ON THE COMPLETENESS OF GENETIC CODE: PART V

Miloje M. Rakočević

Department of Chemistry, Faculty of Science, University of Nish, Serbia
(E-mail: milemirkov@open.telekom.rs; www.rakocevcode.rs)

Abstract. In this fifth part of the work on the completeness of the genetic code, we present further connections and relations between nucleotide doublets and triplets within Genetic Code Table; in all cases through balances of atom number, nucleon number and isotope number.

Starting from Tables 1, 2 and 3 in the previous part of this work (Part IV), in this fifth part, except of correspondence between nucleotide Doublets Table (DT) and nucleotide Triplets Table (TT), we show that the pyrimidine / purine distinctions are followed by the balances of the number of particles – atoms and nucleons, as well as the number of isotopes (nuclides).

1st	2nd letter				3rd
	U	C	A	G	
U	U**U**U / U**U**C / U**U**A / U**U**G **F** / **L**	U**C**U / U**C**C / U**C**A / U**C**G **S**	UA**U** / UA**C** / UA**A** / UA**G** **Y** / CT	U**G**U / U**G**C / U**G**A / U**G**G **C** / CT / **W**	U C A G
C	**C**UU / **C**UC / **C**UA / **C**UG **L**	**C**CU / **C**CC / **C**CA / **C**CG **P**	**C**AU / **C**AC / **C**AA / **C**AG **H** / **Q**	C**G**U / C**G**C / C**G**A / C**G**G **R**	U C A G
A	AU**U** / AU**C** / AUA / AU**G** **I** / **M**	**A**CU / **A**CC / **A**CA / **A**CG **T**	**A**AU / **A**AC / **A**AA / **A**AG **N** / **K**	AG**U** / AG**C** / AG**A** / AG**G** **S** / **R**	U C A G
G	G**U**U / G**U**C / G**U**A / G**U**G **V**	**G**CU / **G**CC / **G**CA / **G**CG **A**	GA**U** / GA**C** / GA**A** / GA**G** **D** / **E**	G**G**U / G**G**C / G**G**A / G**G**G **G**	U C A G
The Pairs: going from pyrimidine to purine coding AAs I. (F-W, L-C, V-G) / II. (P-T, H-K, Q-N) III. (L-A, Y-ct, S-T) / IV. (S-R, I-M, D-E)					

Table 1.1. Distributions of AAs in GCT, in correspondence with pyrimidine / purine distinctions within nucleotide doublets and triplets (I)

1st	2nd letter				3rd
	U	C	A	G	
U	UUU UU**C** **F** U**U**A U**U**G **L**	U**C**U U**C**C U**C**A S U**C**G	UA**U** UA**C** **Y** UA**A** UA**G** CT	U**G**U U**G**C **C** U**G**A CT U**G**G **W**	U C A G
C	**C**UU **C**UC **C**UA L **C**UG	**C**CU **C**CC **C**CA P **C**CG	**C**AU **C**AC **H** **C**AA **C**AG **Q**	**C**GU **C**GC **C**GA R **C**GG	U C A G
A	AU**U** AU**C** I AUA AUG M	**A**CU **A**CC **A**CA T **A**CG	**A**AU **A**AC **N** **A**AA **A**AG **K**	AG**U** AG**C** **S** AG**A** AG**G** **R**	U C A G
G	GU**U** GU**C** **V** GU**A** GU**G**	**G**CU **G**CC **G**CA A **G**CG	GA**U** GA**C** D GA**A** GA**G** E	GGU GGC GGA **G** GGG	U C A G

The Pairs: going from pyrimidine to purine coding AAs
I. (F-W, L-C, V-G) / II. (P-T, H-K, Q-N)
III. (**L-A, Y-ct, S-T**)[1] / IV. (S-R, I-M, D-E)

Table 1.2. Distributions of AAs in GCT, in correspondence with pyrimidine / purine distinctions within nucleotide doublets and triplets (II)

In Table 1.1, in the squares with the dark tones are nucleotide doublets UU, GG, GU and UG, all four in *first* positions within four quadruplets of modified Rumer's Table (as it is shown in Table 2 of Part II of this work). On the other hand, in the squares with light tones are nucleotide doublets CC, AA, AC and CA, all four in *second* positions within four quadruplets of modified Rumer's Table.

In Table 1.2, in the squares with the dark tones are nucleotide doublets CU, AG, GC and UA, all four in *third* positions within four quadruplets of modified Rumer's Table (as it is shown in Table 2 of Part II of this work). On the other hand, in the squares with light tones are nucleotide doublets UC, GA, AU and CG, all four in *fourth* positions within four quadruplets of modified Rumer's Table.

As a very interesting fact, there is a distinction in Table 2.1, in relation to Table 2 in Part IV. As we had complete balance of the number of atoms (in two different classifications) in Table 2

---

[1] The pair S-R shows that the third position within the codon is also an encoding function, not just the first and the second. This fact also supports the hypothesis that the genetic code still in prebiotic conditions was complete.

of Part IV, we got it here also in Table 2.1; there were 160/79 both times, and here it is 125/114 also both times, in both classifications (on the left / on the right).

1	2	3	4	6		Pyrimidine			Purine
M_{11}	F_{14}	I_{13}	V_{10}	L_{13}		F_{14}			W_{18}
W_{18}	Y_{15}		P_{08}	L_{13}		L_{13}	37	24	C_{05}
	H_{11}		T_{08}	S_{05}		V_{10}			G_{01}
	Q_{11}		A_{04}	S_{05}					
	N_{08}		G_{01}	R_{17}		P_{08}			T_{08}
	K_{15}			R_{17}		H_{11}	30	31	K_{15}
	D_{07}					Q_{11}			N_{08}
	E_{10}								
	C_{05}					L_{13}			A_{04}
						Y_{15}	33	21	ct
						S_{05}			R_{17}
						I_{13}			M_{11}
						S_{05}	25	38	R_{17}
						D_{07}			E_{10}
29	96	13	31	70					
	125		114				125	114	
	125 - 114	= 11			Cross		126	113	
	50 + 29	= 79			← Black		50	85	(125+10)
	75 + 85	= 160			← Red		75	29	(114-10)

Table 2.1. Distributions of AAs after the number of coding codons (on the left) and after the splitting into four times of four nucleotide doublets (on the right) (cf. Table 1.1 and Table 1.2).

The pairing process in Table 2.1 is directed from pyrimidine to purine as it is a reality in GCT (cf. Table 1.1 and 1.2). By this, one must notice that the pairs in red color have a vice versa status in relation to the pairs within Table 2 in Part IV; also in relation to the pairs in Tables 2.2, 2.3 and 2.4 in this part of the work. The point is that there are two possibilities; first, the classification by the size of the molecule, and the second one, by direction: the first member of the pair is encoded by a pyrimidine, and the second by a purine nucleotide, as it is shown in Tables 1.1 and 1.2.

1	2	3	4		Small		Large	
M_{75}	F_{91}	I_{57}	L_{57}		F_{91}			W_{130}
W_{130}	L_{57}		V_{43}		C_{47}	139	230	L_{57}
	S_{31}		S_{31}		G_{01}			V_{43}
	Y_{107}		P_{41}					
	H_{81}		T_{45}		P_{41}			T_{45}
	Q_{73}		A_{15}		H_{81}	180	189	K_{72}
	N_{58}		G_{01}		N_{58}			Q_{73}
	K_{72}		R_{100}					
	D_{59}				A_{15}			L_{57}
	E_{73}				ct	46	264	Y_{107}
	R_{100}				S_{31}			R_{100}
	C_{47}							
					M_{75}			I_{57}
					S_{31}	165	230	R_{100}
					D_{59}			E_{73}
205	848	57	333					
1053		**39**0			**0**530		9**1**3	
1443					1443			
1110			333	→	1443 (Shcherbak, 1994)			
$(1443 : 37 = 39)^2$; (6+28+496 = 530) (first three perfect numbers)								
[1443 x 6 = 8658 = 6+28+496 + 8128 (first four perfect numbers)]								

Table 2.2. Distributions of AAs; on the left: after the number of coding codons; on the right: after the splitting into four times of four nucleotide doublets (Table 1.1 and Table 1.2) and in relation to number of nucleons within amino acid side chains.[Nucleon number in first nuclide, as in Shcherbak, 1994.]

In Table 2.2 it is shown that the above said distinctions of AAs are followed by balances of the number of nucleons in the side chains of amino acids. Immediately it is obvious an analogy with the filling of orbitals in an atom: 1053 vs 0530 and 390 vs 913. By this, the patterns 530 and

---

[2] The number 37 as „Prime Quantum 037" in determination of nucleon number within four-codon and non-four-codon amino acids (Shcherbak, 1994).

1443 correspond with perfect numbers, as determinants of genetic code (Rakočević, 1997, p. 60 and www.rakocevcode.rs).

1	2	3	4		Small			Large
M231	F196	I127	L127		F196			W278
W278	L127		V96		C169	368	501	L127
	S85		S85		G03			V96
	Y247		P90					
	H173		T116		P90			T116
	Q173		A34		H173	405	448	K159
	N142		G03		N142			Q173
	K159		R217					
	D161				A34			L127
	E192				ct	119	591	Y247
	R217				S85			R217
	C169							
					M231			I127
					S85	477	536	R217
					D161			E192

509	2041	127	768			
(2550)[3]		**895**			(1369)[4]	(2076)
3445					3445	
(3456 – 3445 = 11) (3456 + 3456 as atom nuber in 64 codons)[5]						
(1655)					(707)	
(1255)[6]					1655 – 707 = 12 x 79	

Table 2.3. Everything is the same as in the previous table (Table 2.2), except that here is the total number of nucleons within AA side chains, in all nuclides (as in Table 7, in Rakočević, 2004, p. 228). [Example of calculation for serine: (3 x H) + (1 x C) + (1 x O) = (3 x 1) + (3 x 2) + (1 x 12) + (1 x 13) + (1 x 16) + (1 x 17) + (1 x 18) = 85.]

---

[3] The result corresponds with the number of nucleons within 20 canonical AAs (2550 vs 1255).

[4] A very significant number because it is a square of Prime Quantum 037 (37 x 37 = 1369).

[5] In the GCT, within two inner as well as two outer columns there are 3456 of atoms (see: Negadi, 2014).

[6] The number of nucleons within 20 canonical AAs.

Analogue with Table 2.2 is Table 2.3, all is the same, except that in Table 2.3 in the question is total number of nucleons, calculated in the manner shown in the legend of Table 2.3.

1	2	3	4		Small			Large
M_{24}	F_{28}	I_{26}	L_{26}		F_{28}			W_{36}
W_{36}	L_{26}		V_{20}		C_{12}	42	82	L_{26}
	S_{11}		S_{11}		G_{02}			V_{20}
	Y_{31}		P_{16}					
	H_{22}		T_{17}		P_{16}			T_{17}
	Q_{23}		A_{08}		H_{22}	55	70	K_{30}
	N_{17}		G_{02}		N_{17}			Q_{23}
	K_{30}		R_{34}					
	D_{16}				A_{08}			L_{26}
	E_{22}				ct	19	91	Y_{31}
	R_{34}				S_{11}			R_{34}
	C_{12}							
					M_{24}			I_{26}
					S_{11}	51	82	R_{34}
					D_{16}			E_{22}
60	272	26	134					
332		160			167		325	
492					492			
332 - 160 = 2 x 86					325 - 167 = 2 x 79			

Table 2.4. Distributions of AAs as in previous tables, but here in relation to isotope number. The patterns (2 x 86) and (2 x 79) as in Tab. 3.1: atom number versus isotope number, what means the self-similarity through the same quantities of AAs.

In Table 2.4 all is the same as in the preceding two tables, except that here in the question is the number of isotopes. For example, for glycine it has been indicated that in the side chain it has two isotopes, because its side chain consists only of one hydrogen atom, having two natural isotopes: protium and deuterium.

Tables 3.1 and 3.2 follow from Table 3 in Part IV, in the manner that is explained in their legends.

3,4	small		1,2	large
I_{13}	F_{14}		M_{11}	W_{11}
L_{13}	C_{05}		W_{11}	L_{11}
V_{10}	G_{01}		F_{11}	V_{11}
S_{05}			L_{11}	
P_{08}	P_{08}		S_{11}	T_{11}
T_{08}	H_{11}		Y_{11}	K_{11}
A_{04}	N_{08}		H_{11}	Q_{11}
G_{01}			Q_{11}	
R_{17}	A_{11}		N_{11}	L_{11}
	ct		K_{11}	Y_{11}
	S_{11}		D_{11}	R_{11}
			E_{11}	
	M_{11}		R_{11}	I_{11}
	S_{11}		C_{11}	R_{11}
	D_{11}			E_{11}
61	61		**86**	**86**
18	18		74	74
79	**79**		160	160

Table 3.1. The Table is the same as Table 3 in Part IV, except the color and underlining. The underlined patterns (2 x 86) and (2 x 79) appear to be determinants of the number of isotopes, as it is shown in Table 2.4. The comparison of left and right side of Table 2.4 (analogously as in Table 3 of Part IV): on the left are the amino acids encoded by 3 or 4 codons and smaller AAs within amino acid pairs, presented on the right side of Table 2.4. On the other hand, on the right side are AAs encoded by 1 or 2 codons and larger AAs within the said amino acid pairs. [Cf. the quantities 61-61 with the quantities 71-71 in Table 3.2.]

1,2	Py		3,4,6	Pu
M	F_{14}		I_{13}	W_{18}
W	L_{13}		V_{10}	C_{05}
F	V_{10}		P_{08}	G_{01}
Y			T_{08}	
H	P_{08}		A_{04}	T_{08}
Q	H_{11}		G_{01}	K_{15}
N	Q_{11}		L_{13}	N_{08}
K			L_{13}	
D	L_{13}		S_{05}	A_{04}
E	Y_{15}		S_{05}	ct
C	S_{05}		R_{17}	R_{17}
			R_{17}	
	I_{13}			M_{11}
	S_{05}			R_{17}
	D_{07}			E_{10}
82	82		71	71
43	43		43	43
125	125		114	114
	(82-71 = 11)	(43-43 = 00)		

Table 3.2. The comparison of left and right side of Table 2.1. On the left are the amino acids encoded by 1 or 2 codons and smaller AAs within amino acid pairs, presented on the right side of Table 2.1. On the other hand, on the right side are AAs encoded by 3 or 4, or 6 codons and larger AAs within the said amino acid pairs. [Cf. the quantities 71-71 with the quantities 61-61 in Table 3.1.]

* * *

All presented facts are such that ones reaffirm the other and vice versa. All together, they favor the recognition that the chemical reactions that determine the GC are not only the reactions in a "test tube", but these reactions are associated with a specific balance of the number of particles (atoms, nucleons and isotopes). Presented facts also support the hypothesis that the genetic code was a complete code from very begining, in prebiotic times and conditions.[7] On the other hand, the knowledge that "the chemistry of living" is actually a harmonized chemistry requires great care in medicine, agriculture and natural environment; all that because genetic code must be reflected in the proteins and cells.

REFERENCES

Dragovich, B. (2011) p-Adic structure of the genetic code, *NeuroQuantology*, 9 (4), 716–727; arXiv:1202.2353v1 [q-bio.OT].

Negadi, T. (2014) The genetic code invariance: when Euler and Fibonacci meet, *Symmetry: Culture and Science*, Vol.25, No.3, 145-288, 2014; arXiv:1406.6092v1 [q-bio.OT].

Rakočević, M. M. (1997) *Genetic code as a unique system*, SKC, Niš and Bina, Beograd, Serbia; www.rakocevcode.rs

Rakočević, M. M. (2004) A harmonic structure of the genetic code, *J. Theor. Biol*. 229, 463-465.

Rakočević, M. M. (2015) On the Completeness of Genetic Code: Part II, viXra:1501.0117.

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.

Weaver, R.F. (2008) *Molecular Biology*, fifth edition, Mc Graw – Hill, New York.

---

[7] The so-called "deviant codes" (Weaver, 2008) represent only a "degree of freedom" in deviation from the standard genetic code. In doing so, it remains only dilemma is whether, perhaps, the standard was preceded mitochondrial code, as more symmetrical (Dragovich, 2011), and then the standard, just because of its small asymmetry, took an evolutionary "course". [Weaver, 2008, pp. 568-569: "These deviant codes are still closely related to the standard one from which they probably evolved".]