Genetic code as an image of the mirror image. Part I

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Φύσις κρύπτεσθαι φιλεῖ (Nature loves to hide).
Heraclitus: fragment 123

Abstract

The paper starts from the established facts about a system consisting of 20 protein amino acids (AAs), arranged according to a hierarchy of chemical similarity (Rakočević, 2019). There, it was shown that the number of atoms in the side chains of AAs given in the arrangement of 5 x 4 is such that it represents a mirror image in a specific way generated sequence of numbers: 02, 13, 24, 16, 05 (20, 31, 42, 61, 50). Further in the paper new insights have been presented to show that mirror symmetry is in many respects an essential feature of the genetic code.

Keywords: Protein amino acids, Amino acid code, Genetic code, Binary tree, Gray code, Golden mean, Fibonacci series, Periodic system, Mirror image, Mirroring.

1. Preliminaries

In the previous three papers we have presented the cipher of the genetic code, the analogies of the genetic and chemical code, and protein amino acids as a complete (periodic) system, with the preliminary idea on the genetic code as an image of the mirror image (Rakočević, 2018a, 2018b, 2019).¹ In this paper, however, we provide additional argumentation that all this is indeed the case, as well as the answer to the question under what circumstances and conditions is this so. It is impossible to know more than that, and therefore not to say. The sense of the appearance of mirror-symmetric and systemic arrangements of AAs cannot be explained from the point of view of physics and chemistry, just as it cannot be explained why only the left AAs (left enantiomers) and not

¹ On the Genetic Code (GC) as image of image see in (Rakočević, 2019, Figure 2 in relation to Tables 2 and 3). There we find the unity of strict chemistry and strict non-chemistry. Namely, the 20 protein amino acids (AAs), strictly ordered by chemical similarity, have so many atoms in their side chains that the number, expressed as a sequence of the number of atoms contained in each four AAs, represents the image of the image – a mirror image of the numbers taken (by strict regularity of "mirroring") from the Periodic System of Numbers (PSN): 02, 13, 24, 16, 05 as 20, 31, 42, 61, 50. This knowledge allows us to more easily understand the fact that codons can encode both chemical and non-chemical entities: amino acids and "stop" events in protein biosynthesis.

the right ones are selected in the genetic code.² However, if it proves to be a systemic thing, the embodiment of a kind of *Aufbau principle*, then at least we sense the circumstances and conditions under which (and under what scenario)³ such a scene could have taken place: principle explains the choice, and the reality of such a choice reveals the validity of the principle. Simply put, such an event scene was a necessary and sufficient condition for the Protein Amino Acid System (PAAS) – generated under prebiotic conditions – to become an integral part of the genetic code system (GC) under biotic conditions, and therefore a condition of life.

The very act of imagining that mirror symmetry is a systemic thing was based on the following logic. The fact that there is a strictly regulated system of chemical elements, ie. of their atoms, arranged so that there is an order of elements: 1st, 2nd, 3rd, etc., has led to the question, is it possible also an adequate system of molecules, made up of these atoms; adequate, in the sense that there is also an order of molecules based on their chemical similarity? On the other hand, if light non-metallic element-atoms exist within two or three short periods of PSE with the balance (equal number) of protons and neutrons in the atoms, is this balance manifested in any way in the system of their molecules – within two or more subsystems; moreover, is there also a corresponding balance number of atoms in the subsystems of the molecules? In the case of confirmation that such a system actually exists (Rakočević, 2019, Table 2, p. 14), and it is known that the "elements" of that system (amino acid molecules) are simultaneously the constituents of the genetic code, then *per se* one must conclude that this, *ipso facto*, also gave the answer to the question of what it was – just on a possible planet (terra nostra, for example), somewhere in the Universe.⁴

The hint that the series of natural numbers makes a hidden (third) alphabet of GC we gave eight years ago (Rakočević, 2011a, b);⁵ and the end result is the finding of the Periodic System of Numbers (PSN), which contains all the essential quantities

² If it was possible to construct a system of amino acid molecules based on such an *Aufbau principle*, which is based on a mirror symmetry, and that the system is capable of doing something "vital", then we simply take that as a fact, just as we take PSE as it is, without wondering why there are four types of orbitals, in sets of 1, 3, 5, 7 respectively, and not otherwise.

³ See the scenario of selecting AAs in the genetic code in (Rakočević, 2018a, Section 2, p. 32).

⁴ Rakočević, 2004, p. 231: "Hypothesis on a complete genetic code ... By this hypothesis, derived from presented facts as we understand them, we support the stand point that genetic code is one and unique, universal, valid for everything living, in fact, it is the condition for origin and evolution of life. Certainly, here we refer to the standard genetic code. According to this hypothesis, regarding other genetic codes (Budisa et al., 1999; Knight et al., 2001) we believe that they present only the expression of a code flexibility and degree of freedom, which is the matter of a separate paper."

⁵ "In determination of the genetic code, except two inherent alphabets – twenty amino acids and four amino bases (two pyrimidines & two purines) – is involved still one 'hidden alphabet', the series of natural numbers, with all its regularities and laws" (Rakočević, 2011a, p. 4).

(Rakočević, 2019) of the System of Protein amino acids (PAAS) as constituent of genetic code, enabled the further researches (Box 1).

Box 1. *The "test tube chemistry" and "system chemistry"*

With the knowledge that a system of molecules with their ordinal number is possible, it inevitably follows the conclusion that in the selection of molecules of life at the scene was not only the chemistry of valence electrons ("test tube chemistry") but also the chemistry of the wholeness of atoms and the completeness of the system of molecules ("system chemistry") – both chemistries in a permanent and inseparable commonalty. Thus, such a commonalty system could be a comparison system and organizational key for all analyzes of protein structures in living systems.

For a better understanding of the said commonalty, we refer to the example quoted by T. Jukes (footnote 11). According to the "test tube chemistry" ornithine would really chemically better match lysine instead of arginine. Both ornithine and lysine each have one amino group and differ only in the fact that lysine has four and ornithine has three methylene groups. In contrast, arginine with three methylene groups contains a very complex guanidino group, derived from guanidine, in which two amino and one imino group are attached to one carbon atom. But with ornithine instead the arginine, a system of AAs with the number of atoms in side chains in such a way that it corresponds 100% to the diagonal (with the number 1 at the end of notation) within PSN, would not be possible: $[(11 + 91 = 102), (21 + 81 = 102), (31 + 71 = 102), (41 + 61 = 102)]$; and just such a system we found in our previous work (Rakočević, 2019, Figure 1, on the right).

Since only the relations with the number of atoms in amino acid molecules are shown in the mirror arrangement of AAs, presented in the previous paper (Rakočević, 2019), we considered it useful to present relations with the number of nucleons as part of this work. In addition, in this paper we show that mirror symmetry characterizes some other essential amino acid arrangements already presented in previous works. First of all, this applies to the Shcherbak's system of four-codon and non-four-codon AAs (Shcherbak, 1994, 2008) as well as to one of our systems, revealed in the form "A harmonic structure of the genetic code" (Rakočević, 2004, Tab. 1)

2. Further insights

2.1. The quantity mirroring

Figure 1 shows the mirror symmetry, "hidden" in Shcherbak's system of two classes of four-codon and non-four-codon AAs (Shcherbak, 1994, Figure 1). An insight into this state comes through the following logic. The number of nucleons in 15 non-four-codon amino acids (on the left: 1110, 1110, 2220) corresponds to the first members of the Fibonacci series: 0, 1, 1, 2, with the rule for the growth of the sequence by summing two antecedents ($0+1=1$; $1+1=2$). Applying this rule, in the next step, the sequence 0, 1, 1, 2, 3, that is 1110, 1110, 2220, 3330 is generated, when we have mirror symmetry with the

number of nucleons within the side chains of 8 four-codon AAs (3330 / 0333). At the same time we also have "hidden" correspondence with the logical square: 0, 1, 2, 3, which we already know from other papers on the genetic code (Swanson, 1984; Shcherbak 2008).⁶ In these papers, however, the validity of the logical square refers not to the amino acid but to the nucleotide component of GC. But better, because it points to the connection of both components, which is realized, as V. Shcherbak also showed, over the number of nucleons (Box 2).

In this case, the first three numbers (1, 1, 2) are the realities, while the last in the sequence, the number "3", as the number 3330, is not a reality, despite being the reality of the 0333 quantity of number of nucleons in eight four-codon AAs, in their side chains (Box 3); it lacks within the set of 23 amino acids,⁷ however, the number 3330, as the reality of the number of nucleons, is found in the set of 24 amino acids, where amino acids K, Y, T, M are included two times each (Figure 2, third quadrant).

Box 2. *Two components of Genetic code: amino acids and nucleotides*

In this paper are presented the mirror distinctions of AAs, determined by the number of nucleons as the product of "Prime Quantum 037" (Shcherbak, 1994). However, since the same determination (via multiples of number 37) occurs within the nucleotide component of GC, the title of this paper applies to that component as well. An argument more, because in the "Scenario of selection of constituents" (Rakočević, 2018a, p. 32) we showed that there is a direct connection in the selection of both constituents – amino acids and nucleotides.

[Shcherbak, 1994, p. 476: "Remarkable relationships between 'amino acid' Table 1 (Prime Quantum 037) and 'triplet' Table 2 (Prime Quantum 007) was found. The product of both Prime Quantums, i.e. 037 x 007 is equal to 259 (which is the third and the final, after 925 and 592, cyclic permutation ...). The DNA canonical pairs A=T and G≡C are, probably, also related to this number. Their baryonic numbers (number of nucleons) are: A + T = 259 and G + C = 259+1..."] [In further studies should analyze the possible relation between these Shcherbak's cyclizations and the circular genetic code, revealed by F. Castro-Chavez (1910).]

⁶ Shcherbak 2008, p. 182: "In order to convert some DNA base sequence into Gamow's *long number* one should replace four bases T, C, A, and G with four quaternary digits 0, 1, 2, and 3." In what way R. Swanson presented the connection of GC with the Boolean logical square 0, 1, 2, 3, we have shown in previous work, at the same time showing correspondence with the logical square in human spoken language, presented by F. de Saussure (Rakočević, 2019, Figure C2, p. 42). Previously, on our side, the logical square of GC was presented in several papers, of which only two cases are quoted here (Rakočević, 1994, p. 8; 1997b, pp. 8 and 161)

⁷ The 23 AAs within the Genetic Code Table (GCT) of the standard genetic code, where amino acids (AAs) leucine, serine and arginine are included twice each, in the amino acids system.

Box 3. *Interrelations between realities of some significant quantities*

The quantity of 3330 nucleons corresponds to the quantity of 330 atoms in the Rumer's nucleotides Table (arranged according to the number of hydrogen bonds in nucleotide pairs: 4–5–5–6) (Rakočević, 2018a, Table 2A, p. 34), as well as to the quantity of 330 atoms in GCT, arranged by pyrimidine-purine nucleotide distinction at positions 1-3 of codons: [(Py-Pu) + (Pu + Pu)] / [(Py-Pu) + (Pu + Py)] (Rakočević, 2004, Table 3a, p. 224). And the said correspondence of the quantities 3330 and 330 is in the sense of the existence of "analogies with quantum physics" (Shcherbak, 1994, p. 476, last passage), because $3330 - 330 = 3000$.

The quantity 3000 corresponds to quantity 300 in Survey 2: $1443 - 1143 = 300$. In addition, Quantity 330 also corresponds to the quantities 033 & 330 found (in 1st and 10th steps, respectively) within the significant Table existing in relation to the Shcherbak's Multiples Table of "Prime Quantum 037" (Rakočević, 2018a, Survey 2, p. 37). But what is most important is the fact that one, the other and the third correspond to the third "orbital" level (00-11-22-33-44-55-66-77-88-99-AA-BB) in the Periodic System of Numbers, PSN (Rakočević, 2019, Fig. A1, p. 28).⁸

2.1.1. The permanent mirroring

The entire calculation process is located on the right side of Figure 1 within the sequence 333-259-592-925, in which the number 333 represents the number of nucleons in 8 side chains of 8 four-codon AAs. The calculation procedure follows the logic of a "Fibonacci series with skipping": the first and second numbers give the third, and the first and third give the fourth. The situation is the same as in our previous paper (Rakočević, 2019, Tab. A2, p. 29). [There we presented namely one variant of a series of numbers for which is valid a rule, similar to Fibonacci's rule, and hence it can be called "Fibonacci series with skipping". It is a series of numbers: 25, 36, 61, 86, 97, as the number of atoms in which the first and second give the third, and the first and third give the fourth number; then the second and third give the fifth number (with "skipping" the fourth).]

In Figure 1, we also see that it makes sense the shosen numbers (in middle area: the products of the number 37) to be designated by a binary unit (1) and not shosen by a binary zero (0). This choice corresponds to the diagonals in Boolean cube; read from opposite sides: 4–1 (100-001) on the left and 6–3 (110-011) on the right. The diagonals of the cubes that intersect with these diagonals are also indicated: 5–0 (101-000) on the left and 7–2 (111-010) on the right. Reading the selected and unselected diagonals together,

⁸ Of course, we can only reach this conclusion after knowlege that the first three levels in PSN have proven to be the most important "mirror" condition for the generation of PAAS, based on the chemical similarity of AAs (Rakočević, 2019, Fig. 2 in relation to Tab. 3). It is also important to note that with the third "orbital" level (00-11-22-33), the first possible (plane) Boolean space is generated, in the form of a logical square, which we otherwise found to be an essential determinant of both genetic and chemical code (cf. Eq. 1 & 2 and Tabs 2, 3 & 4 in (Rakočević, 2018b).

we get two sets of numbers: 5-4-1-0 / 2-3-6-7, the order of which coincides completely with the order of 8 codon families (8 families with 8 codons each) in the Generalized Table of GC (Rakočević, 2019, Table 7, p. 21), corresponding to their positions on binary tree (Rakočević, 1998a, Figure 1): 5-4-1-0 as YGN-YAN-YCN-YUN / 2-3-6-7 as RUN-RCN-RAN-RGN (Remark 1).

Remark 1. In this as in the previous three papers (Rakočević, 2018a, 2018b, 2019) under mirroring the binary sequences we mean the comparison of binary sequences in terms of complementarity. Given that in this comparison, some sequences appear as objects and their images in the mirror, and in accordance with the "if any, then all" principle, we conditionally understand that mirror symmetry applies to all binary sequences. We take as if there is a specific mirror sensitive precisely to complementarity, and in it a complement of the sequence being reflected is obtained. There are three types of complementarity possible: 1. sameness (0/0 or 1/1) [as in: 011/110], 2. differentness (0/1 or 1/0) [as in: 101 / 010]⁹ and 3. the combination of the first two types [as in: 111/100]. (Notice that the diagonals of the sides of the Boolean cube: 011 – 110 and 111 – 100 have the same type of symmetry on two mutually orthogonal sides.)

The point of correspondence via mirror symmetry in Figure 1 is that the original 3330 corresponds to its mirror image 0333 (and vice versa); also that the three plus three permutations are mirror symmetrical as well as the whole arrangement of permutations: two permutations selected plus one unselected (on the right); two permutations unselected plus one selected (on the left). [The permutations that represent the multiples of Shcherbak's "Prime Quantum 037" have the status of "selected permutations" (Shcherbak, 1994, Table 1).]¹⁰

2.1.2.. The cyclicity through mirroring

When the inner area of Figure 1 is arranged in mirror symmetry, with the addition of binary numbers indicating choices (1) and non-choices (0), a system of six permutations gives the following result: two permutations are selected and one is unselected; after that: two were unselected and one was selected. If at the top of each of these two subsystems of permutations we place a mirror and allow superposition, in both cases we have a situation analogous to that already seen in the final column of Periodic system of Numbers (PSN), when we took the first possible Boolean triangle and put the mirror in front of it (Rakočević, 2019, Fig. 2, p. 18):

⁹ Paul Dirac (in Nobel Lecture, December 12, 1933): "On this view the positron is just a mirror-image of the electron, having exactly the same mass and *opposite* charge." (Italic: mmr)

¹⁰ The entire Table of multiples of number 037, expanded with multiples of numbers 3, 33 and 333, we have given in (Rakočević, 2018a, Survey 2, p. 37). [In the mentioned Survey 2, one formal error occurred: in the last, 27th row (in the fourth column), instead of product 858, the product should be $27 \times 33 = 891$.] About multiples of numbers (6, 66, 666), (7, 77, 777), (8, 88, 888) in relation to the product of the number 037 see in (Rakočević, 2008).

(110/011 → 11011) & (001/100 → 00100 (1)

(110/011 → 11011) & (001/100 → 00100 (2)

(110/011 → **101**) & (001/100 → **010**(3)

As we see from solutions (1), (2) and (3), according to the state of affairs in the system of choice and non-choice permutations (binary 1/0), single or multiple superpositions (two digits into one) and/or multiplication (one digit in two) are possible. But, because here is the word about the binary tree (and systems corresponding to it) which, *per se*, contains within itself the complementarity of the left and right sides [(010-101 from the left branch versus 101-010 on the right branch) and (000-000 from the left branch versus 111-111 on the right branch)] in the scene is inevitable the first possible cycling too:

101-010-101 or 010-101-010 (4)

11011-00100-11011 or 00100-11011-00100 (5)

As an example of cyclicity in solution (4) on a six-bit binary tree of genetic code we find the following: UGA codon (on the right of the binary tree), which encodes one of the three stop codons, is in mirror symmetry with the GUC codon (on the left of the binary tree):

UGA / GUC, oxo vs oxo & amino vs amino (6)

101 – 010 / 010 – 101 (7)

As an example of cyclicity in solution (5) we find in Shcherbak's permutations (inner area in Figure 1):

925-592 (952) **592-925** / 529-295 (**259**) 295-529 / **925-592** (952) **592-925**.. (8)

11011 / 00100 / 11011..... (9)

2.2. Dynamic mirroring

We proceed to the analysis of Figure 2. In the first quadrant we find a "dynamic" mirror with possible positions above or below the KYTM series, i.e. before or after a series of specified "boundary" AAs: 189, 289 | 299 | 289, 189 of nucleons in the side chains of 20 amino acid molecules. A unifying of both "mirrors" (third quadrant) results in a total balance, now in a set of 24 AAs: the 2 x 777 nucleon in side chains; and the 2 x 888 nucleons in "heads" of AAs, what is a total of 3330 nucleons. [For multiples of 777 and 888 see footnote 10.]

What is surprising, however, is that the total number of nucleons also corresponds to the total mass of molecules, as 3334. According to our assumption the real molecular

mass for these 24 amino acid molecules is 3333, and the excess of one unit is actually an experimental error, so much small: $3334 - 3333 = 1$ (0.03%) that this is surprising, and in praise to the experimenters. [I did the calculations 15 years ago, with molecular weight values of AAs expressed in two decimal places. If it were recalculated to four decimals now, the accordance would be even better.]

2.3. Non-mirror complementarity

The mirror symmetry is one specific complementarity, so we can say that in the second quadrant of Figure 2 we find an example of non-mirror complementarity. Two of the four AAs are incised above, yielding 10 and 10 complementary AAs, respectively: 10 up and 10 down, with 625 and 630 nucleons, each 10 with molecular mass of 1369 ± 2 , respectively (where 1369 is the square of Shcherbak's prime quantum, number 37). And numbers 625 and 630 represent the central pair in a specific sequence of numbers (Table 1) which proves to be a determinant of not only this but two other amino acid arrangements, presented in the previous work only from the aspect of balance number of atoms (Rakočević, 2019, Fig. 1), and here with both aspects – the balance of the number of atoms and the number of nucleons simultaneously (Figure 3).

As we see two and two of AAs (KM, YT) appear in the function of doubling (third quadrant in Fig. 2) and in the function of creating "a recesses" (second quadrant in Fig. 2), both times for the sake of complementarity (with the first complementarity being mirror and the other not); and, both times for the sake of establishing and/or expressing better balancing and nuancing of physico-chemical properties.

[The notions of balancing and nuancing, related to the state of the genetic code, as well as the circumstances and conditions of the generation of the protein amino acids system (PAAS) are used in this paper in the sense of Definitions 1 and 2, given in our previous paper (Rakočević, 2018a, p. 33). There, we discussed the case of duplication of three AAs (L, S and R) in the GCT of the standard genetic code just as a way of balancing and tinting the physico-chemical properties. As a third significant example, we mention here the duplication of four AAs from three non-alanine stereochemical types: G, P, V, I. By their duplication and unity with the alanine stereochemical type of 16 AAs we have the revelation the relationships of protein AAs with their bioprecursors, and the balance of the number of atoms and nucleons in subsets of essential and non-essential AAs (Rakočević & Jokić, 1996; Rakočević, 1998b; Negadi, 2011).]

2.4. Amino acid "intruders"

T. Jukes was right in saying that arginine is an "intruder" in the set of twenty amino acids.¹¹ But that attitude applies to all three "markers", to all three "border stone" (L, S, R) in the distinctions shown. That is right, arginine is the most pronounced "horn in the bag"¹², overloaded with high diversity functional groups (three methylene, one amino and, and very complex guanidino group); but "intruders," in the context of balancing and nuancing of physicochemical properties, along with arginine are also leucine and serine; leucine, the side chain of which is an iso-butyl group, the first possible case of branching in the hydrocarbon series of alkanes. (Leucine, the only one of the 16 AAs of the alanine stereochemical type with such branching side chain.); and serine, as the first possible case in a set of 20 protein AAs with a hydroxyl functional group.

Let us see now how in this logic are the new two plus two "intruders", KM and YT (Fig. 2). We explained the extremeness of lysine (K) and threonine (T) in previous work.¹³ The extremeness of methionine, however, is that it is the only one of the 20 AAs in the side chain to have a sulfur bridge between two carbon atoms. The extremeness of tyrosine, however, is that it is the only one of the four aromatic AAs that has a functional group (OH) attached to the aromatic ring (not within the ring). And when asked why K with M and T with Y, the answer is this: Among other things, Lys is characterized by methylene groups, and Met by a methyl group. On the other hand, both AAs, Thr and Tyr have an OH group each.

As we can see, it is only with the discovery of amino acid arrangements with the duplication of two or more of AAs that the balancing and nuancing of the properties of AAs come to the full expression, what at the first glance, in a set of 20 AAs, is not easy to see. [The doubling of AAs is analogous to "doubling" into a soldier's platoon. When the platoon commander notices that his three soldiers are "intruders" because they are strikingly protruding from their heights in comparison to the others, he requests from his superiors three more of the similars, to balance the heights.]

¹¹ Jukes, 1973, p 24: "I have suggested that arginine displaced ornithine during the evolution of protein synthesis"; Jukes, 1974, p. 331: "It is speculated that arginine is an 'intruder' into the genetic code, and that it may have displaced another amino acid such as ornithine, or may even have displaced lysine from some of its previous codon assignments". [Note: From the point of view of "test tube chemistry", ornithine could replace arginine, but from a systemic chemistry point of view it would not (cf. Box 1).]

¹² "The only one exception is arginine, handled by class I, which is entered with two of its codons, into the space of amino acids handled by class II synthetases (within Codon Path Cube)" [Rakočević, 2018a, p. 45 in relation to (Rakočević, 1997a, Fig. 1)].

¹³ Rakočević, 2019, p. 19: " ... Lys as the fourth case, instead of the first as in the Ser and Cys case"; Rakočević, 2019, Box 4: "Thr is the only 'black sheep' in the set of 16 AAs of the alanine stereochemical type, given that one of its hydrogen atoms in the CH₂ group, between the head and the body, is replaced by one CH₃ group". [Note: On the four stereochemical types of AAs see in (Popov, 1989) and (Rakočević & Jokić, 1996).]

2.5. Multiple self-similarities

The connecting of different amino acid arrangements through self-similarity is accomplished in various ways. Thus, three duplicate AAs (L-57, S-31, R-100) in GCT have 188 nucleons in their side chains, while in four duplicates (K-72, Y-107, T-45, M-75) within harmonic structure (first quadrant in Figure 2) this amount 299; the difference is determined by Shcherbak's balance: $299 - 188 = 111$ ($111 = 3 \times 037$). However, this does not stop the "game" of establishing connection and interdependence, but continues.

To the number of nucleons in the side chain should be added to the number of nucleons in the "head" (amino acid functional group): $4 \times 074 = 296$ for KYTM and $3 \times 074 = 222$ for LSR. The account goes further: $[(299 + 296 = 595 \text{ and } 188 + 222 = 410; (595 - 410 = 185 \text{ and } 185 - 074 = 111)]$, where the difference (KYTM - LSR = 185) refers to the "intruders".

2.6. "The uncertainty principle"

Interestingly, the duplication of the three AAs in the GCT (L, S, R), parallel to the increase in the degree of balance in the essential chemical properties (Rakočević, 2018a, tabs 5A, 5B, 6A, 6B) also leads to imbalance in codon assignment to AAs. [In standard GC, for example, serine "breaks" the codons that encode arginine into two parts: those that come in front and those that come behind the serine codons.] In a way, the scene is analogous to the validity of Heisenberg's uncertainty principle: the duplication of extreme amino acids results in a balance in chemical properties and an imbalance in codon assignments; and vice versa: without duplication of AAs (in a hypothetical GC) there would be a balance in codon assignments and an imbalance in the chemical properties of AAs.

Imbalances in codon assignment to amino acids where the reason why F. Crick, in his first major work on the genetic code (Crick, 1968), raised the dilemma that, except that it could be that the genetic code was the result of stereochemistry, it could also be a matter of pure chance.¹⁴

2.8. Different entities – the same quantities

However, without invoking the hypothetical code, we can test this new situation (chemical properties versus codon assignments) in a real GC, in a set of 61 of AAs. In this set, all amino acids are duplicated or multiplied; all but two (M and W). In such a situation, the effect of the "intruder" cannot be tested by some additional multiplication.

¹⁴ Crick, 1968, p. 369: "This theory states that the code is universal because it is necessarily the way it is for stereochemical reasons"; p. 370: "In its extreme form, the theory implies that the allocation of codons to amino acids at this point was entirely a matter of 'chance'".

Instead, it makes sense to start (in testing) with codon assignments rather than with chemical properties. The question is: among the four columns of codons in GCT, is there any column that is balanced in codon assignments? We find that it to be the third, with the middle base "A" in codons.

Then there is the additional question: how can we know that the third balanced column affects the whole system (that it affects all four columns) in the GCT? The affirmative answer to this question is contained in Table 2, in the arrangement known as the Codon Path Cube (CPC) (Swanson, 1984; Rakočević, 1997a)¹⁵; moreover, we find that both the Codon Path Cube and the GCT must be viewed in unity, and that both systems-arrangements contain chemistry and non-chemistry unity. How else to interpret the "quantum" balance of the number of molecules and atoms in the three completely different distinctions of AAs in GCT and/or CPC, shown in Surveys 1 and 2?

3. Concluding remark

The presented facts confirm the hypothesis given in the title of the paper that genetic code is a specific image of a specific mirror image. On the other hand, these facts also confirm the hypothesis of V. Shcherbak (1994) that the genetic code contains an analogy with quantum physics. All this goes in support of our hypothesis (Rakočević, 2004) that the genetic code, from the aspect of completeness of the system of its constituents (amino acid and nucleotide constituents), was still prebiotic complete – 20 protein amino acids and four nucleotide molecules in RNA.

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¹⁵ In addition to balancing and nuancing the number of atoms in rows of Codon path cube, as shown here in Table 2, on the balance within its inner and outer space should also be recalled (Rakočević, 2018a, eq. 3 and 4, p. 45).

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FIGURES

Figure 1. Mirror relations in the number of nucleons in two classes of AAs: four-codon and non-four-codon AAs. (Data on the number of nucleons by Shcherbak, 1994, Fig. 1). Notice that on the left side is the direction of the path of non-four-codon AAs downwards, while the direction of the path of four-codon AAs, on the right side, is upwards. (Heraclitus, fragment 60: "The road up and the road down are one and the same".) For details see the text.

	n	M
D N A L →	189	485.49 ≈ 485
R F P I →	289	585.70 ≈ 586
K Y T M →	299	595.71 ≈ 596
H W S C →	289	585.64 ≈ 586
E Q G V →	189	485.50 ≈ 485
	1255	2738.04

	n	M
D N A L →	189	485.49 ≈ 485
R F P I →	289	585.70 ≈ 586
K Y T M →	299	595.71 ≈ 596
	(147+152)	(295.4+301.3)
H W S C →	289	585.64 ≈ 586
E Q G V →	189	485.50 ≈ 485
	1255	2738.04
	n = 625 + 630; M ≈ (1369 -2) + (1369 +2)	

	n ₁	n ₂	n ₃	M
D N A L →	189	296	485	485
R F P I →	289	296	585	586
K Y T M →	299	296	595	596
K Y T M →	29	296	595	596
H W S C →	289	296	585	586
E Q G V →	189	296	485	485
	1554	1776	3330	3334
	(2 x 777)	(2 x 888)	(10 x 333) (≈ 3 x 1111)	

Figure 2. Significant variations of "A harmonic structure of the genetic code". The first quadrant contains the first and last column from Table 1 in (Rakočević, 2004, p. 223): (n₁) "The number of nucleons within 20 AAs side chains, calculated from the first, the lightest nuclide (H-1, C-12, N-14, O-16, S-32); (M) The AAs molecule mass." Additional: (n₂) Nucleon number within AA "heads" (4 x 74 = 296); (n₃) The sum n₁+ n₂. Detailed explanations are given in the text.

[31 + 41 = 2 x (6x6)]					
[61 + 71 = 2 x (66)]					
⁰⁵ S ₃₁	⁰⁸ T ₄₅	¹³ L ₅₇	⁰⁴ A ₁₅	⁰¹ G ₀₁	31 ₁₄₉
⁰⁷ D ₅₉	¹⁰ E ₇₃	¹¹ M ₇₅	⁰⁵ C ₄₇	⁰⁸ P ₄₁	41 ₂₉₅
¹⁵ K ₇₂	¹⁷ R ₁₀₀	¹¹ Q ₇₂	⁰⁸ N ₅₈	¹⁰ V ₄₃	61 ₃₄₅
¹⁴ F ₉₁	¹⁵ Y ₁₀₇	¹⁸ W ₁₃₀	¹¹ H ₈₁	¹³ I ₅₇	71 ₄₆₆
(295 + 345 = 640) (149 + 466 = 615)					
	261	46	56	359	102 / 620
5	91	F	14	15	Y 107
4	57	L	13	04	A 15
3	72	Q	11	08	N 58
2	41	P	08	13	I 57
1	45	T	08	11	M 75
1	31	S	05	05	C 47
2	01	G	01	10	V 43
3	59	D	07	10	E 73
4	72	K	15	17	R 100
5	81	H	11	18	W 130
	289	47	55	346	102 / 635

Figure 3. Two illustrations, within one Figure, correspond to two illustrations in previous work (Rakočević, 2019, Fig. 1, p. 6): the lower illustration to the left there, and the upper illustration to the right. The lower illustration: Cyclic Invariant Periodic System (CIPS I) of AAs, and the upper illustration: CIPS II. Above, at the top, we find the double values of the number of atoms in the side chains of AAs [(6 x 6) and 66], both in the same amounts, respectively (with a change of ± 1) as in the arrangement of "A harmonic structure of genetic code" (Rakočević, 2004, Tab. 9, p. 229), where AAs are classified by basic chemical characteristics: carbon, nitrogen, oxygen and combined. In the illustration above, together with the sign for amino acid also the numbers of particles in the side chains are given: on the left for the number of atoms, and on the right for the number of nucleons. Within the illustration below is the vice versa order. The total number of atoms in the illustration above, in rows, is 31, 41, 61, 71; in the lower, by columns - according to the shaded and unshaded parts, which are given in the mirror symmetry: in the right column 55 and 56, and in the left 47 and 46. The number of nucleons belongs to an ordered number system, with distances of five units each, provided that CIPS I and CIPS II are viewed as a unity, a single entity, as shown in Table 1.

TABLES & SURVEYS

Table 1. The distinctions within CIPS I

<u>2</u>	<u>1</u>	<u>0</u>	<u>0</u>	<u>1</u>	<u>2</u>
615	620	625 = 25 x 25		635	640
		625 – (5) – 630			
		(2)	(2)		
		627	628		
		627 + 628 = 1255			

Legend to Table 1. Three nucleon number pairs. The Table corresponds to the relationships of nucleon number in AAs (within their side chains), in the two arrangements presented in Figure 3. The distance in the determined series of numbers is 5 units, and the distance of the two middle pairs 625-630) and (627-628) is 2 units. This new pair of numbers (2-5), or (010-101), is the same one that allows the emergence of a unique code that is a mirror image (Rakočević, 2019, Fig. 2 in relation to Table 3).

Table 2. Distinctions in CPC					Survey 1. Relations in Tab. 2																									
<table><tr><td>N</td><td>D</td><td>H</td><td>Y</td></tr><tr><td>II</td><td>II</td><td>II</td><td>I</td></tr><tr><td>N</td><td>D</td><td>H</td><td>Y</td></tr><tr><td>K</td><td>E</td><td>Q</td><td>□</td></tr><tr><td>II</td><td>I</td><td>I</td><td></td></tr><tr><td>K</td><td>E</td><td>Q</td><td>□</td></tr></table>				N	D	H	Y	II	II	II	I	N	D	H	Y	K	E	Q	□	II	I	I		K	E	Q	□	41	77 77	<div><div>(7) NDHY KEQ (77) (8) SGRC SGRC (56) (8) TAPS TAPS (50) (8) TAPS TAPS (50) (8) IVLF MVLL (97)</div><div><div>39</div><div>330</div></div></div>
N	D	H	Y																											
II	II	II	I																											
N	D	H	Y																											
K	E	Q	□																											
II	I	I																												
K	E	Q	□																											
				41																										
				36																										
				36																										
<table><tr><td>S</td><td>G</td><td>R</td><td>C</td></tr><tr><td>II</td><td>II</td><td>I</td><td>I</td></tr><tr><td>S</td><td>G</td><td>R</td><td>C</td></tr><tr><td>R</td><td>G</td><td>R</td><td>□</td></tr><tr><td>I</td><td>II</td><td>I</td><td>I</td></tr><tr><td>R</td><td>G</td><td>R</td><td>W</td></tr></table>				S	G	R	C	II	II	I	I	S	G	R	C	R	G	R	□	I	II	I	I	R	G	R	W	28	56 88	<div><div>22</div><div>330-66</div></div> <div>3 x 7 = 21 molecules 77+77+88 = 242</div> <div>5 x 8 = 40 molecules 330 – 77 = 253 253 + 99 = 352 253 / 352 (mirroring)</div>
S	G	R	C																											
II	II	I	I																											
S	G	R	C																											
R	G	R	□																											
I	II	I	I																											
R	G	R	W																											
				28																										
				35																										
				53																										
<table><tr><td>T</td><td>A</td><td>P</td><td>S</td></tr><tr><td>II</td><td>II</td><td>II</td><td>II</td></tr><tr><td>T</td><td>A</td><td>P</td><td>S</td></tr><tr><td>T</td><td>A</td><td>P</td><td>S</td></tr><tr><td>II</td><td>II</td><td>II</td><td>II</td></tr><tr><td>T</td><td>A</td><td>P</td><td>S</td></tr></table>				T	A	P	S	II	II	II	II	T	A	P	S	T	A	P	S	II	II	II	II	T	A	P	S	25	50 50	<div>NDHY KEQ: Amino acids (AAs) in third column of standard GCT.</div>
T	A	P	S																											
II	II	II	II																											
T	A	P	S																											
T	A	P	S																											
II	II	II	II																											
T	A	P	S																											
				25																										
				25																										
				25																										
<table><tr><td>I</td><td>V</td><td>L</td><td>F</td></tr><tr><td>I</td><td>I</td><td>I</td><td>II</td></tr><tr><td>I</td><td>V</td><td>L</td><td>F</td></tr><tr><td>I</td><td>I</td><td>V</td><td>L</td></tr><tr><td>I</td><td>I</td><td>I</td><td>I</td></tr><tr><td>M</td><td>I</td><td>V</td><td>L</td></tr></table>				I	V	L	F	I	I	I	II	I	V	L	F	I	I	V	L	I	I	I	I	M	I	V	L	50	99 97	<div>SGRC: AAs from second and fourth column of GCT.</div> <div>TAPS: AAs in second column of GCT.</div> <div>IVLF: AAs from the first column of GCT.</div> <div>RGW: AAs from the fourth column of GCT.</div>
I	V	L	F																											
I	I	I	II																											
I	V	L	F																											
I	I	V	L																											
I	I	I	I																											
M	I	V	L																											
				50																										
				49																										
				47																										

Legend to Table 2: On the left, in the space bounded by bold lines, a two-dimensional model of Codon Path Cube (CPC) (Rakočević, 1997a), based on a three-dimensional model (Swanson, 1984, Fig. 2) is given. Out of the CPC, in two columns, are the results of summing the number of atoms within side chains of AAs, in rows. Shaded part on the top: AAs encoded by codons with middle base "A". Roman numeral I: amino acids handled by class I of synthetases; and numeral II: amino acids handled by class II of synthetases.

Legend to Survey 1: Current insights into the relationships of the number of atoms in amino acid molecules (in their side chains), in the Codon Path Cube (CPC). The amino acids in the second column of the GCT of standard genetic code appear to be the key for significant distinctions within the CPC. Two sets of AAs are indicated with the number of molecules and atoms, respectively. In the first two areas, the atom number 330 and (330-66) corresponds with the atom number in GCT through the distinction into Py-Pu coding codons (Rakočević, 2004, Tab. 3a, p. 224). In the middle area, the account is made for the separate segments and rows; ultimately for $3 \times 7 = 21$ amino acid molecules (242) and for $5 \times 8 = 40$ molecules (352).

Survey 2. Distinctions within significant arrangements

22 (n) + 39 (p) molecules: $2\bar{2}2 + 3\bar{7}2 = 594$ atoms ($420 + 723 = 1143$)
21 (o) + 40 (i) molecules: $2\bar{3}2 + 3\bar{6}2 = 594$ atoms ($4\bar{2}1 + 7\bar{2}2 = 1143$)
21 (bl) + 40 (nb) molecules: $2\bar{4}2 + 3\bar{5}2 = 594$ atoms ($4\bar{3}1 + 7\bar{1}2 = 1143$)
(Note: $1443 - 1143 = \mathbf{300}$) (Cf. $3330 - 330 = \mathbf{3000}$ in Box 3)
$[22 \pm 0 \text{ (bl)}] + [39 \pm 0 \text{ (nb)}] \text{ mol.} = (330 - 66) + 330 = 594 \text{ atoms}$
$[22 + 10 \text{ (Py-Py \& Pu-Pu)}] \text{ molecules} = 330 \text{ atoms}$
$[39 - 10 \text{ (Py-Pu \& Pu-Py)}] \text{ molecules} = 330 - 66 \text{ atoms}$
(Rakočević, 2004, Tab. 3a, p. 224)

Legend to Survey 2: The upper area, the first two rows: Relationships in GCT expressed through the number of atoms in AAs; on the left: in side chains and on the right: in whole molecules (Rakočević, 2018a, eq. 5-7. p. 45; and Rakočević, 2011b, Eq. 11-14 in relations to Figure A.3, p. 840): n - nonpolar; p - polar; o - outer; i - inner. [Note 1: The polarity of the molecules is expressed by the hydropathy index (Kyte and Doolittle, 1982); Note 2: The number 1443 represents number of nucleons within side chains of 23 AAs (Shcherbak, 1994, Fig. 1, p. 475) whereas the number 1143 represents number of atoms within whole molecules of AAs, in the set of 61 amino acid molecules.] The upper area, the third row: Relationships in CPC (Tab. 2) expressed through the number of atoms in AAs: bl - balanced level [$(3 \times 7 = 21)$ molecules with $77 + 77 + 88 = 242$ atoms]; nb - nonbalanced level [$(5 \times 8 = 40)$ molecules with 352 atoms]. The lower area, the first row: designations as in the third row of the upper area, and the account taken from the first two areas of Survey 1. The lower area, the second and third rows as in (Rakočević, 2004, Tab. 3a, p. 224).