The Patterns of Base Sequences in the Nucleic Acids of Prokaryotes and Eukaryotes Reflect Features of their Abiotic Past

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The base sequences of the nucleic acids corresponding to ten proteins (aconitase, alcohol dehydrogenase, enolase, fumarase, isocitrate dehydrogenase, lactate dehydrogenase, phosphofructokinase, phosphoglycerate mutase, pyruvate kinase and succinate dehydrogenase) belonging to a total of 154 species, ranging from prokaryotes to vertebrates, were compared with the base sequences of oligoribotides whose growth rates were calculated by a chemical kinetics model. It was shown that oligoribotides grown according to the kinetics model have a fraction of repetitive bases larger than expected from random processes. The base sequences of nucleic acids of prokaryotes and eukaryotes retain, in decreasing proportions, this feature of their abiotic past. Chemically synthesized pentameric stretches with repetitive bases are slightly more abundant than those present in prokaryotes. Genetic drift and natural selection, operating as fundamental laws even for the most primitive living systems, reduced the original, chemically controlled, repetitive base frequency in prokaryotes, which was further reduced for eukaryotes.

Key words: Nucleic Acids, Oligoribotide, Abiotic Past