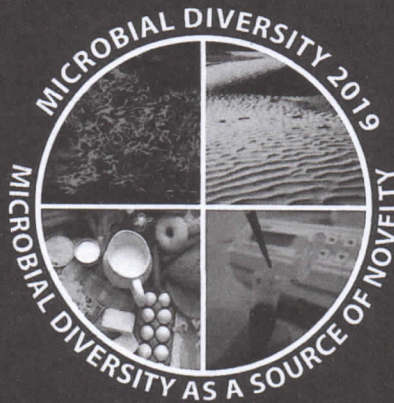


# MICROBIAL DIVERSITY 2019

MICROBIAL DIVERSITY AS A SOURCE OF NOVELTY:  
FUNCTION, ADAPTATION AND EXPLOITATION



**MD 2019**

## Comparative Genome Analysis of *Lactococcus lactis* isolated from Trentino cheese and environment adaptation

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**Introduction.** *Lactococcus lactis* is one of the most important microorganisms in the dairy industry for the cheese fermentation, because it is responsible for cheese acidification and for product properties such as flavor and texture. *L. lactis* has adapted from plant to the milk environment and its evolution has been associated with genome reduction and the acquisition of genes involved in protein and lactose metabolism. In a previous work, we have isolated different strains belonging to *L. lactis* species from spontaneous dairy fermentation in "wild" high mountain cheeses called "malga" cheeses (Trentino, Italy). These isolates showed phenotypical traits different from commercial *L. lactis* and in particular they were able to growth to high temperature (up to 45 °C), they were slow acidifiers and were able to produce complex and heterogeneous flavors in milk.

**Materials and Methods:** In order to find a further niche adaptation of "malga" cheese *L. lactis* to the high mountain dairy environment, we sequenced the draft genomes of 47 *L. lactis* strains and compared these strains with 38 publicly available fully sequenced *L. lactis* genomes obtained from dairy samples. A total of 85 genomes (47 in this study and 38 from public database) were annotated de novo using the Prokka pipeline to prevent gene calling and functional annotations discrepancies. Prokka annotations for all genomes were inputted to Roary for producing the *L. lactis* pan-genome presence/absence gene matrix (listing each gene and which samples it is present in). The pan-

genome genes were functionally annotated using ARGOT and EggNog softwares. A pan-Genome-wide association study (pan-GWAS) was performed with selected phenotypes using Scoary.

**Results:** The average number of coding sequences of the 47 malga strains was 2811. The Enrichment analysis performed using Scoary with a Bonferroni correction showed that, of the 2811 identified OGs, 59 were conserved among all the 47 malga strains and identified as significantly different from the other public *L. lactis* genomes. Amongst these 59 OGs, 31 were annotated as "hypothetical proteins". The remaining 28 OGs encoded, several stress proteins (ClpB proteins) and enzymes involved in the cell membrane components biosynthesis like lipopolysaccharides, teichoic acid that is useful in giving resistance to high range of temperature and exopolysaccharide that could give protection for growth at low temperatures and in high salinity environment.

**Conclusions:** The analysis of the genome sequences of a niche set of *L. lactis* strains allowed us to identify some specific genes that were not identified earlier in this species. The analysis of functional properties could be useful for industrial strain discovery and selection processes.