

## TRADITIONAL MOLDOVAN CHEESE MICROFLORA

Anatoli CARTASEV<sup>1\*</sup>, ORCID: 0000-0002-3592-3919

<sup>1</sup>*Comrat State University, Comrat, UTA Gagauzia, Republic of Moldova*

\*Corresponding author: Anatoli Cartasev, email: [anaticartasev@gmail.com](mailto:anaticartasev@gmail.com)

Moldovan cheese, named “Brinza” is a traditional cheese made from cow’s, goat’s and sheep’s milk. Moldovan cheese is part of the cultural heritage of our country but still isn’t registered as a Protected Geographical Indication. It is produced in several variants, while the main cheese made from unpasteurized milk. The quality of cheese is largely influenced by the origin of microflora of milk and traditional technological process of production, which has a crucial effect on development of microflora.

The aim of current study was to update the knowledge about diversity and concentration of lactic acid bacteria in Moldovan cheese at different levels of maturity. For the quantification of lactobacilli, lactococci, yeasts, molds and accompanying contaminating microflora (*E. coli*, coagulase-positive staphylococci) was used culture analysis. Selected isolates of estimated lactobacilli and lactococci were identified using polymerase chain reaction (PCR) and DNA sequencing. To characterize prokaryotic and eukaryotic diversity of microbial communities, we used culture analysis.

In samples of sheep cheese, were found that the concentration of lactic acid bacteria reached values of  $1 \times 10^6$  UFC/g already after the first day of ripening, but pH value were found on the 2nd and 3rd days of ripening (5.1–4.8), corresponding with the recommended range. Also, was observed increased concentrations of *E. coli* and yeasts in cheese and several colonies of *Streptococcus aureus* correspond to the fact that the cheeses were made from unpasteurized milk without added support culture and the suppression of undesirable microorganisms was left to competition and the effect of matrix acidification.

A total of 40 colonies of presumed lactococci and 20 colonies of presumed lactobacilli were identified from each sample of cheese by species multi-stage multiplex PCR, or by amplification and sequencing of the 16S rDNA section.

Were identified the highest number of selected colonies as *Lactococcus lactis subsp. Lactis* and *Lactobacillus plantarum*. Other identified species were *Lb. paracasei*, *Lb. brevis*, *Lc. lactis subsp. cremoris*, *Lb. fermentum*, *Lb. rhamnosus*, *Lb. delbrueckii* and *Lb. casei*.

Through cultivation analysis, were found that the main component of bacterial microflora of cheese are lactococci (mainly *Lc. lactis subsp. lactis*), lactobacilli (mainly *Lb. paracasei*, *Lb. helveticus*, *Lb. brevis* and *Lb. plantarum*), further *Streptococcus thermophilus*, and bacteria from the genera *Leuconostoc* and *Enterococcus*. Other highly identified yeast genera were *Yarrowia spp.* (esp *Y. lipolytica*), and *Kluyveromyces spp.* (especially *K. lactis* and *K. marxianus*).

On this basis, maybe assume the presence of metabolites and products of autolysis, including enzymes that they contribute to the creation of a typical profile of aromatic substances of the product.

**Keywords:** lactic acid bacteria, PCR, microbiota, brinza.