Complete genome and two plasmids sequences of *Lactiplantibacillus plantarum* L55 for probiotic potentials
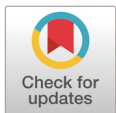
Bogun Kim[1], Kiyeop Kim[2], Xiaoyue Xu[1], Hyunju Lee[1], Duleepa Pathiraja[1], Dong-June Park[3], In-Geol Choi[1]* and Sejong Oh[2]*

[1]*Department of Biotechnology, College of Life Sciences and Biotechnology, Korea University, Seoul 02841, Korea*
[2]*Division of Animal Science, Chonnam National University, Gwangju 61186, Korea*
[3]*Korea Food Research Institute, Wanju 55365, Korea*

*Corresponding author
In-Geol Choi
Department of Biotechnology, College of Life Sciences and Biotechnology, Korea University, Seoul 02841, Korea.
Tel: +82-2-3290-3152
E-mail: igchoi@korea.ac.kr

Sejong Oh
Division of Animal Science, Chonnam National University, Gwangju 61186, Korea.
Tel: +82-62-530-2116
E-mail: soh@jnu.ac.kr

ORCID
Bogun Kim
https://orcid.org/0000-0002-5493-1674
Kiyeop Kim
https://orcid.org/0000-0002-1072-4032
Xiaoyue Xu
https://orcid.org/0000-0001-9654-8676
Hyunju Lee
https://orcid.org/0009-0000-5423-4812

Abstract

In this study, we report the complete genome sequence of *Lactiplantibacillus plantarum* L55, a probiotic strain of lactic acid bacteria isolated from kimchi. The genome consists of one circular chromosome (2,077,416 base pair [bp]) with a guanine cytosine (GC) content of 44.5%, and two circular plasmid sequences (54,267 and 19,592 bp, respectively). We also conducted a comprehensive analysis of the genome, which identified the presence of functional genes, genomic islands, and antibiotic-resistance genes. The genome sequence data presented in this study provide insights into the genetic basis of *L. plantarum* L55, which could be beneficial for the future development of probiotic applications.

Keywords: *Lactiplantibacillus plantarum*, L55, Complete genome sequence, Probiotics

Lactic acid bacteria (LAB) are known for their ability to convert carbohydrates to lactic acid, which helps to maintain the appropriate environment of the host gut and can have beneficial effects on the health of humans and animals. *Lactiplantibacillus plantarum*, formerly named *Lactobacillus plantarum*, can be found in various environments such as dairy products, fermented sausages, meat, fish, vegetables, and human feces. The *L. plantarum* strain is also present in the gut microbiota of healthy individuals and has been shown to have various health benefits for its host. Some of the benefits include improved digestion, enhanced immune system function, and reduced inflammation [1,2]. *L. plantarum* L55 is a probiotic strain of bacteria that has been isolated from kimchi and has been found to be highly resistant to acidic conditions and bile salts, making it a good candidate for use as a probiotic supplement and starter culture for yogurt.

The genome of *L. plantarum* is relatively large, ranging from 2.8 to 3.3 megabases, and exhibits high variability among different strains. The *L. plantarum* genome encodes for a diverse array of genes, which are involved in a range of biological processes, including carbohydrate metabolism, amino acid biosynthesis, and stress responses. This genetic diversity is thought to contribute to the adaptability of *L. plantarum* to different environments and its ability to compete with other bacteria.

Duleepa Pathiraja
https://orcid.org/0000-0001-6239-5958
Dong-June Park
https://orcid.org/0000-0001-9452-9391
In-Geol Choi
https://orcid.org/0000-0001-7403-6274
Sejong Oh
https://orcid.org/0000-0002-5870-3038

Competing interests
No potential conflict of interest relevant to this article was reported.

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

Authors' contributions
Conceptualization: Choi IG, Oh S.
Data curation: Kim K, Choi IG, Oh S.
Formal analysis: Kim B.
Methodology: Kim B, Pathiraja D.
Software: Kim B, Xu X, Lee H, Pathiraja D.
Validation: Kim B, Xu X, Lee H, Pathiraja D.
Investigation: Kim K.
Writing - original draft: Kim B, Choi IG, Oh S.
Writing - review & editing: Kim B, Kim K, Xu X, Lee H, Pathiraja D, Park DJ, Choi IG, Oh S.

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

Using de Man-Rogosa-Sharpe (MRS) medium (Becton, Dickinson, Rungis, France), *L. plantarum* L55 was grown for 24 h at 37℃. HiGene™ Genomic DNA Prep kit (BIOFACT, Daejeon, Korea) was used to extract genomic DNA in accordance with the manufacturer's instructions. We used an Illumina® DNA Prep kit to assemble our short-read sequencing library (Illumina, San Diego, CA, USA). Short-read sequencing (300 base pair [bp], paired-end) was carried out on the Illumina MiSeq platform with the Illumina MiSeq reagent kit V3 (Illumina). The Oxford Nanopore Ligation Sequencing kit was used for the library preparation of long-read sequencing (Oxford Nanopore, Oxford, UK). The MinION sequencing instrument (Oxford Nanopore) with a MinION flow cell (R9.4.1) was used for the long-read sequencing (Oxford Nanopore). 675,276 paired-end reads (165,535,022 bp) were obtained from Illumina short-read sequencing, while 251,401 reads averaging 1,342 bases in length were obtained from Oxford Nanopore long-read sequencing.

The *de novo* genome sequence was assembled using a Flye assembler (v. 2.9) [3] with default options. Adapter sequence removal and quality control of short-reads were performed using TrimGalore (v. 0.6.7) [4] with the "paired" parameter. The quality of the draft genome assembly was improved by correcting errors with Pilon (v. 1.24) [5] with default parameters. Gene predictions for the chromosome and plasmid sequences were performed with Prokka (v. 1.14.5) [6]. An assessment for genome assembly completeness was conducted by BUSCO (v. 5.2.2) [7] using the OrthoDB v10 bacterial (bacteria_odb10) lineage dataset.

The complete genome sequence of *L. plantarum* L55 consisted of one circular chromosome (3,301,852 bp) with an overall GC content of 44.5% and two circular plasmid sequences of 54,267 bp and 19,592 bp, respectively (Table 1).

The sequences of the genome and the plasmids predicted a total of 3,231 genes, including 3,149 genes that code for proteins, 16 genes for ribosomal RNA, and 66 genes for transfer RNA (Fig. 1).

Functional annotation of the predicted genes was performed with EggNOG-mapper (v. 2.1.9) [8] using EggNOG database version 5.0.2 [9]. Within the total of 3,149 protein-coding genes, biological functions were defined for 2,678 (85.04%). Annotated genes were associated with transcription (290), translation (168), cellular envelope biogenesis (155), energy production (116), secretion (62), signal transduction (53) and secondary metabolite biosynthesis (15). Moreover, each gene was assigned with a putative function.

Folate and riboflavin biosynthesis, molybdopterin biosynthesis, sulfur metabolism, cellulose degradation, terpenoid and polyketide biosynthesis, and bacteriocin production were some of the functions that were postulated to be carried out by *L. plantarum* L55.

NUCLEOTIDE SEQUENCE ACCESSION NUMBER

The complete genome sequence has been deposited in the NCBI GenBank under the accession number GCA_026153115.1. The BioProject accession number is PRJNA893861 and the

Table 1. Genome features of *Lactiplantibacillus plantarum* L55.

	Length (bp)	GC (%)	Depth	CDSs	tRNA	rRNA
Chromosome	3,301,852	44.5	66.0	3,079	66	16
Plasmid1	54,267	39.1	327.0	48	0	0
Plasmid2	19,592	40.5	405.0	22	0	0
Total	3,375,711	44.4	72.2	3,149	66	16

bp, base pair; G, guanine; C, cytosine; tRNA, transfer RNA; rRNA, ribosomal RNA.
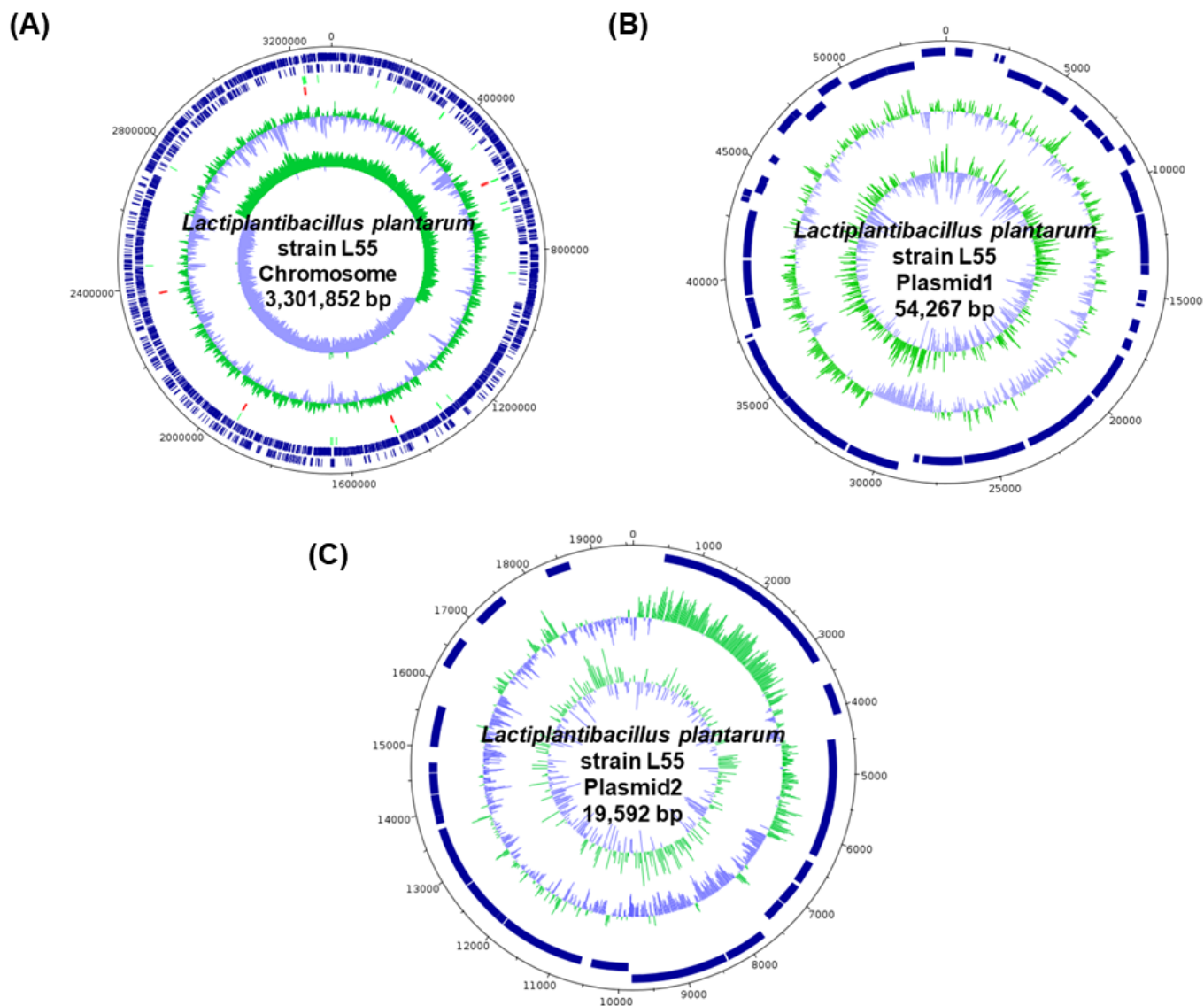
Fig. 1. Circular chromosome and plasmid maps of *Lactiplantibacillus plantarum* L55. From the periphery to the center, marked features are as follows: protein-coding sequences on the forward strand, protein-coding sequences on the reverse strand, tRNA, rRNA, GC ratio, and GC skew. (A) Chromosome, (B) plasmid1, (C) plasmid2. bp, base pair; G, guanine; C, cytosine; tRNA, transfer RNA; rRNA, ribosomal RNA.

BioSample accession number is SAMN31433308.

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