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Comparative genomics analysis of 29 Lactococcus *lactis* strains

Schermann Sabine
DuPont Nutrition and Health, France

Lactococcus *lactis* is a lactic acid bacterium widely used in the dairy industry to produce diverse cheeses. Several decades of meticulous microbial selection have provided large collections of strains with appropriate technological attributes such as fast milk acidification, improved bacteriophage resistance and desired aroma production. The objective of this study is to link specific phenotypes to the genetic content of select strains using a pan-genome approach following whole genome sequencing. Whole genome sequences were generated for 29 L. *lactis* subsp. cremoris or subsp. *lactis* proprietary strains using Illumina sequencing. The 29 draft genomes ranged in size between 2.40 and 2.90 Mb (mean: 2.57 Mb) and were organized into 94 to 332 contigs, reflecting a varying content of repeated sequences, notably insertion sequences. The number of predicted CDS varied between 2,644 and 3,521 per genome (mean: 2,813). In most genomes, putative plasmid-based contigs could be detected, although this prediction of plasmid nature is not trivial. Overall, 81,578 CDS were classified into 10,604 gene families (pan-genome), including 1,142 core genes and 4,769 unique genes. In this study, many novel genes and functions could be identified easily within a set of 29 L. *lactis* strains having a potential for industrialization. Although this species is well-known for its small genome size, our data indicate a significant strain-to-strain genetic diversity in agreement with already observed physiological distinctive features thus paving the way for further genomic analyses.

Biography

Schermann Sabine obtained her Master's Degree in Bioinformatics at Université Paul Sabatier (Toulouse, France) in 2011. Just after her studies, she joined the DuPont Company as a Bioinformatician. She works in the Research and Development Department-Nutrition and Health division of the same company. Her team works on the selection and study of lactic acid bacteria aimed to be used in the dairy industry. Her main missions are tool development, Linux server maintenance and the conduction of genomics analyses.

sabine.van.dillen@dupont.com

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