GENETIC CODE AS A BOOLEAN SPACE

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(plus two additional illustrations)

Remark 2.2. The binary symmetry $A \leftrightarrow A'$ (or $A \leftrightarrow B$) in this paper is still understood, except by S. Marcus, in the sense used by P. Hilton and J. Pederson (1989, pp 73-74) so that the given entity from the pair *A*, *A'* (or *A*, *B*) "may admit several different combinatorial structures and each structure will be regarded as combinatorially distinct. You should thus be warned that [*entities*] which we regard as *the same* (i.e. combinatiorially equivalent), you may hitherto have regarded as *different* (see Fig.1(a)); and [*entities*] which we regard as different (i.e.combinatorially distinct), you may hitherto have regarded as the same (see Fig.1(b))." For a better understanding of this we present a possible correspondence between their Fig.1 and our Fig.1. The entity on the left side of their Fig.1(a) - "the cube" - correponds to the pyrimidine entity (in 32 combinations, or to be more correct, variations) on the left branch of the binary tree in our Fig.1; their right side entity ("the prism") corresponds to our purine entity on the right side (also in 32 variations). The entity on the left side of any one of the 4+4 "rossete" (or classes) codons on the binary tree in our Fig.1 corresponds to their left entity in their Figure 1(b); a simpler cube model corresponds to our simpler pyrimidine (U) and/or purine (A) entity; their right entity - a more complex cube model - corresponds to our more complex pyrimidine (C) and/or purine (G) entity on the right side (cf analogous "cubes" and "prismes" in Fig. 3.5 in Dubinin, 1985, p 81).

Remark 2.3. Since the genetic code can be reduced to the Gray code model (Fig.1 in Swanson, 1984,p 188) and to a binary tree (Fig.1 in this paper), with a starting codon UUU 000000 and a final codon GGG 111111, it follows that as to questions of symmetry in relation to the genetic code *the mathematical group theory* holds only partially (our hypothesis and a prediction of this - *Prediction* 1 - remains for further, that is, future research). This results from the fact that set Q of rational numbers, including zero, does not form *a group* with respect to a multiplication operation. The above mentioned is the reason why we won't use the mathematical group theory to research the symmetries of the genetic code in this paper.

3. GENETIC CODE AS A BOOLEAN SPACE

A more detailed analysis of (experimental) facts shows that the nature of the genetic code is such that the two contradictory views stated in the 8-th question in the *Introduction* hold true simultaneously: for the characteristics of the genetic code, which, being as they are, are "the result of the mathematical structure", in other words, they are not that, they didn't originate "from any mathematical formula" but are the result of the "biochemical properties of nucleotides". The genetic code, in fact, represents a unity of both one and the other: the relations of the characteristics of the genetic code are such that they correspond to an ideal (one or more) mathematical model; "correspond" in the sense that they are correspondent of and in accordance with the model. (With this a hypothetical answer has been given to question 8 in the *Introduction*, with proof being that of the arguments which, given through all the seven

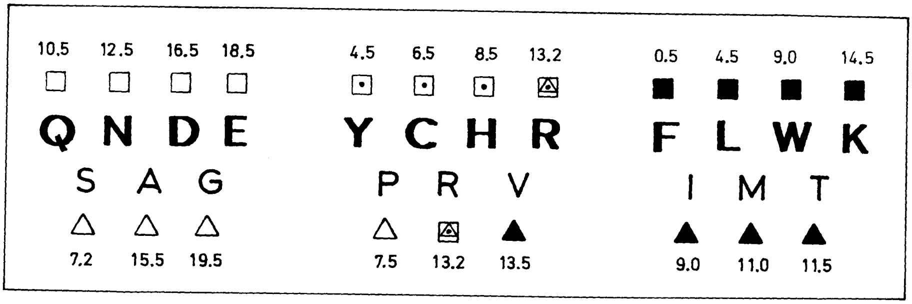

Figure 5(II) *Here are given amino acids from Space-3 and Space-4 as in previous Figure but here are taken the collective binary values (cf Rakočeviæ, 1980, p 10). In case of nonexistence of such values, the categorization (3 x 3) would not make any sense for Space-3, but only the categorization (2 x 4). Note that the sequences (Q, N, D, E) and (S, A, G, P) are the same as in Mutation ring.*

With this we have total and definitive proof for the existence of the *Input* (Essential amino acids) - *Output* (Essential, semiessential and non-essential amino acids) relation presented in the second working hypothesis (Chapter 2). Of course, here it is understood that, for organisms which first came into being, all the amino acids had to be essential (in other words, non-essential, depending on the view; they were non-essential in the sense that the organisms themselves were able to synthesize all of them).

It is important to notice that with the systemization of amino acids, as given in Figure 5, the problem of amino acid classification is solved, and from the aspect of essentiality, that has been achieved according to the model 10 : 10 or the model 8 : 4 : 8 (4 semiessential amino acids). The surprisingly large number of different views about this problem, which we have mentioned in a previous study (Rakoèeviæ, 1994, pp 84-85) now acquires a simple solution: amino acids must first of all separate into those of Space-3 and Space-4; only then can their essentiality be analyzed.

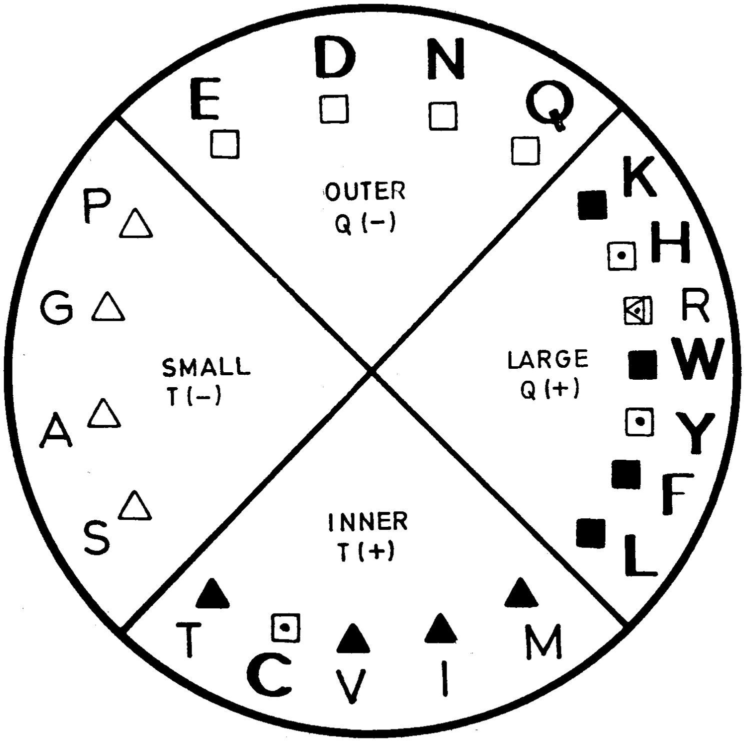

Figure 6 *Mutation ring II. This Ring could be regarded the Mutation ring II provided that R. Swanson's Mutation Ring (Swanson, 1984, Fig. 2) is regarded the Mutation Ring I; Everything is the same as on Mutation Ring I, only the S.T.-Q.K. line is shifted by one step on both ends in relation to Mutation Ring I; and P.E.-M.L. line is shifted only on one (the other) end. The squares designate the amino acids from Space-4 and triangles designate the amino acids from Space-3. The empty squares and empty triangles designate the nonessential amino acids, otherwise they designate the essential amino acids; the dots designate the semi-essential amino acids. The lines strictly separate non-essential from yes-essential amino acids; then the lines strictly separate the Space-3 amino acids from Space-4 amino acids. There are the two exceptions: C is full-strayed; R is semi-strayed. One should note that the complementarity principle is applied as follows: outer-inner: non-essential amino acids from Space-4 are complementary with the essential amino acids from Space-3, etc.*

Surprises, however, do not stop here. We can see in Figure 6 how the arranged system of essential amino acids, determined by Space-3 and Space-4, brings order to the relations among the amino acids within the mutation ring. The essentiality of amino acids and the relation between Space-3 and Space-4, in fact, reveals that the Mutation ring (Fig. 3 in Swanson, 1984, p 191 - Mutation ring I) must exist in yet another form, as

Table A. Isotope number: "bottom" Space–3 and "top" Space–4

Q_{23} N_{17} D_{16} E_{22} **Y_{31} C_{12} H_{22} R_{34}** **F_{28} L_{26} W_{36} K_{30}**
S_{11} A_{08} G_{02} P_{16} R_{34} V_{20} I_{26} M_{24} T_{17}

78 / 21 **99** / 70 **120** / 67

297 / 158 → 455 [455 = 421 + R 34]

Table B. Designations: "outer" atom number and "inner" isotope number

11	08	07	10		15	05	11	17		14	13	18	15
+1	+1	+2	+2		+1	+2	±0	±0		±0	±0	±0	±0
23	17	16	22		31	12	22	34		28	26	36	30
Q	**N**	**D**	**E**		**Y**	**C**	**H**	**R**		**F**	**L**	**W**	**K**
S	A	G			P	R	V			I	M	T	
11	08	02			16	34	20			26	24	17	
$\boxed{+1}$	±0	±0			±0	±0	±0			±0	$\boxed{+2}$	$\boxed{+1}$	
05	04	01			08	17	10			13	11	08	
a	(up 56 / 88); (dn 18 / 59) → [56 + 59 = (87 + 11)+R 17] [88 + 18 = (117 - 11]												
i	(up 121 / 176); dn 37 / 121) → [121 + 121 = (210 – 2) + R 34] [176 + 37 = 211+2]												
a	(up 56 / 88); (dn $\boxed{24}$ / 53) → [56 + 53 = 110 - 01] [88 + $\boxed{24}$ = 111 + 01]												
i	(up 121 / 176); dn $\boxed{52}$ / 106) → [121 + 106 = 22$\underline{7}$] [176 + $\boxed{52}$ = 22$\underline{8}$] → **455**												