

1 **Genome Announcement**

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3 **Complete genome and two plasmids sequences of *Lactiplantibacillus***
4 ***plantarum* L55 or probiotic potentials**

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20 **Abstract**

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

29 **Keywords:** *Lactiplantibacillus plantarum*; L55; complete genome sequence; probiotics

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

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

49 Using de Man-Rogosa-Sharpe (MRS) medium (Becton, Dickinson, France), *L. plantarum*
50 L55 was grown for 24 h at 37 °C. HiGene™ Genomic DNA Prep kit (BIOFACT, Daejeon,
51 Korea) was used to extract genomic DNA in accordance with the manufacturer's instructions.
52 We used an Illumina® DNA Prep kit to assemble our short-read sequencing library (Illumina,
53 San Diego, USA). Short-read sequencing (300 bp, paired-end) was carried out on the
54 Illumina MiSeq platform with the Illumina MiSeq reagent kit V3 (Illumina). The Oxford

55 Nanopore Ligation Sequencing kit was used for the library preparation of long-read
56 sequencing (Oxford Nanopore, Oxford, UK). The MinION sequencing instrument (Oxford
57 Nanopore) with a MinION flow cell (R9.4.1) was used for the long-read sequencing (Oxford
58 Nanopore). 675,276 paired-end reads (165,535,022 bp) were obtained from Illumina short-
59 read sequencing, while 251,401 reads averaging 1,342 bases in length were obtained from
60 Oxford Nanopore long-read sequencing.

61 The de novo genome sequence was assembled using a Flye assembler (v. 2.9) [1] with default
62 options. Adapter sequence removal and quality control of short-reads were performed using
63 TrimGalore (v. 0.6.7) [2] with the “paired” parameter. The quality of the draft genome
64 assembly was improved by correcting errors with Pilon (v. 1.24) [3] with default parameters.
65 Gene predictions for the chromosome and plasmid sequences were performed with Prokka (v.
66 1.14.5) [4]. An assessment for genome assembly completeness was conducted by BUSCO (v.
67 5.2.2) [5] using the OrthoDB v10 bacterial (bacteria_odb10) lineage dataset.

68 The complete genome sequence of *L. plantarum* L55 consisted of one circular chromosome
69 (3,301,852 bp) with an overall GC content of 44.5% and two circular plasmid sequences of
70 54,267 bp and 19,592 bp, respectively (Table 1).

71 The sequences of the genome and the plasmids predicted a total of 3,231 genes, including
72 3,149 genes that code for proteins, 16 genes for ribosomal RNA, and 66 genes for transfer
73 RNA (Fig. 1).

74 Functional annotation of the predicted genes was performed with EggNOG-mapper (v. 2.1.9)
75 [6] using EggNOG database version 5.0.2 [7]. Within the total of 3,149 protein-coding genes,
76 biological functions were defined for 2,678 (85.04%). Annotated genes were associated with
77 transcription (290), translation (168), cellular envelope biogenesis (155), energy production

78 (116), secretion (62), signal transduction (53) and secondary metabolite biosynthesis (15).

79 Moreover, each gene was assigned with a putative function.

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

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84 **DISCLOSURE STATEMENT**

85 No potential conflicts of interest were reported by the authors.

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93 **DATA AVAILABILITY**

94 The complete genome sequence has been deposited in the NCBI GenBank under the accession
95 number GCA_026153115.1. The BioProject accession number is PRJNA893861 and the
96 BioSample accession number is SAMN31433308.

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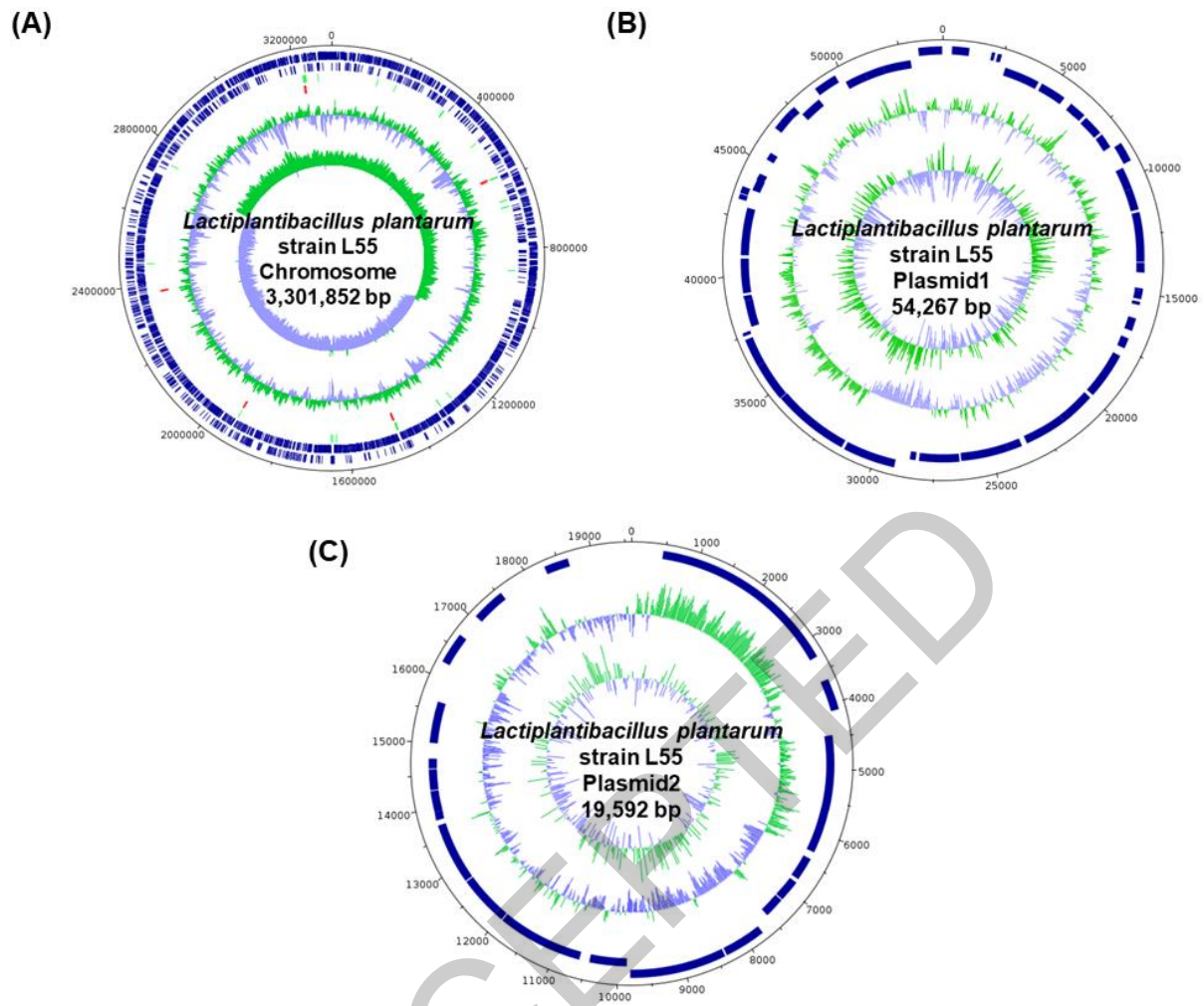
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121 Table 1. Genome features of *Lactiplantibacillus plantarum* L55.

	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

122 bp: base pair; G: guanine; C: cytosine; tRNA: transfer RNA; rRNA: ribosomal RNA.

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