

## **Study of lactobacteria's genomes evolution**

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Lactobacillus is a genus of the gramm-positive faculty anaerobic bacteria. They are among the most important group of lactic acid bacteria, the majority of which converts lactose and other carbohydrates into lactic acid (Makarova & Koonin, 2007). Comparing the genomes of species's representatives can help identify structural changes in the conduct of the genome of the symbiotic existence. For our study we took 20 strains of the 14 species of the genera Lactobacillus, part of which is a symbiotic relationship with a man, another are free-living. Based on the proteomes of all strains, we have built series of orthologous genes for each species, so called, orthological ranks. We used two programs for this: OrthoMCL and Protheinortho. It turned during comparing the results that this programs give different clusters, both in quantity and quality. In particular, the program Protheinortho calculates no clusters that contain only one species genes. The frequency distribution graph representation of the number of species in different clusters had small rise in the middle in both cases (fig .1), it is characteristically for the analysis of closely related strains. Total taxonomic tree was constructed using all the genes that were present in full orthological clusters (fig .2). Gene flow was estimated to find genes, that acquired and lost in the process of evolution on the branches of a tree.

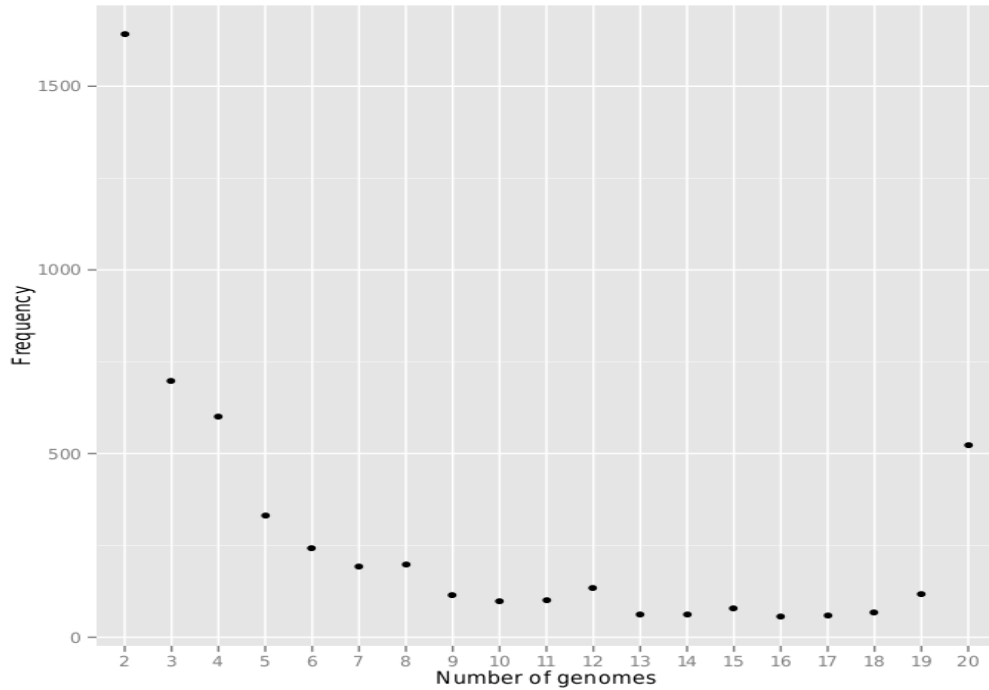


Figure 1. The frequency distribution of the representation of the number of genomes in clusters

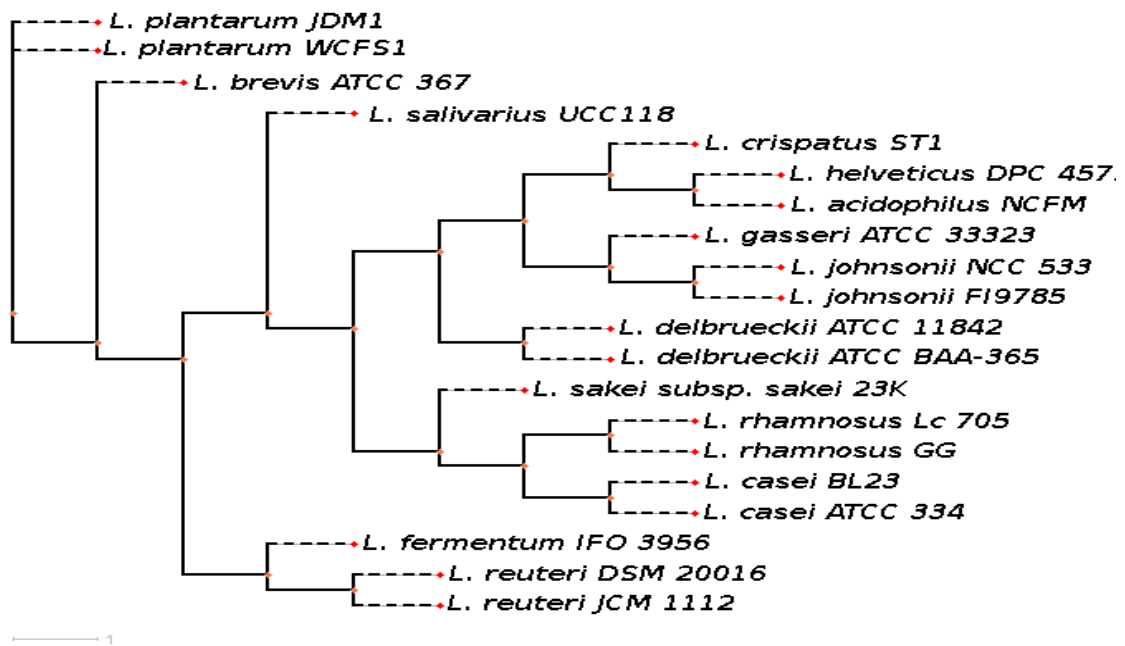


Figure 2. A phylogenetic tree of all types used in this work

1. Makarova, K. S., & Koonin, E. V. (2007). Evolutionary genomics of lactic acid bacteria. *Journal of Bacteriology*, 189(4), 1199–1208.