Complete Genome Sequence of *Lactobacillus acidophilus* MN-BM-F01

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Lactobacillus acidophilus MN-BM-F01 was originally isolated from a traditional fermented dairy product in China. The characteristics of this bacterium are its low post-acidification ability and high acid-producing rate. Here, we report the main genome features of *L. acidophilus* MN-BM-F01.

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*L*actobacillus acidophilus is a lactic acid bacterium widely used by the dairy industry as a starter culture to obtain high-quality fermented products (1–3), such as cheeses and yogurt. *L. acidophilus* MN-BM-F01 was isolated from a traditional fermented dairy product called dairy fan, in the region of Yunnan province, China. The low post-acidification ability and high acid-producing rate of *L. acidophilus* are useful for dairy products, which can extend shelf life and shorten the milk coagulation time.

Whole-genome sequencing of *L. acidophilus* MN-BM-F01 was performed using the whole-genome shotgun strategy with Pacific Biosciences RS II sequencing platform (Pacific Biosciences, Menlo Park, CA, USA). A 10-kb single-molecule real-time (SMRT) bell library was prepared from sheared genomic DNA using a 10-kb template library preparation workflow. SMRT sequencing was conducted on a PacBio RS II sequencing platform using the C4 sequencing chemistry and P6 polymerase with 1 SMRT cell. *De novo* assembly of the PacBio read sequences was carried out using continuous long reads following the Hierarchical Genome Assembly Process (HGAP) workflow (PacBioDevNet; Pacific Biosciences) as available in SMRT Analysis version 2.1. The complete genome sequence of *L. acidophilus* MN-BM-F01 contains a circular 1,875,071-bp chromosome, with a GC content of 49.71%. In total, there are 2,121 predicted genes in the chromosome, including 2,010 protein-encoding genes, 87 tRNA-encoding genes, and 24 rRNA-encoding genes (4, 5).

The functions of predicted proteins were annotated based on the comparison of homologues to the NCBI-nr, Pfam, and KEGG databases. We have found that, of all the proteins in *L. acidophilus* MN-BM-F01, 507 have homologues in the eggNOG databases and

have been assigned proper terms. The remaining have no orthologous groups (with E-value <1E−5). Gene Ontology and KEGG analyses were performed by Blast2GO (6), and 981 and 968 genes, respectively, were assigned to proper terms.

Nucleotide sequence accession number. The sequence and annotation of the *Lactobacillus acidophilus* MN-BM-F01 genome is available from GenBank under accession number CP013610.

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