

# THE VARIABILITY OF GENES OF OPERON *plnABCD* OF STRAINS *LACTOBACILLUS PLANTARUM*

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The aim of the research was to study of variability of genes belonging to the regulatory operon *plnABCD*.

To analyse the sequence of bacteriocins loci of *Lactobacillus plantarum* strains represented in the GenBank database as a genome-wide were selected.

The phylogenetic analysis was carried out using the method of the Minimum Evolution (Minimum Evolution) and the evolutionary model JTT (Jones-Taylor-Thornton). The analysis was made in the program Mega 5. The amino acid sequences were used to construct the trees. Similar combinations of methods and models were used both for phylogenetic analysis of the operon *plnABCD* sequences as well as for analysing a set of sequences of each gene.

The obtained topologies of phylogenetic trees for operon indicates the formation of several separate clusters, the significance of which is confirmed by the high level of reliability of the results of the bootstrap analysis (66 - 98 %).

By analyzing the topology of phylogenetic trees for each gene, we noted the formation of stable clusters. The fluctuations of the confidence level of formation of internal nodes were insignificant.

The maximum indicators of the attitude  $K_n/K_s$  were obtained when we analysed the sequences of the operon as a whole (1,73 – 2,0) and gene *plan* encoding plantaricin A (1,24 – 1,37). For other genes index force of selection was significantly lower (0,06 – 0,5). At the same time noted the uneven distribution of synonymous and non synonymous substitutions for each individual gene.

The maximum calculated values of nucleotide diversity ( $\pi$ ) and the value of the criterion Tajima (D) were also noted for the whole operon and gene *plnA*.