

GENE LOSS AND ACQUIRING IN EVOLUTION OF PROKARYOTIC COMMUNITIES – MODELING WITH EVOLUTIONARY CONSTRUCTOR PROGRAM

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Motivation and Aim: Prokaryotes are – the world of tiny genomes and huge size communities. Consuming external nonspecific substrate (NS) populations of various species divide functions in community and act as compartments in associated metabolic reactions. By virtue of exchange of metabolites and other specific substrates (SS) various species form trophic networks (graphs) [1]. Reduction of genome size is considered to be one of the major trends of prokaryotic evolution, as the replication determines reproduction rate (i), and specialization of species in community facilitates loss of functions and, consequently, genes (ii). In the present study the role of both ecocenotic and genetic factors in evolution of prokaryotic genomes size was investigated *in silico*.

Methods and Algorithms: The modeling tool “Evolutionary constructor” – “EC” [2] was used for computer simulations of evolution.

Results: We have modeled evolution of trophic networks of haploid organisms’ populations, providing each other with SS and consuming the common NS. The time of evolution simulation was up to 30000 generations. Growth rate of a population depended on number of consumable SS, efficiency of SS/NS consumption/utilization (both factors are genetically determined), and total genome size of population cells (bigger genomes get bigger penalties). Deficiency of NS in environment could be partially compensated with an excess of SS. Against the backdrop of NS concentration oscillations (from sublethal to excess) both gene loss and horizontal gene transfer (HGT) could occur. It has been shown that trend of gene reduction is adaptive only in conditions of NS excess. In this case it involves all members of community. In conditions of NS deficiency the adaptive trend is increase of genomes size owing to HGT. In normal conditions events of gene loss and transfer redistributed genes in populations-members of community which changed proportions of their sizes.

Conclusion: In highly-integrated community genome size reduction becomes a major trend in comfortable conditions, and occasionally occurs in sub-comfortable ones. However in non-comfortable conditions integrated metabolism conduces community members to acquire genes.

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References:

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