Complete Genome Sequence of the Probiotic Strain *Lactobacillus salivarius* LPM01

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Lactobacillus salivarius LPM01 (DSM 22150) is a probiotic strain able to improve health status in immunocompromised people. Here, we report its complete genome sequence deciphered by PacBio single-molecule real-time (SMRT) technology. Analysis of the sequence may provide insights into its functional activity and safety assessment.

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The role of probiotics in the establishment of a well-balanced microbiota in humans has been widely demonstrated (1, 2). Results highlighting the functional effect of some probiotics in boosting the immune system (3) have led to the attempt to study the effect of probiotics on the amelioration of immunosupression therapy side effects.

The breast milk isolate *Lactobacillus salivarius* LPM01 (DSM 22105) has shown desirable traits for improving health status in drug-immunocompromised people by ameliorating immuno-suppression therapy digestive side effects, including a strong lactase activity (our unpublished data). Whole-genome analysis has been carried out as a part of safety assessment study in accordance with FAO/WHO guidelines (4). These data will also help us to elucidate its functional mechanisms. Here, we present the complete genome sequence of this probiotic strain.

In order to carry out the complete genome sequencing of *L. salivarius* LPM01, we used the massive sequencing technology as implemented at the PacBio platform (Pacific Biosciences, Menlo Park, CA). Purified DNA was obtained, and a 20-kb library was constructed. One single-molecule real-time (SMRT) cell was sequenced using P6-C4 chemistry and a data collection time of 4 h. Once filtered by quality, the sequencing run provided 92,286 sequences with an accuracy of Q20 and a mean read length of 23,939 nucleotides (nt). The total output was 1.88 Gb. A *de novo* assembly employed the default parameters with the Hierarchical Genome Assembly Process (HGAP) approach. The assembly process rendered two contigs of 1.788 Mb and 0.245 Mb, with coverage of 521×. The 0.245-Mb contig was circularized and suggested as a potential plasmid, showing 98% identity (63% coverage) to plasmid pMP1046A (*L. salivarius* JCM 1046, accession no. CP007647.1) and 94% identity (70% coverage) to plasmids pHN3 (*L. salivarius* CECT 5713, accession no. CP002037.1) and pMP118 (*L. salivarius* UCC 118, accession no. CP000234.1).

The assembled genome sequences were annotated using Prokka annotation pipeline (version 1.11 [5]), predicting tRNA, rRNA, and mRNA genes and signal peptides in the sequences using Aragorn, RNAmmer, Prodigal, and SignalP, respectively (6–9). Based on their similarity, putative gene products were assigned to the protein-coding genes (CDSs). CDSs were annotated by BLAST searching against the MvirDB database (virulence factors) and the CARD database (antibiotic resistance genes). GO terms were obtained by matching them to the reference proteins in the Swiss-Prot database.

The chromosome of strain LPM01 contains 1,813 elements, where 1,712 are open reading frames (ORFs) (1,570 canonical and 391 noncanonical), and 101 are structural RNAs (21 rRNA and 79 tRNA). The plasmid contains 250 elements (249 ORFs and one tRNA). The genome was compared with the reference strain *L. salivarius* UCC 118 (genome accession no. CP000233) with BLASTP (10), and 389 elements were not present in strain *L. salivarius* UCC 118. Specific plasmid ORFs were detected in 0.245-kb contig, confirming its status of plasmid. No remarkable antibiotic resistance or virulence-associated genes were found.

Accession number(s). The results of the whole-genome project have been deposited at the European Nucleotide Archive under the accession numbers LT604074 to LT604075. The version described herein is the first version.

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