Genome Sequence of *Lactobacillus amylovorus* GRL1118, Isolated from Pig Ileum[▽]

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***Lactobacillus amylovorus* is a common member of the beneficial microbiota present in the pig gastrointestinal tract. Here, we report the genome sequence of the surface layer (S-layer) protein-carrying and potentially probiotic strain *L. amylovorus* GRL1118, which was isolated from porcine ileum and which shows strong adherence to pig intestinal epithelial cells.**

The porcine gastrointestinal tract is colonized by a complex mixture of bacteria, which performs various functions that are beneficial to the host. Unlike in humans, lactobacilli are the dominant lactic acid bacteria (LAB) in the pig intestine (12). Comparative genomics of LAB has revealed the existence of a large inter- and intraspecies genomic diversity (9, 15), and the actual capacities of these microbes can be predicted by their genome sequences.

L. amylovorus is an abundant *Lactobacillus* species found in the intestines of piglets that has exhibited several potential probiotic properties, such as antimicrobial activity against enteric pathogens, in both *in vitro* and *in vivo* trials (10, 11, 17). *L. amylovorus* GRL1118 is a Gram-positive, nonmotile, anaerobic, rod-shaped bacterium that was isolated from porcine ileum (14). It shows features typical of homofermentative *Lactobacillus* species, like the production of large quantities of lactic acid and small amounts of acetic acid but no gas from glucose. It requires a number of vitamins for growth. *L. amylovorus* does not exhibit oxidase-, catalase-, or nitrate-reducing activities (16) and is a member of the *L. acidophilus* group (8).

S-layers are considered to protect the cell from hostile environmental agents and aid in maintaining cellular integrity, as they are the outermost paracrystalline structure (2). S-layer proteins from *Lactobacillus brevis*, *Lactobacillus crispatus*, and *Lactobacillus acidophilus* have been shown to confer adherence to host epithelial cells and extracellular matrix components (3, 6, 18).

L. amylovorus is one of the dominant S-layer-carrying *Lactobacillus* species in pigs, showing strong adherence to the pig intestinal epithelial cells and being of interest because of its potential probiotic properties (7, 13).

The entire genome of *L. amylovorus* GRL1118 was sequenced using a Roche 454 Life Sciences GS FLX system (27× coverage). The obtained sequences were assembled using

Newbler, and the gaps between contigs were closed by sequencing direct PCR or linker PCR products using BigDye chemistry and an ABI3730 capillary sequencer (Applied Biosystems). PCR products containing long repetitive areas were cloned using a BigEasy v2.0 linker cloning kit (Lucigen Corp.). The obtained clones were sequenced using a template generation system II kit (Finnzymes, Finland) (5). The viewing and editing of the sequences were done using Gap4 in the Staden package (19).

Coding sequences (CDSs) were predicted using a combination of GeneMark and Glimmer3 (4, 14) followed by manual curation of the start sites. The remaining intergenic regions were reanalyzed for missed CDSs by using BlastX (1). Annotation transfer was performed based on a BlastP search, followed by PGAAP analysis (http://www.ncbi.nlm.nih.gov/genomes/static/Annotation_pipeline_procedures.txt) and manual verification.

The genome of *L. amylovorus* GRL1118 contains a single circular chromosome of 1,894,401 bp and two circular plasmids of 78,145 bp and 4,541 bp (the plasmid sequences are not included in this article). The overall G+C content of the chromosome is 38.1%. The chromosome contains 1,842 protein-coding genes, 62 tRNA genes, and 12 rRNA genes. A putative function could be predicted for 1,347 (73.13%), whereas 495 (26.87%) of the CDSs were annotated as hypothetical proteins.

Nucleotide sequence accession number. The complete genome sequence of *L. amylovorus* GRL1118 is available in GenBank under accession number CP002609.

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