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Unknown symmetries and fractals in long DNA-texts; Genetics and quantum informatics

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The lecture shows an unknown class of hidden symmetries and fractal structures in long sequences of oligonucleotides of single stranded DNA from their wide set. These symmetries are an addition to symmetries described by the second Chargaff's parity rule (%A = %T and %G = %C). These new symmetries and their rules concern collective probabilities of oligonucleotides from special tetra-groups and their subgroups in long DNA-texts including complete sets of chromosomes of human and some model organisms. These rules of tetra-group probabilities are considered as possible candidacies for the role of universal rules of long DNA-sequences. A quantum-informational model of genetic symmetries of these collective probabilities is proposed using the known quantum-mechanic statement that quantum state of a multicomponent system is defined by the tensor product of quantum states of its subsystems. In this model, nitrogenous bases C, T, G, A of DNA are represented as computational basis states of 2-qubit quantum systems. A model explanation of the second Chargaff's rule from the standpoint of quantum informatics is proposed. Elements of quantum-information genetics are under developing. Considerations are given on the biological sense of these quantum-information phenomena of genetic symmetries. From the proposed standpoint, biological organisms are quantum-information essences. The results give new abilities to use mathematics of quantum informatics and quantum computing in synthetic biology and also to search bio-information patents of nature for technologic applications including medicine and devices of artificial intelligence.

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