Evolution of trophically linked populations of unicellular organisms; translation efficiency in unicellular organisms.

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The comparative modeling of populations' adaptivity and biodiversity dynamics is carried out. Populations consist of symbiotic unicellular haploid asexual organisms inhabiting in a biotope of limited volume in which the nonspecific substrate (NS) inflows externally. Organisms consume NS and it is necessary for every of them. Symbiosis is provided by intra-populational exchange of specific substrates. Using the original software package "Evolutionary Constructor"[1] allowing varying both genetic and trophic structure of a model, we have shown that under sub-lethal conditions (NS deficiency) populations with compensatory metabolism (NS deficiency can be compensated by symbiont coevolution) have the better adaptivity (mutation in some single can save all symbiont populations) but gradually lose biodiversity. Another model deals with origin of cells encapsulating exterior community metabolism into interior intercellular one. The origin of such cells could be the one of significant stages in evolution and possible eukaryotes origin. We considered simple ring-like symbiotic community of three members feeding each other and simulated its evolution during 15 thousand generations. During evolutionary process horizontal genes transfer could stochastically occur which lead to genes exchange and possible origin of a novel population. If a cell has both genes of synthesis and utilization for a particular substrate, its metabolic strategy is as follows. Cell tries to saturate itself with this substrate and only then secretes remains of these substrates, if they are. So cells could accumulate genes and enclose a part of metabolism in them, getting some benefit.

In order to estimate gene expression efficiency as a function of its nucleotide content the Elongation efficiency index (EEI) [2] was used. Nucleosome formation potential (NFP) values were estimated by Recon method. We have analyzed relations between NFP and EEI on the sample of all yeast ORFs (6301 sequences from GenBank). Profiles of correlation coefficients between NFP (5'-UTR) and EEI (coding sequences) were constructed for (-600; +600) regions in relation to translation start. Both for all genes and for high-expressing genes (10% of EEI-highest genes) we have shown reliable negative correlation between NFP (in a part of promoter region) and EEI. For low-expressing genes (10% of EEI-lowest genes) we have shown reliable positive correlation between NFP and EEI. We suggest such correlation to be explained by expression optimization. In high-expressing genes (high EEI) the transcription initiation should be facilitated – to maximize mRNA number, i.e. nucleosome packaging should not be condensed; and vice versa for low-expressing genes.

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List of publications:

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