

EVOLUTION OF GENOME CONTAINING MOBILE GENETIC ELEMENTS

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High concentration of mobile genetic elements (MGE) is a characteristic feature of eucariotic genome. These mobile genetic elements may considerably influence genome evolution. In this work the results of phylogenetic and contextual analysis of nucleotide sequences of MGE of archbacteria, prokaryotes and eukaryotes which provide understanding of some aspects of MGE general origin are presented.

Some problems of MGE connection with prokaryotic and eukaryotic organisms are discussed. In particular, investigations of possible ways of evolution reveal that the known peculiarities of mobile elements structural functional organization are difficult to explain, if the hypothesis that eukaryotic organisms originated from prokaryotic ones is true.

The results of mathematical modeling of MGE intragenome dynamics taking into account their influence on organisms fitness due to insertional mutagenesis and processes of recombination determined by MGE are introduced. While studying properties of real MGE classes it was shown that if we assume that the transposition of these mobile elements is not regulated there emerge a significant genetic load, and its value may induce degeneration of populations of organisms where there are MGE of this type. This indicates that certain regulatory molecular mechanisms reducing the value of genetic load emerge during evolution. The similarity of such regulatory mechanisms for eukaryotes is confirmed by the found connections between the number of copies and the frequency of mobile elements transpositions in genomes of various organisms. The

rate of emergence and dynamic properties of possible and known real molecular mechanisms of MGE transposition regulation are investigated with the help of mathematical methods. The analysis of factors responsible for emergence of such mechanisms has been carried out both for prokaryotes and eukaryotes. Estimations of dynamic and structural properties of regulatory mechanisms, allowing to reduce negative influence of recombinational processes with MGE participation on fitness were obtained. The results of comparison with experimental data are introduced. The observed tendency of multicopied MGE families to form dispersed clusters in genome is explained.

The properties of such regimes when mobile genetic elements can be a factor of populations evolutionary non-degeneration in conditions of periodic and occasional stress influences of the environment because of the correlation between the frequency of MGE transpositions and conditions of the environment are investigated by methods of mathematical modelling (basing on the previously done analysis of nucleotide MGE sequences). The situations when it is profitable to have regulatory sites responding on stress changes of the environment comprised in mobile genetic elements and not in conservative location in the genome is analysed.