Genetic code as an image of the mirror image. Supplement 2

Miloje M. Rakočević

University of Niš, Faculty of Sciences and Mathematics, Department of Chemistry,
Višegradska 33, 18000 Niš, Serbia

Abstract

In this (second) Supplement are given the further new insights on mirror symmetry within Genetic Code (GC). The main result is the correspondence of the binary tree of GC and the Standard GC Table in such a way that it follows that it makes no sense to talk about the evolution of GC from the aspect of test tube chemistry (of performing chemical reactions in nature and/or laboratory), but only makes sense to talk about prebiotic chemical evolution of GC in a manner analogous to the evolution of the chemical code i.e. Periodic system of chemical elements. Taken together, an even more important conclusion is that all the physical and chemical laws we know represent immediate causality, while in the case of GC on the scene is an indirect causality, realized through multiple mirror symmetry.

Keywords: Protein amino acids, Genetic code, Binary tree, Golden mean, Periodic system, Mirror image. Mirroring.

In Supplement 1 of this paper, we outlined the arrangement of amino acid pairs, in the order from the last to the first amino acid (AA) in the GC binary tree (Suppl. 1, Fig. 3 in relation to Fig. 1)¹. In doing so, the first member of the pair was selected with strict adherence to two Mendeleevian principles - the principle of minimum change and the principle of continuity. [The only exception is the choice of asparagine rather than lysine because asparagine is a pair-member of aspartic acid, despite aspartic acid being previously paired with glutamic acid.]

In the meantime, we have presented the distinction of amino acid molecules by the formula: $[(6+3)+(3+4)+4]^2$ (Rakočević, 2020a), where subset {6+3} represents native AAs, subset {3+4} no-native AAs; both subsets within the set of {16} AAs of the alanine stereochemical type. The last number in summation is a set of {4} AAs of non-alanine stereochemical types.³ Now it makes sense to combine the two distinctions (the order of

¹ Figure 3 in Suppl. 1, here is Figure 1. Table 1 and Table 2 here contain the distribution of AAs in Table of standard GC. Table 3 shows, among other things, the pairs of AAs by chemical similarity. In relation to the pairing in Figure 1, here is the original chemical pairing: S-T and K-R but in Figure 1 the pairing is S-R and T-K. And, there is another pairing: here, in Table 3, the pairs are G-G (because glycine is the only one AA in the glycine stereochemical type; P-P (because proline is the only one in the proline type), V-I (because they are the only two AAs in the valine stereochemical type). In Figure 1, the pairs are G-V and P-I, as in CIPS 2 (Rakočević, 2019a; Fig. 1, p. 6).

² It should be noted that number 4 is a neighbor, i.e. a follower of number 3 in the series of natural numbers (which is a condition for the validity of two Mendelian principles). We will hereafter refer to this formula as the Kinship Formula. Our prediction is that the Kinship Formula is a unique situation in a specific arithmetic system, which we will address in the next paper (Rakočević, 2020b).

³ On the four stereochemical types of AAs see in (Popov, 1989; Rakočević and Jokić, 1996).

the amino acid pairs on the binary tree and the *in-out* arrangement in Table of GC), and look at how they correspond to each other. This relationship is shown to be reality, so here we present it in Figure 1 in relation to Tables 1 and 2.

Figure 1 is the same as that presented in Suppl. 1 as Fig. 3, with new distinctions given here; there were differences in relation to the golden mean of the binary tree of GC, and here are the distinctions to the chemical affinity of amino acids as constituents of GC (Rakočević, 2020a). In two columns, there are 60 ± 1 atoms in the amino acid molecules (in their side chains) at odd positions of the total number of atoms of distinct amino acid classes (designated by different colors), respectively. [(14+27+18 = 59); (18+18+25= 61).] In even positions: 47 and 37, respectively. [(17+30 = 47); (18+19 = 37).]⁴ (Box 1)

Box 1. Explanation of Figure 1

This Figure corresponds to Figure 3 in Suppl. 1. All pairs of AAs within alanine stereochemical type correspond to pairs in the arrangement given in Table 3, except in two cases. The positions of AAs on the binary tree are such that the restructuring of S-T and K-R pairs into S-R and T-K is inevitable. The generation of two pairs within non-alanine stereochemical types is explained in footnote 1.

And the total generation of the pairs is as follows: Going from right to the left, from end towards the beginning of the binary tree of GC (Fig. 1 in Suppl. 1) we first encounter glycine (G), and then look for its pair-member, amino acid valine (V); then, in the same way we find R-S and then D-E; we skip K, and take derivatives of pair D-E, which is pair N-Q. Only then do we return to skipped lysine (K) and, going forward, look for its new pair-member, threonine (T). After selecting lysine (K), the first following AA is tryptophan (W). We take it and go looking for its pair-member histidine (H). Then comes cysteine (C), whose pair-member methionine (M) is located far from there. The following is tyrosine (Y) whose pair-member phenylalanine (F), exists at the very beginning of the binary tree.

The next unselected AA is alanine (A), which we take as the next, along with its pair-member leucine (L). Finally, there is isoleucine (I), in the immediate vicinity of which is its pair-member, proline (P).

Six native aliphatic AAs are marked in red; orange: three native aromatic; follow 3+4 non-native AAs (blue plus green, respectively). Altogether: 16 AAs of alanine stereochemical type, in color; plus 4 AAs of non-alanine stereochemical type, without color.

Notice also direct and cross balances within columns: (51+55 = 107-1); (41+57 = 97+1); (51+57 = 107+1); (41+55 = 97-1). These relations correspond to the arithmetic system presented in: (Rakočević, 2019a, Tab. A2, p. 29);

⁴ That the principles of nuancing and balancing are valid here is more than obvious (footnote 2 in Suppl. 1).

The arithmetic form of the results that came from the linear order of AAs on a binary tree is analogous to the result obtained in chemically relevant distinctions of amino acid molecules in the Standard GC Table, realized not in linear but in *inner-outer* arrangement (Tables 1 and 2 in relation to Survey 1).

In Survey 1 it is shown that the positions of AAs on the binary tree of GC and in the Standard GC Table are interconnected by multiple mirror symmetries, which symmetries are expressed over the notations of the number of atoms in the side chains of amino acid molecules.

From the presented results it follows that there is no point in talking about the evolution of GC from the aspect of *test tube chemistry* (of performing chemical reactions in nature and / or in the laboratory), but only makes sense to talk about system chemistry, that means to talk about prebiotic chemical evolution of GC in a manner analogous to the evolution of the chemical code i.e. Periodic system of chemical elements.⁵ Taken together, an even more important conclusion is that all the physical and chemical laws we know represent immediate causality, while in the case of GC on the scene is an indirect causality, realized through multiple mirror symmetry.⁶

Everything presented goes in support of the conclusion of the original paper of which this is the Supplement. First, in support of the working hypothesis contained in the title of the article, and also in support of the hypothesis of the analogy of GC with quantum physics, and the hypothesis that GC was still prebiotic complete.

⁵ See the original paper of this Supplement for the *test tube chemistry* and *system chemistry* (Rakočević, 2019b, Box 1).

⁶ When it comes to mirror symmetry within the binary number system, which we have dealt with in the three works mentioned in 2019, then we have presented not only direct mirroring according to the notations [(010/010) (101/101)], but also indirect, by the opposite of the digits, analogous to Dirac's mirror symmetry positron / electron, in the following sense: [(010/101) (101/010)] (Rakočević, 2019b, footnote 9).

51		41	
G	01	10	V
R	17	05	S
E	10	07	D
N	08	11	Q
K	15	08	T
W	18	11	H
C	05	11	M
Y	15	14	F
A	04	13	L
I	13	08	P
55		57	

14		18
17		18
27		18
30		19
18		25
60 - 01		60 + 01
47		37

Figure 1. The Pairs of AAs taken from the binary tree of GC, going from right to left, i.e. from end to beginning. In selecting the first member, in the mating process, two Mendeleevian principles, the minimum change principle and the continuity principle, are respected. The second member of the pair automatically joins (from close proximity or, for a leap, from distance), wherever it is on a binary tree. The same rule applies to the classes of AAs in this Figure. For example, the number of atoms in the amino acids (in their side chains) located in the first red region are automatically joined, in the summation process, by the number of atoms from all the following red areas, as shown on the right side of the Figure. [We used the same procedure to read and take 7 "golden" AAs and their 7 complements, as well as 6 non-complements, on the binary tree of GC (Rakočević, 1998, 2011). A, also the same procedure for reading 20 AAs in the Standard GC Table, when equilibrium determination of AA classes was shown in even seven parameters (Rakočević, 2004, Tables 7 and 8, p. 228.)]

Table 1. Amino acid positions in standard GC (I)

F ₁₄ L ₁₃	S ₀₅	Y ₁₅	C ₀₅ W ₁₈
L ₁₃	P ₀₈	H ₁₁ Q ₁₁	R ₁₇
I ₁₃ M ₁₁	T ₀₈	N ₀₈ K ₁₅	S ₀₅ R ₁₇
V ₁₀	A ₀₄	D ₀₇ E ₁₀	G ₀₁
61 / 61 [59, 61] 61 - 59 = 02 61 - 61 = 00 122 - 120 = 02			

All AAs in outer (red) area are nonpolar measured by cloister energy; in inner (blue) area polar are all, except one: histidine is ambivalent in cloister energy, but polar in hydropathy. In amino acids (within their side chains) at outer/inner areas there are 61/61 atoms, respectively. Polar/nonpolar squares: 4 ± 0 . (The polarity/nonpolarity data in Table 3.) [The Table represents the reduced form of Table 3 in (Rakočević, 2017).]

Table 2. Amino acid positions in standard GC (II)

F ₁₄ L ₁₃	S ₀₅	Y ₁₅	C ₀₅ W ₁₈
L ₁₃	P ₀₈	H ₁₁ Q ₁₁	R ₁₇
I ₁₃ M ₁₁	T ₀₈	N ₀₈ K ₁₅	S ₀₅ R ₁₇
V ₁₀	A ₀₄	D ₀₇ E ₁₀	G ₀₁
59 / 58 [59, 61] 59 - 47 = 12 / 21 58 - 37 = 21 / 12		59 - 37 = 22 58 - 47 = 11	

All AAs in right (pink) area plus dark-green are polar, measured by cloister energy and hydropathy. On the left in light-green area are nonpolar. Polar/nonpolar squares: 4 ± 1 . In amino acids (within their side chains), in right/left areas there are 59/58 atoms, respectively. [The Table represents the reduced form of Table 4 in (Rakočević, 2017).]

Table 3. Pairing process between 16 AAs of alanine stereochemical type and two times 4 AAs of non-alanine stereochemical types

CE	HP	I	II	HP	CE
-0.16	-0.4	G 01	01 G	-0.4	-0.16
-0.09	+1.8	A 04	13 L	+3.8	-0.54
-0.52	+4.2	V 10	13 I	+4.5	-0.56
		III	IV		
+0.24	-0.8	S 05	08 T	-0.7	+0.27
-0.73	+2.5	C 05	11 M	+1.9	-0.57
-0.52	+4.2	V 10	13 I	+4.5	-0.56
		V	VI		
+0.69	-3.5	D 07	10 E	-3.5	+0.71
+0.52	-3.5	N 08	11 Q	-3.5	+0.91
+1.46	-3.9	K 15	17 R	-4.5	+0.87
		VII	VIII		
+0.46	-1.6	P 08	08 P	-1.6	+0.46
± 0.00	-3.2	H 11	18 W	-0.9	-0.25
-0.56	+2.8	F 14	15 Y	-1.3	+0.42

After (Rakočević and Jokić, 1996, p. 346): On the full line, as well as on the dotted line, there are 118 atoms; HP: hydropathy index on a number unnamed scale (Kyte and Doolittle, 1982); CE: cloister energy in kcal/mol (Swanson, 1984).

Survey 1. Arithmetic relations of positions of AAs
on the binary tree and in the Standard GC Table

Above left are the sums of the number of atoms (59, 61; 47, 37) in AAs on the binary tree of GC, calculated according to Figure 1; on the right (61, 61; 59, 58) according to Tables 1 and 2, respectively. Mirror symmetries ("hidden") appear through the addition and/or subtraction operations as visible patterns.

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