

Complete Genome Sequence of *Lactobacillus helveticus* R0052, a Commercial Probiotic Strain

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***Lactobacillus helveticus* R0052 is a commercially available strain that is widely used in probiotic preparations. The genome sequence consisted of 2,129,425 bases. Comparative analysis showed that it was unique among *L. helveticus* strains in that it contained genes encoding mucus-binding proteins similar to those found in *Lactobacillus acidophilus*.**

Lactobacillus helveticus R0052 was deposited at the Institut Pasteur Collection Nationale de Cultures de Micro-organismes as strain I-1722. It was initially identified as a *Lactobacillus acidophilus* strain based on its phenotypic characteristics, but subsequent DNA-DNA hybridization and multilocus sequence typing indicated that this strain was an *L. helveticus* strain (6). It was isolated in March 1990 by Institut Rosell from a sweet acidophilus milk.

The samples were prepared for sequencing by growing the *L. helveticus* R0052 anaerobically overnight at 37°C in de Man Rogosa Sharpe broth (catalog no. CM0361; Oxoid). Genomic DNA was extracted using the DNeasy blood and tissue kit (catalog no. 69504; Qiagen) according to the manufacturer's recommended protocol for Gram-positive bacteria. The quantities of DNA obtained were determined using a Nanodrop spectrophotometer ND1000; typically, 1 to 5 µg of DNA was sent to Genome Quebec (Montréal, QC, Canada) for sequencing according to their specifications.

Three different kinds of library were prepared for sequencing on the 454 GS FLX Titanium system: a standard library, a 3-kb-insert paired-end library, and an 8-kb-insert paired-end library. These libraries yielded 341,383 unpaired reads, 16,330 3-kb-insert paired-end reads, and 82,711 8-kb-insert paired-end reads for a total of 108 million bases (amounting to a 51-fold coverage of the genome). These reads were assembled with version 6.0 of the wgs assembler (5), which yielded 2 scaffolds made of 21 contigs. By comparison with an optical map of this strain (Opgen, Inc., Gaithersburg, MD), the correctness of the assembly could be confirmed and the remaining gaps were closed through the standard techniques of primer design, PCR, and Sanger sequencing. The genome was annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). There were a total of 1,980 coding sequences, including 73 RNA coding sequences. Comparison was made with the genomes of *L. helveticus* CNRZ-32 (J. R. Broadbent, personal communication), *L. helveticus* DPC 4571 (accession no. NC_010080.1), *L. helveticus* H10 (accession no. NC_017467.1), *L. helveticus* DSM 20075 (accession no. NZ_ACLM00000000), *L. acidophilus* 30SC (GenBank accession no. NC_015214.1), *L. acidophilus* ATCC 4796 (GenBank accession no. NZ_ACHN00000000), and *L. acidophilus* NCFM (GenBank accession no. NC_006814.3).

R0052 contained a 6,414-nucleotide cryptic plasmid which we previously reported (2), and the strain is unique among *L. helveticus* strains in that it only carries one of the four cell envelope-

associated proteinases, prtH4 (1). It also has a unique surface-layer protein which has been shown to inhibit the adhesion of *Escherichia coli* O157:H7 to human cells (3). There were 83 genes shared between R0052 and the *L. acidophilus* strains that were not observed in any of the other fully sequenced strains of *L. helveticus*, notably the genes encoding three mucus-binding protein (MUB) precursors. These proteins are thought to play an important role in the adhesion to the intestinal mucus layer (4) and may demonstrate that this particular strain is able to persist in the gut.

Nucleotide sequence accession number. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number CP003799. The version described in this paper is the first version.

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