The Structure of DNA Taking Into Account the Higher Dimension of Its Components

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INTRODUCTION

Deoxyribonucleic acid (DNA), as a chemical substance, it was isolated by Johann Friedrich Micher in 1869 from the remains of cells contained in the pus. He singled out a substance that includes nitrogen and phosphorus. When Misher determined that this substance has acid properties, the substance was called nucleic acid (Dahm, 2005). Gradually it was proved that it was DNA, and not proteins, as previously thought, and which is the carrier of genetic information. One of the first decisive proofs was the experiments of Oswald Avery, Colin MacLeod and McLean McCarthy (1944) on the transformation of bacteria.

The structure of the double helix DNA it was proposed by Francis Crick and James Watson in 1953 on the base of the X-ray structural data obtained by Maurice Wilkins and Rosalind Franklin and the "Chargaff rules" according to which in each DNA molecule the strict relationships connecting the quantity of nitrogenous bases of different (Watson, & Crick, 1953a, b). For outstanding contributions to this discovery, Francis Crick, James Watson and Maurice Wilkins were awarded the 1962 Nobel Prize in Physiology or Medicine. Deoxyribonucleic acid (DNA) is a biopolymer, the monomer of which is the nucleotide (Albert, et al., 2002; Butler, 2005). Each nucleotide consists of a phosphoric acid residue attached to sugar deoxyribose, to which one of the four nitrogen bases is attached also. The bases that make up the nucleotides are divided into two groups: purines (adenine [A] and guanine [G]) and pyrimidines (cytosine [C] and thymine [T]) are formed by combined five - and six - membered heterocycles.

They managed to show that the DNA isolated from the pneumococci corresponds to the so-called transformation (the acquisition of pathogenic properties by a harmless culture as result of the addition of dead pathogenic bacteria to it). The experiment of American scientists Alfred Hershey and Martha Chase (Hershey - Chase experiment, 1952) with radioactively labeled proteins and bacteriophage DNA showed that only the phage nucleic acid is transmitted to the infected cell, and the new generation of phage contains the same proteins and nucleic acid, as the initial phage (Hershey & Chase, 1952). Deciphering the structure of DNA (1953) has become one of the turning points in the history of biology.

In 1986, Frank-Kamenetskiy in Moscow showed how a double-stranded DNA folds into a so-called H - shape, composed not of two but three strands of DNA (Frank – Kamenetskiy, 1986, 1988). Deoxyribonucleic acid (DNA) is a biopolymer, the monomer of which is the nucleotide (Albert et al., 2002; Butler, 2005).

Nucleotides are long polynucleotide chains covalently linked. These chains in the overwhelming majority of cases (except for some viruses possessing single - stranded DNA genomes) are combined pairwise by means of hydrogen bonds into a secondary structure, called the double helix (Watson & Crick, 1953 a, b; Berg, Tymoczko & Stryer, 2002). Each base on one of the chains is connected to one definite base on the second chain. This specific binding is called complementary. Purines are complementary to pyrimidines (that is, they are capable of forming hydrogen bonds with them): adenine forms bonds

only with thymine, and cytosine - with guanine. In a double helix, chains are also linked by hydrophobic interactions and stacking, which do not depend on the DNA base sequence (Ponnuswamy & Gromiha, 1994). Complementarity of the double helix means that the information contained in one chain is also contained in another chain. Different base pairs form a different number of hydrogen bonds. In the future, the existence of nucleic acids differing in the length of the period and shape with rotation of the spiral both to the right and to the left was experimentally established (Ha, et al., 2005; Cantor, & Schimmel, 1980; Frank – Kamenetskiy, 2010).

Watson and Crick postulated the spiral form of the DNA molecule, but they did not discuss the reasons for the formation of such a DNA molecule. Until now there have been no works explaining the existence of a spiral in the DNA molecule.

In the book (Zhizhin, 2017), the molecules of practically all the elements of the periodic system were studied in detail and it was shown that many of them, including magnesium and calcium, form compounds of higher dimension (see also Zhizhin, 2015 a, b; Zhizhin, & Diudea, 2016; Zhizhin, Khalaj, & Diudea, 2016). In the works (Zhizhin, 2016 a, b), the structures of biomolecules, which also form compounds of higher dimension, are also studied. When analyzing the metric space of nucleic acid structures, one should use the representations of their constituents in the form of polytopes of higher dimension. This primarily applies to the phosphoric acid residues and the D - ribose molecules, since nitrogenous bases have a dimensionality of 2 and do not have a significant effect on the geometric structure of nucleic acids.

The determination of the geometric forms of chemical compounds according to the Euler-Poincaré (Poincare, 1895) relation translates classical stereochemistry in three-dimensional space into sulfur chemistry in a space of higher dimension. Here new discoveries are possible in the laws of chemical compounds. Consideration of the geometry of molecules using spaces of higher dimension makes it possible to explain the facts observed in reality, which previously had no clear explanations. In the book (Zhizhin, 2017), for example, showed that the rotation of the plane of light polarization in tartaric acid is due to the difference in the shapes of the molecules of D - tartaric acid and L - tartaric acid, which is clearly visible in their images in five - dimensional space, since their dimension is five. Pasteur (Pasteur, 1960) also tried to explain the rotation of the polarization plane of light in liquid tartaric acid by the difference in the structures of the crystals of D - tartaric acid and L- tartaric acid. This book received an explanation for the fact that there is no branching in the chain of glucose molecules, if they are bound in β - glycoside linkage. If these molecules are bound in α – glucoside linkage, branching of the chain is possible. It is shown that, because of the higher dimensionality of glucose molecules in the case of a β – glycoside linkage, the centers of possible branching of the chain are blocked by glucose molecules. In this time, with α – glycoside linkage the possible branching points of the chain remain free.

The concept of the geometric correspondence of the structure of substances in the formation of a chemical compound is essential for the form of the compound. However, the complementarity of DNA spirals when connecting spirals can not be the reason for the formation of these spirals. The geometric shape of the constituent parts of the spiral itself must be important here. They are phosphoric acid residues and D - ribose molecules. This paper is devoted to the investigation of this problem. In this case it is necessary to take into account the dimension of these parts, which, as shown in (Zhizhin, 2017), is higher than three. It should be noted, that there is no contradiction in the representation of the structure of DNA as a spiral in a three - dimensional space with the highest dimension of its components. The point is that according to the geometry of Riemann (Riemann, 1854), a space of higher dimension has a boundary. Therefore, a space of a smaller dimension can be located outside this space.

The higher dimensionality of molecules can be considered as an example of Big Data. The concept of Big Data has become widespread in computer science in recent times (Kosrapohr, 2003; Hughes,

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