



Genome Sequence of *Lactobacillus plantarum* KB1253, a Gamma-Aminobutyric Acid (GABA) Producer Used in GABA-Enriched Tomato Juice Production

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ABSTRACT Here, we present the draft genome sequence of *Lactobacillus plantarum* KB1253, isolated from a traditional Japanese pickle. Its genome comprises 3,097 genes and 3,305,456 nucleotides, with an average G+C content of 44.4%.

Gamma-aminobutyric acid (GABA), a 4-carbon nonproteinaceous amino acid found ubiquitously in nature, is associated with several well-characterized physiological functions (1–4). Many microorganisms can produce GABA, including bacteria, fungi, and yeasts, although lactic acid bacteria (LAB) are the most utilized GABA producers (5–8). GABA-producing LAB have been a focus of research in recent years because they possess unique physiological properties and are regarded as safe for use in the food industry (6, 9–11). Many food-derived lactobacilli produce GABA, including several strains of *Lactobacillus brevis* (12–16), *L. plantarum* (17–21), *L. buchneri* (6, 22–24), *L. paracasei* (13, 18, 21, 25), and single strains of *L. rhamnosus* (21, 25), *L. delbrueckii* (18, 25), and other species (25–29). Currently, there are no reports on the genetic basis of the technological and safety aspects of lactobacilli used in GABA-enriched tomato juice production.

We diluted a traditional Japanese pickle in saline, incubated the diluted solution on a de Man-Rogosa-Sharpe (MRS) agar (Oxoid, Cambridge, UK) plate for 24 h at 30°C, and obtained a single colony of strain KB1253. Genomic DNA was isolated from this single colony, which was grown in MRS broth overnight at 30°C under anaerobic conditions. DNA was extracted using a Genomic-tip 500/G kit (Qiagen, Valencia, CA). Detailed genome analyses will help elucidate the genetic basis of GABA production, favorable flavor, and food safety.

Libraries for sequencing were prepared at Genewiz, Inc. (South Plainfield, NJ), using a Nextera XT DNA library preparation kit (Illumina, San Diego, CA) following the manufacturer's recommended procedures. The sequencing libraries were sequenced on an Illumina MiSeq instrument using the MiSeq reagent kit version 2 for 2 × 250-bp paired-end reads. Sequence reads were trimmed to remove nucleotides with poor quality at the 3' end (error rate, <0.05). If there were two nucleotides with poor quality (error rate, <0.05), these nucleotides and all downstream nucleotides were removed. After trimming, reads with <100 bases were removed from subsequent assembly. A total of 30,678,684 reads were generated and assembled into 82 contigs using CLC Genomics Workbench 9.0 (Qiagen, Valencia, CA), with an N_{50} value of 120,850 bp and average read coverage of 1,654-fold. The 16S rRNA sequence from the assembled genome was compared to the NCBI 16S rRNA database via a blastn search, identifying the best hit to the *Lactobacillus plantarum* subsp. *plantarum* NBRC 15891 sequence (GenBank accession number [NR_113338](https://www.ncbi.nlm.nih.gov/nuccore/NR_113338); query coverage, 100%; identity, 99.93%). The genome annotation was performed by the DDBJ Fast Annotation and Submission Tool (DFAST) (30), an annotation server optimized for *Lactobacillus* spp. (6). The default

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settings were used. The final sequence is composed of 3,305,456 bp with 3,097 putative open reading frames (ORFs) and a G+C content of 44.4%.

The genome of strain KB1253 contains two *gadB* genes coding for glutamate decarboxylase. One is located next to *gadC* and likely regulated as a whole operon with *gts* (glutamyl-tRNA synthetase) and *gadR* (transcriptional regulator), as reported for *L. brevis* strains (31, 32); the other gene is located far from the operon. These genes may be involved in GABA synthesis in this strain. The genome also revealed the presence of gene clusters homologous to genes associated with the production of bacteriocins such as plantaricin.

We also surveyed the KB1253 genome for genes related to transferable antibiotic resistance and virulence factors, according to a previous report (33); however, as with previously sequenced *L. plantarum* strains, none were found. These data, supported by *in vivo* studies, confirm that KB1253 can be considered “generally recognized as safe” (GRAS) with “qualified presumption of safety” (QPS) status.

The genome sequence of *L. plantarum* KB1253 is a promising resource for further identification of genes involved in beneficial processes, such as the production of GABA and other metabolites related to favorable flavor during fermentation with tomato juice. In addition, these data contribute to the availability of GABA-producing *Lactobacillus* genome sequences and enable a better understanding of their potential technological and biofunctional properties.

Data availability. This whole-genome sequence was deposited at DDBJ/EMBL/GenBank under the accession numbers [BIFE01000001](#) to [BIFE01000082](#). The version described in this paper is the first version, BIFE01000000. Raw data were deposited in the Sequence Read Archive (SRA) under BioSample number [SAMN11080842](#) and SRA run number [SRR8693953](#), which are part of SRA study number [SRP187802](#).

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