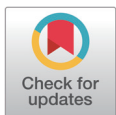


# Genome analysis of *Limosilactobacillus fermentum* JN2019 applied to tumeric fermentation for animal feed

Heeseop Yoo<sup>1,2#</sup>, Cheng Chung Yong<sup>2#</sup> and Sejong Oh<sup>2\*</sup>

<sup>1</sup>JNBIO, Jeongeup 56212, Korea

<sup>2</sup>Division of Animal Science, Chonnam National University, Gwangju 61186, Korea



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#These authors contributed equally to this work.

## \*Corresponding author

Sejong Oh

Division of Animal Science, Chonnam National University, Gwangju 61186, Korea.

Tel: +82-62-530-2116

E-mail: soh@jnu.ac.kr

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## ORCID

Heeseop Yoo

<https://orcid.org/0000-0003-2905-6676>

Cheng Chung Yong

<https://orcid.org/0000-0003-0531-6381>

Sejong Oh

<https://orcid.org/0000-0002-5870-3038>

## Competing interests

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

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## Abstract

*Limosilactobacillus fermentum* JN2019, formerly named *Lactobacillus fermentum* JN2019, was isolated from kimchi. Its genome was completely sequenced using the PacBio RSII sequencing system to explore beneficial phenotypes. In a previous study, *L. fermentum* JN2019 was used to ferment the by-product of tumeric for use in livestock feed. The 2.3 Mb genome had a high guanine (G) + cytosine (C) content of 50.6% and a 30 kb plasmid. The data will inform the comprehensive understanding of JN2019 and provide insights for potential applications.

**Keywords:** *Limosilactobacillus fermentum*, Kimchi, Whole-genome sequencing, Feed, *Lactobacillus*

## ANNOUNCEMENT

*Limosilactobacillus fermentum* (formerly named *Lactobacillus fermentum* JN2019) is commonly found in fermented food products and is generally considered safe [1]. *L. fermentum* has been regularly used for acid-producing starter cultures and acts as a food preservative [2]. In addition, JN2019 increases the bioavailability of curcumin, the active component of turmeric, while reducing cytotoxicity through fermentation [3]. In the present study, the JN2019 genome was sequenced to explore its genetic characteristics.

JN2019 was isolated from local fermented kimchi in Korea and grown in de Man-Rogosa-Sharpe (MRS) medium (Merck, Darmstadt, Germany). Genomic DNA (gDNA) was extracted with DNeasy Ultraclean microbial kit (Qiagen, Hilden, Germany), according to the manufacturer's instructions. The gDNA was sequenced using single molecular real-time (SMRT) portal (v.2.3) with the PacBio RS II system (Pacific Biosciences, Menlo Park, CA, USA). A total of 43,479,132 reads (6,565,348,932 total bases) were generated using SMRT sequencing. Gene neighborhood analysis illustrating the closest genome to JN2019 was *L. fermentum* strain DR9 (98.26%), followed by strain FTDC 8312 (85.60%). Although pronounced similarity to strain DR9 was observed, the value fell below the species recognition threshold of 98.6% [4], clarifying the identity of JN2019 as *L. fermentum*. The genome sequences were annotated by the NCBI Prokaryotic Genomes Annotation Pipeline.

The complete genome of JN2019 consists of two contigs within the 2.3 Mb genome (G + C content

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Not applicable.

**Availability of data and material**

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

**Authors' contributions**

Conceptualization: Oh S.  
Data curation: Yoo H, Yong CC.  
Formal analysis: Yoo H, Yong CC.  
Methodology: Yoo H.  
Investigation: Yoo H.  
Writing - original draft: Yong CC, Oh S.  
Writing - review & editing: Yong CC, Oh S.

**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 *Limosilactobacillus fermentum* JN2019**

	Chromosome	Plasmid
Genome size (bp)	2,298,221	29,243
G + C content (%)	50.6	40.8
Gene	2,359	34
Pseudogene	206	6
Protein	2,077	28
rRNA	15	-
tRNA	58	-
Other RNA	3	-

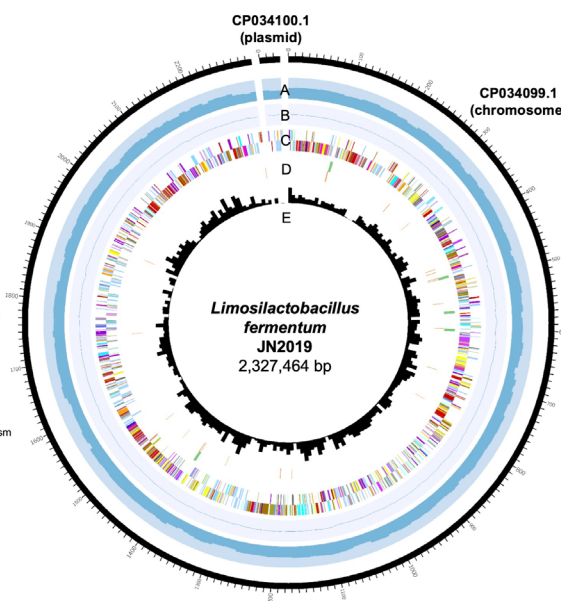
G, guanine; C, cytosine.

A : GC contents  
B : GC skew  
C : All annotated ORFs are colored differently based on the COG assignments  
+ strand upper layer, - strand lower layer

- J : Translation, ribosomal structure and biogenesis
- A : RNA processing and modification
- K : Transcription
- L : Replication, recombination and repair
- B : Chromatin structure and dynamics
- D : Cell cycle control, cell division, chromosome partitioning
- Y : Nuclear structure
- V : Defense mechanisms
- T : Signal transduction mechanisms
- M : Cell wall/membrane/envelope biogenesis
- N : Cell motility
- Z : Cytoskeleton
- W : Extracellular structures
- U : Intracellular trafficking, secretion, and vesicular transport
- O : Posttranslational modification, protein turnover, chaperones
- X : Mobilome: prophages, transposons
- C : Energy production and conversion
- G : Carbohydrate transport and metabolism
- E : Amino acid transport and metabolism
- F : Nucleotide transport and metabolism
- H : Coenzyme transport and metabolism
- I : Lipid transport and metabolism
- P : Inorganic ion transport and metabolism
- Q : Secondary metabolites biosynthesis, transport and catabolism
- R : General function prediction only
- S : Function unknown

D : Green = rRNAs  
Orange = tRNAs

E : Variant frequency from  
*Limosilactobacillus fermentum* JN2019  
(bin size : 10,000 bp)



**Fig. 1. Circular genome map of *Limosilactobacillus fermentum* JN2019.** Circles from the outside to the center denote (A) G + C content, (B) G + C skew, (C) annotated open reading frames colored differently based on the COG assignments, (D) rRNAs (green) and tRNAs (orange), and (E) variant frequency. G, guanine; C, cytosine; ORF, open reading frame; COG, clusters of orthologous group.

of 50.5%), a single chromosome of 2.3 Mb with a G + C content of 50.6% and a 30 kb plasmid with a G + C content of 40.8% (Table 1). The 2.3 Mb genome corresponds to 2,359 genes, 2,077 proteins, 15 rRNAs, 58 tRNAs, and 3 other RNAs. These 2,359 genes are specifically clustered into 26 Clusters of Orthologous Groups of proteins-based functional categories (Fig. 1).

The genome information of JN2019 provides fundamental knowledge to inform discoveries of its beneficial properties and industrial applications. The complete genome sequence of JN2019 is available from NCBI/GenBank under BioSample accession number SAMN10417155 or directly via the assembly accession number CP034099.1 (chromosome) and CP034100.1 (plasmid).

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