

Genome Sequence of *Lactobacillus mucosae* LM1, Isolated from Piglet Feces

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***Lactobacillus mucosae* LM1, isolated from stool samples of a healthy piglet, displays good *in vitro* mucin adhesion and antimicrobial activity against pathogenic bacteria. To elucidate its antimicrobial effects and to find its epithelial cell and mucin adhesion genes, the genomic sequence of *L. mucosae* LM1 was investigated.**

Lactobacillus mucosae, found in the mammalian gastrointestinal tract, has been shown to have the ability to adhere to mucosal surfaces (2, 3, 9). Previous reports have identified *L. mucosae* as having the ability to attach tightly to the epithelium of the human intestine and to produce antimicrobials and a biofilm when exposed to the physiological conditions of the gut (4). The adhesion of lactobacilli to gastrointestinal mucus makes them a good choice for probiotics since it increases their ability to colonize the gut efficiently, modulate the intestinal immune system, and inhibit pathogenic bacteria (1, 4, 9).

L. mucosae LM1 was isolated from stool samples from a healthy piglet (6). Preliminary trials regarding the adhesion and antibacterial activity of *L. mucosae* LM1 demonstrated good mucin-binding activity *in vitro* and antibacterial activity against pathogenic bacteria. The genome of *L. mucosae* LM1 was determined using a Roche 454 GS FLX sequencer and Illumina GA IIx platform. All reads were assembled into 55 contigs by *de novo* assembly. The initial draft assembly was prepared from the libraries of 22,092,187 reads (950× coverage) using Newbler Assembler 2.3 (Roche), CLC Genomics Workbench 4.8 (CLCbio), and CodonCode Aligner (CodonCode Co.). A functional annotation was performed by the Rapid Annotation using Subsystem Technology (RAST) server and BLASTP-based comparisons with the KEGG and COG databases.

The draft genome of *L. mucosae* LM1 included 2,213,697 bp with a 45.87% G+C content, 2,039 protein-coding genes, and 56 tRNA-encoding genes. Functions were assigned to 64.6% (1,318) of the total coding sequences; 8.7% (428) were found to be hypothetical proteins that are unique to this strain. A phylogenetic tree produced from the 16S rRNA genes revealed that strain LM1 is most closely related to *L. mucosae* CCUG 43169 (8). Likewise, 16S rRNA analysis showed strong homology to other *Lactobacillus* species with completed genomes, including *Lactobacillus reuteri* DSM 20016 (NCBI reference NC_009513.1), with 94% similarity, and *Lactobacillus fermentum* IF03956 (GenBank reference AP008937.1), with 95% similarity. The 16S rRNA gene sequence was extracted from whole-genome shotgun assemblies derived from the EzTaxon-e database (5).

An analysis of the *L. mucosae* LM1 genome revealed that LM1 has a specific mucus-binding protein (*mub*) gene (LBLM1_04370), which showed 95% coverage and 93% similarity to the best-matched *L. reuteri mub* gene. The mucus-binding activity induced by this *mub* gene has antimicrobial effects through cell surface protection (7, 8). Moreover, the *L. mucosae* LM1 genome includes a putative ABC transporter and adhesin-like protein (LBLM1_10110) with signifi-

cant homology (100% coverage and 93% similarity) to *L. mucosae* ABC 2745, which has specific affinity for the human blood group antigens A and B and which protects against the attachment of pathogenic bacteria (9). The *mub* and adhesin-like protein homologs in the *L. mucosae* LM1 genome indicate that LM1 may be useful in competitive exclusion against pathogens through blood group antigen receptors in the human gastrointestinal mucosa (9).

Nucleotide sequence accession number. The draft genome sequence of *L. mucosae* LM1 has been deposited in NCBI GenBank under accession number AHIT00000000.

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