

Microbial analysis of ovine cheese by next generation sequencing

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Ovine cheese is a good source for isolation of wild lactobacilli-potential starter cultures. This study aimed to analyse microbiota of the ovine cheese (Slovak Bryndza) and to investigate the presence of *Lactobacillus* antibiotic resistance, virulence or probiotic genes by pyrosequencing.

The V1-V3 regions of the 16S ribosomal DNA were amplified from different ovine cheeses using PCR. In all samples, the microbial populations consisted of *Lactobacillus helveticus*, *Lb. acidophilus*, *Lb. plantarum*, *Lb. rhamnosus*, *Lb. brevis*; *Lactococcus lactis*, *L. raffinolactis*, *L. garviae*; *Enterococcus italicus* and *E. camelliae*; *Streptococcus salivarius*, *St. thermophilus*, *St. caballi* and *St. ferus*.

Furthermore, the genomes of selected *Lb. plantarum*, *Lb. brevis*, *Lb. paracasei* were pyrosequenced. The assembly of *L. plantarum* resulted in 203 contigs longer than 1,000 bp (D'Auria et

al., 2014). There were identified probiotic proteins as an alpha amylase (PF00128), peptidase (PF01433), catalase (PF00199), heat shock protein 33 (PF01430). Nevertheless, there was discrepancy between *Lb. plantarum* ampicillin sensitivity and the presence of serine beta-lactamase like superfamily (PF00144). No virulence factors were detected. Results indicated new properties of lactobacilli, which were not occurred by phenotyping testing.

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References

D'Auria G, Džunkova M, Moya A, Tomaška M, Kološta M, Kmet V (2014). Genome Sequence of *Lactobacillus plantarum* 19L3, a Strain Proposed as a Starter Culture for Slovenska Bryndza Ovine Cheese. *Genome Announc.* **2**(2):e00292-14. <http://dx.doi.org/10.1128/genomeA.00292-14>