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REVIEW ARTICLE

THREE-DIMENSIONAL MODEL OF THE GENETIC CODE

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Abstract

The classical table of the genetic code does not reflect all the relations among the codons. This paper demonstrates that the three-dimensional topological model — cube enveloping a sphere — is the source of all the relations within the genetic code: eight cognate codons, disposed at the corners, make up the main cube; then, according to the superposition principle, these eight cubes make up a bigger (common) cube containing all the 64 codons. The topological relation between the cube and the sphere inscribed in the cube is expressed by Euler's theorem of homeomorphic translation. Using this three-dimensional model, a new table and a new matrix of the genetic code can be worked out, representing the relations among encoding words (codons), in the actual DNA and RNA molecules far more precisely than the classical ones.

Introduction

In spite of its adequate name from the very beginning of investigations in molecular biology, the genetic code has not been sufficiently and comprehensively explored as a code, i.e. as a mathematical essence of the relations. This task, however, has been present since 1963, when all the 64 codons were practically known. The fact that the genetic code is in full accordance with the mathematical model for generating three-letter words out of a four-letter alphabet (third class variations with repetition, out of a four-element set 4^3), led to further necessary and evident deductions. So, after 1966, when the genetic code table was finally established, it was necessary to search for a solution of the obvious problem of two sites in the table being „occupied” by serine and two by arginine. The main purpose of both the previous (Rakočević, 1988a; 1988b) and this work was actually that necessary deduction, based on appropriate theoretical and experimental data.

The whole project has proved to make sense, since it has led to a significant result, which may be summarized as follows:

The genetic code, as a unity of a nucleotide and an amino acid component (the encoding words and encoded elements from the first and the second alphabet, respectively) is in full accordance with the three-dimensional topological model of a cube with an inscribed sphere, their mutual relation being described by Euler's theorem of homeomorphic translation. The degree of difference between codons (which occupy the cube corners on the topological model) corresponds precisely to mutual distances between the corners: 1 step (or 1 bit in the binary record) if the codons are at opposite ends of the edges; 2 steps, if they are at opposite ends of face diagonals, and 3 steps if they are at opposite ends of the cube diagonals. In the matrix of distances between the codons (Table 1), which is derived directly from this three-dimensional model, zeros are consistently situated on the diagonal (one does not differ from itself), while unities follow as the next number sequence along the diagonal. They testify to the optimum quality of the genetic code revealed in the regular one-unit distance between adjacent codons, according to similarity-dissimilarity criterium.

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