



Complete genome sequence of *Lactobacillus plantarum* SK151 isolated from kimchi

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김치로부터 분리한 *Lactobacillus plantarum* SK151의 유전체 염기서열 해독

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Lactobacillus plantarum is a Gram-positive, facultative heterofermentative, nonspore-forming nonmotile bacterium found in a wide range of environmental niches. Here we present the complete genome sequence of *L. plantarum* SK151 isolated from kimchi, which shows high adhesion to intestinal epithelial cells. The genome is 3,231,249 bp in length and has a GC content of 44.6%. The genome contains genes related to cell adhesion and a complete operon for riboflavin biosynthesis.

Keywords: *Lactobacillus plantarum*, adhesion, kimchi, riboflavin synthesis

Lactobacillus plantarum is a Gram-positive, facultative heterofermentative nonmotile rod (de Vries *et al.*, 2006; Siezen and van Hylckama Vlieg, 2011). It is found in a wide range of environmental niches (Siezen *et al.*, 2010), including vegetables (Jeon *et al.*, 2017; Son *et al.*, 2017), dairy products (Jia *et al.*, 2017), human saliva (Kleerebezem *et al.*, 2003), and the gastrointestinal tract (Ahrné *et al.*, 1998).

Many *L. plantarum* strains have been studied for their potential as a probiotic. In addition, some strains of *L. plantarum* are

found to be capable of producing riboflavin (vitamin B₂). This vitamin plays an important role as precursor of flavin mononucleotide and flavin adenine dinucleotide which are coenzymes for several reduction-oxidation reactions (Akimoto *et al.*, 2006; Arena *et al.*, 2014). Riboflavin should be supplied via foods because humans cannot synthesize this vitamin in the body (Arena *et al.*, 2014). Up to now, the biosynthetic mechanism of riboflavin in *L. plantarum* has not been studied extensively yet. A complete riboflavin operon was observed in *L. plantarum* SK151, showing high adhesion to intestinal epithelial cells, which was isolated from kimchi previously (unpublished data). Here we present the complete genome sequence of *L. plantarum* SK151.

L. plantarum SK151 was grown in de Man, Rogosa and Sharpe (MRS, Difco Laboratory) broth at 37°C for 12 h. The genomic DNA was prepared as described previously (Valeriano *et al.*, 2017), and the DNA concentration and quality were checked using a spectrophotometer (UV-1601PC; Shimadzu). The genomic DNA of strain SK151 was sequenced using the PacBio RSII platform (ver. 2.0; Pacific Biosciences). The PacBio reads (1,159,300,410 bases; 150,226 reads) were *de novo* assembled using the RS hierarchical genome assembly

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Table 1. Genome features of *Lactobacillus plantarum* SK151

| Attribute | Value |
|----------------------|-----------|
| Genome size (bp) | 3,231,249 |
| GC content (%) | 44.6 |
| No. of contigs | 1 |
| Total genes | 3,074 |
| Protein-coding genes | 3,043 |
| tRNAs | 68 |
| rRNAs | 16 |

process (HGAP ver. 3.0), which produced one large circular scaffold (Fig. 1). Genome annotation was conducted with Rapid Annotation using Subsystem Technology (RAST) using default parameters (Aziz *et al.*, 2008). Functional annotations of protein coding sequences were predicted and categorized using the SEED Viewer (Overbeek *et al.*, 2014). Transfer RNAs (tRNAs) were predicted using tRNAscan-SE 2.0 (Lowe and Chan, 2016), and ribosomal RNAs (rRNAs) were searched using the Basic Rapid Ribosomal RNA Predictor (BARRNAP

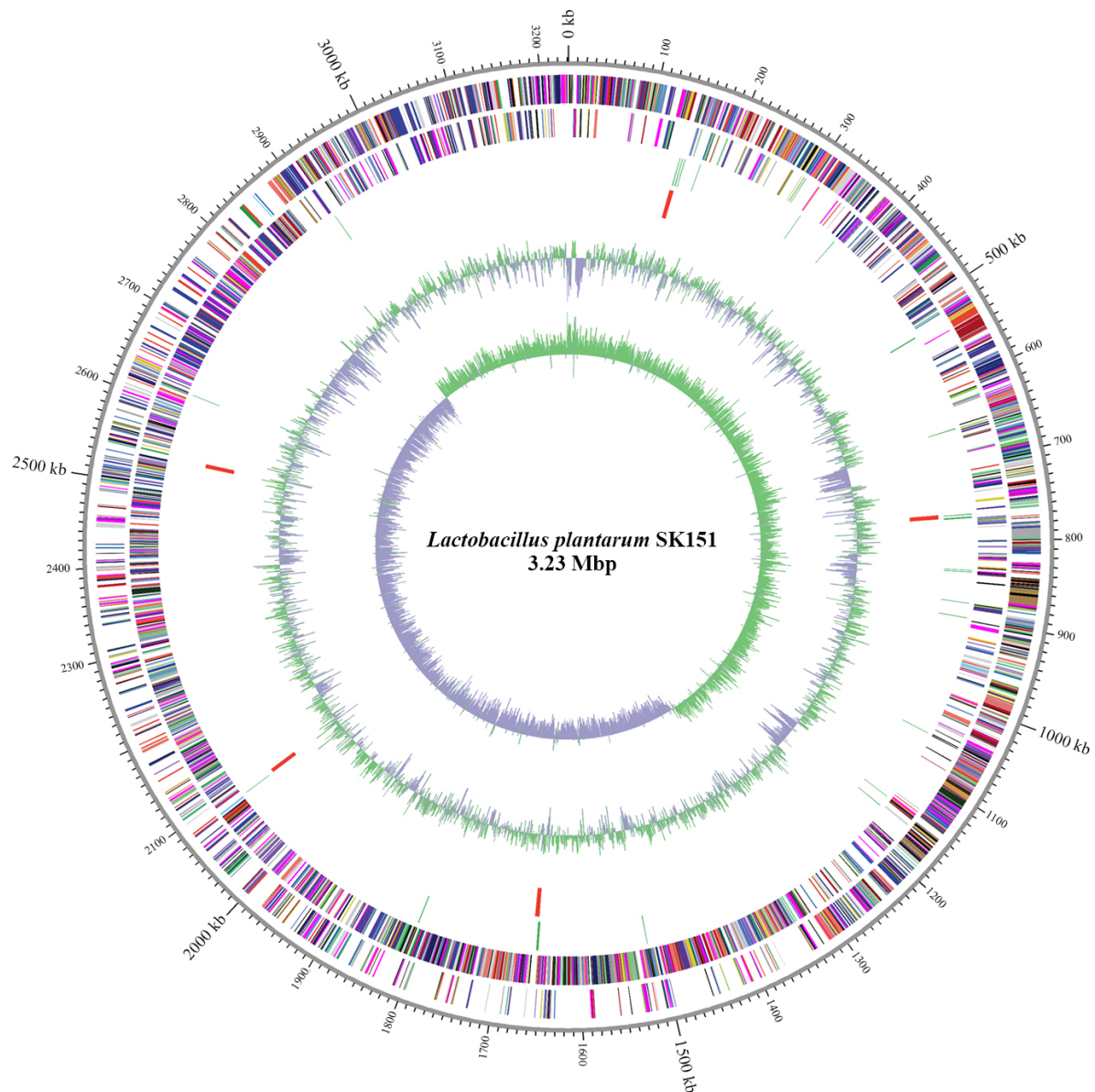


Fig. 1. Chromosome map of *Lactobacillus plantarum* SK151. Circles illustrate the following characteristics from the outside to the center: (1) coding sequences on forward strand, (2) coding sequences on reverse strand, (3) Transfer RNAs (tRNAs), (4) ribosomal RNAs (rRNAs), (5) GC content, and (6) GC skew.

ver. 0.7). The complete genome of *L. plantarum* SK151 is 3,231,249 bp in length and has a GC content of 44.6% (Table 1). A total of 3,043 predicted coding sequences (CDS), 16 rRNAs, and 68 tRNAs were annotated (Table 1).

Genes involved in cell adhesion, such as fibronectin binding protein, chaperonin, several putative internalin genes with mucin-binding protein (MucBP) domain, and a putative internalin with LPXTG motif were identified. In addition, the genome contained oxidative stress response genes such as catalase, nicotinamidase, ferroxidases, organic hydroperoxide resistance transcriptional regulator, peroxidase stress regulator PerR, and putative Holliday junction resolvase YggF. Furthermore, a complete riboflavin operon was found within the genome: *ribG* [bifunctional di-aminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase], *ribB* (riboflavin synthase), *ribA* (3,4-dihydroxy-2-butanone 4-phosphate synthase), and *ribH* (6,7-dimethyl-8-ribityllumazine synthase). The genomic information of *L. plantarum* SK151 will be helpful to understand the biosynthetic mechanism of riboflavin in lactobacilli as well as adhesion into intestinal epithelial cells.

Nucleotide sequence accession number

The whole-genome sequence was deposited in GenBank under accession number NZ_CP030105.

적 요

*Lactobacillus plantarum*은 그람 양성, 비운동성의 이형발효세균이며, 다양한 환경에서 서식하고 있다. *L. plantarum* SK151은 장관상피세포 흡착능이 우수한 균주로서, 김치로부터 분리되었다. SK151 균주의 유전체 길이는 3,231,249 염기 쌍이며, G + C 함량은 44.6%이었다. SK151 균주의 유전체에는 비타민 B₂ (리보플라빈) 생합성에 필요한 유전자군이 완벽하게 존재하고 있었으며, 세포 흡착과 관련된 유전자도 다수 존재하고 있었다.

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