

COMPUTER MODELING OF GENOME EVOLUTION

Summary

A dozen years of computer simulations of age structured populations composed of individuals represented by their diploid genomes show how evolution of the genetic pool of populations depends on the population size, intragenomic recombination rate and promiscuity. The cross-over rate and the effective population size decide about the probability of separation of genes located on one chromosome during the reproduction. If this probability is low, the genes are inherited as a cluster. Purifying selection, which tries to minimise the number of mutations by eliminating defective genes from a cluster, seems to be the more costly strategy and genomes may chose the strategy of complementation. Switching between the two strategies – purifying selection and complementation of haplotypes – has a character of transition. Results of the human chromosome analyses suggest that our chromosomes evolve in conditions close to this transition and formation of clusters

and their complementation should be expected. The distribution of genes in the complementing clusters is not random and it is specific for evolving populations. Sympatric speciation, where one species splits into several within the same territory, should be considered as a very common phenomenon in spatially distributed populations and, in fact, it is observed during the computer simulations. In neo-Darwinian theory of evolution, sympatric speciation has been considered as an improbable and negligible phenomenon just because in the mean field models of very large Mendelian populations (panmictic, with very high intragenomic recombination rate) these effects cannot be observed. Computer modeling also showed that the shrinking of the Y chromosome observed during genome evolution of mammals is connected with promiscuity in the strategy of their reproduction.