From genome to phenotype: an integrative approach to evaluate the natural diversity of *Lactococcus lactis* subsp. *lactis*

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*Lactococcus lactis* is one of the most extensively used Lactic Acid Bacteria in manufacture of dairy products and a promising candidate for non-food processes such as white biotechnology or health. Delineating the natural diversity of *L. lactis* could help rational selection of new strains in regards to specific tasks. Through the integration of genotypic and phenotypic analyses, we assessed the diversity of *L. lactis* subsp. *lactis*, lactococcal subspecies of economic interest.

154 strains with unique PFGE fingerprint were subjected to MLST analysis. Data revealed that strains might be classified in two groups: the “domesticated” strains (isolated from dairy products or commercial starters) of low genetic diversity, and the “environmental” strains (isolated from plants, animals, but also from raw milk) that are the essential contributors of the genetic diversity of the subspecies *lactis* (1).

As expected, the phenotype investigation of “environmental” strains revealed high diversity in carbohydrate metabolism, especially in plant-derived carbohydrates (2). Moreover, strains isolated from raw milk have some technological properties, such as milk acidification capacity and ability to produce bacteriocins and aroma (3). These results highlight the potential of “environmental” strains among which news starters might be selected.

The phenotypic diversity of several “domesticated” strains was accessed by monitoring 82 variables such as physiological descriptors, production of metabolites, and volatile organic compounds (VOCs). Statistical analysis led us to select the 20 most significant phenotypic markers, all related to VOCs, and integrate these markers to MLST data to obtain a robust strain discrimination method (4).

References


