

# Draft Genome Sequence of *Lactobacillus plantarum* BFE 5092 Isolated from Maasai Fermented Milk

Folarin A. Oguntoyinbo,<sup>a,b</sup> Gyu-Sung Cho,<sup>a</sup> Erik Brinks,<sup>a</sup> Gregor Fiedler,<sup>a</sup> Jan Kabisch,<sup>a</sup> Sabrina Koberg,<sup>a</sup> Wilhelm Bockelmann,<sup>a</sup> Horst Neve,<sup>a</sup> Youn-Goo Kang,<sup>c</sup> Doyeon Yun,<sup>c</sup> Ah-Ram Kim,<sup>c</sup> Arjan Narbad,<sup>d</sup> Charles M. A. P. Franz<sup>a</sup>

Department of Microbiology and Biotechnology, Max Rubner-Institut, Federal Research Institute of Nutrition and Food, Kiel, Germany<sup>a</sup>; Department of Microbiology, Faculty of Science, University of Lagos, Lagos, Nigeria<sup>b</sup>; School of Life Science, Handong Global University, Pohang, South Korea<sup>c</sup>; Gut Health and Food Safety Program, Institute of Food Research, Norwich, United Kingdom<sup>d</sup>

**The draft genome of *Lactobacillus plantarum* BFE 5092 isolated from the Maasai traditional fermented milk product kule naoto was sequenced, and sequence analysis showed the assembled genome size to be 3,285,094 bp, containing a predicted total of 3,111 protein-encoding genes, 17 rRNAs, and 70 tRNAs.**

Received 18 April 2016 Accepted 28 April 2016 Published 2 June 2016

**Citation** Oguntoyinbo FA, Cho G-S, Brinks E, Fiedler G, Kabisch J, Koberg S, Bockelmann W, Neve H, Kang Y-G, Yun D, Kim A-R, Narbad A, Franz CMAP. 2016. Draft genome sequence of *Lactobacillus plantarum* BFE 5092 isolated from Maasai fermented milk. *Genome Announc* 4(3):e00481-16. doi:10.1128/genomeA.00481-16.

**Copyright** © 2016 Oguntoyinbo 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 Charles M. A. P. Franz, [charles.franz@mri.bund.de](mailto:charles.franz@mri.bund.de).

*Lactobacillus plantarum* is a lactic acid bacterium that has been isolated from diverse ecosystems, such as vegetables, meat, fish, dairy products, and the gastrointestinal tract (1). This species is known for its high phenotypic, genomic, and metabolic diversity, the consequences of which are central to the success of its industrial application. This versatility of the species is largely based on the presence of so-called genomic “lifestyle islands” that consist of numerous functional gene cassettes, particularly for carbohydrate utilization, which can be acquired, shuffled, substituted, or deleted in response to niche requirements (1).

*L. plantarum* BFE 5092 was isolated from a fermented sour milk product, kule naoto, produced by the Maasai in Kenya. The strain is considered to have potential as a probiotic strain, as it was found to survive gastrointestinal passage in an *in vitro* model, showed antimicrobial activity toward and coaggregation with pathogens, and adhered well to HT29 MTX cells in cell culture (2–4). The strain was also shown to possess genes for the production of two plantaricins (i.e., EF and JK) (5) and is currently investigated for its potential as a starter culture for the fermentation of African leafy vegetables. Currently, there are genome sequences of 34 *L. plantarum* strains available, of which 7 have been completed. The genome of strain BFE 5092 was sequenced in order to assess its technological and functional properties and to compare its genome sequence with those of other sequenced *L. plantarum* strains from different sources.

The genomic DNA of *L. plantarum* BFE 5092 was isolated using the Qiagen Genomic-tip 100/G kit (Qiagen, Manchester, United Kingdom). The library was prepared with an Illumina Nextera XT library prep kit (Illumina, San Diego, CA), and genome sequencing was done with an Illumina MiSeq sequencer. In total, 2,909,131 paired-end sequence reads of 500 bp in length were obtained with 117-fold coverage. The template-based assembly was performed using Andrew And Aaron’s Awesome Assembly pipeline (A5-miseq, version 20140604), which yielded 66 scaffolds. The largest scaffold was 425,807 bp in size. The  $N_{50}$  was

122,578 bp. The genome of *L. plantarum* BFE 5092 is 3,285,094 bp in size, with a 44.39 mol% G+C content. The genome sequence was annotated using the Rapid Annotations using Subsystems Technology (RAST) server (<http://rast.nmpdr.org/>) (6, 7). The genome contains 3,111 protein-coding genes, 17 rRNAs, and 70 tRNAs. Four hundred thirty-three genes are involved in sugar metabolism, including genes for 11 phosphoenolpyruvate (PEP)/phosphotransferase systems (PTS) for the utilization of *N*-acetylglucosamine, mannose, sucrose, maltose, and glucose, beta-glucoside sugars, cellobiose, trehalose, mannitol, galactitol, fructose, as well as glucitol and sorbitol sugars. The genome information for this wild-type strain will be useful for its further development and application as a multifunctional starter culture.

**Nucleotide sequence accession number.** This whole-genome shotgun project has been deposited at the European Nucleotide Archive (ENA) under the accession no. [FJVL01000000](https://ena.ebi.ac.uk/ena/record/FJVL01000000).

## ACKNOWLEDGMENTS

We thank the Georg Forster Fellowship for Experienced Researcher of the Alexander von Humboldt Foundation, Germany, for funding a research visit of F. A. Oguntoyinbo.

## FUNDING INFORMATION

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

## REFERENCES

- Siezen RJ, van Hylckama Vlieg JET. 2011. Genomic diversity and versatility of *Lactobacillus plantarum*, a natural metabolic engineer. *Microb Cell Fact* 10(Suppl 1):S3. <http://dx.doi.org/10.1186/1475-2859-10-S1-S3>.
- Vizoso Pinto MG, Franz CMAP, Schillinger U, Holzapfel WH. 2006. *Lactobacillus* ssp. with *in vitro* probiotic properties from human faeces and traditional fermented products. *Int J Food Microbiol* 109:205–214. <http://dx.doi.org/10.1016/j.ijfoodmicro.2006.01.029>.
- Vizoso Pinto MG, Schuster T, Briviba K, Watzl B, Holzapfel WH, Franz CMAP. 2007. Adhesive and stimulatory properties of potentially probiotic *Lactobacillus* strains. *J Food Prot* 70:125–134.

4. Mathara JM, Schillinger U, Guigas C, Franz C, Kutima PM, Mbugua SK, Shin HK, Holzapfel WH. 2008. Functional characteristics of *Lactobacillus* spp. from traditional Maasai fermented milk products in Kenya. *Int J Food Microbiol* 126:57–64. <http://dx.doi.org/10.1016/j.ijfoodmicro.2008.04.027>.
5. Cho GS, Huch M, Hanak A, Holzapfel WH, Franz CMAP. 2010. Genetic analysis of the plantaricin EFI locus of *Lactobacillus plantarum* PCS20 reveals an unusual plantaricin E gene sequence as a result of mutation. *Int J Food Microbiol* 141 (Suppl. 1):S117–S124. <http://dx.doi.org/10.1016/j.ijfoodmicro.2010.02.022>.
6. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formisma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:. <http://dx.doi.org/10.1186/1471-2164-9-75>.
7. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). *Nucleic Acids Res* 42:D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.