ON THE COMPLETENESS OF GENETIC CODE: PART VI

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Abstract. In this sixth part of the work on the completeness of the genetic code, we present further relationships within Rumer Table and modified Rumer Table of nucleotide doublets within genetic code.

In Table 1 are given nucleotide doublets within modified Rumer's Table; all is the same as in a previous Table (Table II/2)[1], except it is indicated here the splitting into odd and even rows of the Table. With that indication it becomes immediately obvious that the quantities of atom number correspond to the quantities obtained in splitting presented in Part V. In fact, there (Table V/2.1) were obtained results (125/114) and (135/104), and here the preceding result (115/124), which is once more confirmation of analogy of filling of atomic orbitals. In addition, the indicated balances (the changes in the number of atoms for 00, 01 and 10) establish modification of Rumer's Table, because such balances cannot be obtained in original Rumer's Table (cf. Table II/1 with Table II/2).

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. St.**	
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**	

Table 1. The modified Rumer's Table: the balances of the number of atoms in amino acids (their side chains), corresponding with two octets of nucleotide doublets.

[1] With Roman numerals we denote the part of the work; hence, the Roman numeral II here refers to Part II.

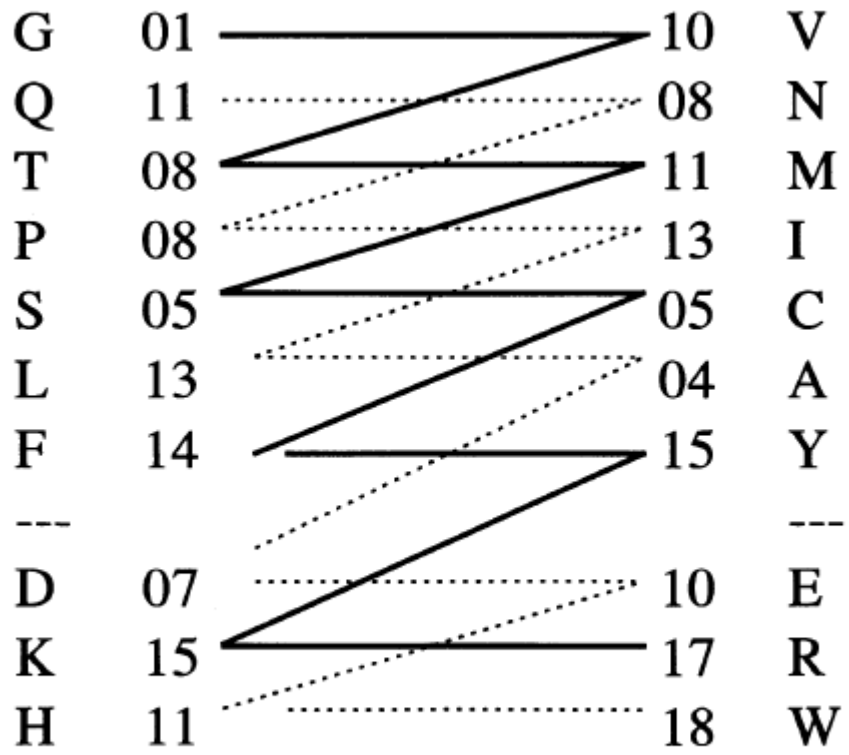
It is interesting that the three sums of the number of atoms in three columns of AAs in Table 1 (66, 78 and 60 + 35) are in correspondence with the three sums that get in the determination of the binary tree of GC with golden mean (cf. Figure 1 in Rakočević, 1998 and Table 3 in this Part of the work). And this is an example more of the similarity and self-similarity of quantities in genetic code.

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 Stop
(35)	(40)	(43)	(36)	(38)
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
(40)	(37)	(30)	(39)	(45)
125	**36** 106	**120**	**84** 118	114
330-66		**330±00**		

Table 2. The Rumer's Table of nucleotide doublets: the key quantities in the set of 23 AAs (black) and in the set of 61 AAs (blue color). Cf. the results 330-66 and 330±00 with the same results in Figure I/1 and Table I/1.1.

The comparing Table 1 and Table 2 shows that the modification of Rumer Table does not apply to splitting into top and bottom part of the Table. Table 2 is the original Rumer's Table, with the quantities which are identical in the modified table.

Amino acid quantities, as number of all atoms in the amino acid side chains, in Table 2, are calculated as follows. Upper left column: Gly 01 + Pro 08 + Arg 17 + Ala 04 = **30**; upper middle and right column: [(Phe 14 + Asn 08 + Ile 13 + Tyr 15) = 49 + 01] + [(Leu 13 + Lys 15 + Met 11) = 49 – 10)] = **89** (30 + 89 = 119); Lower left column: Thr 08 + Val 10 + Ser 05 + Leu 13 = **36**; lower middle and right column: [(His 11 + Cys 05 + Asp 07 + Ser 05) = 28 x 1] + [(Gln 11 + Trp 18 + Glu 10 + Arg 17) = 28 x 2)] = **84** (36 + 84 = 120).[2]



Scheme 2. **Survey 2.1.** *Atom number balance directed by Golden mean route on the binary-code tree (I).*

Table 3. Atom number balance directed by Golden mean on the binary code tree (after: Rakočević, 1998, p. 289). Notice that on the two zigzag lines there are 102±1atoms.

[2] Notice the difference 120 – 119 = 01

Analogously are calculated the quantities as the number of all atoms in the nucleotide doublets (116/108 versus 106/118).[3]. Finally, it remains to show the balance of atomic quantities of the AAs along two diagonals: 30 + 84 = **114** versus 89 + 36 = **125**. It is expected that the reader will see that the pattern 114/125 appears also in Table V/2.1, although in a completely different arrangement of AAs.

Amino acid quantities, as number of hydrogen atoms in amino acid whole molecules, in Table 2, are calculated as follows. Upper left column: Gly 05 + Pro 09 + Arg 14 + Ala 07 = 35 **(**the number in parentheses); upper middle column: Phe 11 + Asn 08 + Ile 13 + Tyr 11) = 43 **(**the number in parentheses); upper right column Leu 13 + Lys 14 + Met 11 = 38 **(**the number in parentheses) [35 + 43 + 38 = **116**]; Lower left column: Thr 09 + Val 11 + Ser 07 + Leu 13 = 40; lower middle column: His 09 + Cys 07 + Asp 07 + Ser 07) = 30; lower right column: Gln 10 + Trp 12 + Glu 09 + Arg 14 = 45 (40 + 30 + 45 = **115**).[4]

Analogously are calculated the quantities as the number of all hydrogen atoms in the nucleotide doublets. (Above: 40 +36 = 76; down: 37 + 39 = 76).[5]

In Table 3 the first seven amino acids, on the left, are 'golden' amino acids, while on the right are their complements; below are three amino acid pairs as non-complements. Within seven 'golden' amino acids (side chains) there are 60 atoms; within their seven pairing complements there are [60 + (1x 6)] atoms, and within six non-complements there are [60+(1x6)] + (2 x 6) of atoms. [Notice that the differences are 1x6, 2x6 and 3x6.]

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The above presented examples of balances, correspondences, interrelationships, similarity and self-similarity, with everything stated in the previous parts of this work, also make a contribution to understanding the completeness of the genetic code.

REFERENCES

Rakočević, M. M. (1997) Two classes of the aminoacyl-tRNA synthetases in correspondence with the codon path cube, *Bulletin of Mathematical Biology*, 59, 645-648.

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

[3] Atom number in four bases is: U = 12, C= 13, A = 15, G = 16 (cf. Table 2 in Rakočević, 1997, p. 647).

[4] Notice the difference 116 – 115 = 01

[5] Hydrogen atom number in four bases is: U = 4, C= 5, A = 5, G = 5. Notice the difference 76 – 76 = 00.