

## **Molecular-genetic analysis of lactic acid bacteria compositions in fermented food**

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The foods or beverages produced by regulated microorganisms growth and enzymatic conversion of primary and secondary food components are defined as the fermented food. Nutritional and functional properties of such products are improved

during fermentation. These properties include improved availability of minerals, vitamins and antioxidants, as well as increasing organoleptic features and safety.

The consumption of fermented milk products has been going on for thousands of years, using the biochemical activity of microorganisms present in raw milk. Lactic acid bacteria represent the majority of the microbial content in dairy products. Among these are lactobacilli, lactococci, bifidobacteria and others. Besides, various *Enterococcus* species are also detected.

The study, analysis and identification of lactic acid bacteria and bifidobacteria inhabiting in complex microbial ecosystems by conventional methods is time consuming and it is based on the study of phenotypic characteristics of these microorganisms. This approach limits the possibility of qualitative and quantitative analysis of the taxonomic composition of the microbiome in natural substrates and does not allow evaluating the biodiversity of microorganisms that inhabit a particular ecosystem.

Modern systematics and identification techniques and methods use the analysis of genetic structures of microorganisms, which allows qualitatively and quantitatively assess the diversity of bacterial groups in a particular ecosystem.

The aim of the presented research was to evaluate the diversity of lactic acid bacteria in dairy products using molecular-genetic methods.

For this purpose samples of milk and feta cheese were selected for the analysis. To detect bacteria of the genera *Enterococcus*, *Lactobacillus* and *Bifidobacterium*, PCR with genus specific primers was carried out. Amplification was performed using total DNA isolated from dairy products.

As a result of PCR-analysis it was shown that enterococci and lactobacilli are present in all analyzed samples. Bifidobacteria were found only in home-made feta cheese and milk. Quantitative analysis of relative content of *Enterococcus* species in analyzed products revealed that the number of bacteria is higher in feta cheese in comparison with milk samples.

Thus, the obtained results suggested that molecular-genetic methods can be effectively used for qualitative and quantitative evaluation of microorganisms in dairy products.