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Book of Abstract

Exploring the genomic biodiversity of *Lactococcus lactis* from mountain cheeses for application in microencapsulation and cheesemaking

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Lactococcus lactis is a key bacterial species in dairy fermentations, contributing to acidification, flavor development, and microbial stability in cheese. While industrial strains are well characterized, *L. lactis* populations from artisanal and natural environments remain underexplored, despite their potential to enhance the genetic and functional diversity of starter cultures. This study investigated the genomic diversity of 27 *L. lactis subsp. lactis* strains isolated from traditional mountain cheeses produced in Trentino (Italy), via spontaneous fermentation in microbiologically closed environments where local microbial ecosystems naturally evolve. These niche conditions provide a unique opportunity to explore native biodiversity and its potential food applications. Our comparative pan-genomic analysis identified a total of 5,765 genes, including 1,767 core, 2,818 accessory, and 1,180 unique genes. Key findings include genes involved in stress response (e.g., thioredoxins, cold shock proteins), flavor compound production (e.g., acetoin and diacetyl biosynthesis pathways), and antibacterial activity (e.g., nisin biosynthesis via the NisK-NisR regulatory system). Carbohydrate metabolism was well represented, with conserved transport and catabolic systems for glucose, fructose, lactose, and mannose, essential for growth and acidification in milk. Importantly, the accessory genome contained genes related to phage resistance, environmental adaptation, and metabolic flexibility, highlighting the evolutionary dynamics of *L. lactis* in artisanal cheese environments. The rich functional diversity uncovered in these wild strains suggests promising opportunities for their incorporation into cheese production. Moreover, their metabolic versatility and resilience make them potential candidates for encapsulation in microcapsules aimed at targeted delivery of bioactive compounds in complex food matrices. Our findings underscore the value of biodiversity-driven approaches for developing robust, multifunctional starter cultures and bioactive carriers to support innovation in the production of high-quality, naturally fermented foods.

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