

EVOLUTION OF GENOMES AND THE ORIGIN OF NEW GENES

Summary

Genomes of Bacteria and Archaea are extremely compact, almost devoid of noncoding DNA. Sizes of these “prokaryotic” genomes span only two orders of magnitude and their evolution is characterized by: strong pressure for the removal of non-functional DNA, frequent structural rearrangements resulting in randomization of gene order, profound differences in gene content between related forms and ubiquitous horizontal gene transfer (HGT). Genome sizes in Eukaryotes vary enormously, spanning five orders of magnitude. A relatively weak correlation between the genome size and organismal complexity in Eukaryotes, known as the C-value paradox, results from interspecific differences in the amount of noncoding DNA, composed of introns, repetitive sequences and mobile elements. The plausible explanation for the disparities between prokaryotic and eukaryotic genomes are the differences of the effective population sizes be-

tween organisms, which affect efficiency of natural selection. The accumulation of “extra” DNA is weakly deleterious and it is efficiently removed by selection in huge populations of Bacteria and Archaea. In smaller populations of eukaryotes, particularly multicellular organisms, drift overcomes selection, rendering this “extra” DNA effectively neutral, enabling its accumulation and consequently increase of genome size. New genes may emerge through multiple mechanisms. In bacteria and Archaea HGT is very important in this respect. In Eukaryotes duplications, both whole genome and segmental, are of utmost importance. One copy of a duplicated gene most often accumulates deleterious mutations and becomes a pseudogene. However, sometimes both duplicated copies are retained – one of them evolves a new function in the process of neofunctionalization or each copy undergoes specialization in the process of subfunctionalization.