ENIGMAS OF THE GENETIC CODE, ENIGMA 2: A SECOND HIDDEN ARITHMETICAL ALGORITHM (Version 1)

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Abstract

This second enigma is standing in relation to enigma 1 in our previous communication. It is relating to total number of atoms (204) in side chains of 20 protein amino acids, within standard genetic code.

INTRODUCTORY NOTES

1. From the aspect of symmetry, the relation between the numbers 2 and 5 appears to be special (Table 1). Namely, in the binary numbering system, the pair 2-5 is the first possible pair with both symmetry – direct (vertical) and indirect (horizontal):

010

$$0 1 0 / 1 0 1$$
 (1)

101

2. It is known that the balances of atom number and/or nucleon number in amino acid molecules (within genetic code) are determined by the differences for 00, 01, 10 and/or 11, writing in decimal numbering system [see about that in our works; for example, References in Note 1 (version 2) in our site (www.rakocevcode.rs)].

3. The question is whether the standpoints of point 1 and point 2 may be related? The answer to this question incorporates arithmetic system presented in Table 2.

THE PROBLEM

Find such an arrangement of amino acids (5 x 4) that the number of atoms (in the side amino acid chains), in five rows (Table 3), corresponds to 10^{th} event within the system in Table 2. (Hint: In a series of even natural numbers just 10^{th} case is the number 20.)

COMMENT

The solutions of this enigma give the satisfaction to our hypothesis that the genetic code was complete from the very beginning and that it represents a unique (full and whole) system in which the position of each amino acid is strictly determined, and that with several different aspects (Rakočević, 2004).

(1) (2)	0 1	1 0				
(2) (5)	0 1	1 0	0 1			
(5) (10)	0 1	1 0	0 1	1 0		
(10) (21)	0 1	1 0	0 1	1 0	0 1	
(21) (42)	0 1	1 0	0 1	1 0	0 1 1 0	

Table 1. The pairs of numbers (from the sequence of natural numbers) that have mutual symmetry [*see* binary number presentation (1)].

00	02	04	06	08	10	12
11	13	15	17	19	21	23
22	24	26	28	30	32	34
11	16	21	26	31	36	41
00	05	10	15	20	25	30
44	60	76	92	108	124	140
	12	14	16	18	20	22
	23	25	27	29	31	33
	34	36	38	40	42	44
	41	46	51	56	61	66
	30	35	40	45	50	55
	140	156	172	188	<u>204</u>	<u>220</u>
	22	24	26	28	30\	/32
	33	35	37	39	41	43
	44	46	48	50	52 \	54
	66	71	76	81	86 /	91
	55	60	65	70	75/	80
	220	236	252	268	<u>284</u>	\ <u>300</u>
	32	34	36	38	40	42
	43	45	47	49	51	53
	54	56	58	60	62	64
	91	96	101	106	111	116
	80	85	90	95	100	105
	300	316	332	348	364	380

Table 2. A specific arithmetical system. Start with 00-11-22-11-00, and then adding the number 2 in the first three cases, and number 5 in the last two cases. As a result we have 10^{th} event, correspondent with number of atoms within 4 x 5 amino acids as it is shown in Table 3. (Notice, that the pair 220-284 is the first pair of friendly numbers; cf. Figures A.1 and A.2 in Appendix A.)

20 $a_1 \ a_2 \ a_3 \ a_4$ \rightarrow b_1 b_2 b_3 b_4 \rightarrow 31 $c_1 c_2 c_3 c_4$ 42 \rightarrow $d_1 d_2 d_3$ d_4 61 50 e1 **e**₂ **e**₃ e₄ \rightarrow 51-1 51+1 51-1 51+1

Table 3. The number of atoms within side chains of five rows of amino acids $(a_1-a_4, b_1-b_4, ..., e_1-e_4)$ corresponds to the five results in 10^{th} case of an arithmetical system presented in Table 2.

REFERENCES

- Rakočević, M. M. (1998) The genetic code as a Golden mean determined system, Biosystems 46, 283-291.
- Rakočević, M. M. (2004) A harmonic structure of the genetic code, J. Theor. Biol. 229, 221–234.

APPENDIX A

The six-bit binary code tree of the genetic code (Rakočević, 1998) in Figure A.1 and its determination with third perfect number (496) as well as first pair of friendly numbers (220, 284) in Figure A.2.

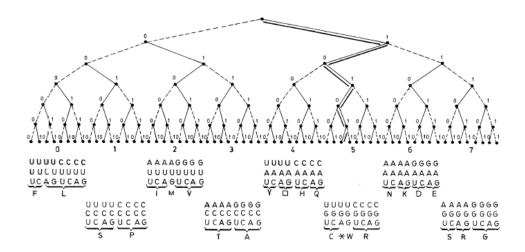


Figure A.1. The six-bit binary code tree of the genetic code (Rakočević, 1998)

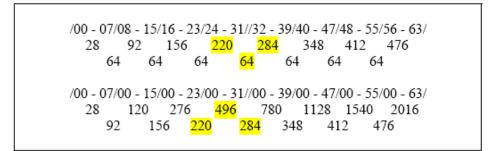


Figure A.2. The determination of six-bit binary code tree (Figure A.1) with third perfect number (496) and with first pair of friendly numbers (220, 284).