

Genome Sequence of *Lactococcus raffinolactis* Strain 4877, Isolated from Natural Dairy Starter Culture

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The nonstarter lactic acid bacterium *Lactococcus raffinolactis* is prevalent in a wide range of environments, such as the dairy environment, but little is known about this species. Here, we present the draft genome of *Lactococcus raffinolactis* strain 4877, isolated from a natural mesophilic dairy starter culture.

The mesophilic lactic acid bacterium *Lactococcus raffinolactis* is present in a wide range of environments, such as foods (meat, fish, milk, vegetable), animals, and plant materials (2, 5, 7, 10). In the dairy environment, this species has been found in raw milks (cow, ewe, goat, and camel), natural dairy starter cultures, and a great variety of cheeses (3, 4, 6, 8, 9). Despite the prevalence of this bacterium in dairy foods, little is known about this species, possibly due to its “nondominant” status compared to other lactococci.

The genome sequence of *Lactococcus raffinolactis* strain 4877 was determined by Roche 454 GS (FLX System) pyrosequencing performed at Eurofins Genomics (Germany). A total of 284,392 reads (totaling ~159 Mb) were obtained, providing a 20-fold coverage of the genome. The reads were assembled by using Celera software at Eurofins Genomics, and the Consed software was used for final assembly. A total of 127 large contigs were generated, ranging from 1,116 to 78,092 bp in size and with an average length of 17,958 bp. The annotation of the contigs was obtained from the RAST (Rapid Annotation using Subsystem Technology) server (1).

The draft genome of *Lactococcus raffinolactis* strain 4877 is composed of 2,280,761 bp with an overall G+C content of 38.7%. The number of predicted open reading frames (ORFs) is 2,418, covering 83.5% (1,905,337 bp) of the genome and with an average length of 788 bp. There are 1,785 ORFs (73.8%) annotated as encoding proteins with known functions and 633 ORFs (26.2%) annotated as encoding hypothetical proteins. There are 48 predicted tRNAs, and 25 phage-related genes were found, although no complete prophage could be identified.

The genome is represented by 315 RAST subsystems, with many of them related to amino acid and carbohydrate metabolisms. Genome analysis of *Lactococcus raffinolactis* strain 4877 revealed the presence of the complete set of genes for lactate fermentation and genes involved in the oligopeptide ABC transporter.

A more detailed analysis of the genome of *Lactococcus raffinolactis* strain 4877 and comparative genomics with other species of *Lactococcus* will highlight specific features of this species and improve our knowledge of this important food and environmental species.

Nucleotide sequence accession number. The complete draft

genome sequence of *Lactococcus raffinolactis* strain 4877 is accessible at GenBank under accession number [CALL000000000](https://www.ncbi.nlm.nih.gov/nuccore/514848100).

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