

## Genome Sequence of *Lactobacillus johnsonii* PF01, Isolated from Piglet Feces<sup>∇</sup>

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***Lactobacillus johnsonii* PF01, an autochthonous bacterium of the gastrointestinal tract, was isolated from a fecal sample from a piglet. The strain adhered specifically to the duodenal and jejunal epithelial cells of the piglet and had high bile resistance activity. Here we report the genomic sequence of *L. johnsonii* PF01.**

Lactobacilli, important bacteria of the natural gut microbiome in animals, as well as humans, have been extensively investigated for their health-promoting properties (9). *Lactobacillus johnsonii* PF01, which was isolated from piglet feces, was previously identified as *L. acidophilus* (1). This strain adheres specifically to duodenal and jejunal epithelial cells in piglets and inhibits the growth of *Escherichia coli* K88 and *Salmonella* spp. (1). In addition, the strain has high bile resistance *in vitro* through bile salt hydrolase (BSH) activity against tauroconjugated bile salts. To elucidate these probiotic properties and to compare *L. johnsonii* PF01 with identical species of human origin, we determined the genomic sequence of the strain.

The genome of *L. johnsonii* PF01 was sequenced using a Roche 454 GS FLX platform. The initial draft assembly was prepared from the libraries of 419,265 reads (82-fold coverage; mean read length, 392 bp) using Newbler assembler 2.3 (Roche) and CodonCode Aligner (CodonCode Co.). Gap closure was carried out using standard PCR. The full annotation was performed by the RAST (rapid annotation using subsystem technology) server to predict open reading frames (ORFs) using Glimmer 3 (2, 3, 10). The predicted ORFs were annotated by searching against the Clusters of Orthologous Groups and SEED databases (4).

The genome consists of one chromosome (three contigs, 1,882,804 bp, 34.6% G+C) and two plasmids, pLJPF01L (25.8 kb) and pLJPF01S (13.9 kb). The chromosome has 1,846 coding sequences, 34 tRNA genes, and 9 rRNA genes. Among the 1,846 predicted protein-coding sequences in the chromosome, 405 ORFs (21.9%) matched hypothetical protein sequences in the public database. Among the 1,846 genes, 31 (1.6%) were

unique to *L. johnsonii*. A phylogenetic tree based on 16S rRNA genes showed that strain PF01 is most closely related to *L. johnsonii* DPC 6026, which was also isolated from a porcine small intestine (6). The metabolic capabilities and biosynthetic pathways of PF01 are in accordance with the surrounding nutrient environment (6). The strain has several phosphotransferase systems and ABC transporters, enabling the utilization of sugars in the gastrointestinal tract, similar to other *L. johnsonii* strains and the closely related genomes of the acidophilus complex (6). The large plasmid (pLJPF01L) consists of 31 ORFs and is similar to *L. johnsonii* FI9785 plasmid p9785L (GenBank accession number FN357112); in fact, 39% of the sequences overlapped. However, the small plasmid, consisting of 15 ORFs, has no homology with any known plasmid.

Sequencing of the genome revealed genes implicated in bile acid tolerance. A reduced serum cholesterol concentration induced by BSH is one of the known probiotic effects of lactobacilli (5, 7). We found three different types of BSH genes, including choloylglycine hydrolase, and two types of bile transporter genes, including *uhpC* (5, 8), suggesting its potential as a probiotic bacterium.

**Nucleotide sequence accession number.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AFQJ00000000. The version described in this paper is the first version (accession no. AFQJ01000000).

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