

Draft genome sequences of *Lactiplantibacillus plantarum* strains KABP062 and KABP063 isolated from human feces

Pol Huedo,^{1,2} Erola Astó,¹ Marta Perez,¹ Maria Rodriguez-Palmero,¹ Jordi Espadaler-Mazo^{1,2}

AUTHOR AFFILIATIONS See affiliation list on p. 2.

ABSTRACT We present the draft genome sequences of *Lactiplantibacillus plantarum* strains KABP062 and KABP063, two fecal isolates with probiotic potential.

KEYWORDS probiotics, microbiota, microbiome, genomics

Lactiplantibacillus plantarum is a metabolically versatile, nomadic lactic acid bacterium with relevance in the food industry and human health (1). Genome sequencing of novel *L. plantarum* strains is essential to explore their probiotic potential.

L. plantarum strains KABP062 and KABP063 were isolated in 2005 from fecal samples from two different healthy Peruvian kids (Cajamarca, Perú, 7°9'49.6" S, 78°30'1" W), whose legal tutors gave informed, explicit consent. Fresh fecal samples were diluted in phosphate-buffered saline and seeded onto de Man, Rogosa, and Sharpe (MRS) agar plates and incubated at 37°C for 48 h in anaerobic jars. Bacterial species were firstly identified through 16S rDNA sequencing using primers 27F (5'-AGAGTTTGATC MTGGCTCAG-3') and 1492R (5'-TACGGYTACCTTGTACGACTT-3') (2), amplicons being queried against the 16S RNA sequences database in BLAST (3). Genomic average nucleotide identity was verified with JSpecies (4). Antibiotic susceptibility was performed by the broth microdilution method following ISO 10932:2010 (5), as recommended by EFSA (6).

Isolated colonies were inoculated into 10 mL of MRS medium and cultured as indicated above. Cultures were centrifuged, and genomic DNA was extracted from pellets using the QIAamp DNA Blood Mini Kit (Qiagen, USA) following manufacturer instructions. Whole-genome sequences were obtained at Macrogen (Korea). Genome libraries were prepared by Nextera XT DNA Preparation kit and sequenced by Illumina NovaSeq 6000 generating 2 × 150 bp paired-end reads. Trimmomatic v0.38 (7) was used to remove adapter sequences and low-quality reads. *De novo* assembly was performed using SPAdes v3.15.0 (8). The assembled genomes were validated using BWA-MEM v0.7.17-r1188 aligner (9) and BUSCO v5.1.3 analysis (10). Annotation was performed through NCBI Prokaryotic Genome Annotation Pipeline v6.7 (11). Default parameters were used except where otherwise noted.

Results of genome sequencing are shown in Table 1. Both strains KABP062 and KABP063 showed MICs below EFSA cut-off values for *L. plantarum* (6). Specifically, they exhibited 0.5 µg/mL for ampicillin, 4 µg/mL for gentamicin, 16 µg/mL for kanamycin, 0.5 µg/mL (KABP062) and 0.25 µg/mL (KABP063) for erythromycin, 0.5 µg/mL for clindamycin, 8 µg/mL (KABP062) and 4 µg/mL (KABP063) for tetracycline, and 4 µg/mL (KABP062) and 2 µg/mL (KABP063) for chloramphenicol.

Further *in vitro* and clinical validation will be required to confirm probiotic activity of *L. plantarum* strains KABP062 and KABP063.

Editor Vanja Klepac-Ceraj, Wellesley College, Wellesley, Massachusetts, USA

Address correspondence to Pol Huedo, huedo@ab-biotics.com.

P.H., E.A., M.P., M.R.-P., and J.E.-M. are full time employees of AB-BIOTICS SA (part of Kaneka Corp.).

Received 17 February 2026

Accepted 28 March 2026

Published 20 April 2026

Copyright © 2026 Huedo et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

TABLE 1 Genome assembly, annotation, and quality metrics of *Lp*^a strains KABP062 and KABP063

Feature	<i>Lp</i> KABP062	<i>Lp</i> KABP063
Total reads	17,856,196	20,853,774
Number of contigs	53	38
Genome size (bp)	3,262,171	3,251,349
N50 (bp)	130,217	247,484
Depth	175×	190×
G + C content (%)	44.5	44.4
BUSCO completeness	98.39% complete (122 C, 2 D, 0 F, 0 M; 124 total)	98.39% complete (122 C, 2 D, 0 F, 0 M; 124 total)
Total genes (Prokaryotic Genome Annotation Pipeline)	3,152	3,149
Protein-coding sequences	3,020	3,011
tRNA genes	66	66
5S rRNA	5	6
16S rRNA	3	1
23S rRNA	1	1
16S rRNA sequencing best hit (%)	99.93 (<i>Lp</i> JCM 1149)	99.93 (<i>Lp</i> JCM 1149)
Average nucleotide identity of <i>L. plantarum</i> ATCC 14917 (%)	98.83	98.83

^a*Lp*, *Lactiplantibacillus plantarum*.

ACKNOWLEDGMENTS

This work has been funded by AB-BIOTICS SA (part of Kaneka Corporation).

AUTHOR AFFILIATIONS

¹R&D Department, AB-Biotics S.A. (Part of Kaneka Corporation), Barcelona, Spain

²Basic Sciences Department, Universitat Internacional de Catalunya, Barcelona, Spain

AUTHOR ORCIDs

Pol Huedo  <http://orcid.org/0000-0002-2933-0586>

AUTHOR CONTRIBUTIONS

Pol Huedo, Conceptualization, Funding acquisition, Investigation, Project administration, Software, Supervision, Writing – original draft, Writing – review and editing | Erola Astó, Formal analysis, Investigation, Validation, Writing – review and editing | Marta Perez, Conceptualization, Project administration, Writing – original draft, Writing – review and editing | Maria Rodriguez-Palmero, Conceptualization, Funding acquisition, Project administration, Resources, Supervision, Writing – original draft, Writing – review and editing | Jordi Espadaler-Mazo, Conceptualization, Formal analysis, Funding acquisition, Project administration, Resources, Supervision, Validation, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

The whole-genome sequencing project for *L. plantarum* KABP062 has been deposited at GenBank under accession number [JBUPYW000000000](https://www.ncbi.nlm.nih.gov/nuclseq/JBUPYW000000000). The raw sequencing data are available in the Sequence Read Archive (SRA) database under accession

number [SRR3708484](https://www.ncbi.nlm.nih.gov/sra/SRR3708484). The whole-genome sequencing project for *L. plantarum* KABP063 has been deposited at GenBank under accession number [JBUPYV000000000](https://www.ncbi.nlm.nih.gov/genbank/JBUPYV000000000). The raw sequencing data are available in the SRA database under accession number [SRR3708484](https://www.ncbi.nlm.nih.gov/sra/SRR3708484). The associated BioProject accession number is [PRJNA1418146](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1418146).

ETHICS APPROVAL

All procedures of isolation complied with the current laws of the country and adhered to the principles of the Declaration of Helsinki. At that time, the participating institutions did not require ethics review for minimal-risk non-invasive sampling, and all samples were anonymized in situ with no identifiable information available to the authors.

REFERENCES

1. Martino ME, Bayjanov JR, Caffrey BE, Wels M, Joncour P, Hughes S, Gillet B, Kleerebezem M, van Hijum SAFT, Leulier F. 2016. Nomadic lifestyle of *Lactobacillus plantarum* revealed by comparative genomics of 54 strains isolated from different habitats. *Environ Microbiol* 18:4974–4989. <https://doi.org/10.1111/1462-2920.13455>
2. Frank JA, Reich CI, Sharma S, Weisbaum JS, Wilson BA, Olsen GJ. 2008. Critical evaluation of two primers commonly used for amplification of bacterial 16S rRNA genes. *Appl Environ Microbiol* 74:2461–2470. <https://doi.org/10.1128/AEM.02272-07>
3. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *J Mol Biol* 215:403–410. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2)
4. Richter M, Rosselló-Móra R, Oliver Glöckner F, Peplies J. 2016. JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison. *Bioinformatics* 32:929–931. <https://doi.org/10.1093/bioinformatics/btv681>
5. International Organization for Standardization. 2010. ISO 10932:2010 - milk and milk products - determination of the minimal inhibitory concentration (MIC) of antibiotics applicable to bifidobacteria and non-enterococcal lactic acid bacteria (LAB). Vol. 2010.
6. EFSA. 2018. Guidance on the characterisation of microorganisms used as feed additives or as production organisms. *EFSA J* 16:1–24. <https://doi.org/10.2903/j.efsa.2018.5206>
7. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>
8. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>
9. Li H, Durbin R. 2009. Fast and accurate short read alignment with Burrows–Wheeler transform. *Bioinformatics* 25:1754–1760. <https://doi.org/10.1093/bioinformatics/btp324>
10. Simão FA, Waterhouse RM, Ioannidis P, Kriventseva EV, Zdobnov EM. 2015. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics* 31:3210–3212. <https://doi.org/10.1093/bioinformatics/btv351>
11. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>