

*Complete genome sequence of
Lactobacillus plantarum 10CH, a potential
probiotic lactic acid bacterium with potent
antimicrobial activity*

Article

Published Version

Creative Commons: Attribution 4.0 (CC-BY)

Open Access

El Halfawy, N. M., El-Naggar, M. Y. and Andrews, S. C. (2017) Complete genome sequence of *Lactobacillus plantarum* 10CH, a potential probiotic lactic acid bacterium with potent antimicrobial activity. *Genome announcements*, 5 (48). e01398-17. ISSN 2169-8287 doi: <https://doi.org/10.1128/genomeA.01398-17> Available at <http://centaur.reading.ac.uk/74392/>

It is advisable to refer to the publisher's version if you intend to cite from the work. See [Guidance on citing](#).

To link to this article DOI: <http://dx.doi.org/10.1128/genomeA.01398-17>

Publisher: American Society for Microbiology

All outputs in CentAUR are protected by Intellectual Property Rights law, including copyright law. Copyright and IPR is retained by the creators or other copyright holders. Terms and conditions for use of this material are defined in the [End User Agreement](#).

www.reading.ac.uk/centaur

CentAUR

Central Archive at the University of Reading

Reading's research outputs online



Complete Genome Sequence of *Lactobacillus plantarum* 10CH, a Potential Probiotic Lactic Acid Bacterium with Potent Antimicrobial Activity

Nancy M. El Halfawy,^{a,b} Moustafa Y. El-Naggar,^a  Simon C. Andrews^b

Department of Botany and Microbiology, Faculty of Science, University of Alexandria, Alexandria, Egypt^a;
School of Biological Sciences, University of Reading, Reading, United Kingdom^b

ABSTRACT *Lactobacillus plantarum* 10CH is a bacteriocin-producing potential probiotic lactic acid bacterium (LAB) strain isolated from cheese. Its complete nucleotide sequence shows a single circular chromosome of 3.3 Mb, with a G+C content of 44.51%, a 25-gene plantaricin bacteriocin gene cluster, and the absence of recognized virulence factors.

Lactobacillus plantarum is an inhabitant of the human gastrointestinal tract (1) and is used as a probiotic, since it is generally regarded as safe, confers beneficial health effects in humans, and exhibits antimicrobial activity against microbial pathogens (2, 3). From 50 novel lactic acid bacterium (LAB) isolates, the extracellular products of *L. plantarum* 10CH (isolated from cheese) gave the highest antimicrobial activities against a panel of 13 indicator strains, including *Listeria monocytogenes*, *Staphylococcus aureus*, *Enterococcus faecium*, *Enterococcus faecalis*, and *Salmonella enterica*, characteristic of bacteriocin production.

Genomic DNA of *L. plantarum* 10CH was isolated using a GeneJET purification kit and assessed using a NanoDrop ND-1000 spectrophotometer and by electrophoresis. Genome sequencing was performed by Microbes NG (University of Birmingham, UK) using MiSeq and HiSeq 2500 platforms (Illumina, UK). The genome sequencing yielded 968,127 reads, with a median insert size of 489 bases and 123-fold coverage of the genome. The reads were trimmed using Trimmomatic (4) by identification of adapter sequences, and the quality of the trimmed reads was assessed using in-house scripts combined with the bwa-mem software (5). These reads were *de novo* assembled with SPAdes software version 3.7.0 (6), yielding 48 large contigs (>1,000 bp). The quality of the genome assemblies was assessed using the Quality Assessment Tool for Genome Assemblies (QUAST) (7). The draft genome was mapped against the published reference genome of *L. plantarum* WCSF1 (GenBank accession number AL935263), which was found to be the closest neighbor by the NCBI server using the CONTIGuator mapping tool (8). Based on the Artemis Comparison Tool view, contigs were arranged, and the intrascaffold gaps were then determined. Thirty-two pairs of PCR primers were designed to fill the putative gaps between the contigs, and the PCRs were carried out using high-fidelity CloneAmp HiFi PCR premix (TaKaRa, Japan). The resulting amplicons were analyzed by gel electrophoresis and sequenced by Eurofins Genomics. The sizes of the amplified gaps ranged from 900 bp to ~5.5 kb. SeqBuilder (Lasergene) was used to fill the gaps using the resulting sequences of the amplified PCR products.

The sequencing results were consistent with the presence of a single circular replicon of 3,311,056 bp (no plasmids were found). The complete genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and the Pathosystems Resources Integration Center (PATRIC) Web server (9, 10). This revealed a total of 3,192 protein-

Received 6 November 2017 Accepted 6 November 2017 Published 30 November 2017

Citation El Halfawy NM, El-Naggar MY, Andrews SC. 2017. Complete genome sequence of *Lactobacillus plantarum* 10CH, a potential probiotic lactic acid bacterium with potent antimicrobial activity. Genome Announc 5:e01398-17. <https://doi.org/10.1128/genomeA.01398-17>.

Copyright © 2017 El Halfawy 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/).

Address correspondence to Simon C. Andrews, s.c.andrews@reading.ac.uk.

coding genes, along with 6, 5, and 5 5S, 16S, and 23S rRNA genes, respectively, 67 tRNA genes, and 100 pseudogenes. Four prophage loci ranging in size from 26 to 51 kb were also identified in the chromosome using the PHAST Web server (11). Five adjacent plantaricin gene clusters were predicted (*plnRLKJ*, *plnMNOP*, *plnABCD*, *plnIFE*, and *plnGHTUVW*) using Vector NTI Express (Invitrogen) and are responsible for the production of plantaricins A, EF, and JK. Similar bacteriocin clusters are found in *L. plantarum* ST-III (GenBank accession number CP002222), C11 (X94434), and V90 (FJ809773). No classical virulence genes were identified in the *L. plantarum* 10CH genome, which, together with its strong and broad-spectrum antimicrobial activity, indicates its potential suitability as a probiotic strain.

Accession number(s). The complete genome sequence of *L. plantarum* 10CH has been deposited at GenBank with the accession number [CP023728](https://doi.org/10.1093/nar/gkr485).

ACKNOWLEDGMENTS

This research was financially supported by the Newton-Mosharafa program, co-funded by the British Council and Ministry of Higher Education, Egypt.

We thank Microbes NG for the performing the Illumina sequencing.

REFERENCES

- Ahrné S, Nobaek S, Jeppsson B, Adlerberth I, Wold AE, Molin GJ. 1998. The normal *Lactobacillus* flora of healthy human rectal and oral mucosa. *J Appl Microbiol* 85:88–94. <https://doi.org/10.1046/j.1365-2672.1998.00480.x>.
- Arena MP, Silvain A, Normanno G, Grieco F, Drider D. 2016. Use of *Lactobacillus plantarum* strains as a bio-control strategy against food-borne pathogenic microorganisms. *Front Microbiol* 7:464. <https://doi.org/10.3389/fmicb.2016.00464>.
- Cunningham-Rundles S, Ahrné S, Bengmark S, Johann-Liang R, Marshall F, Metakis L, Califano C, Dunn AM, Grasseley C, Hinds G, Cervia J. 2000. Probiotics and immune response. *Am J Gastroenterol* 95:S22–S25. [https://doi.org/10.1016/S0002-9270\(99\)00813-8](https://doi.org/10.1016/S0002-9270(99)00813-8).
- 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>.
- 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>.
- 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>.
- Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUASt: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
- Galardini M, Biondi EG, Bazzicalupo M, Mengoni A. 2011. CONTIGuator: a bacterial genome finishing tool for structural insights on draft genomes. *Source Code Biol Med* 6:11. <https://doi.org/10.1186/1751-0473-6-11>.
- 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>.
- Wattam AR, Abraham D, Dalay O, Disz TL, Driscoll T, Gabbard JL, Gillespie JJ, Gough R, Hix D, Kenyon R, Machi D, Mao C, Nordberg EK, Olson R, Overbeek R, Pusch GD, Shukla M, Schulman J, Stevens RL, Sullivan DE, Vonstein V, Warren A, Will R, Wilson MJC, Yoo HS, Zhang C, Zhang Y, Sobral BW. 2014. PATRIC: the bacterial bioinformatics database and analysis resource. *Nucleic Acids Res* 42:D581–D591. <https://doi.org/10.1093/nar/gkt1099>.
- Zhou Y, Liang Y, Lynch K, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <https://doi.org/10.1093/nar/gkr485>.