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LOGIC CORE OF GENETIC CODE

A b s t r a c t

Transformation of nucleotides dual numeric form is proposed as a model of genetic code. Extraction of digrams (covering first and second nucleotide in codon) leads to a matrix of translation, where 20 amino acids are enframed by 16 RNA-digrams.

INTRODUCTION

By *genetic code* (GC) one understands, basically, „*translation*" – meaning transformation of the three „transcripts" of DNA genic memory (iRNA, tRNA and rRNA) into amino acids (AA).

Logic dealt with in this paper is a specific type of quaternary numeric logic, presented as *Dual Logic* (DL)[1], developed by us as sensory software – particularly for perception of color mixtures.

Analogy among GC and sensory DL appears fascinantingly close. Essential difference between GC and *sensory code* (SC) lies in direction: while SC presents *ENcoding* of (specific modal) *space*, GC means *DEcoding* nucleic *memory* of pre-biotic or phylogenetically selected amino acids and their trains.

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[1] Not published, in preparation.

In the following text, numerical description of codon space, based upon order of iRNA *di-grams* (DG) and Ordinal Numbers (ON) of AA, is presented.

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In Figure 1, according to transformations $T_{I, II}$ and T_{III}, numerical values of DGs consisting of first (I) and second (II) nucleotide in codon (CD) are given. The role of the third nucleotide (III) has been sketched, leaving *codon space* for further examination, emphasis laid on smooth line of natural numbers, from 0 to 16, given in quaternary system, with a meaningful „hole" at 8. (*Nota bene*: Codons are written from right, but read from left!)

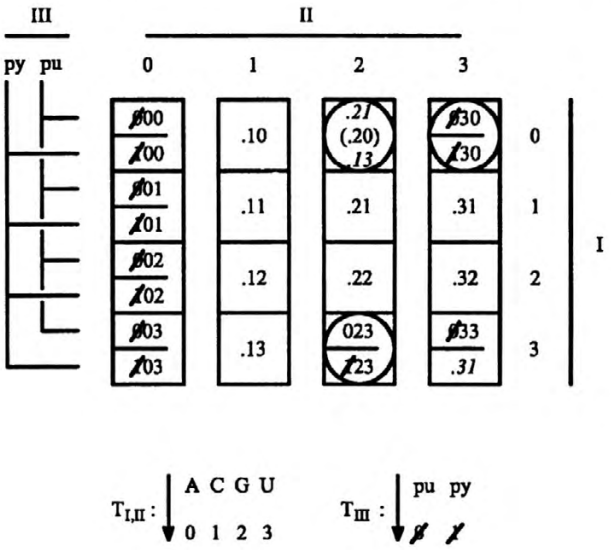


Fig. 1 (Explanation in text)

In our code, functions of three different RNAs (i-, t-, r-) correspond neatly to ordinal numbers of „target" AAs, at DG level of iRNA. Such correspondence is depicted in Figure 2.

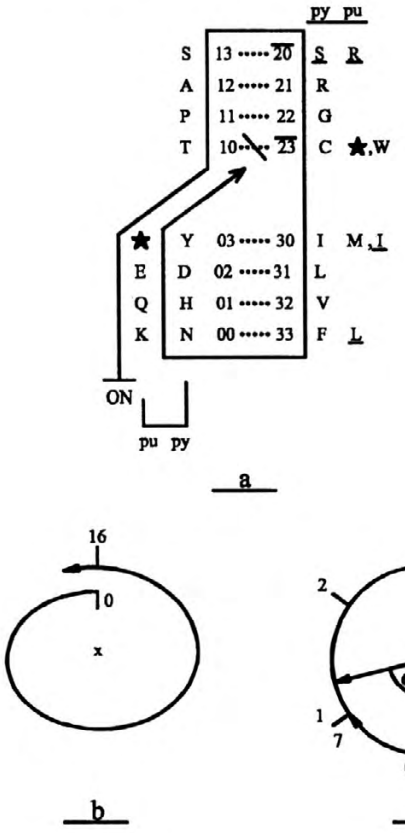
By Figure 2/a, the cycle of DGs is presented, and the spiral of CDs demonstrated to the number 19, with the „inverse" appearance of number 20.

The DGs, as well as CDs, have been arranged in complementary pairs, connected by dots.

Figure 2/b suggests *cylindrical spiral* form of codon functions, whereby DG-sequence, on the perpendicular cross-section of the cylinder, appears cyclic.

The cyclic DG-projection of codon space resembles suggestively color projection of visual space. Basic relation of both, as well as other sensory and biophysical phenomena, is presented in Figure 2/c. There, numbers: 6, 7 and 0, „octaves" and „dodecaves", colorist palettes,... perhaps many other percepts and memory functions of three independent variables, seem to be coded hierarchically: „II" selects a full-angle sector, and „I" it's spin. So, DG of iRNA codons, as well as „constant" colors of visual space, appear as single whole numbers – symbols of angle a, or placed along the *perimeter as geometric place*. So, ordinal number is a single-meaning dimension of codon space.

Codons, in interaction with ribosome, as an interface to tRNA, fixing the rotation of CD-space cylinder, also determine the polar coordinates of polypeptides. The 3-dimensional *stereochemical space*, determining position of acting AA, is so reduced to two dimensions.



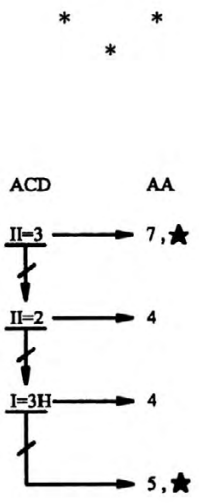


Fig. 2 (Explanation in text)

Fig. 3 (Explanation in text)

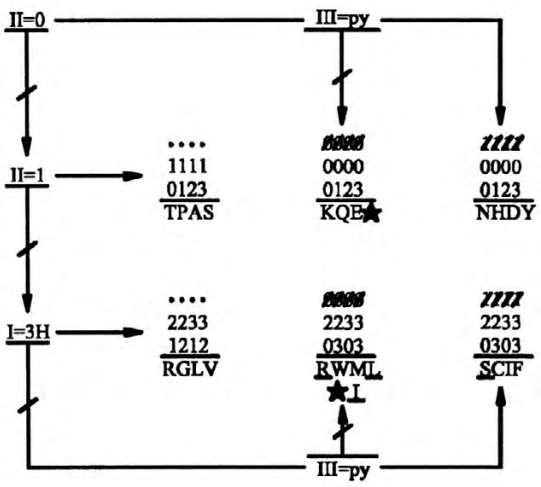


Fig. 4 (Explanation in text)

Nucleotides serve as hardware carriers of phylogenetic memory data. Concerning organic evolution, crucial question is: *on account of which property have nucleotides been selected for genetic memory*? Different physicochemical and stereochemical parameters have been tried to this end. Though, in our opinion, complemental pair digram/antidigram (DG – ADG) should be taken as a frame; within it, the three nucleotides (I, II, III) may have four properties: purinity (pu), pyrimidinity (py), 3H-bondage (3H), 2H-bondage (2H). Considering dominating properties, one finds basic branching at II position in CD: pu, 2H or py, 3H (A or C); in I position, 3H or 2H matters; in position III, relevant are *py* or *pu*.

Translation „seen from anticodon (ACD)" gives rise to amino acids as shown in Figure 3. Measured by ACD (tRNA), there should be 20 AAs and 2 stop-codons, as there are.

Figure 4 represents an alternative to binary *Tree* of codons, resp. AAs. It is an *algorithm of dual branching*, whereby different criteria decide at II, I, and III positions in codon.

Dr Miloje Rakočević has painstakingly „read" our model and established its correspondence with physicochemical parameters of amino acids – which I am grateful for. It is encouraging biophysicist (i. e. non-chemist) to realize such correspondence, which means legitimity of black-box analysis of input-output relations from tables of classic (hardware) measurements.