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Mini Review

Hidden Nucleic Acid Bond Order?

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Abstract

The author examines a polytopic of hereditary information presented earlier by the author. It is shown that in the space of the polytope of hereditary information of dimension 13, only five coordinate planes are possible in which each of the flat pairs of nitrogenous bases can be located. This leads to a coordination of the number of nucleotides and the number of amino acids without the need for a genetic code.

Keywords: Hereditary Information; Nucleic Acids; Polytopes; Sugar Molecules; Genetic Code

Introduction

In [1], it was established that a polytope of hereditary information exists between two nucleic acids in each region of their bond with nitrogen bases. The dimension of this polytope is 13, its type is a cross-polytope. This polytope has 12 flat coordinate planes, i.e. exactly as many different pairs of connected nitrogenous bases [2] exist:

$$A:U,U:A,G:C,C:G,G:U,G:A,U:U,U:C,A\cdot A,A\cdot C,U:G,A:G. \quad (1)$$

(the number of points between the bases indicates the number of bonds between the bases).

The polytope of hereditary information is the result of combining two sugar molecules located in two nucleic acids in the antiparallel position. In this work, examining the geometry of the polytopic of hereditary information, it was found that out of 12 coordinate planes of 13 - cross - polytope pairs of flat nitrogenous bases can be located in only five coordinate planes.

Investigation of the possible location of canonical pairs of nitrogenous bases in the polytope of hereditary information

A simplified image of two sugar molecules with antiparallel ribs is shown in figure 1 [1,3].

A complete image of the polytopic of hereditary information can be found [1,4]. The blue color in figure 1 indicates 12 coordinate planes passing through the vertices of the polytope, including through the vertices between which flat nitrogenous bases could be located in the coordinate planes. From figure 1 it follows, however, that not all 12 coordinate planes can have flat nitrogenous bases. They could be located only between the vertices of the polytope belonging to different sugar molecules closest to each other,

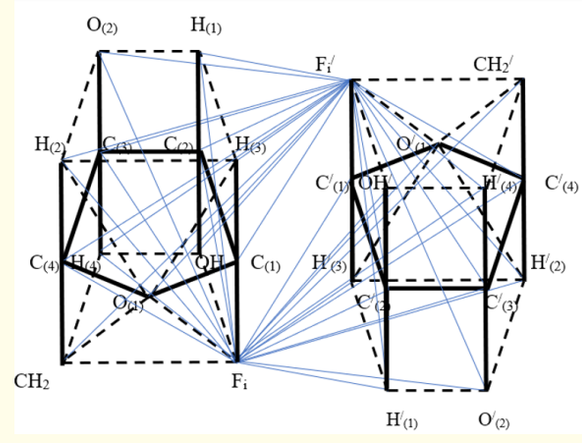

Figure 1: The two sugar molecules in a simplified form with anti-parallel edges.

i.e. between the planes OH - $H_{(3)}$ - $H_{(1)}$ - F_i and OH' - $H_{(3)}{}'$ - $H_{(1)}{}'$ - F_i'. Between the distant peaks located on the opposite planes of sugar molecules, the location of flat nitrogenous bases is difficult, due to the obstacles encountered in the form of sugar molecule atoms and covalent chemical bonds. Therefore, out of the 12 possible coordinate planes, only five coordinate planes designated by the vertices of the polytope:

$$\begin{matrix} F_i'H_{(1)} & , & F_i'C_{(2)} & , F_i'H_{(3)} & , & F_i'C_{(1)} & , F_i'OH \\ H_{(1)}'F_i & & C_{(2)}'F_i & H_{(3)}'F_i & & C_{(1)}'F_i & (OH)'F_i \end{matrix} . \quad (2)$$

If among 12 pairs (1) canonical [5,6] (Watson-Crick) base pairs for linked DNA molecules are distinguished, then there are only 4 of these pairs

$$A:U, G:C, C:G, U:A. \quad (3)$$

If RNA molecules are linked, then in (3), base U must be replaced with base T.

Considering that there are 4 canonical base pairs, and there are 5 planes in which each pair can be located, the total number of base pairs location options is 20, i.e. exactly as many different amino acids exist. Thus, each variant of the arrangement of base pairs corresponds to a certain amino acid connected in the ribosome to transport RNA. As is known [2], the attachment of an amino acid to transport RNA carries out a specific enzyme that recognizes the amino acid and its corresponding transport RNA when they are combined. In this case, transport RNA is associated with messenger RNA, and between these RNAs at the junction point there again exists a polytopic of hereditary information. Thus, information on the state of messenger RNA is transmitted by transport RNA, on which the given amino acid joins. As we see in this process, there is no need to use the concept of a genetic code to describe it. The latter was introduced as an attempt to explain the difference in the number of canonical base pairs from the number of amino acids. However, this concept together with the concept of the codon does not explain anything. Taking into account the dimension of the polytope of genetic information allows us to determine the internal (hidden) order in the location of the bases. The situation is similar to the situation with the discovery of quasicrystals. X-ray diffraction patterns of some intermetallic compounds revealed a lack of translational symmetry in them [7]. This caused a stormy reaction of the scientific community. Such intermetallic compounds were called quasicrystals. However, in works [8,9] it was shown that translational symmetry immediately appears if we consider diffractograms as projections onto a two-dimensional plane of a structure of higher dimension (a hidden order of diffractograms is revealed).

Currently, there are no results of special experiments to determine a unique correspondence between the location of this pair of bases in the polytopic of hereditary information and a specific amino acid. However, one can qualitatively confirm the existence of five different arrangements of base pairs using experimental data on the correspondence of codons (nucleotide triplets) to amino acids [2]. If we assume that the average nucleotide in the codon plays the main influence in this correspondence, then five amino acids correspond to triplets with an average nucleotide U: Phe, Leu, Ile, Met, Val. Since each amino acid corresponds to one of the positions of nucleotide U, it turns out that these directions exist 5. A similar situation is repeated with triplets with an average nucleotide C. They correspond to 5 amino acids: Ser, Pro, Thr, Ala, Cus. For triplets with an average nucleotide G there correspond the amino acids: Ser, Cys, Trp, Arg, Gly. Triplets with an average nucleotide A correspond to 7 amino acids: Tyr, His, Glu, Asn, Lys, Gln, Asp. Some violations of the strict unambiguous equality of 5 amino acid numbers to each nucleotide can be explained by the influence of lateral nucleotides in triplets and noncanonical parasitic bases.

It should be noted that taking into account the highest dimension of the polytopic of hereditary information is also necessary in the analysis of pandemics in which viral RNA penetrates the cell and forces the ribosomes to produce proteins necessary for viruses to reproduce.

Conclusion

A detailed examination of the geometry of the nucleic acid compound region led to the construction of a hereditary information polytope and then to the determination of an almost unambiguous correspondence between nucleic acid nucleotides and amino acids. This destroys the idea of the correspondence of triplets to certain amino acids, introduced logistically, in order to avoid the contradiction between a small number of nucleotides and a large number of amino acids. It turned out that the polytop of hereditary information has an internal (hidden) degree of freedom in the form of a different arrangement of pairs of flat nitrogen base in the space of higher dimension. Consideration of this internal degree of freedom is necessary when analyzing the transmission of hereditary information and analyzing the spread of viral infectious diseases.

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