MODELING CELL AUTONOMISM ORIGIN IN PROKARYOTES USING EVOLUTIONARY CONSTRUCTOR PROGRAM

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Motivation and Aim: Progressive evolution involves an organism's complication and its metabolism intensification. Whence and evolutionary ways of complex life forms on the Earth are the significant scientific problems. Many studies using complete genome data of eubacteria, archaebacteria and eukaryotes go in evidence that lots of eukaryotic domains originated rather from bacteria than from mitochondria and plastids. Hence, a eukaryotic cell has been formed owing to autonomism of a member of complex syntrophic prokaryotic community via its self-closure of base regulatory pathways. As an experimental study of evolution is too complex, mathematical modeling becomes the main tool used;

Methods and Algorithms: To model the origin of cell autonomism the previously developed software package "Evolutionary Constructor" (EC) [1] was used. EC is designed for modeling of coevolution in trophically linked populations of haploid organisms. It combines imitation and generalized modeling approaches which allow changing structure of modeled system immediately during the calculation process. In turn it allows us to model such evolutionary processes as mutation and horizontal transfer of gene material (HT);

Results: We have studied long-term evolution of trophic system being represented at starting time as closed "ring" of populations, feeding each other. Each population utilized only one specific (for that population) substrate and produced only one specific (for that population) product. During the calculation a HT might occur with a certain probability. HT could lead to beginnings of novel populations which could utilize more substrates and/or produce more products. It has been shown that in long view the ultimate advantage (the highest population size) obtained the populations having "most complete genome" (i.e. populations utilizing and producing maximal number of substrates/products in given trophic system) or populations having "almost complete genome". In long view such populations eliminated all other members from trophic system while the common metabolism rate grew up.

Conclusion: It was shown that HT in the stable environmental conditions transforms common metabolism of trophic ring to inner metabolisms of separate species becoming autonomous. Selection supplies autonomism, but the novel populations cause trophic ring disintegration to a set of autonomous populations. At that time common metabolism rate grows up. Consequently the criteria of progressive evolution are presented here.

References:
1.   S.A. Lashin, V.V. Suslov, N.A. Kolchanov, Yu.G. Matushkin (2007) Simulation of coevolution in community by using the "Evolutionary Constructor" program. *In Silico Biology*, **7:** 261-275.