

Draft Genome Sequence of *Lactobacillus plantarum* Strain WJL, a *Drosophila* Gut Symbiont

Eun-Kyoung Kim, Young Min Park, Oun Young Lee, Won-Jae Lee

School of Biological Science, Seoul National University and National Creative Research Initiative Center for Symbiosystem, Seoul, South Korea

Lactobacillus plantarum strain WJL, a member of the symbiotic gut bacteria, was isolated from the intestine of the fruit fly, *Drosophila melanogaster*. Here, we report the draft genome sequence of *L. plantarum* WJL.

Received 7 October 2013 Accepted 22 October 2013 Published 21 November 2013

Citation Kim E-K, Park YM, Lee OY, Lee W-J. 2013. Draft genome sequence of *Lactobacillus plantarum* strain WJL, a *Drosophila* gut symbiont. *Genome Announc.* 1(6):e00937-13. doi:10.1128/genomeA.00937-13.

Copyright © 2013 Kim et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Won-Jae Lee, lwj@snu.ac.kr.

Lactobacillus plantarum is a Gram-positive, lactic acid-producing bacterium that is found in a variety of environmental niches (1). Interestingly, *L. plantarum* is frequently observed as a member of commensal bacteria in the metazoan gut, ranging from the fly to the human gastrointestinal tract (2, 3). Although this bacterium is generally considered to be a symbiont that induces beneficial effects in its host, the molecular mechanism by which *L. plantarum* impacts host physiology is largely unknown. *Drosophila*, a classical animal model for developmental biology and innate immunity, is now being introduced to the field of gut-microbiota interactions (4). *L. plantarum* strain WJL was originally isolated as a member of the symbiotic bacteria from the *Drosophila* gut (5). This bacterium is capable of colonizing gut epithelia without provoking host gut immunity (6). Recent genetic analyses further showed that *L. plantarum* WJL stimulates the target of sirolimus kinase activity in the host, especially under poor nutritional conditions, to promote systemic larval growth by optimizing integrated hormone signaling pathways (7). In the current study, the genomic information of *L. plantarum* WJL is presented, which is essential to determine the bacterial genes required for a positive impact on the host physiology.

The genome sequence of *L. plantarum* WJL was analyzed using a 100-bp paired-end library (4,567,308 reads) with the Illumina HiSeq 2000 (Illumina, San Diego, CA). The sequence reads were assembled into 102 contigs using the CLC Genomics Workbench 5.1 (CLC bio, Denmark). The total coverage over the whole genome reached ~198-fold. Functional annotation of the predicted genes was performed using the RAST server (8) and COG (9) database. The genome of *L. plantarum* WJL was estimated to be 3,477,495 bp, and 3,410 open reading frames (ORFs) were identified, which include 4 rRNA genes and 71 tRNA genes. Among the 3,410 ORFs, only 2,356 (69%) were identified with predicted functions based on homologies to previously known proteins. The G+C content of the genome is 44.24 mol%. Deducing the sequence information improves the feasibility of performing genetic analyses of this bacterium as well as comparative genomics with other *Drosophila* gut-colonizing lactobacilli, which will provide novel insights into the molecular interactions between lactobacilli and *Drosophila* gut epithelia.

Nucleotide sequence accession numbers. The result of this whole-genome shotgun project has been deposited at GenBank under the accession no. [AUTE00000000](https://www.ncbi.nlm.nih.gov/nuccore/AUTE00000000). The version described in this paper is the first version, AUTE01000000.

ACKNOWLEDGMENTS

This study was supported by the National Creative Research Initiative Program from the National Research Foundation of Korea and the BK 21 Plus program of the Ministry of Education, South Korea.

REFERENCES

1. Siezen RJ, Tzeneva VA, Castioni A, Wels M, Phan HT, Rademaker JL, Starrenburg MJ, Kleerebezem M, Molenaar D, van Hylckama Vlieg JE. 2010. Phenotypic and genomic diversity of *Lactobacillus plantarum* strains isolated from various environmental niches. *Environ. Microbiol.* 12:758–773.
2. Ahrné S, Nobaek S, Jeppsson B, Adlerberth I, Wold AE, Molin G. 1998. The normal *Lactobacillus* flora of healthy human rectal and oral mucosa. *J. Appl. Microbiol.* 85:88–94.
3. Lebeer S, Vanderleyden J, De Keersmaecker SC. 2008. Genes and molecules of lactobacilli supporting probiotic action. *Microbiol. Mol. Biol. Rev.* 72:728–764, Table of Contents.
4. Lee WJ, Brey PT. 2013. How microbiomes influence metazoan development: insights from history and *Drosophila* modeling of gut-microbe interactions. *Annu. Rev. Cell Dev. Biol.* 29:571–592.
5. Ryu JH, Kim SH, Lee HY, Bai JY, Nam YD, Bae JW, Lee DG, Shin SC, Ha EM, Lee WJ. 2008. Innate immune homeostasis by the homeobox gene caudal and commensal-gut mutualism in *Drosophila*. *Science* 319:777–782.
6. Lee KA, Kim SH, Kim EK, Ha EM, You H, Kim B, Kim MJ, Kwon Y, Ryu JH, Lee WJ. 2013. Bacterial-derived uracil as a modulator of mucosal immunity and gut-microbe homeostasis in *Drosophila*. *Cell* 153:797–811.
7. Storelli G, Defaye A, Erkosar B, Hols P, Royet J, Leulier F. 2011. *Lactobacillus plantarum* promotes *Drosophila* systemic growth by modulating hormonal signals through TOR-dependent nutrient sensing. *Cell Metab.* 14:403–414.
8. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paccian 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* 9:75. doi:10.1186/1471-2164-9-75.
9. Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, Kiryutin B, Koonin EV, Krylov DM, Mazumder R, Mekhedov SL, Nikolskaya AN, Rao BS, Smirnov S, Sverdlov AV, Vasudevan S, Wolf YI, Yin JJ, Natale DA. 2003. The COG database: an updated version includes eukaryotes. *BMC Bioinformatics* 4:41. doi:10.1186/1471-2105-4-41.