

Complete genome sequence of *Lactobacillus plantarum* SK156, a candidate vehicle for mucosal vaccine delivery

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Competing interests

No potential conflict of interest relevant
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Abstract

Lactobacillus plantarum SK156 was isolated from traditional Korean food. The genome of SK156 strain consists of a circular chromosome (3,231,383 bp) with guanine (G) + cytosine (C) content of 44.56%. Among the predicted 2,991 protein-coding genes, the genome included genes encoding for α -amylase, which hydrolyzes α -bonds of polysaccharides. Genomic sequencing of *L. plantarum* SK156 will give information on the mechanism involved in the enzymatic degradation of polysaccharides and its application for improving feed efficiency.

Keywords: Genome, *Lactobacillus plantarum*, α -Amylase

In our previous study, *Lactobacillus plantarum* SK156, originally isolated from traditional Korean food, was revealed to be an effective host for the expression of bioactive substances in the intestine [1]. The SK156 strain expressed the antigens of porcine epidemic diarrhea virus on its cell surface, which causes acute watery diarrhea in pigs, inducing both immune responses in mice following oral administration (unpublished data); these findings suggested that SK156 is a promising candidate vehicle for mucosal vaccine delivery in animals. For complete genome analysis, *L. plantarum* SK156 was grown in de Man, Rogosa, and Sharpe (MRS) Broth (Difco, Franklin Lakes, NJ, USA) at 37°C for 12 h. Genomic DNA of SK156 strain was prepared as described previously [2] and its quality was validated using spectrophotometry (UV-1601PC, Shimadzu, Kyoto, Japan). The genomic DNA of *L. plantarum* SK156 was sequenced using the PacBio RSII platform ver. 2.0 (Pacific Biosciences, Menlo Park, CA, USA) at Macrogen (Seoul, Korea), and then all reads were *de novo* assembled using the RS HGAP Assembly ver. 3.0 protocol [3]. Functional annotation was performed using the InterProScan ver. 5.30–69.0 (<http://www.ebi.ac.uk/interpro/>), GO (<http://geneontology.org/page/go-database>), BLAST ver. 2.6.0+ (<http://blast.ncbi.nlm.nih.gov/>) with UniProt ver. 2018_06 (<http://www.uniprot.org/>), and EggNOG ver. 4.5 (<http://eggnogdb.embl.de/#/app/home>) databases. The genome of *L. plantarum* SK156 was submitted into GenBank (<https://www.ncbi.nlm.nih.gov/>) under accession no. CP059473.

The genome of SK156 strain consists of a circular chromosome (3,231,383 bp) with guanine (G) + cytosine (C) content of 44.56% (Table 1), and no plasmids were detected (Fig. 1). A total of 2,991 protein-coding sequences, 65 tRNAs and 16 rRNAs were annotated (Table 1). Genomic sequence analysis showed that SK156 possessed genes encoding for α -amylase enzyme, which hydrolyzes α -bonds of polysaccharides and generate malto-oligosaccharides in animal feed [4–6]. Genomic sequencing of *L.*

Availability of data and material

Upon reasonable request, the datasets of this study can be available from the corresponding author.

Authors' contributions

Conceptualization: Hwang IC, Kim SH, Kang DK.

Data curation: Kim SH.

Formal analysis: Hwang IC, Kim SH.

Methodology: Hwang IC, Kim SH.

Validation: Kang DK.

Investigation: Kim SH.

Writing - original draft: Hwang IC, Kim SH, Kang DK.

Writing - review & editing: Kang DK.

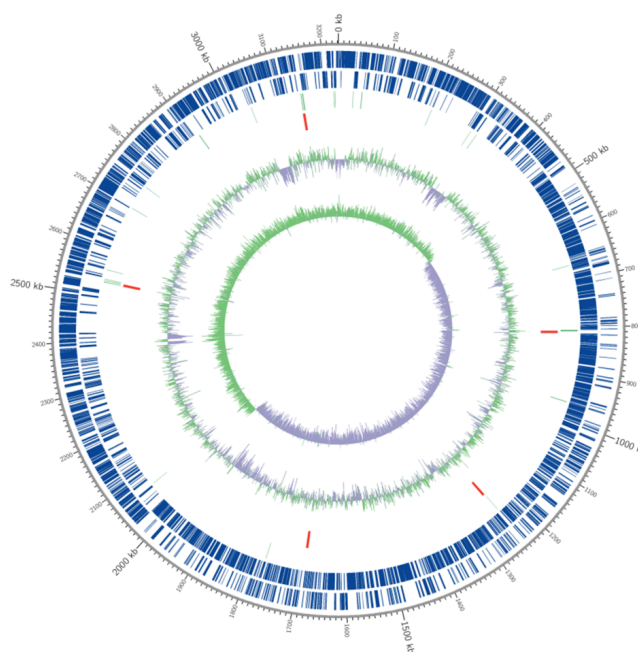
Ethics approval and consent to participate

This article does not require IRB/IACUC approval because there are no human and animal participants.

Table 1. Genome features of *Lactobacillus plantarum* SK156

Attribute	Value
Genome size (base pair)	3,231,383
GC content (%)	44.56
Number of contigs	1
Total genes	3,072
Protein-coding genes	2,991
tRNAs	65
rRNAs	16

GC, guanine-cytosine.



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.

Fig. 1. Chromosome map of *Lactobacillus plantarum* SK156. GC, guanine-cytosine.

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