ON THE COMPLETENESS OF GENETIC CODE: PART IV

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 fourth part of the work about the completeness of the genetic code, we present further connections and relations between nucleotide doublets and triplets within Genetic Code Table.

In Table 1 are designated nucleotide doublets from modified Rumer's Table (Part II): with brown color four 1st, blue color with four 2nd, dark tones with four 3rd and light tones with four 4th doublets. These four areas correspond with four classes of AAs, presented through chemically meaningful pairs (right side of Table 2).

1st	2nd letter				3rd
	U	C	A	G	
U	UUU **F** UUC UUA **L** UUG	UCU UCC UCA UCG **S**	UAU **Y** UAC UAA CT UAG	UGU UGC **C** UGA CT UGG **W**	*U* *C* *A* *G*
C	CUU CUC CUA **L** CUG	CCU CCC CCA **P** CCG	CAU **H** CAC CAA CAG **Q**	CGU CGC CGA **R** CGG	*U* *C* *A* *G*
A	AUU AUC **I** AUA **M** AUG	ACU ACC ACA **T** ACG	AAU AAC **N** AAA AAG **K**	AGU AGC **S** AGA AGG **R**	*U* *C* *A* *G*
G	GUU GUC GUA **V** GUG	GCU GCC GCA **A** GCG	GAU **D** GAC GAA **E** GAG	GGU GGC GGA **G** GGG	*U* *C* *A* *G*

Table 1. Distributions of AAs within four times four codon quadruplets of GCT in connection with nucleotide doublets, presented in Table 2 in Part II (Rakočevič, 2015).

At left side of Table 2 has presented the splitting into four classes of AAs: one-codon, two-codon, three-codon and four-codon amino acids (AAs), respectively; at right side, as in Table 1.

As it is self-evident from Table 2 two splittings are followed by a specific balance (near to be 2:1) in both cases: [2 x (80±0)] : [1 x (80-1)].

1	2	3	4		Small		Large	
M W	F L S Y H Q N K D E R C	I	L V S P T A G R		F C G	20	41	W L V
					P H N	27	34	T K Q
					A ct S	09	45	L Y R
					M S D	23	40	I R E
29	131	13	66					
160		**79**			**79**		**160**	

Table 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) and in relation to number of atoms within amino acid side chains.

In addition there are other partial balances, such as these: (20+41+27+34 = 122 and (09+45+23+40 = 117) versus (20+27+45+40 = 122+10 and (41+34+09+23 = 117-10). Also the balances and relationships, presented in Table 3 and in Surveys 1, 2 and 3.

3,4	small		1,2	large
I	F		M	**W**
L	C		**W**	**L**
V	**G**		F	V
S			**L**	
P	**P**		S	T
T	H		Y	**K**
A	N		H	**Q**
G			**Q**	
R	**A**		N	L
	ct		**K**	Y
	S		D	**R**
			E	
	M		**R**	I
	S		C	R
	D			E
61	61		86	86
18	18		74	74
79	79		160	160

Table 3. The comparison of left and right side of Table 2. Here are on the left the amino acids (AAs) encoded by 3 or 4 codons and smaller AAs within amino acid pairs, presented on the right side of Table 2. On the other hand, here, on the right are AAs encoded by 1 or 2 codons and larger AAs within the said amino acid pairs.

ILVTR (61) = FCHNMSD (61)	
I**LVT**R (61) + **FCHN**MSD (61) = 122 **LVT** (31) + **FCHN** (38) = 69 IR (30) + MSD (23) = 53	**FC**G W**LV** P**HN** **T**KQ (122) **FCLVHNT** (69) + GWPKQ (53) = 122

Survey 1. The results of comparison of the first and the second column on the left side of Table 3.

MFSYHNDEC (86) = VTLYIRE (86)	
MFS**<u>Y</u>**HND**<u>E</u>**C (86) + VTL**<u>Y</u>**IR**<u>E</u>** (86) = 122 + 50 **<u>YE</u>** (25) + **<u>YE</u>** (25) = 50 MFSHNDC (61) + VTLIR (61) = 122	ILVTR (61) = FCHNMSD (61) [Survey 1, first row] VTLIR (61) = MFSHNDC (61) [Survey 2, last row]

Survey 2. The results of comparison of the first and the second column on the right side of Table 3.

61 + 86 = 147 18 + 74 = 92	**147** **92**	137 102	127 112	**117** **122**	107 132	97 142	87 152

Survey 3. The "intermediated" results of final atom number sums, given in Table 3 (first and second column); within the fifth column is the real result from right side of Table 2 (up/down summarizing); all other results appear to be our prediction – in future one will find such splitting in GCT.

* * *

All presented balances and relationships go in favor of our hypothesis that the genetic code still in prebiotic conditions was complete.

REFERENCE

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