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**Sequence-specific local structural organization of DNA and its role for analog coding of genetic information.**

Encoding of genetics information is the multilevel process. The time and positions for translation, namely for the formation of RNA nucleotide sequences, complementary to the deoxynucleotide sequences of triplets in DNA, is regulated by DNA-protein interactions.

The RNA sequences encode proteins with definite sequences of amino acids, according to the digital trilateral codes. At the same time the unique structural and mechanical properties of DNA, which are needed for accuracy of complex formation with regulatory proteins, realizes the analog coding for translational processes. Such coding in a great extent is defined by the sequence-specific conformational dynamics and has high level of degeneration.

We have found the common characteristics of DNA structure, which define it as a promoter for RNA polymerase II. For these purpose we have used sets of the animal promoters (23360 promoters for *H. sapiens*, 21239 promoters for *M. musculus*, 15073 promoters for *D. melanogaster*, 10728 promoters for *D. rerio*, 7120 promoters for *C. elegans*); plant promoters (10229 promoters for *A. thaliana*) and fungi promoters (4324 promoters for *S. cerevisiae* and 3440 promoters for *S. pombe*) [1]. For comparison of the promoter structures from different species we constructed profiles representing the mean values of each physical parameter for the set of the core promoter sequences for every species. These profiles show the alteration of different local properties at the levels of base-pair, di-, tetra- and hexanucleotides: the frequencies of nucleotide occurrence, duplex stability, mechanical characteristics, 3D structural organization and the ultrasonic [2, 3], and DNase I cleavage intensity [4] in each complementary strand along the sequence of the core promoters.

We have found that the fragments of the core promoters, responsible for interaction with regulatory proteins, in all species have unique 3D structural and mechanical properties, despite the differences in the nucleotide sequences. Thus the analog structural code shows high level of degeneration.

The regions of TATA-box and TSS are detached from each other by two turns of the B-form helix with the unique level of conformational motion asymmetry in the complementary strands in all metazoan. But there is a fine distinction between structural organization of metazoan and eukaryotic fungi that correlates with the data on the differences of their biochemical and genetic systems. This reveals the plasticity of analog coding of genetic information which is needed for the processes of evolution.

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