Genome Sequence of *Lactobacillus johnsonii* PF01 Isolated from Piglet Feces

Je Hee Lee¹, Jong Pyo Chae⁴, Ji Yoon Lee⁵, Jong-Sung Lim⁵, Geun-Bae Kim⁶, Jun-Sang Ham⁷,
Jongsik Chun¹,²,³, and Dae-Kyung Kang⁴*

¹ Chunlab, Inc., Seoul National University, Seoul, Republic of Korea
² Institute of Molecular Biology and Genetics, Seoul National University, Seoul, Republic of Korea
³ School of Biological Sciences & Institute of Bioinformatics (BIOMAX), Seoul National University,
  Seoul, Republic of Korea
⁴ Department of Animal Resources Science, Dankook University, Cheonan, Republic of Korea
⁵ National Instrumentation Center for Environmental Management, Seoul National University, Seoul,
  Republic of Korea
⁶ Department of Animal Science and Technology, Chung-Ang University, Anseong, Republic of
  Korea
⁷ National Livestock Research Institute, Rural Development Administration, Suwon, Republic of
  Korea

* To whom correspondence should be addressed:

Dae-Kyung Kang, Ph.D.
e-mail: dkkang@dankook.ac.kr
Department of Animal Resources Science, Dankook University, #29 Anseo-dong, Cheonan,
Chungnam-do 330-714, Korea
Tel: 82-41-550-3655
Fax: 82-41-564-3655
Lactobacillus johnsonii PF01, an autochthonous bacterium of the gastrointestinal tract, was isolated from a fecal sample of piglet. The strain adhered specifically to the duodenal and jejunal epithelial cells of the piglet and had high bile resistance activity. Here, we report a genomic sequence of L. johnsonii PF01.

Lactobacilli, important bacteria of the natural gut microbiome in animals, including 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 activity in vitro through bile salt hydrolase (BSH) of 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 Rapid Annotation using Subsystem Technology (RAST) server to predict open reading frames (ORFs) using Glimmer 3 (2, 3, 10). The predicted ORFs were annotated by searching against clusters of orthologous group 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 CDSs, 34 tRNA genes, and 9 rRNA genes. Among the 1,846 predicted protein-coding sequences in the chromosome, 405 (21.9%) ORFs matched hypothetical protein sequences in the public database. Among the 1,846 genes, 31 (1.6%) were unique to L. johnsonii spp. 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 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 PTS systems and ABC transporters enabling the utilization of sugars in the GI 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 choloeylglycine 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 the accession AFQJ00000000. The version described in this paper is the first version, AFQJ01000000.

**Acknowledgements**

This work was supported by a grant from the Next-Generation BioGreen 21 Program (PJ00812701), Rural Development Administration, Republic of Korea.

**References**


