JOURNAL OF BACTERIOLOGY, Feb. 2011, p. 789–790 0021-9193/11/\$12.00 doi:10.1128/JB.01365-10 Copyright © 2011, American Society for Microbiology. All Rights Reserved.

## Genome Sequence of Lactobacillus amylovorus GRL1112<sup>∇</sup>

Ravi Kant, 1\* Lars Paulin, 2 Edward Alatalo, 2 Willem M. de Vos, 1,3 and Airi Palva 1\*

Department of Veterinary Biosciences, Faculty of Veterinary Medicine, FIN-00014 University of Helsinki, Helsinki, Finland<sup>1</sup>; Institute of Biotechnology, FIN-00014 University of Helsinki, Helsinki, Finland<sup>2</sup>; and Laboratory of Microbiology, Wageningen University, Wageningen, Netherlands<sup>3</sup>

Received 17 November 2010/Accepted 19 November 2010

Lactobacillus amylovorus is a common member of the normal gastrointestinal tract (GIT) microbiota in pigs. Here, we report the genome sequence of *L. amylovorus* GRL1112, a porcine feces isolate displaying strong adherence to the pig intestinal epithelial cells. The strain is of interest, as it is a potential probiotic bacterium.

Recently, a new abundant Lactobacillus species was identified in the intestine of piglets and found to possess probiotic properties, like antimicrobial activity against enteric pathogens in both in vitro and in vivo trials (9, 10, 14). While first classified as Lactobacillus sobrius, subsequent taxonomic studies revealed it to belong to the Lactobacillus amylovorus group that is abundant among Lactobacillus species originating from porcine intestine (7). L. amylovorus is an anaerobic, Gram-positive, nonmotile, non-spore-forming, and rod-shaped bacterium that grows in short chains. It shows features typical of homofermentative Lactobacillus species, like 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 nitratereducing activities (13). According to taxonomic studies, L. amylovorus is a member of the L. acidophilus group. Regarding the cell surface structures of lactobacilli, L. amylovorus has also been suggested to be one of the dominant S-layer-carrying Lactobacillus species in pigs (8).

As the outermost paracrystalline structures, S-layers are considered to protect the cell from hostile environmental agents and to aid in maintaining cellular integrity (2). Several *Lactobacillus* S-layer proteins (Slp), like those from *L. brevis*, *L. crispatus*, and *L. acidophilus*, have also been shown to confer adherence to host epithelial cells and extracellular matrix components (4, 6, 15).

L. amylovorus strain GRL1112 was originally isolated from porcine feces and found to be an abundant colonizer of the gastrointestinal tract (GIT) in pigs (11). Being an Slp carrier, GRL1112 also displays a strong adherence to the pig intestinal epithelial cells and has been further studied for its potential probiotic properties (11).

The GRL1112 genome was sequenced (14-times coverage) using a 454 pyrosequencer with GS FLX chemistry (Roche). The contig order was confirmed, and gaps were filled by se-

The genome of *L. amylovorus* GRL1112 contains a single circular chromosome of 2.07 million base pairs (Mbp) and two circular plasmids of 25 kbp and 33 kbp (the plasmid sequences are not included in this article). The overall G+C content of the chromosome is 38.2%, whereas two plasmids have G+C contents of 36.3% and 31.8%. The chromosome contains 2,054 CDSs, 60 tRNA genes, and 4 rRNA operons. Out of the predicted CDSs, a putative function was assigned to 1,441 (70.2%), whereas 613 (29.8%) of the CDSs were annotated as hypothetical proteins, and of those 317 were novel. Based on the orthologous grouping, about 470 (22.8%) of the CDSs encoded by GRL1112 have no detectable homologs in any of the complete *Lactobacillus* genomes published to date.

**Nucleotide sequence accession number.** The genome sequence of *L. amylovorus* GRL1112 was deposited in GenBank under accession number CP002338.

Work was supported by Center of Excellence in Microbial Food Safety Research (MiFoSa), Academy of Finland (R.K.).

R.K. thanks Ilkka Palva for valuable discussions and for reading the manuscript.

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quencing PCR fragments from the genomic DNA template using ABI 3730 and BigDye chemistry (Applied Biosystems). Genomic data were processed using the Staden Package (16) and gsAssembler (Roche). Coding sequences (CDSs) were predicted using a combination of GeneMark and Glimmer3 (5, 12) 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. Orthologous groups between the different lactobacillar proteomes were identified using EDGAR (3).

<sup>\*</sup> Corresponding author. Mailing address: Department of Veterinary Biosciences, Faculty of Veterinary Medicine, P.O. Box 66, FIN-00014 University of Helsinki, Helsinki, Finland. Phone for Ravi Kant: 358919157054. Fax: 358919157033. E-mail: ravi.kant@helsinki.fi. Phone for Airi Palva: 358919157058. Fax: 358919157033. E-mail: airi .palva@helsinki.fi.

<sup>&</sup>lt;sup>▽</sup> Published ahead of print on 3 December 2010.

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