

In this research we observe bacterial carbohydrate metabolism genes. The goal was to obtain a realistic scheme of all kinds of carbohydrate metabolism gene co-evolution and co-functioning patterns in bacteria. A convenient classification system for all such genes was built based on their functional, structural and orthological characteristics. Patterns of their co-evolution were investigated based on the gene co-location on bacterial chromosomes. Matrices of pairwise co-occurrence of the orthological-structural families of genes belonging to different major functional classes were built, and their structure was studied providing data on types of different family behavior among different matrices and data on the whole matrices concerning, for example, "peak" rate (where peaks relate to co-evolution tendencies), in particular, in terms of deviation from the expected values. Lists of natural loci and all types of sub-loci containing several carbohydrate metabolism genes (from 2 to about 20) were also built and sorted by their abundance. We also constructed virtual possible loci structures based on real co-occurrence frequencies of its genes. We allocated some of the loci and sub-loci on the bacterial phylogenetic tree in order to study their distribution and possible cases of horizontal transport.

Overall, we made a suitable classification of carbohydrate metabolism genes; identified the most stable combinations (loci and sub-loci) of such genes; defined groups of bacteria that have similarities in the organization of those combinations; defined gene families that have similarities in their preferences towards co-location with other families; made assumptions about co-evolutionary patterns, built virtual possible gene combinations of genes that might "work" together well and allocated some of the loci and their variations on a phylogenetic tree to assess the distribution of the different loci of bacteria and identify cases of horizontal transfer of loci and their parts.