

[6] Rakočević, 2004, p. 231: . "Hypothesis on a [prebiotically] complete genetic code (CGC): By this hypothesis ... we support the stand point that CGC must be based on several key principles. ... 1. The

After the selection of phenylalanine (at the beginning of the first column of GCT) , as the first possible aromatic AA with a six-membered ring, its first possible derivative, tyrosine, is selected (at the beginning of the third column of GCT). It possesses the hydroxy group in the most stable para position (and not in a less stable ortho or meta position). Following two Mendeleev principles – the continuity and minimum of change – one should expect a derivative with a nitrogen functional group (amino group), instead of the oxygen (hydroxyl) group. But in such a case we would have a functional group with three instead with two atoms, what would not be in accordance with the principles of balancing and nuancing, which, in the case of genetic code, are also valid, as we will further show.

If we see the beginning and the end of GCT as complementary to each other (see below), then we see that, as the first minimal change in the set of arenes occurs at the beginning, so does the very first minimal change in the set of alkanes. [It is, therefore, the complementarity of the two most stable classes of hydrocarbons; one that is very complex, with hybridized chemical bonds and delocalized electron orbitals (arenes) and others that are very simple, with simple chemical bonds and localized electron orbitals (alkanes).][7]

As in the beginning, a minimal change occurs in which from Phe follows Tyr, so the same or similar process occurs at the end: the substitution of a hydrogen atom in Gly (last in the fourth column), with one methyl group (Comment 2), follows Ala (last in second column), which is "automatically" (as explained above) in relation to Phe. Moreover, the substitution of hydrogen atom in the Gly with an isopropyl group (III in Fig. 2) appears Val (last in the first column). At the "same time", together with valine was generated proline (Comment 3); and in a parallel process, in the first row, as a direct derivative of alanine, follow Ser, the first in second column, and Cys in the fourth one (Comment 4).

Comment 2. Within the side chain of Gly, as the first in the set of AAs, there is one atom only; in next amino acid, Ala, the 4 atoms. As we see, the numbers 2 and 3 are "forbidden" due to the four valences of the carbon. The question arises whether the set of number of atoms is chaotic or nonchaotic. Our researche shows that valid is the second response – not chaotic (Rakočević, 2017a, Table 3, p. 16).

Comment 3. The generating of proline is realized through isopropyl group, whose "triangle" is connected to the head of AA: in the case of valine with the vertex, and in the case of proline with the side. (For details see in Rakočević & Jokić, 1996.). [See Section 2.3.2.]

Comment 4. On a spatial-spheric model of the Genetic Code Table, the first and last rows are neighbors, as well as the first and last columns. This is, *mutatis mutandis*, as in LIGHT (Logical-Information-Geometric-Homeomorphic-Topological) model of the genetic code (Rakočević, 1994, Fig. 4.1, p. 54).

---

principle of systemic self-related and self-similar organization. …" [Note: This hypothesis best corresponds with the same such hypothesis of V.V. Sukhodolets (1985).]

[7] "Contraria sunt complementa." (A motto at Niels Bohr's own coat of arms, which featured a taijitu, symbol of yin and yang, designed in 1947.

Already with the selection of the first aromatic AA (Phe), we see the correspondence with two Py nucleotide bases, because the pyrimidine is a benzene derivative. As can be seen from Figure 1, the selection of a two-nitrogen pyrimidine (VII) is preferable than one-nitrogen pyridine (V). Two chemical reasons can be crucial here. Pyrimidine is more than a weaker base, but, more importantly, its far greater ability is to establish hydrogen bonds in potential dimers, which are actually found in natural DNA and RNA. One and the other is a distinct advantage for further balancing and nuancing. [As the "sowing" through the Darwin sieve, in the selection of chemical elements of the second period of the PSE, stopped before the fluorine, which, with its high reactivity, "burns" life before it arises, so this has also been shown here that the sieve was non-selective for stronger organic bases, which also lack the ability for balancing and nuancing in dimerization.]

2.2.2. Diversity enriching and economicity

With the selection of the third (Trp) and the fourth (His) aromatic AAs, the correspondence with two Pu nucleotide bases is also evident. In addition, it is also evident that in Darwin's prebiotic (chemical) evolution the selectivity of the sieve is "enriched" so that two additional principles apply: the principle of economicity and the principle of the enriching of diversity by increasing the degree of multi-meaning in relationships. The influence of both these principles is seen in the act of selection of tryptophan. In the case of Trp, we have a fusion of benzene with pyrrole into a two-ring indole (I + VI = IX), rather than with pyridine in double-strand quinoline (I + V = Quinoline); in the case of histidine, imidazole (VIII) is selected as similar to pyrrole (VI).

In addition to the stated reasons for the non-ability of pyridines, the reason are also the two quoted principles: by selection a five-membered aromatic ring (in both cases, in the case of pyrrol, as well as imidazole), instead of the six-member, molecular diversity increases, and in addition, imidazole provide an aromatic electronic sextet which possess the benzene too; moreover, the selection of this new type of electronic sectet enriches the multi-meaning relations within the genetic code (Box 1).

Both five-membered rings, pyrrole and imidazole, in fused compounds, within the constituents of genetic code, provide approximately equal acidity / basicity with a lower reactivity. Imidazole (VIII) is found in purine (X), in two purine bases, but also, as already mentioned, in the fourth aromatic AA histidine (the fourth in this discussion).

Additionally, one more point is needed here. When we discuss the analogy of six-membered and five-membered aromatic rings, apart from the similarities presented, we also mean the coherence of structural patterns (structural motives) and the similarity in the "flow" of delocalized electrons and electronic densities in the molecule. Thus, for pyrimidine (VII) and imidazole (VIII), except for the possession of an aromatic sextet, we say that they are analogs with the fact that they both have non-adjacent nitrogen

atoms. [The pyrimidine is not analogous to the pyrazole (the imidazole isomer) because both the pyrazole nitrogen atoms are adjacent.]

Box 1. *The economicity of aromatic five-membered rings*
L. G. Wade, Jr, Organic Chemistry, 8th International Edition, New York, 2013, p. 731: "Pyridine is an aromatic nitrogen analogue of benzene. It has a six-membered heterocyclic ring with six pi electrons. ... Pyridine shows all the characteristics of aromatic compounds. ... Because it has an avaiable pair of nonbonding electrons, pyridine is basic." Ibidem, p. 732: "Pyrrole is an aromatic five-membered heterocycle, with one hydrogen atom and two double bonds. ... Although it may seem that pyrrole has only four pi electrons, the nitrogen atom has a lone pair of electrons. The pyrrole nitrogen atom is sp^2 hybridized, and its unhybridized *p* orbital overlaps with the *p* orbitals of the carbon atoms to form a continuous ring. The lone pair on nitrogen occupies the *p* orbital, and (unlike the lone pair of pyridine) these electrons take part in the pi bonding system. These two electrons, added to the four pi electrons of the two double bonds, complete an aromatic sextet." Ibidem, p. 733: "Imidazole is an aromatic five-membered heterocycle with two hydrogen atoms. The lone pair of one of one of the nitrogen atoms (the one not bonded to hydrogen) is in a sp^2 orbital that is not involved in the aromatic system; this lone pair is basic. The other nitrogen uses its third sp^2 orbital to bond to hydrogen, and its lone pair is part of the aromatic sextet. Like the pyrrole nitrogen atom, this imidazole N–H nitrogen is not very basic. ... Purine has an imidazole ring fused to a pyrimidine ring. Purine has three basic nitrogen atoms and one pyrrole-like nitrogen."

2.3. The branching structures

Above we analyzed that part of the scenario that relates to the selection of Py-Pu bases and four aromatic AAs. Now we are going to analyze the generating, i.e. the selection of those AAs, which have a "pure" hydrocarbon side chain, a standard series (Ala, Leu, Val, Ile) and two AAs with a non-standard side chain (Gly, Pro)(Comment 5.) We assume that the logic of selection by the principle of matching the same or similar structural patterns here is also valid. Through analyzing these six AAs, we will continue to "keep on eye", for comparison, the remaining eight non-sulfur AAs (Section 2.3.1).

Comment 5. About four diversity types of AAs can be seen in Rakočević, 2011b, p. 822: (GP), (ALVI), (CMFYWH), (RKQNEDTS). Within the sub-set ALVI, all four AAs have a "pure" hydrocarbon side chain, and hence all four are nonpolar. Within the sub-set GP, for Gly we say that the non-standard hydrocarbon amino acid is hence because its hydrocarbon originates only from the head, and not from the body. (Hence its semi-polarity, as explained in Comment 7). The proline is also non-standard hydrocarbon AA, but through other reasons. By having three methylene groups in the body, that is, in the side chain, it is a hydrocarbon AA; but because the sequence of three methylene groups binds to the head, it is not a "pure" hydrocarbon AA. From the same reason, such a structure makes proline a semi-polar AA. This insight was necessary for the complete interpretation of "A harmonic structure of the genetic code" (Rakočević, 2004, Tables 3 & 4 and Section 3.3).

2.3.1. The "mapping" from the head to the body

Observing the structure of methane, the simplest alkane (III, Fig. 1), we see that it is a form that we find in the amino acid functional group (in the "head" of AA), as already mentioned above. Even more than that, we note that the generating of the body (side chain) of the remaining eight AAs can be understood as a "mapping" of partial functional groups from the head to the body. And, the mappings are as follows: the amino group leads to the generating of Lys & Arg; hydroxyl to Ser & Thr; carboxyl to Asp & Glu; and, finally, the fusion of the carbonyl and amino groups forms two amides (Asn & Gln), the derivatives of the two carboxylic AAs.

2.3.2. The pure hydrocarbon AAs

We return to the problem of generating four standard hydrocarbon AAs (Ala, Leu, Val, Ile) and two non-standard (Gly, Pro). We continue to observe the structure of the methane molecule (III, in Fig. 1) and note that this structure does not resemble the structure of the following members of the homologous series of alkanes (ethan and propane). Paradoxically, the methan looks like the fourth member, not as n-butane but as iso-butane. Despite the fact that, after Ala, as methyl derivatives, it is expected that AAs, which are ethyl and propyl derivative, are selected, this, however, does not happen; such AAs exist not in the set of protein AAs.

In Figure 2, the structures of the methyl and iso-butyl groups (I, II, in Fig. 2) are given. We see that the accordance is complete; the only difference is the size of electronic density on three "branches". Therefore, it becomes understandable why, after alanine, with the simplest hydrocarbon sequence of one methyl group, the expected derivatives with the atomic groups of ethyl, n-propyl, n-butyl come not, but iso-propyl and isobutyl derivatives, as well as one nitrogen analogue (II, III and IV in Fig. 2). [The nitrogen analogue is in arginine, by analogy of the iso-propyl group and the guanidine molecule.]

Iso-butane derivatives are the only two isomeric AAs, Leucine and Isoleucine; Leucine as the second AA in the series of AAs of the alanine stereochemical type and Isoleucine as a second one in series of AAs of the valin stereochemical type. [The generating of the first AA in the alanine type (Ala) on the methane pattern was explained above; also of the generating of the first, and only one AA in the glycine type (Gly). The explanation, however, for the first AA in the valine type (Val) and the first, and only one in proline type (Pro) on the iso-propil pattern, we gave in one of the previous papers (see Comment 3).]

3. NUCLEOTIDE TABLES AND THEIR FACES

3.1. The 24 permutations of four Py-Pu bases

In the set of four Py-Pu bases (UCAG) there are 24 permutations, each with three possible sequencing: 16 of the same bases in the first, or second, or third codon position. Of the 24 permutations, the chemical hierarchy (from the aspect of the complexity of molecules) corresponds only to the first (UCAG), which has a very distinct Py-Pu hierarchy, and all others, if it makes sense to analyze, then only in relation to the first permutation. Such permutations are UACG, with a strict hierarchy: *two* vs *three* hydrogen bonds; and CAUG, also with a strict hierarchy: *amino* vs. *oxo* functional group. The half-inversion UCAG/CUGA has no chemical meaning because "C" is a more complex molecule than "U". The same goes for UACG/AUGC, because (for an equal number of hydrogen bonds, A = 2 and U = 2), "A" is a more complex molecule.

In the third case, the half-inversion CAUG / ACGU has a chemical sense. In the first case at the beginning is Py molecule "C" as less complex; in the second one, the Pu molecule "A" as poorer in the functional groups than Py molecule "C". [Adenine does not have two but only one functional group (amino group).] Chronologically, "an alternative model of translation" within genetic code was presented via ACGU permutation (Damjanović, 1998; Damjanović & Rakočević, 2005, 2006, 2007); and then a "p-adic model of ... genetic code" via CAUG permutation (Dragovich et al ., 2006, 2010, 2017).

Bearing in mind, once more, that there are 24 permutations of four Py-Pu bases, each with three forms, from that aspect, F. Crick (1966, 1968) must first be acknowledged, which in the act of revealing the complete GCT, presented the best possible solution, from the aspect of the physico-chemical properties of the molecules, the builders of the genetic code (Crick, 1966, 1968). But the acknowledgement to R. Swanson that she realized that Py-Pu distinctions in the Gray Code model of the genetic code, and consequently on the binary tree, as well as in GCT, also (from the physical-chemical aspect) must follow Crick's model (Swanson, 1984).[8] [Today we can say that a large number of works have been confirmed the Crick's model, from which we list here only some, which, *mutatis mutandis*, correspond with this our work (Brimacombe, et al., 1965; Nirenberg, et al., 1966; Woese, et al., 1966; Rumer, 1966; Swanson, 1984; Doolittle, 1985; Sukhodolets,1985; Leunissen and De Jong,1986; Brains, 1987; Taylor & Coates, 1989; Alvager et al., 1989; Koruga,1992; Shcherbak, 1994, 2008; Négadi, 2009, 2011, 2014; Castro-Chavez, 2010; Petoukhov, 2016).]

3.2. The nucleon number balances

Starting from the said Crick's GCT model and the Swanson's Py-Pu distinctions, it was easy for us to show that these rules follow not only for the distinctions for 64 codons

[8] About chemical sense of 24 permutation of UCAG see also in (Rakočević, 2007, Table 1).

on a six-bit binary tree (Rakočević, 1998a), but also for the binary records of 16 nucleotide doublets (Table 1.2). On the other hand, it was possible to show that only in the GCT constructed via the first permutation UCAG, with four columns (NUN, NCN, NAN, NGN), each column with 16 codons, it can be shown in the GCT two significant nuance balancing splittings.

In the first (Rakočević, 2004, Fig. 5, p. 226), the GCT is diagonally (and symmetrically) splitted into the upper part with 12 amino acid molecules (in which there are 888 nucleons) and the lower part with 11 molecules, which in the side chains possess 555 nucleons (here: Figure 3, on the left). In the second, nuance-balancing splitting (Rakočević, 2006, Fig. 7) (here: Figure 4)], the GCT splits into 9 four-codon spaces, where 9 single amino acids are encoded, and 7 four-codon spaces where are encoded 7 pairs of AAs. For better and more light the current analysis, we give here a complete legend for the first splitting, which leads to a sophisticated nuancing and balancing:

"The nucleon number balance within two complementary parts (sub-systems?) of Standard Genetic Code Table. Up, in 12 AAs molecules (side chains), there are 888 nucleons (in first nuclide): F91 + L57 + S31 + Y107 + C47 + W130 + P41 + H81 + Q72 + R100 + S31 + R100 = 888. Down, in 11 AAs molecules (side chains), there are 555 nucleons: G01 + E73 + D59 + K72 + N58 + A15 + T45 + V43 + M75 + I57 + L57 = 555. [Cf. the possible relations with patterns (quantums) in the system of four-codon AAs (888–555=333) and non-four-codon AAs (555+555=1110), in Shcherbak, 1994, Fig. 1, p. 475]" (Rakočević, 2004, Legend to Figure 5, p. 226).

This interpretation, given 14 years ago, today we are able to expand and supplement. We read as follows. If one diagonal splits GCT into the upper part with 12 amino acid molecules (FLSYCWPHQRSR) and the lower part with 11 molecules (LIMVTANKDEG) [here: Figure 3, on the left], then in 12 molecules, in their side chains, has 888 nucleons, and 11 molecules have 555 nucleons. The sense of the balancing, through harmonization with two Mendeleev principles (continuity and minimum change) is this: **555**–666–777–**888**, where two external patterns "play", and two internal ones do not.[9] And the same, "just a little different" (Mendeleev's continuity and minimum change), we find in the orthogonal splitting of GCT into four columns and four rows: within 1 & 4 rows as well as 2 & 3 columns of GCT there are 654 nucleons, while in 2 & 3 rows as well as in 1 & 4 columns 789 nucleons. In the question is, then, the sequence 456–**789** / 987–**654**, in which in one case "plays" the original, and in the second one the mirror image (Verkhovod, 1994; Rakočević, 2006, Fig. 7, p. 24) (here: Figure 4).

[9] More than a curiosity: the sum 555 + 888 = 1443 (number of nucleons within side chains of 23 AAs) corresponds with the sum of the first four perfect numbers: 6 + 28 + 496 + 8128 = 6 x 1443. [About the hypothesis that the perfect numbers can be the determinants of the genetic code see in (Rakočević, 1997b, p. 60) and in (Rakočević, 2017c, Chapter 7, p. 2/43).]

By comparison Shcherak's findings in Rumer's Table of nucleotide doublets (Shcherbak, 1994, Figure 1) with our findings in the standard GCT (Rakočević, 2004, Figure 5, p. 226), we see the quantitative relationships as follows. [By comparison, the left and right side in the Rumer's Table it will be observed, as well as the upper and lower diagonally distinct parts in GCT (here: Table 2.1 vs Figure 3, left side).] On the right side of the Rumer's Table, in the "16-1" non-four-codon AAs, in their side chains, as well as in their heads, there are 1110 nucleons each, while in the diagonally distinct lower part of the GCT it has exactly one half of that quantity (1110: 2 = 555); if this quantity is added to the total number of nucleons in 8 ± 0 four-codon AAs (existing on the left side of the Rumer's Table), in their side chains (555 + 333 = 888), the quantity 888 is obtained, as it is the exact number of nucleons in the upper diagonally separated part of the standard GCT. (In both halves there are 555+888 = 1443 nucleons.)

Bearing in mind that the above quoted result (from our previous paper) for the number of nucleons is obtained by separating via left diagonal, in this paper we go a step further, analyzing the state of the number of nucleons in relation to the separation via the right diagonal too. In addition, we analyze the state of the number of atoms in both types of separation (Figure 3). For the number of nucleons, we obtain the result 555 + 49 and 888-49, which is also a kind of uniqueness, as demonstrated in Survey 1. [Results for the number of atoms in both separations are presented directly in Figure 3.]

For further evidence of the existence of correspondence in nuancing and balancing between the nucleotide doublet and the nucleotide triplet Table, it is also important to note the other uniqueness of the sequence 555-333-888, which had not been previously discussed (Survey 1); and also to notice that our series 555-333-888 (in form 333-555-888) is included in the set of multiples of Shcherbak's "Prime quantum 037" (Survey 2).

With the insight in Survey 2, we find the following relationships. The quantities of the number of nucleons that are valid for the lower and upper parts of GCT, 555 & 888, are in the immediate neighborhood of the quantities 592 & 925, respectively, valid for four-codon AAs. In other words, the difference is exactly for one "Prime quantum 037" (592 -555 = 037 and 925 - 888 = 037); with a valid neighborhood also for two referent points: (592 - 333 = 259 and 555-333 = 222) (259 - 222 = 037). As we see, nucleotide doublet and triplet Tables are balanced not only within themselves, but they are balanced one to other, through the Pythagorean triple: (3 ^ 2) x 037 = 333; (4 ^ 2) x 037 = 592; (5 ^ 2) x 037 = 925; (592 - 333 = 259).[10]

[10] Regardless of Shcherbak's work, which announced that the multiples of "Prime quantum 037" (in form of a Table of number triplets) appear to be a determinant of the Genetic Code, I found the same Table but with the number singlets (analog to Table in Survey 2). I presented the Table at Scientific conference of the Montenegrin Academy of Sciences and Arts in Cetinje, 27-30. September 1993. An integral article was published in Proceedings of Scientific Conferences of the Montenegrin Academy of Sciences and Arts (CANU), 1995, Book 35, Department of Art CANU, Book 12, pp. 245-265 (as Table 2). The Shchrbak's Table I found just in the year in which it was published (Shcherbak, 1994).

3.3. The atom number balances

For the analysis of the relationships of the nucleotide doublets and the nucleotide triplets Table, we start with the Rumer's double Table (Table 2.1) and we compare it first with Tables 3 & 4, in which the codons from Table 1.1 (in the form of nucleotide doublets) are mapped. We see that the separation into the upper and lower half of the Table 2.1 is dictated by hydrogen bonds, while in Table 4 it is dictated by the positions of the doublets on the binary tree (Rakočević, 1998, Figure 1). This is important because in Table 5.1, which is mapped from Table 4, we have the same balance of the number of atoms in the corresponding amino acids as in Table 2.1 (120: 119); all that in situation when the distinctions between the amino acid molecules are dictated by the polarity.

It is obvious that in the quantities "120 atoms" and "119 atoms," in two Tables, not all AAs are the same, so it is important to analyze what the difference is. Within the quantity "120 atoms" in Table 2.1 there are T+V+S+S = 28 and within Table 5.1 it is A+G+N+K = 28 atoms. Within both Tables there are L+R+D+E+C+W+H+Q = 92 atoms; altogether 28+92=120 atoms. On the other side, within the quantity "119 atoms" we have a vice versa situation: in Table 2.1 there are A+G+N+K = 28 atoms and in Table 5.1, it is T+V+S+S = 28 atoms. Within both Tables there are P+R+F+I+Y+L+M=91 atoms; altogether 28 + 91 = 119 atoms.

The difference between "quantity 92" and "quantity 91" comes from two different sequences, which differ by one molecule and one atom: D+E+C+W+H+Q=62 and P+F+I+Y+M = 61 atoms. The same sequence in "quantity 92" and "quantity 91" is the sequence L+R = 30 atoms. If we bring this fact in relation to the upper sequence T+V+S+S = 28, it becomes clear that the amino acids L, R and S are duplicated in GCT just for balancing and nuancing.

Following these comparisons, it makes sense to compare the "faces" of the nucleotide doublet Tables (Table 2.1 and Table 5.1) with the "faces" of the nucleotide triplet Table (Table 1.1, Table 1.3 and Figure 3). We see that the nuance-balancing, as in each individual Table, and among them, is determined by the middle pair of the number of atoms in the side chains of the AAs, in a set of "23" AAs, by shifting "the tongue on the scale" by ± 10 in the first as well as for ± 10 in the second step. [We can split the number of 239 atoms (within the side chains of 23 AAs) into the pairs, where 119-120 is the middle pair (0, 1, 2, 3, 4, ..., 119-120, ..., 235, 236, 237, 238, 239).][11]

Bearing in mind the fact that the number of atoms determines the number of nucleons, it is necessary, with the given results, to give one note more. In both cases, Shcherbak's as well as Verkhovod's result on the scene is a "block" exchange of quantities, analogously to that we first presented in the work on essential and non-essential AAs (Rakočević & Jokić, 1996), and later in other works. Future researches should show if these "block" exchanges remain within the limits of nuancing and

[11] This again resembles "The Little Gauss" algorithm in the process of adding numbers from 1 to 100, which was given to a nine-year-old Gauss by his teacher (Rakočević, 2011b, p. 833).

balancing, or, additionally, they themselves "represent analogies with quantum physics" (Shcherbak, 1994), as we stated in the Introduction.

3.4. The sense of the modification of Rumer's Table

In a previous work (Rakočević, 2013b), we have shown that the "mapping" of nucleotide doublets from the Modified Rumer's Table (Table 2.2) into GCT corresponds to the nuancing balance of polarity of the correspondent AAs, measured by the Cloister energy parameter (Swanson, 1984).[12] Thus, each first doublet, of four quartets, within the Modified Rumer's Table occupies one of the four (4±0) external four-codon-spaces in GCT, filled with nonpolar AAs: GG – Gly, UU – Phe & Leu, GU – Val, UG – Cys & Trp; each second doublet occupies one of the four (4±0) internal four-codon-spaces, filled with polar AAs: CC – Pro, AA – Asn & Lys, AC – Thr, CA – His & Gln; each third plus forth doublet occupies one of the four plus four [(4+1) & (4-1)] intermedial four-codon-spaces, filled with (4+1) polar, and (4-1) non-polar AAs; polar: UC – Ser, UA – Tyr, CG – Arg, AG – Ser & Arg, GA – Asp & Glu; non- polar: GC – Ala, AU – Met & Ile, CU – Leu.

Intermedial amino acids are listed in a continuous circular order, starting from Serine with the lowest value for polarity (the lowest value in the set of 5 intermedial and polar AAs), and going in the clockwise direction. The nuancing-balancing as follows: S= **0.24**; Y = **0.42**; [R=0.87; S=0.24; R=0.87] (R+S+ R) /3 = **0.66**; D = **0.69**; E = **0.71**; A = - 0.09; M = - 0.57; I = - 0.56; L = - 0.54 (Notice that A & L are the first and the last, respectively) (Comment 6).

External amino acids can also be listed with a growing sequence of values. Namely, the nuancing-balancing is as follows: C= - 0.73; F= - 0.56; V= - 0.52; G= - 0.16; W= - 0.25. As we see, the exception is where the listing has been started: Trp is more non-polar than Gly (Comment 7).

Internal amino acids cannot be listed in a rising sequence, but via the "broken" line, the zigzag periodicity: H = 0.00; T = 0.27; P = 0.46; N = 0.52; Q = 0.91; K = 1.46. As we see, here there are His as first and Lys as last in their column (the first and last in the set of internal AAs); Thr as the next is on the left in the previous column; Gln as next in the column; Gln vs Pro as the next on the left; and, finally, Asn as the next in its column (Comment 8).

Comment 6. In the set of four intermedial non-polar AAs, the exception in the falling series of values of the cloister energy parameter is Ala. It is signficant that Ala is also an exception by its specificity of molecular structure within the set of 16 AAs of the alanine stereochemical type. All of them are characterized by the existence of the CH_2 group between the head and the body.

[12] Cloister energy is "a formal free energy of transfer of the amino acid from the outside of a protein to the inside … I use cloister energy in preference to other measures of amino acid hydrophobicity/philicity because it is an in situ measure of the property of interest" (Swanson, 1984).

"Reading" so for alanine, it turns out that it has a body of glycine. On the other hand, if the hydrogen atom in the glycine is substituted by isopropyl group, a valine (valine type) is formed. However, as Valine is an "inversion" of proline, as a result we have that all four types are interconnected, what represents their similarity and self-similarity.

Comment 7. This exception at the end of the non-polarity sequence, expressed in relation to Gly-Trp, corresponds with the exception of the polarity of these two AAs when the polarity is measured by the index of hydropathy. Namely, these two AAs by the hydropathy are not non-polar but polar (cf. their hydropathy values in Table 5.1). The reason for this disagreement lies in the fact that (by their chemical structure) both AAs are semi-polar. Namely, Trp has at the same time a nonpolar benzene ring and a polar pyrrole ring. On the other hand, the side chain of Gly is a hydrogen atom that is nonpolar. But this atom, together with another one, is at the same time in the head of AA. Hence the polarity. All together, it results in semi-polarity.

Comment 8. We said that the internal amino acids are *polar*. However, it would be more correct to say that they are *not nonpolar*. It is because of His who has a zero value. It is, therefore, an exception; and it is an exception in the whole set of canonical AAs, since the only one contains only a five-membered aromatic ring. [This is not the case with Trp, because it has a six-membered benzene ring together with the five-membered pyrrole one.]

The nuancing-balancing through polarity, presented above, are followed by the nuancing-balancing of the number of nucleons and atoms. Irrespectively of the modified Table of nucleotide doublets, V. *sh*Cherbak (2008, Fig. 10, p. 173) showed that it makes sense a codons display into GCT exactly as we shown here for nucleotides doublets: four squares at the corners and four squares in the center; then, eight squares in middle, i.e. in "between" positions. After *sh*Cherbak's view, the balance of the number of nucleons is the next: AAs in four squares in the corners as well as AAs in four squares in the center have 369 nucleons each [(F91 + L57 + V43 + G01 + W130 + C47 = 369); (P41 + T45 + K72 + N58 + Q72 + H81 = 369)].

To this *sh*Cherbak's insight, we now add: the same quantity give the AAs in right site, in relation to the diagonal F–G, in the spaces of the doublets UC, UA, CG and AG (S31+Y107+R100+S31+R100 = 369). On the left side of the diagonal (in spaces CU, AU, GC and GA) there are 336 nucleons (L57+I57+M75+A15+D59+E73=336), what means 33 nucleons less, in relation to 369. With this emergence of difference of "33" on the scene appears a specific self-similarity because the number 33 is an important determinant of the number of atoms in the rows and columns as we shown in Table 2.1, down (Comment 9).

Comment 9. If we consider the set of "61" of AAs, then in the rows, YNR & RNY, there are **8 x 33** = 264, and in the others, YNY & RNR, **10 x 33** = 330 atoms. On the other hand, in two pyrimidine columns, NYN, there are **(9 x 33) – 1** = 297-1, and in two purine ones, NRN, **(9 x 33) + 1** = 297 of atoms (Rakočević, 2004, Tab. 3a, p. 224) (Y for pyrimidine, R for purine and N for all four types of nucleotides). [Notice that the numbers 264, 297 and 330, we can find also in a unique Table, presented in Survey 2 (positions: 8, 9 and 10).]

To these nuancing-balancing by nucleon number we now also add the nuancing-balancing by the atom number: AAs in four squares in the corners as well as in the center of GCT have 61 atoms in amino acid side chains (F14 + L13 + V10 + G01 +W18 + C05 = 61); (P08 + T08 + K15 + N08 + Q11 + H11 = 61)]. In relation to the diagonal F–G there are 58 and 59 atoms, respectively; on the left: L13 + I13 + M11 + A04 + D07 + E10 = 58, and on the right: S05 + Y15 + R17 + S05 + R17 = 59. These quantities (58 and 59) are the same as the quantities of hydrogen atoms in Sukhodolets' system (what is a further nuancing-balancing): 58 in two inner and 59 hydrogen atoms in two outer rows (Sukhodolets, 1985; Rakočević, 2011b Table 7, p. 830). [Notice that 58 + 59 = 117 is total number of hydrogen atoms in 20 canonical AAs of GC, within their side chains, what is the nuancing-balancing once more.]

4. A SPECIFIC CHEMICAL COMPLEMENTARITY AS THE CIPHER

Bearing in mind the Gray Code model of the genetic code, Binary-code tree and the Scenario, presented in Chapter 2, just their possible connection, a generalized standard Genetic Code Table (as Table 1.1) can be generating; also that a sophisticated analysis of the Rumer's nucleotide doublet Table is possible (as in form of Table 2.1), as well as a modification of Rumer's Table (as in form Table 2.2); such a modification that the modified form with the original makes the inseparable whole. On the other hand, it was proved by a justified and necessary of generating another arrangement that would represent a unifying arrangement of the binary code tree and GCT (Table 3). Such an arrangement makes sense to be named CIS (Canonical Invariant System) since the canonical amino acids in it are strictly determined and possess positions which it cannot be changed.

In the next step it makes sense to bring together the CIS and the Rumer's Table, so that the one-meaning doublets will be separated from the two-meaning ones (Table 4); such a procedure in order to analyzing the interrelations of splitted doublets from the aspect of two types of arrangements: according to their positions in the CIS and according the number of their hydrogen bonds.

Now about the interrelation between Table 2.1 and Table 2.2. Both tables contain four doublet quartets. In both Tables, the two upper quartets start with GG/UU doublets, and the two lower ones start differently: with AC/CA at first and with GU/UG in the second case; we say that in the first case the lower quartets follow by *dissimilarity*, and in the second case by the *similarity* of nucleotide bases.

In addition, the order of the remaining two and two doublets, as well as the corresponding amino acids, have also changed; in total the changes are subject to three pairs. Thus, in Table 2.1, we have Thr–Val, Arg–Ala and Ser–Leu, whereas in Table 2.2 there are: Val–Thr, Ala–Arg and Leu–Ser. [Observed by individual amino acids, their order in Table 2.1 better suits to the order in the binary tree (reading in reverse order);

however, observed by the amino acids pairs, better suits the order in Table 2.2. (Cf. order of AAs in Table 5.1).]

4.1. Three types of distinct chemical complementarity

Observing the Table of nucleotide triplets (Table 1.1) and the Table of nucleotide doublets (Tables 2.1 & 2.2), we note that the pairing and/or interconnection of the nucleotides is characterized by three distinct chemical complementarities: 1. Being Py or Pu, 2. The Py-Pu interconnection and/or pairing with two, or with three hydrogen bonds, 3. The pairing over *oxo* or *amino* functional groups. All three distinct complementarities are expressed into three key systems (the three modes of presentation) of the Genetic code: 1. In the standard GCT (Crick, 1968), 2. At Gray code model of GC (Swanson, 1984), 3. On the Binary tree of GC (Rakočević, 1988, Figure 31, pp. 120; and 1998, Figure 1, p. 284).

The third type of complementarity (Py-oxo with Pu-oxo; and Py-amino with Pu-amino) and the third type of presentation of genetic code (on the Binary-code tree) appear now to be the key to seeing the existence of the genetic code cipher and its key. Namely, the cipher key represents the positions of the nucleotide doublets and their associated AAs on the binary tree, and the cipher itself represents the specific complementarity of both – the doublets and the amino acids (Comment 10). In addition, complementarity follows in this order: 0-15, 1-14, 2-13, ..., 6-9, 7-8, as shown in Tables 1, 3 and 4. The complementarity described herein ("external complementarity") on the hypercube (B^4), as a Boolean model,[13] can be understood as summing up until the same sum, to the number 15, or up to the number 1111 in the binary record (middle part in Table 4).

Comment 10. In this hierarchy the term (and notion) "genetic code" remains what has been from the beginning: a connection between four-letter alphabet (four Py-Pu nucleotides, in form of codons) and a twenty-letter alphabet (twenty amino acids).

4.2. Nuancing and balancing of chemical structures and properties

The specificity of the chemical complementarity, which we are talking about here, is expressed as complementarity of the nucleotide doublets as well as the corresponding amino acids on each two vertices on the Boolean hypercube (B^4) whose binary values give the sum 1111 in the binary record (corresponding to the number 15 in decimal one). In the question are the nuanced and balanced chemical complementarities, both through chemical structures, and through the chemical properties of molecules. Examples are already listed in the second section of this paper (in the Scenario), and here we again present some characteristic examples in the new meaning (cipher – key of the cipher).

[13] The details on how GC can be understood as Boolean space can be seen in two of our studies (Rakočević, 1994, 1997b), both installed on our site.

Thus, we see that the initial (zeroth) doublet UU is complementary to the last doublet GG, which is the complementarity through the chemical difference.

4.2.1. The chemical hierarchy in the set of four nucleotides

Of the two pyrimidines, uracil is simpler because it has two the same functional groups (oxo functional groups), while cytosine possesses two different functional groups – oxo and amino. Of two purines, glutamine is more complex because it possesses both of these groups, while adenine has only one amino group.[14] Paradoxically, the simplest doublet, UU, encodes Phe, very complex AA, in whose side chain is very complex benzene ring. On the other hand, the most complex doublet, GG, encodes Gly, the simplest within the set of 20 protein AAs, with only one hydrogen atom in side chain.

4.2.2. Similarity in Dissimilarity

We might say that complementarity, shown above, is complementarity through dissimilarity. However, a deeper chemical insight shows that this complementarity is a complementarity through *similarity in dissimilarity*. In the case of two dissimilar nucleotides (as Py vs Pu), UU vs GG, the similarity is that both possess the oxo group; in the case of two dissimilar AAs (Phe vs Gly), the similarity is in a similar structural pattern within both molecules. The matter becomes clearer when it is seen that the doublet UU does not encode only Phe than Leu (formulas II and III in Figure 1, in relation to formulas I and II in Figure 2). [In reality the codons code for amino acids. Thus, Gly is encoded with the four most complex codons (GGN). On the other hand, chemically very complex AA, Phe, is encoded with only two simplest codons, UUU & UUC.]

Within the CH_3 group of toluene, one hydrogen atom is substituted by an amino acid functional group. Hence, a H-C-H group is formed between the head and the body. In this case, a C atom from the amino acid functional group and a C atom from the benzene ring are bonded vertically for the C atom in H-C-H group. All together, a form analogous to structures I and II in Figure 2 is obtained.

As we see, in the case of nucleotides, the dissimilarity is derived from the difference between their two dissimilar types (pyrimidine vs purine), and the similarity is derived from the same functional group. In the case of AAs, the dissimilarity arises from the difference of molecular classes involved in the construction of the amino acid side chain, and the similarity commes from the similarity in molecular structural patterns.

4.3. The chemical complementarity as a neighborhood logic

[14] These chemical distinctions are important from the aspect of the answer to the question of which form of GCT is the best (cf. Section 4.3.1).

In order to be able to analyze other examples of complementarity in the standard GCT, we must first answer the question of which GCT arrangement must be presented; in other words, which of 72 possible the arrangements, is the best; the best in terms of respecting the chemical hierarchy, from the aspect of less or more molecular complexity. It is only after answering this question that it makes sense to look at the state of chemical complementarity of nucleotide and/or amino acid molecules (Sections 3.1 and 4.3.1).

The correct answer to the raised question was already given in 1966 in the form of the above presented tables, the Nucleotide Triplet Table (Crick, 1966, 1968) and the Nucleotide Doublets Table (Rumer, 1966). In the presentation of these Tables, both authors went from experimental facts, which in practice, *mutatis mutandis*, already led to the Genetic Code Table (Brimacombe et al, 1965; Nirenberg et al., 1966), in which "the best present version of the code is shown", as Crick wrote in his second paper on GCT (Crick, 1968, Section:" The Structure of the Present Genetic Code ", p. 367).

4.3.1. The best possible permutation arrangement

The meaning of the above-quoted Crick's sentence is that only with the arrangement of the first permutation (UCAG) and codons with the same base in the middle position (16 times), the logic of the neighborhood within the four columns is achieved: 1st N**U**N, 2nd N**C**N, 3rd N**A**N, 4th N**G**N. Only in this case neighboring codons are mutually similar, and they can encode the same or similar AAs. And what was in force in 1966 and 1968, is valid today, with all in the presence the so-called deviant codes (Box 2). This is truly the best arrangement, the only neighborhood in wich codons similarities correspond to the similarities in chemical structures and properties (see Section 4.2.1 and footnote 14).

Only after these considerations and refinements can we continue with the analysis of specific chemical complementarity, valid for the standard genetic code. Namely, the nuancing and balancing of chemical structures (and properties) through complementarity becomes obvious only if we in the first and second columns (of the GCT) go downward, and in the last and the first to last – upward. By this act, there is an immediate obviousness that the "neighborhood logic" of codons and correspondent AAs, valid for columns, extends also to rows. Even more than the neighborhood logic also applies in diagonal connections (Comment 11)

Comment 11. The presentation of chemical similarities ("connections") in columns, rows, and diagonals completely correspond to the presentation of chemical similarities between the chemical elements, as Mendeleev drew in the PSE Table just a year after the discovery of PSE (1870 vs 1869), drawing not only periods and groups, but also diagonal connections [Photocopy VIII in (Kedrov, 1977) or in (Rakočević, 2017c, p. 341).]

The examples as follows. Phe and Leu are (through complementarity logic) in connection with Gly, as we said above. However, according to the logic of the neighborhood, they are at the same time in connection with Ser and Pro; Leu even more

with Thr. In Phe the bonding between the head and the body was achieved on a methane and isobutane pattern; In Leu, the body itself is that pattern. In the Ser we have the first possible derivation of the methan pattern by the introduction of the hydroxyl group. [This introduction of a hydroxyl group chemically can also be understood as the substitution of one hydrogen atom in the CH_3 group of Ala.] A "step further" is realized in the Thr – it is formed by replacing one hydrogen atom in the CH_2 group of the Ser by a methyl group. Hence, in the Thr between the head and the body is not H-C-H, but H-C-CH_3 group. [This also explains the similarity of Thr, both with Ala and with Pro, what corresponds to their positions in the GCT.] In the Pro, the side chain consists of three methylene (CH_2) groups, analogous (in its commonality, as a sequence of three such groups) with the structure of the isopropyl group. ["... just as a $–CH_2–$ group in a molecule is called a methylene group" (Wade, 2013, p. 166). By respecting the principle of self-similarity, the side chain of Pro can be chemically "read" as a pyrrolidine, which is a non-aromatic analogue of pyrrole (VI in Figure 1).]

Box 2. *The deviant genetic codes*
At that very first time (from 1966 until 1979) the Genetic Code Table was considered to be the Table of a universal genetic code. However, later with the discovery of alternative genetic codes, the Table was renamed in GCT of standard genetic code. The universality of the genetic code was first challenged in 1979, when mammalian mitochondria were found to use a code that deviated somewhat from the "universal" (Barrell et al., 1979; Attardi, 1985). Our opinion about "deviant codes" we have expressed in one of the previous works (Rakočević, 2004), and we still think the same today, that they represent only a "degree of freedom" in deviation from the standard one. [Knight at al., 2001, p. 49: "The genetic code evolved in two distinct phases. First, the 'canonical' code emerged before the last universal ancestor; subsequently, this code diverged in numerous nuclear and organelle lineages"; Weaver, 2012, pp. 568-569: "These deviant codes are still closely related to the standard one from which they probably evolved".]

After phenylanaline, going from the left to the right in the rows, we find a very characteristic case of simultaneous linear and diagonal neighborhoods between the three remaining aromatic AAs: Tyr, His and Trp.

After phenylanaline and leucine in the first column, isoleucine and methionine come in a complementarity relationship with arginine. In other words, when we go upstairs, in the last column, we encounter the arginine for which we saw that in the side chain it possesses a structural motif analogous to the structural motif of the isolpropyl group (II and III in Figure 2). The same motif we find in Val at the bottom of the first column, as also, mutatis mutandis, a motif of iso-propyl and iso-butyl group branching we find at the top of the last column (Cys, Trp).

With this movement – downward, upward, lateral and diagonal, we have the resolution for the position of the serine, the explanation of how it is located in two distant

and chemically different places in the GCT. Serine is at the beginning of the second column as the diagonal adjacent to leucine. On the other hand, serine is adjacent to arginine, and arginine is located at the second end of the Leu-Arg complementarity line ("1-14"). It becomes clear that in the same serine column there is cysteine, which is its chalcogenic analog (both elements, oxygen and sulfur are in VI group of PSE).

4.3.2. Dissimilarity in similarity

At the beginning, as well as at the end of GCT, we have relations between two and two AAs, with the minimum change: Phe-Tyr and Gly-Ala, respectively, as explained in the Scenario in Chapter 2. We have the complementarity of two and two AAs, but not through the addition operation, but through the subtraction on the Binary tree (15 - 7 = 8 and 8 - 0 = 8). Tyrosine as the derivative of Phenilalanine, like alanine as derivative of glycinne, both represent the minimal possible change (as explained in the scenario, in Section 2.2.1 (Paragraph in front of Comment 2). Hence, this is complementarity by *dissimilarity in similarity*. [Notice that this complementarity expresses relationships between the first and third, as well as between the second and fourth columns in the GCT. The cases that follow, listed simultaneously, in the upper and lower parts of Table 3 can be analyzed in the same or similar manner, as to "chemical eyes" are directly apparent. But this remains for some other occasions if it appears that there is of an interest of the scientific public.]

The specificity of the chemical complementarity, which we are talking about here, is expressed as complementarity of the nucleotide doublets as well as the corresponding amino acids on each two vertices on the Boolean hypercube (B^4) whose binary values give the sum 1111 in the binary record (corresponding to the number 15 in decimal one).

4.4. The cipher in relation to particles balance

Table 4 directly corresponds with Rumer's Table (Table 2.1), in the sense that the classification of dublets is given into one-meaning (left) and two-meaning ones (right). On the left side, each four-codon family encodes one AA and the right one for two. [The exception is the family in the 7^{th} position that is really two-meaning, but encodes one AA and termination signal.] In Table 4, nucleotide doublets are given in the order of the binary tree of the genetic code, while in the Rumer's Table they are classified from the aspect of the number of hydrogen bonds: two quartets in the upper and two in the lower half of the Table; two upper with different (4 and 6), and two lower with the same number of hydrogen bonds (5 and 5). And these different classifications, with such grait differences in the type of organizational arrangements, were followed by nuancing and balancing in the number of atoms (in a set of 23 AAs): in the upper and lower half of the

two arrangements, they differ by ± 0 (left) and ± 1 (right). [30 & 36 versus 30 & 36 and 89 & 84 versus 88 & 85 with a crossing.]

The classification into one-meaning and two-meaning four-codon families, that is, four-codon and non-four-codon AAs, was followed by already well-known balance in the number of nucleons mediated by Pythagorean triples (Shcherbak, 1994) (Score 1110 vs 1110 at the bottom of Table 4). Moreover, by balancing and nuancing, the correspondence of this classification with Py-Pu distinctions in the standard GCT was established in a set of 61 of AAs. [See the result (330-66 = 264) vs 330 at the bottom of Table 2.1; cf. with result (330-66 = 264) vs 330 in (Rakočević, 2004, Table 3a, p.224); see also here in Survey 2 on the positions 8 & 10.] It is obvious that all these balancings and shadings are at the same time in the function of harmonization with the principles of similarity and self- similarity.

5. THE POLARITY IN RELATION TO THE CIPHER KEY

In the last paragraph of the Introduction of this paper, we were told that we are starting from the hypothesis, according to which the chemical affinity between codon and amino acids in the genetic code is mediated by a specific cipher and its key. In the subsequent sections, arguments are given for making the cipher specific chemism in the form of a specific chemical complementarity; and that the cipher's key represents a sequence of codon positions and correspondent amino acids on the binary-ode tree of the genetic code (Rakočević, 1988, Fig. 31 on page 120; 1998, Fig. 1 on page 284). The following four Tables (5.1, 5.2 & 6.1, 6.2) contain the result, the final result, which supports that evidence. What is common in these tables is that it is directly apparent[15] that the key of cipher splits AAs into two groups: a group in which the AAs are strictly differentiated into polar and nonpolar, and another group, in which this is not the case. What are different are changes through balancing and nuancing, expressed in changes in the number of molecules and atoms.

5.1. The final result

The division of amino acids into two groups, in Table 5.1, is completely symmetrical. It is divided into the outer and inner space, each of four columns. Nuancing and balancing we find in interactions of Table 2.1, Table 4 and Table 5.1 are expressed by a change of ± 0 and ± 1 in the number of atoms by groups ("blocks") of AAs, with a crossover.[16] The change is such that it also reflects the cyclicity of the system: in Table 4, the positions on the cipher key, from 10 to 14, participate in the balance, while in Table

[15] "A picture is worth a thousand words"

[16] Dzivo Gundulic (Giovanni Gondola), Dubrovnik poet (1589–1638): "Tko bi gori, eto je doli, a tko doli gori ustaje" ("Who was up, now is down / and who was down, now is up.")

5.1 we have a "block" movement for exactly one block. The block "1-14" appears to be out of the "game" and the block "6-9" comes in, so that now the positions 9 to 13, as an internal space, come to participate in the balance. In one cyclic movement, the block "1-14" from the upper part of the Table is moved to the bottom; that is, together with the lower part makes the outer space. This is enabled by the same number of atoms of AAs H & Q and S & R (both times 22 atoms in their side chains); as well as by the difference in the number of atoms L-13 vs T-8 (for 5 atoms), whereby the previous result of "30" becomes as a new result 36-1, corresponded with the result 36, with an balance change for ± 1. [The changes for the ± 0 and ± 1 listed here, as in the previous sections, correspond with the same such changes (nuancing and balances) and in other systems and/or arrangements of the genetic code (Section 5.2)]

In the dark spaces of Table 5.1, the separation into polar and nonpolar AAs is complete. On the other hand, in the internal unshielded spaces, the separation is such that on one side we have a little polar AAs, and on the other side, the very polar. There is only one case where one opposite to the other we have non-polar AAs: a highly non-polar valine versus far less polar cysteine; and to make the separation more complete, tryptophan is added.

The eight amino acids, which correspond to eight "one-meaning" nucleotide doublets (AAs in the upper part of Table 5.1), make sense to name - the single amino acids. In such a case, tyrosine joins them because it is also the only AA in the four-codon UA space (Table 5.2).[17] As we see, this small change, this "tongue on the scale" causes new sophisticated shading and balancing, making "jumps" from one system to another, from one arrangement to another.

The changing of Table 5.1 in Table 6.1 is that purine encoding AAs are excluded, those that are encoded by codons that have purine in the third position. The result (number of atoms) in the upper part of the two Tables has not changed since the same AAs remained. But in the lower part it is. Instead of 88, now we have 44 (which is again a symmetry and balance!). On the other hand, instead of 85, we now have 31, correspondent with the result 31 in the upper part. The difference 85 - 31 = 54 is in correspondence with the result of 44 atoms. The whole thing becomes clear when we compare Table 5.1 with Table 6.2 where pyrimidine encoding AAs are excluded: we have a balance in one crossing: 54 vs 44 and 41 vs 31.

The differences from the aspect of the inclusion / exclusion of the block of Py / Pu amino acids have also been shown to be significant in other arrangements of the Genetic Code. So, this was demonstrated in the case of the classification of AAs into two classes, handled by two classes of enzymes of aminoacyl-tRNA synthetases (Damjanović and

[17] In this definition, it is only important that the doublet UA can encode only one AA, irrespective of the fact that it can encode also the termination signal.

Rakočević, 2005, 2006, 2007) (Box 3), and also in the case of the analysis of "p-adic model of ... genetic code " (Dragovich et al., 2006, 2010, 2017).

*

In Table 5.1, it should be noted that at the main "block" of the change, at positions "1-14", there are amino acids L, S, R, precisely those that are doubled in the set of "23" AAs. Only with their duplication (Comment 12) is it easier to nuance and balance chemical properties, which could be a kind of "intelligent design" (Box 4). Now, the meaning of their duplication is seen: non-polar Leu vs polar Ser & Arg. In sequence "0-15", we again have Le to "help" in establishing a relationship between non-polar Phe and polar Gly. The same applies to Arg, which, as polar, reappears in sequence "4-11" versus non-polar Ile and Met; Finally, Ser is also in the sequence of positions "2-13" in order to be, as slightly polarized against the high polar Asp and Glu. [For relations of the final result with some previous ones, see in Section 5.2.]

Comment 12. In the standard GCT the amino acids L, S, R appear twice each; in an extremely nuance reading of the standard GCT the Isoleucine appears also twice (Rakočević, 2007, Table 7; Wohlin, 2015, Table 2); within a "doublet-triplet" arrangement of protein AAs where reveals a connection between AAs and their biosynthetic precursors, the four AAs from non-alanine stereochemical type (G,P,V,I) also appear twice (Survey 1 and Table 1 in Rakočević and Jokić, 1996).

In Tables 5.1 & 5.2; then 6.1 & 6.2, we showed the nuancing and balancing in the number of atoms in the distinction of AAs to "single AAs" and "double AAs". In Tables 7 & 8, however, we showed nuancing and balancing in the "natural environment" of encoding amino acids, in the genetic code, from the aspect of as many as seven different parameters. These are the same two Tables that we published in one of the previous papers, but now more sophisticated, indicating the specific values for the hydropathy index.

*

The divisions, given by one and the same hatching within the six Tables (5.1 & 5.2; then 6.1 & 6.2, and in Tables 7 & 8), show that over the same division there is a specific proof of the correctness of the hypothesis about the necessity of distinguishing the genetic code on the code, the cipher and the key of the cipher. In a certain way, one confirms the other: the values of the hydropathy index confirm the validity of the cipher key, and the cipher key confirms the validity of the experimentally determined values of the hydropathy index (Kyte & Doolitle, 1982).

Box 3. *Pyrimdine/purine distinctions in relation to two classes of AAs*

„A further classification is also a proof for the wholeness within a holistic system of genetic code, the classification in relation to the base type in third position of the belonging codon. Thus, in class II there are AAs whose codons do not possess purine in third position (first subclass): N, D, F, H ... with 40 atoms within their side chains; then AAs whose codons possess purine in third position (second subclass): K, P, A, S, T, G ... with 40+01 atoms. On the other hand in class I there are AAs whose codons possess either pyrimidine or purine in third codon position (first subclass): V, L, R, also with 40 atoms within their side chains; then AAs whose codons possess only purine in third codon position (second subclass): M, Q, E, W with 40+10 atoms; as a third subclass there are AAs whose codons possess only pyrimidine in third codon position: C & Y with 40-20 atoms within their side chains. Out of the classification within class I there is isoleucine which belongs to the first subclass within standard genetic code and to the third subclass within mitochondrial genetic code ..." (Damjanović and Rakočević, 2005, p. 517; 2006 in arXiv:q-bio/0611033 [q-bio.OT], p.12; 2007, p. 121).

Box 4. *The Spontaneous Intelligent Design*

Castro-Chavez, 2010, p. 718: "We can conclude that the genetic code is an intelligent design that maximizes variation while minimizing harmful mutations."

Rakočević, 2013 and 2015, p. 18: "With insight into the results … one is forced to propose a hypothesis (for further researches) that here, there really is a kind of intelligent design; not the original intelligent design, dealing with the question – intelligent design or evolution (Pullen, 2005), which is rightly criticized by F.S. Collins (2006). Here, there could be such an intelligent design, which we could call "Spontaneous Intelligent Design" (SPID) that is consistent with that design which was presented by F. Castro-Chavez (2010), and is also in accordance with the Darwinism. ... Actually, it can be expected that the hypothetical SPID, contained in the results …, is in accordance with an identical (or similar?) SPID, presented in the only diagram, in Darwin's book "Origin of Species" (Darwin, 1859), as we have shown through an analysis of that diagram in one of our books (Rakočević, 1994; www.rakocevcode.rs). [In the case of the statement that spontaneity and intelligent design are mutually opposite, one must ask the question: isn't it true that human intelligence is the result of a spontaneous evolutionary process?]"

5.2. The final result in relation to some previous ones

In one of the previous papers (Rakočević, 1997a, p. 645) we have shown that the distribution of amino acids within the "Codon path cube" (Swanson, 1984) is followed with a strict distinctiion into inner and outer space. Within inner space there are AAs handled by class I of enzymes aminoacyl-tRNA synthetases, whereas in outer one the AAs handled by class II. [The only one exception is arginine, handled by class I, which is entered with two its codons, into the space of amino acids handled by class II synthetases.] Within the two and two sub-spaces, in both spaces, the differences in the number of atoms in AAs (in their side chains) are also ±0 i ±1 (in relation to the mean value):

I: [(M_{11}+I_{39}+V_{40}+L_{78} = **168±0)**; (Y_{30}+Q_{22}+E_{20}+R_{68}+C_{10}+W_{18} = **168±0**)] (1)

II+R_{34}: [(T_{32}+A_{16}+P_{32}+S_{20} +F_{28}=**129-1**); (N_{16}+D_{14}+H_{22}+K_{30}+S_{10}+G_{04}+R_{34}=**129+1**)] (2)

In another paper (Rakočević, 2011b, p. 838 and 840) we have shown that the external (o) and inner (i) space of the standard GCT is in relation to the space of nonpolar (n) and polar (p) AAs, respectively (also measured by the index of hydropathy), through the distinction in the number of atoms in AAs (in their whole molecules) which amount is exactly ±1:

(n) [(V_{76}+M_{20}+I_{66}+A_{52}+L_{132}+F_{46}+C_{28}=**420**];

(o) [(V_{76}+M_{20}+I_{66}+A_{52}+Y_{48}+R_{104}+W_{27}+C_{28}= **421**)] (3)

(p) [(G_{40}+K_{48}+N_{34}+P_{68}+Y_{48}+R_{156}+W_{27}+E_{38}+D_{32}+T_{68}+S_{84}+Q_{40}+H_{40} = **723**]

(i) [(G_{40}+K_{48}+N_{34}+P_{68}+L_{132}+F_{46}+E_{38}+D_{32}+T_{68}+R_{52}+S_{84}+Q_{40}+H_{40} = **722**] (4)

In the same paper (Rakočević, 2011, Figure 6, p. 832 and Figure 7, p. 833) we have presented the CIPS (Cyclic Invariant Periodic System)[18] of protein AAs, the canonical AAs within the genetic code. Cyclicism exists there in the sense that in the middle of the system there are chalcogenic amino acids (ST-CM), and further, in cyclic circles, there are two by two AAs from the same subclass, ending with two aromatic AAs and two aromatic heterocyclic (FY-HW).

The obtained cyclic rings split then into two superclasses: superclass I with AAs of lower chemical complexity (GP-VI + AL-KR) and Superclass II with AAs of more chemical complexity (ST-CM + DE-NQ + FY-HW). The number of atoms in two superclasses and two classes is well balanced with the difference of ± 0:

Class II: {[(G_{01}+P_{08})+(A_{04}+K_{15}) = 28] + [(S_{05}+T_{08})+(D_{07}+N_{08})+(F_{14}+H_{11}) = 53]} = **81**
Class I: {[(V_{10}+ I_{13})+(L_{13}+R_{17}) = 53] + [(C_{05}+M_{11})+(E_{10}+Q_{11})+(Y_{15}+W_{18}) = 70]} = **123** (5)

Sup.cls I: {[(G_{01}+P_{08})+(A_{04}+K_{15}) = 28] + [(V_{10}+ I_{13})+(L_{13}+R_{17}) = 53]} = **81**
Sup.cls II: {[(S_{05}+T_{08})+(D_{07}+N_{08})+(F_{14}+H_{11})=53]+[(C_{05}+M_{11})+(E_{10}+Q_{11})+(Y_{15}+W_{18}) = 70]} = **123** (6)

It is obvious that this is a "block" exchange between two classes and two superclasses (Rakočević, 2011b, Figure 7, p. 833).[19]

6. CONCLUDING REMARKS

The facts about a specific chemical complementarity of the constituents of the genetic code, given throughout this paper provide evidence to support the hypothesis, given in the title of this paper that the genetic code can be interpreted as the unity of the three entities: the code, the cipher of the code and the key of the cipher. Just only with this understanding, we can find, within the two main Genetic Code Tables (of the nucleotide

[18] CIPS follows from determination of genetic code by Golden mean on the Binary-code tree (Rakočević, 1998, 2011b), which tree appears now as the key of the ciher of the Genetic code.

[19] According to our *prediction*, these relationships will be, in the future, a referent system for protein structure researches.

doublets and nucleotide Triplets) the sophisticated nuancing and balancing in the properties of the constituents of GC, including the balance of the number of molecules, atoms, and nucleons.

All this also confirms our hypothesis, given in one of the previous paper (Rakočević, 2004) that the genetic code, from the beginning, in prebiotic conditions, was complete. Out of the millions of possible aggregations of molecules, the potential builders of GC, on "the card of life" played the one that potentially possessed all the chemical complementarities, we have exposed here.[20]

Our expectation is that this work could be joined to works that are on the way to solving open problems of existence and the essence of genetic code; such problems related to the search for answers to questions of origin and evolution of life; in particular, those works that open up new fronts of research in biology, extending the theme of genetic code on topics of *The codes of life*, or, more broadly, to *The biological codes* (Barbieri, Hofmeyr et al., 2008, 2018).

Acknowledgements

I am grateful to Vladimir Ajdačić, Branko Dragovich, Djuro Koruga, Nataša Mišić, Tidjani Négadi and Dejan Raković for helpful, stimulating discussions and benevolent critique.

[20] "Each of that aggregations could (and must) have its own 'evolution', but only one could have been selected – the one that gained the characteristic of self-reproduction (by which, through trial, error and success it became everything); all other, not selected, could not have any chance ..., they became nothing" (Rakočević, 2004, p. 232).

REFERENCES

Alvager, T. et. al. (1989). On the Information Content of the Genetic Code. *Bio Systems*, 22, 189-196.

Attardi, G. (1985). Animal Mitochondrial DNA: an Extreme Example of Genetic Economy. *Int. Rev. Cytol*. 93, 93-145.

Barbieri, M., (2018) What is code biology?, *BioSystems*, 164, 1–10.

Barbieri, M., Edit. (2008) The Codes of Life, *Biosemiotics*, Vol. 1, pp. 1-437, Springer.

Barbieri, M., Hofmeyr, J.-H.S., Edits (2018) Code Biology, *BioSystems*, Edited by Marcello Barbieri and Jan-Hendrik S. Hofmeyr, Vol. 164, pp. 1-226.

Barrell, B.G., Bankier, A.T., Drouin, J. (1979) A different genetic code in human mitochondria, *Nature*, 282, 189–194.

Brains, W. (1987) Codon distribution in Vertebrate genes may be used to predict gene length, *J. Mol. Biol*., 197, 379-388.

Brimacombe, R., Trupin, J., Nirenberg, M., Leder, P., Bernfield, M., Jaouni, T. (1965) RNA codewords and protein synthesis, VIII. Nucleotide sequences of synonym codons for arginine, valine, cysteine, and alanine, *Proc. Nat. Acad. Sci. US*, 54, 3, 954–958.

Castro-Chavez, F. (2010) The rules of variation: amino acid exchange according to the rotating circular genetic code, *J. Theor. Biol*. 264, 711-721.

Collins, F.S. (2006) The Language of God, Free Press, Bethesda, Maryland, USA.

Crick, C. H. F. (1966) The genetic code yesterday, today and tomorrow, *Cold Spring Harbor Symposia on Quantitative Biology*, 31, 3-9.

Crick, C.H. F. (1968) The Origin of the Genetic Code, *J. Mol. Biol*. 38, 367-379.

Damjanović, Z. (1998) Logic core of genetic code, *Proceedings (Glasnik) of the Section of Natural Sciences of Montenegrin Academy of Sciences and art* (CANU), 12, 5-8.

Damjanović, Z. M., Rakočević, M. M. (2005) Genetic code: an alternative model of translation, *Annals of New York Academy of Sciences*, 1048, 517-523.

Damjanović, Z. M., Rakočević, M. M. (2006) Genetic Code: A New Understanding of Codon - Amino Acid Assignment, arXiv:q-bio/0611033 [q-bio.OT].

Damjanović, Z. M., Rakočević, M. M. (2007) Genetic Code: A New Understanding of Codon - Amino Acid Assignment, *Proceedings (Glasnik) of the Section of Natural Sciences of Montenegrin Academy of Sciences and art* (CANU), 17, 121-153.

Darwin, Ch. (1859) *On the Origin of Species*, John Murray, London.

Doolittle, R.F. (1985) Proteins, *Scientific American*, 253, 74-85.

Dragovich, B., Dragovich, A. (2006) p-Adic Model of DNA Sequence and Genetic Code, arXiv:q-bio/0607018v1 [q-bio.GN].

Dragovich B., Dragovich A. (2010) p-Adic modeling of the genome and the genetic code. *The Computer Journal*; 53 (4): 432-441. arXiv:0707.3043 [q-bio.OT].

Dragovich, B., Khrennikov A. Yu., Mišić N. Ž. (2017) Ultrametrics in the genetic code and the genome, *Applied Mathematics and Computation*, 309, 350-358. arXiv:1704.04194 [q-bio.OT].

Jukes, T. H. (1973) Possibilities for the evolution of the genetic code from a preceding form, *Nature*, 246, 22-27.

Kedrov, B. M. (1977) *Predictions of Mendeleev in atomism – unknown Elements*, Atomizdat, Moscow [in Russian].

Kyte, J., Doolittle, R. F. (1982) A simple method for displaying the hydropathic character of a protein. *J. Mol. Biol*. 157, 105-132.

Knight, R.D., Freeland, S.J., Landweber, L.F. (2001) Rewiring the keyboard: evolvability of the genetic code, *Nature Reviews Genetics*, Jan., 2001, Vol. 2, no 1, pp. 49-58.

Koruga, D.L. (1992) Neuromolecular Computing. *Nanobiology*, 1, 5-24.

Leunissen, J. A., De Jong, W.W. (1986) Phylogenetic trees constructed from hydrophobicity values of protein sequences. *J. Theor. Biol*. 119, 187-196.

Mišić, N.Ž. (2011) Nested numeric/geometric/arithmetic properties of shCherbak's prime quantum 037 as a base of (biological) coding/computing, *Neuroquantology* 9(4), 702–715.

Négadi, T. (2009) The genetic code degeneracy and the amino acids chemical composition are connected, *Neuroquantology*, Vol. 7, 1, 181-187; arXiv:0903.4131v1 [q-bio.OT].

Negadi, T. (2011a) The multiplet structure of the genetic code, in one and small number, arXiv:1101.2983v2 [q-bio.OT] (Submited to Neuroquantology Journal).

Négadi, T. (2011b) On Rakočević's Amino Acid Biosynthetic Precursors Relations, *Neuroquantology* 9 (4), 772–798.

Negadi, T. (2014) The genetic code invariance: when Euler and Fibonacci meet, *Symmetry: Culture and Science*, Vol.25, No.3, 145-288, 2014; arXiv:1406.6092 [q-bio.OT].

Nirenberg, M., Caskey, T., Marshall, R., Brimacombe, R., Kellogg, D., Doctor, B., Hatfield, D., Levin, J., Rottman, F., Pestka, S., Wilcox, M., Anderson, F. (1966) The RNA code and protein synthesis, *Cold Spring Harb Symp Quant Biol.,* 31: 11–24.

Petoukhov, S. (2016) The system-resonance approach in modeling genetic structures, *BioSystems*, 139, 1–11.

Popov, E. M. (1989) *Strukturnaya organizaciya belkov*. Nauka, Moscow (in Russian).

Pullen, S. (2005) *Intelligent design or evolution?* Free Press, Raleigh, N. Carolina, USA.

Rakočević, M. M. (1988a) Three-dimensional model of the genetic code, *Acta Biologiae et Medicinae Experimentalis,* (Prishtina), 13, 109-116 [An excerpt in: http://www.rakocevcode.rs).]

Rakočević, M. M. (1988b) Genes, Molecules, Language (in Serbian with an English Language Supplement), Naučna knjiga, Belgrade. (http://www.rakocevcode.rs)

Rakočević, M. M. (1994) *Logic of the Genetic Code*, Naučna knjiga, Belgrade. (http://www.rakocevcode.rs

Rakočević, M. M. (1997a) Two classes of the amino acyl-tRNA synthetases in correspondence with the Codon path cube. *Bull. Math. Biol*. 59, 645-648.

Rakočević, M.M. (1997b) *The genetic code as a unique system*, Studentski kulturni centar, Niš (www.rakocevcode.rs)

Rakočević, M.M. (1998a) The genetic code as a Golden mean determined system, *Biosystems*, 46, 283-291.

Rakočević, M. M. (1998b). Whole-number relations between protein amino acids and their biosynthetic precursors. J. Theor. Biol. 191, 463 – 465.

Rakočević, M. M. (2000) The factors of the classification of protein amino acids, *Proceedings, (Glasnik) of the Section of Natural Sciences of Montenegrin Academy of Sciences and art* (CANU), 13, 273-294. (arXiv:q-bio/0611004 [q-bio.BM])arXiv:q-bio/0703011v2 [q-bio.OT].

Rakočević, M.M. (2004) A harmonic structure of the genetic code, *Journal of Theoretical Biology*, 229, 221– 234.

Rakočević, M. M. (2006) Genetic Code as a Harmonic System, arXiv:q-bio/0610044 [q-bio.OT] [Also in MMR, 2017b, Chapter 1, pp. (1–26) (4–29)]

Rakočević, M.M. (2007) A New Genetic Code Table, arXiv:q-bio/0703012 [q-bio.GN].

Rakočević, M.M. (2011a) Genetic Code: Four Diversity Types of Protein Amino Acids, arXiv:1107.1998v2 [q-bio.OT].

Rakočević, M.M. (2011b) Genetic code as a coherent system. *Neuroquantology* 9 (4), 821–841.

Rakočević, M. M. (2013a) Harmonic mean as a determinant of the genetic code, arXiv:1305.5103v4 [q-bio.OT].

Rakočević, M. M. (2013b) Golden and Harmonic Mean in the Genetic Code, *Proceedings of the 2nd International Conference "Theoretical Approaches to BioInformation Systems"* (TABIS.2013), September 17–22, 2013, Belgrade, Serbia. (Also in: OSF Preprints, DOI 10.17605/OSF.IO/2PFE7.)

Rakočević, M. M. (2015) Enigma of Darwin Diagram, www.rakocevcode.rs, stored on 2015-01-06. Also stored in: OSF Preprints, 2017-11-29 (UTC); DOI 10.17605/OSF.IO/QZG69.

Rakočević, M. M. (2017a) Analogies of Genetic and Chemical Code. www.rakocevcode.rs (stored also in: OSF Preprints 2017-08-09; and a new, minimally modified version 2017-10-02, DOI 10.17605/OSF.IO/MXECJ).

Rakočević, M. M. (2017b) Harmony of genetic code (Vol. 1), OSF Preprints, 2017-12-9). DOI 10.17605/OSF.IO/C38RG

Rakočević, M. M. (2017c) Harmony of genetic code (Vol. 2), OSF Preprints, 2017-12-13). DOI 10.17605/OSF.IO/89UAH.

Rakočević, M.M., Jokić, A. (1996) Four stereochemical types of protein amino acids: synchronic determination with chemical characteristics, atom and nucleon number. *J. Theor. Biol*. 183, 345–349.

Rumer, Yu, B. (1966) O sistematizacii kodonov v geneticheskom kode, *Doklady Akad. Nauk. SSSR*, 167, 1393-1394.

Shcherbak, V.I. (1994) Sixty-four triplets and 20 canonical amino acids of the genetic code: the arithmetical regularities. Part II, *J. Theor. Biol*., 166, 475-477.

Shcherbak, V. I. (2008) The arithmetical origin of the genetic code, in: M. Barbieri (ed.), The codes of life: the rules of macroevolution (pp. 153-181), Springer, Berlin.

Swanson, R. (1984) A unifying concept for the amino acid code, *Bull. Math. Biol*. 46, 187–207.

Sukhodolec, V.V. (1985) The meaning of the genetic code: the reconstruction of the stages of prebiological evolution (in Russian), *Генетика*, XXI, 10, 1589 – 1599.]

Swanson, R. (1984) A unifying concept for the amino acid code, *Bull. Math. Biol*. 46, 187-207.

Taylor, R.J.F., Coates, D. (1989) The code within codons. *Biosystems* 22, 177–187.

Verkhovod, A. B. (1994) Alphanumerical divisions of the universal genetic code: new divisions reveal new balances, *J. Theor. Biol*. 170, 327-330.

Wade, L. G, Jr (2013) *Organic Chemistry*, 8th international Edition, New York.

Weaver, R.F. (2012) *Molecular Biology*, fifth international edition, McGraw-Hill, New York.

Wetzel, R. (1995) Evolution of the Aminoacyl-tRNA Synthetases and the Origin of the Genetic Code. *J. Mol. Evol*., 40, 545-550.

Woese, C.R., et al. (1966) On the fundamental nature and evolution of the genetic code. In: Cold Spring Harbor Symp. *Quant. Biol*., 31, 723-736.

Wohlin, Åsa (2015) Numeral series hidden in the distribution of atomic mass of amino acids to codon domains in the genetic code, *J. Theor. Biol.* 369, 95–109.

T A B L E S

Table 1.1. The generalized nucleotide triplets Table

U	**C**	**A**	**G**	
UUN (**0**) **F** II **L** I	UCN (**2**) **S** II	UAN (**8**) **Y** I ct	UGN (**10**) **C** I ct **W** I	(11) **120 + 10**
CUN (**1**) **L** I	CCN (**3**) **P** II	CAN (**9**) **H** II **Q** I	CGN (**11**) **R** I	
AUN (**4**) **Ile** I **M** I	ACN (**6**) **T** II	AAN (**12**) **N** II **K** II	AGN (**14**) **S** II **R** I	(12) **119 -10**
GUN (**5**) **V** I	GCN (**7**) **A** II	GAN (**13**) **D II** **E I**	GGN (**15**) **G** II	
(11-1) **119 - 20**		(12+1) **120 + 20**		
53		77		
46		63		

The number of atoms within amino acid side chains corresponds to the number of atoms in the Rumer's Table of nucleotide doublets, both vertically and horizontally, and diagonally. The changes are for ±10 and ±10 once more. The changes in molecules number for 1 and ±1. The relations to arrangements in Tables 2.1 & 2.2 as follows. The diagonal relation: 53 + 63 = 115+1 and 46 + 77 = 124-1 versus 115 & 124 in the modified Rumer's Table (Table 2.2) and 125 & 114 in the original Rumer's Table (Table 2.1).

Table 1.2. The nucleotide doublet Table with binary records

Y–Y (Py–Py)				Y–R (Py–Pu)			
UU	0000	UC	0010	UA	1000	UG	1010
CU	0001	CC	0011	CA	1001	CG	1011
AU	0100	AC	0110	AA	1100	AG	1110
GU	0101	GC	0111	GA	1101	GG	1111
R–Y (Pu–Py)				R–R (Pu–Pu)			

Table 1.3. The Py-Pu and odd-even arrangement of amino acids within standard Genetic Code Table (GCT)

I	$\underline{\mathbf{L_1}}$+ V_2 + $\underline{\mathbf{S_3}}$ + P_4 + $\underline{\mathbf{T_5}}$ + A_6 + $\underline{\mathbf{Y_7}}$ + R_8 + $\underline{\mathbf{G_9}}$ = $\underline{\mathbf{42}}$ + 39 = 81 $\mathbf{F_Y}$ + M_R + $\underline{\mathbf{H_Y}}$ + K_R + $\underline{\mathbf{D_Y}}$ + W_R + $\underline{\mathbf{S_Y}}$ = $\underline{\mathbf{37}}$ + 44 = 81 $\underline{\mathbf{L_R}}$ + I_Y + $\underline{\mathbf{Q_R}}$ + N_Y + $\underline{\mathbf{E_R}}$ + C_Y + $\underline{\mathbf{R_R}}$ = $\underline{\mathbf{51}}$ + 26 = $\underline{77}$
II	(**FL**)$_{\underline{\mathbf{1}}}$+(MI)$_2$+(**HQ**)$_{\underline{\mathbf{3}}}$+(KN)$_4$+(**DE**)$_{\underline{\mathbf{5}}}$+(WC)$_6$+(**SR**)$_{\underline{\mathbf{7}}}$ = (**37+51)**+(44+26) = $\underline{\mathbf{88}}$ + 70
III	($\underline{\mathbf{42}}$ + $\underline{\mathbf{88}}$ = $\underline{120}$ + *10*) (39 + 70 = $\underline{119}$ – *10*)
IV	($\underline{\mathbf{88}}$ – $\underline{77}$ = 11) (81 – 70 = 11)

The Table corresponds with Table 5.2. In both Tables are the same amino acid singlets, but here their order is according to the positions in GCT, and in Table 5.2 according to positions on the binary tree. Sector I: In the first row there are amino acid singlets ("lonely" AA in four-codon space), in the order as in GCT. In the second and third row are amino acid doublets (per two AAs within four-codon space). Sector II: The amino acid doublets. In Sector III it is shown that number of atoms in amino acid singlets and doublets is determined by the middle pair of the total number of atoms within the set of 23 AAs (0, 1, 2 , 3, 4, ..., 119-120, ..., 235, 236, 237, 238, 239), with a change for ± 10. In Sector IV the following ratio of the number of atoms was shown: the difference in the number of atoms in all doubled AAs at odd positions (88) and the number of atoms in purine and doubled AAs at even positions (77) is equal to the difference in the number of atoms in all single AAs (81) [or in all pyrimidine and doubled AAs (81)] and all purine and doubled AAs at even positions (70). The nuance balance is self-evident.

Table 2.1. The Rumer's nucleotide doublets Table (Rumer, 1966)

114	**30** 116	**(119)**	**89** 108	125
Gly Pro Arg Ala	GG (6) CC (6) CG (6) GC (6)	Phe Asn Ile Tyr	UU (4) AA (4) AU (4) UA (4)	Leu Lys Met ct
Thr Val Ser Leu	AC (5) GU (5) UC (5) CU (5)	His Cys Asp Ser	CA (5) UG (5) GA (5) AG (5)	Gln Trp Glu Arg
125	**36** 106	**(120)**	**84** 118	114
330-66		**330±00**		
125 + 114 = 239 125 – 114 = **11**				

The one-meaning nucleotide doublets and corresponding four-codon amino acids on the left; and the two-meaning (UG as three-meaning) doublets and corresponding non-four-codon amino acids on the right. Four quartets (of nucleotide doublets) in relation to the number of hydrogen bonds. In the set of 23 AAs there are above 30 + 89 = 119 atoms in 11 amino acid molecules, within their side chains; and down: 36 + 84 = 120 atoms in 12 molecules; diagonally: 30 + 84 = 114 atoms in 12 molecules, and 36 + 89 = 125 atoms in 11 molecules. Within Py-Pu bases there are 106 + 116 atoms on the left and 108 + 118 on the right. [U = 12, C = 13, A = 15, G = 16; all as in (Rakočević, 1997a).] At the bottom (shaded) – the number of atoms in the amino acid molecules (side chains): within 32 amino acid molecules on the left and 29 on the right, within the set of "61" amino acid molecules. [Note: In originsl Rumer's Table only the number of hydrogen bonds (4 & 6 and 5 & 5 in brackets) is calculated; all other calculations are ours.]

Table 2.2. The modified Rumer's Table: the balances of the number of atoms in amino acid side chains, corresponding with odd/even positions

01. G	GG (6)	**02. F**	UU (4)	**03. L**	Odd **(115)** / Even **(124)**
04. P	CC (6)	**05. N**	AA (4)	**06. K**	
07. A	GC (6)	**08. Y**	UA (4)	**09.ct**	
10. R	CG (6)	**11. I**	AU (4)	**12. M**	
13. V	**GU** (5)	**14. C**	**UG** (5)	**15. W**	
16. T	AC (5)	**17. H**	CA (5)	**18. Q**	
19. L	CU (5)	**20. S**	AG (5)	**21. R**	
22. S	UC (5)	**23. D**	GA (5)	**24. E**	
28	(10)	**39**	(00)	**48**	(01)
38		39		47	
66		**78**		**60+35**	

The odd positions of nucleotide doublets and corresponding AAs are shaded. On the odd/even positions there are 115/124 atoms, respectively, in a balance correspondence with the "diagonal result" in the original Rumer Table (125/114 and Table 2.1). The result within the columns (60, 66, 78 atoms within the amino acid side chain) corresponds with the number of atoms within 7 "golden" AAs, 7 their complements and 6 non-complements respectively (as in: Rakočević, 1998a, Scheme 2, p 289; cf. Survey 3 in this paper). A "surplus" of 35 atoms is a "balance fraction" which, when passing from 204 atoms in the set of 20 AAs to 239 atoms in the set of 23 AAs, corresponds to the quantity for three doubled AAs ($L_{13} + S_{05} + R_{17} = 35$).

Table 3. The Canonical Invariant Sistem (CIS) of codons and corresponding amino acids, according their positions on the binary-code tree (Rakočević, 1998a)

0	UUN	F, L	**8**	UAN	Y	**15**	GGN	G
1	CUN	L	**9**	CAN	H, Q	**14**	AGN	S, R
2	UCN	S	**10**	UGN	C, W	**13**	GAN	D, E
3	CCN	P	**11**	CGN	R	**12**	AAN	N, K
		53 46			77 63			63 77
4	AUN	I, M	**12**	AAN	N, K	**11**	CGN	R
5	GUN	V	**13**	GAN	D, E	**10**	UGN	C, W
6	ACN	T	**14**	AGN	S, R	**9**	CAN	H, Q
7	GCN	A	**15**	GGN	G	**8**	UAN	Y
(53+46 = 119 - 20) (53+77 = 120+10) (77+63 = 120 +20) (46+63 = 119 - 10)						Left 46 56 Right 53 84		
(53+63 =115+1) (46 + 77 = 124-1)						46 + 56 = 102 53 + 84 = 102 + 35		

The number of atoms in the upper and lower part of the Table corresponds to the number of atoms in GCT (Table 1.1). Diagonal result (115 + 1 & 124-1 vs 115 & 124 in Table 2.2). A "surplus" of 35 atoms is a "balance fraction" which, when passing from (102 + 102 = 204 atoms) in a set of 20 AAs to 239 atoms in a set of 23 AAs, corresponds to the quantity for three doubled AAs (L13 + S05 + R17 = 35).

Table 4. The vertical CIS display into one-meaning and two-meaning nucleotide doublets and corresponding amino acids

an	on_2	on_1	c_1	aa	s	aa	c_2	on_1	on_2	an
13	**1**	0001	CUN	L	(15) 1111	S, R	AGN	1110	**14**	22
05	**2**	0010	UCN	S	(15) 1111	D, E	GAN	1101	**13**	17
08	**3**	0011	CCN	P	(15) 1111	N, K	AAN	1100	**12**	23
10	**5**	0101	GUN	V	(15) 1111	C, W	UGN	1010	**10**	23
36										85
08	**6**	0110	ACN	T	(15) 1111	H, Q	CAN	1001	**9**	22
04	**7**	0111	GCN	A	(15) 1111	Y, ct	UAN	1000	**8**	15
17	**11**	1011	CGN	R	(15) 1111	I, M	AUN	0100	**4**	24
01	**15**	1111	GGN	G	(15) 1111	F, L	UUN	0000	**0**	27
30										88
	(333 + 592 = 925) (1110 +1110) 259 000									
	(36 + 88 = **124**) (30 +85 = **115**)									

The designations: an – number of atoms within amino acid side chain; on_1 – ordinal number in binary records; on_2 – ordinal number in decimal records; c_1 – codons with containing one-meaning nucleotide doublets; c_2 – codons with containing two-meaning nucleotide doublets; aa – amino acids.

Table 5.1. The horizontal CIS display into one-meaning and two-meaning nucleotide doublets and corresponding amino acids (I)

1	**2**	**3**	**5**	**6**	**7**	**11**	**15**
L	S	P	V	T	A	R	G
+3.8	-0.8	-1.6	+4.2	-0.7	+1.8	-4.5	-0.4
-0.8 -4.5	-3.5 -3.5	-3.5 -3.9	+2.5 -0.9	-3.2 -3.5	-1.3	+4.5 +1.9	+2.8 +3.8
S R	D E	N K	C W	H Q	Y	I M	F L
14	**13**	**12**	**10**	**9**	**8**	**4**	**0**

Final result	LARG = 36-1 SRYIMFL = 88	35+85 = 120 88+31 = 119	SPVT = 30+1 DENKCWHQ = 85

All is the same as in Table 4, with an additional distinction of amino acid molecules through their polarities, measured by the hydropathy index (Kyte & Doolittle, 1982). Notice a diagonal balance in which it is shown that number of atoms in amino acid singlets and doublets is determined by the middle pair of the total number of atoms within the set of 23 AAs (0, 1, 2 , 3, 4, ..., 119-120, ..., 235, 236, 237, 238, 239); all that in a strict distinction into polar and non-polar AAs.

Table 5.2. The horizontal CIS display into one-meaning and two-meaning nucleotide doublets and corresponding amino acids (II)

1	**2**	**3**	**5**	**6**	**7**	**8**	**11**	**15**
L	S	P	V	T	A	Y	R	G
+3.8	-0.8	-1.6	+4.2	-0.7	+1.8	-1.3	-4.5	-0.4
-0.8 -4.5	-3.5 -3.5	-3.5 -3.9	+2.5 -0.9	-3.2 -3.5		±0.0	+4.5 +1.9	+2.8 +3.8
S R	D E	N K	C W	H Q		Θ	I M	F L
14	**13**	**12**	**10**	**9**		**8**	**4**	**0**

F.R. II	LAYRG = 50 SRIMFL = 73	50 + 31 = 81 73+85 = 123 + 35	SPVT = 31 DENKCWHQ = 85

All is the same as in Table 5.1, with an exception: the amino acid tyrosine is above instead down. Notice here a specific balance in which it is shown that the number of atoms in amino acid singlets (9 AAs above) equals 81 as in 10 AAs of class II, handled by class II of enzymes of aminoacyl-tRNA synthetases; On the other hand, the quantity of the number of atoms in 14 doublet AAs is 123 + 35, where the number 123 corresponds to the number of atoms in class I of AAs, handled by class II of enzymes aminoacyl-tRNA synthetases and the number 35 is a "surplus" of 35 atoms is a "balance fraction" which, when passing from 204 atoms in the set of 20 AAs to 239 atoms in the set of 23 AAs, corresponds to the quantity for three doubled AAs (L13 + S05 + R17 = 35). [About classification into two classes of AAs, handled by two classes of enzymes aminoacyl-tRNA synthetases, one can see in: Wetzel, 1995; Rakočević, 1997a; Rakočević, 1998a, Survey 4, p. 290.]

Table 6.1. The horizontal CIS display into one-meaning and two-meaning nucleotide doublets and corresponding amino acids (III)

L	S	P	V	T	A	R	G
+2.8	-0.8	-1.6	+4.2	-0.7	+1.8	-4.5	-0.4
-0.8	-3.5	-3.5	+2.5	-3.2	-1.3	+4.5	+2.8
S	D	N	C	H	Y	I	F

F.R. III	LARG = 35 SYIF = **44**	SPVT = 31 DNCH = **31**	

It is all the same as in Table 5.1, except that purine-coding amino acids are excluded in the bottom row.

Table 6.2. The horizontal CIS display into one-meaning and two-meaning nucleotide doublets and corresponding amino acids (IV)

L	S	P	V	T	A	R	G
+2.8	-0.8	-1.6	+4.2	-0.7	+1.8	-4.5	-0.4
-4.5	-3.5	-3.9	-0.9	-3.5	±0.0	+1.9	+3.8
R	E	K	W	Q	Θ	M	L

F.R. IV	LARG = 35 RML = **41**	SPVT = 31 EKWQ = **54**	
(44 + 10 = 54) (31 + 10 = 41)			

It is all the same as in Table 5.1, except that pyrimidine-coding amino acids are excluded in the bottom row.

Table 7. The AAs sequence taken from GCT as well as from binary-code tree of Genetic Code (Rakočević, 1998a; 2004)

F	L	**I**	M	**V**	Y	**H**	Q	**N**	K
+2.8	+3.8	**+4.5**	+1.9	**+4.2**	-1.3	**-3.2**	-3.5	**-3.5**	-3.9
-0.8	-1.6	**-0.7**	+1.8	**+2.5**	-0.9	**-4.5**	-0.4	**-3.5**	-3.5
S	P	**T**	A	**C**	W	**R**	G	**E**	D

After AAs encoded by middle "U" codons come AAs encoded by middle "A" codons; then follow AAs encoded by middle "G" and "C" in a cyclic organized system. The system can be seeing also as a sequence of the pairs (F-S, L-P, etc.). The sign "+" and "–" for nonpolar and polar AAs, respectively (after hydropathy index) (Rakočević, 2004, Table 7, p. 228).

Table 8. The results of calculations from data given in Table 7

	AN	MM	NN-T	NN-1	PN	IN	CN
Odd	**102-1**	**1369-1**	**15*1*3**	**627-1**	**343-1**	**210-1**	**203+1**
Even	102+1	1369+1	15*0*3	628+1	343+1	211+1	202-1

The designations: AN-the number of atoms within AA side chain; MM – the molecule mass of AA molecule; NN-T – the total nucleon number within AA side chain; NN-1– the nucleon number within first nuclide; PN – the number of protons; IN– the number of isotopes (nuclides); CN – the number of conformations, as in Popov (1989, Table 8, p. 88). The sums are given for AAs pairs in odd (bold) as well as in even positions within the system in Table 7. For example, within five AAs pairs [(F–S), (I–T), (V–C), (H–Y), (N–E)], existing in odd positions, there are 10 AAs molecules with molecules mass of 1368 units and with atom number of 101 atoms, etc., as it is presented in this table. The balances are self-evident.

F I G U R E S

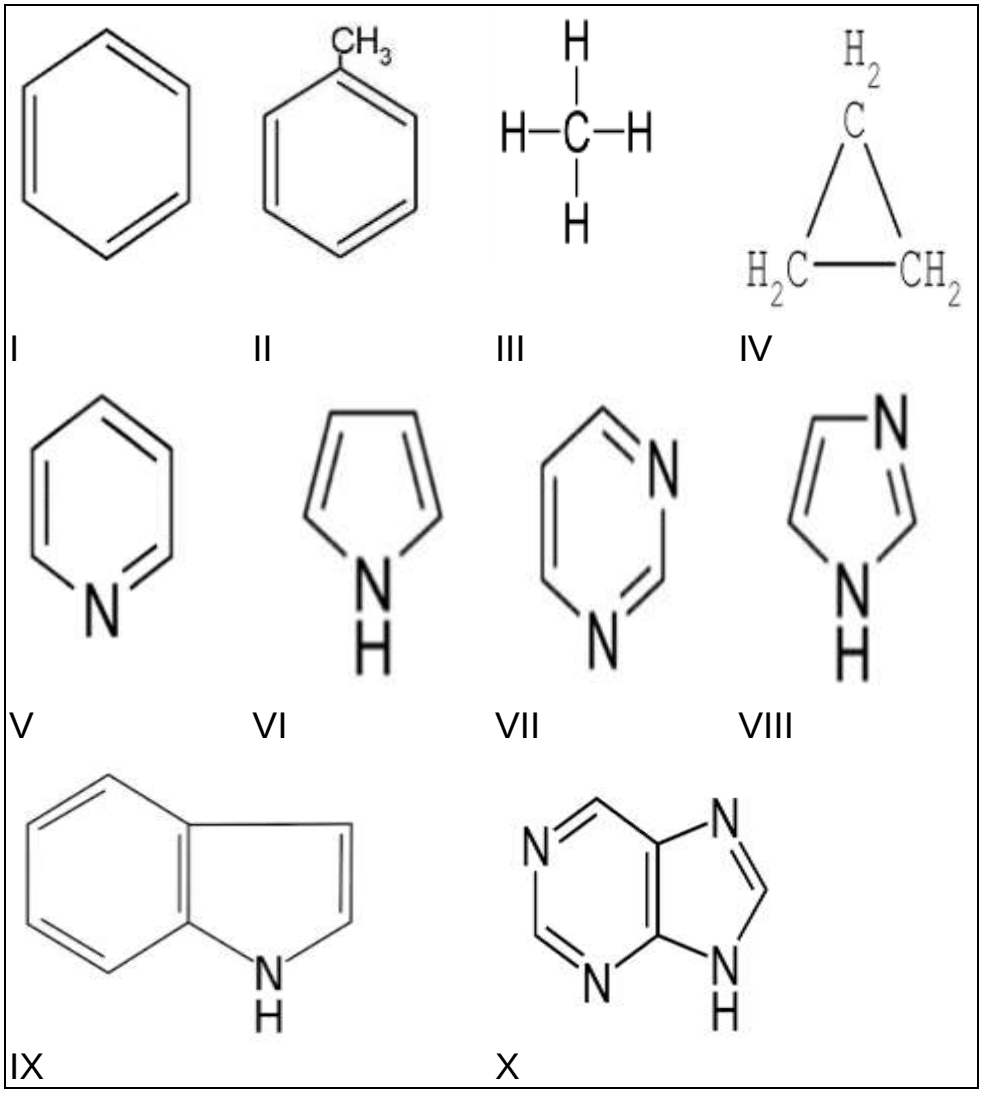

Figure 1. Correspondent molecules for 20 protein AAs (16 aliphatic and 4 aromatic) and/or for two and two (4 aromatic) Py-Pu bases. The designations: I. benzene; II. toluene; III. methane; IV. cyclopropane; V. pyridine; VI. pyrrole; VII. pyrimidine; VIII. imidazole, IX. indole, X. purine.

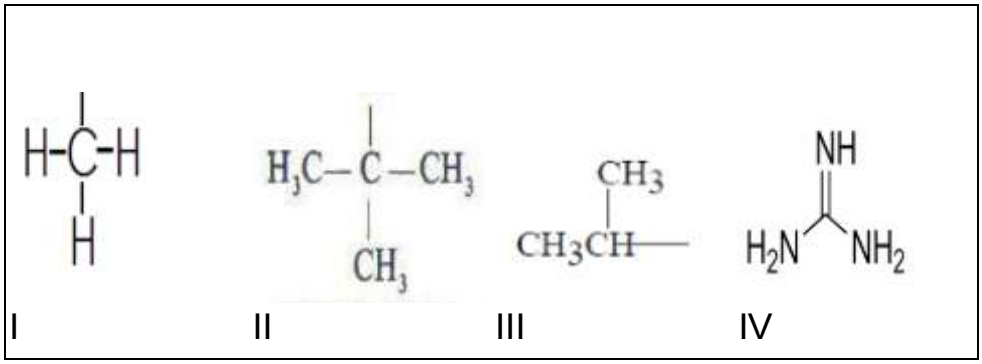

Figure 2. Atom groups and guanidine molecule, correspondent for some protein AAs. The designations: I. methyl group; II. isobutyl group; III. isopropyl group; IV. guanidine molecule.

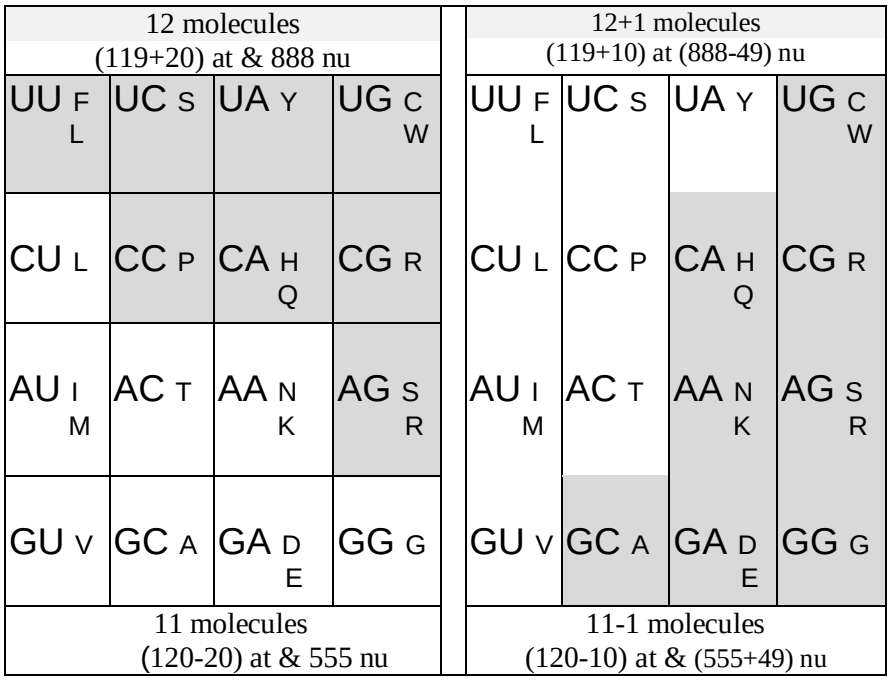

Figure 3. Left side: The illustration is the same as in (Rakočević, 2004, Figure 5, p. 226), except one difference: in that previous paper in the question is only the number of nucleons, but in this paper both – the number of atoms (at) and the number of nucleons (nu). Right side: It is all the same as on the left side, except here are relations via right diagonal.

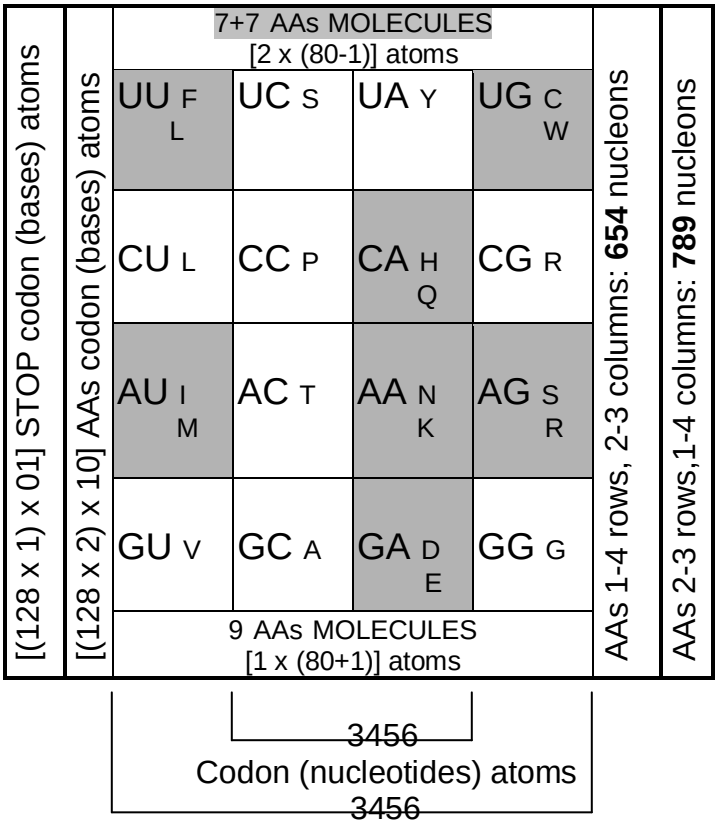

Figure 4. The number of atoms and nucleons within GCT. The number of atoms and nucleons in the classes and subclasses of amino acids corresponds to the parts of sequences of natural numbers, with principle of minimum (unit) change. The external vertical row on the left: the number of atoms in three "stop" codons, calculated to bases (U = 12; C = 13; A = 15; G = 16). The internal vertical row on the left: number of atoms in the remaining 61 codons, which have amino acid meaning. Two vertical rows on the right: the number of nucleons in the GCT according to (Verkhovod, 1994, Figure 2). Dark tones: two-meaning nucleotide doublets, each with two encoded amino acids [in total: two times (8-1) amino acids with 123+35 atoms]. Light tones: one-meaning nucleotide doublets, each with one encoded amino acid [in total: (8+1) molecules, with 81 atoms]. The bottom of Figure shows that in two and two columns, as well as in two and two rows, there are 3456 atoms in the codons, calculated to nucleotides (UMP = 34; CMP = 35; AMP = 37; GMP = 38). Notice that the distinctions into 9 single AAs (white areas) and 14 doublet AAs (dark tones) is the same as in Table 5.2.

S U R V E Y S

Survey 1. The uniqueness of the sequence of the number of nucleons in the two diagonally separated halves of GCT in Figure 3

(1221)	(999)	222	206	216	$16 = (4)^2$
(999)	(555)	444	417	427	$27 = (5.20)^2$
(777)	(111)	666	628	638	$38 = (6.16)^2$
(555)	(333)	888	8**39**	8**49**	**$49 = (7)^2$**
3,5,8 3,8,5 **5,3,8**	5,8,3 8,3,5 8,5,3	19 59	29 69	39 79	**$49 = (7)^2$** 89 99
(0,1,1), (1,2,3), (3,5,8), (8,13,21), ...					

The uniqueness of the sequence of the number of nucleons in the two diagonally separated halves of GCT [555 + 888 = 1443 in relation to the sequence (555 + 49) + (888-49) = 1443] manifests itself through similarity and self-similarity (849 vs 839) as well as through uniqueness of the number 49. Also, through the relation with the Fibonacci series (down, left), observed in the form of triples with one overlap. This insight is significant if we already have evidence that the GC was determined by the Golden mean, contained in the Fibonacci series (Rakočević, 1998a: Binary tree on Figure 1, contained "golden" AAs in relation to Farey tree on Figure 2, contained Fibonacci series as the key determinant).

Survey 2. The multiples of "Prime Quantum 037" and to it correspondent numbers

27	78	**9**	858	**99**	8991	**999**
26	78	26/3	858	286/3	8658	962
25	75	25/3	825	275/3	8325	925
24	72	**8**	792	**88**	7992	**888**
…						
16	48	16/3	528	176/3	5328	592
15	45	**5**	495	**55**	4995	**555**
…						
10	30	10/3	**330**	110/3	3330	370
9	27	**3**	**297**	**33**	2997	*333*
8	24	8/3	**264**	88/3	2664	296
7	21	7/3	231	77/3	2331	259
6	18	**2**	198	**22**	1998	**222**
5	15	5/3	165	55/3	1665	185
4	12	4/3	132	44/3	1332	148
3	9	**01**	66	**11**	999	**111**
2	6	2/3	66	22/3	666	074
1	3	1/3	33	11/3	333	037
		1/3		11/3		111/3
"Steps"	→	1st		2nd		3rd

The multiples of numbers 3, 33, 333 and 1/3, 11/33, 111/3, in relation to multiples of Shcherbak's "Prime Quantum 037". The explanations in the text.

Survey 3. "Golden" amino acids, their complements and non-complements

F 14		15 **Y**
L 13	(66–1)	04 **A**
Q 11		08 **N**
P 08		13 **I**
T 08		11 **M**
	(60+1)	
S 05		05 **C**
G 01		10 **V**
D 07		10 **E**
K 15	(78 ± 0)	17 **R**
H 11		18 **W**

Presented is the modified Survey 2.1, given in Rakočević, 1998a, p. 289. Originally, "Golden" amino acids (dark tones) are given in the order they have on the binary tree; and here according to the growing mass of their molecules. Over the "golden" AAs, there are their complements, and at the bottom non-complements. The number of atoms in side chains of amino acids is as follows: GSTPQLF = **60**, VCMINAY = 60 + (1 x 6) = **66**, DEKRHW = [60 + (1 x 6)] + (2 x 6) = **78.** Here, however, is shown that one other distinction is possible with the same patterns of the number of atoms (self-identity!); such a change that leads to a minimum change, for ± 1.