Draft Genome Sequence of *Lactobacillus brevis* Strain EW, a *Drosophila* Gut Pathobiont

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 brevis* strain EW, a gut pathobiont, was isolated from the fruit fly *Drosophila melanogaster*. Here, we report the draft genome sequence of *L. brevis* EW.**

*L*actobacillus brevis is a Gram-positive rod-shaped species of lactic acid-producing bacteria. Many strains of *L. brevis*, such as ATCC 367 [1], KB290 [2], and *L. brevis* subsp. *gravesensis* ATCC 27305, have been shown to exert a probiotic effect in humans and animals. *L. brevis* strain EW was originally isolated from the gut epithelia of *Drosophila melanogaster* [3]. Although the presence of lactobacilli is generally considered to be beneficial to the host, *L. brevis* EW acts as a pathobiont (i.e., a resident gut bacterium that is generally benign within a normal community structure but is pathogenic under certain deregulated conditions) in the *Drosophila* gut [4]. A recent study showed that germfree *Drosophila* monoassociated with *L. brevis* EW exhibited severe gut cell apoptosis and early host death [4]. The *L. brevis* EW-induced host pathology is a result of the chronic activation of a reactive oxygen species-producing enzyme, dual oxidase (DUOX). Since bacterium-derived uracil acts as a ligand for DUOX activation in *Drosophila* gut immunity [4], it has been hypothesized that *L. brevis* EW releases uracil in a constitutive manner, which in turn induces chronic DUOX-dependent reactive oxygen species (ROS) generation in the gut. However, it is unclear as to why *L. brevis* EW secretes uracil, as certain other lactobacilli do not. In the current study, the genomic information for *L. brevis* EW is presented, which is essential for elucidating the mechanism by which *L. brevis* EW provokes gut-microbe dysbiosis through chronic DUOX activation.

The genome sequence of *L. brevis* EW was determined using a 3-kb paired-end library (175,405 reads, ~10.92-fold coverage) with the Genome Sequencer FLX system (Roche Diagnostics, Branford, CT) and a 100-bp paired-end library (6,924,211 reads, ~362.4-fold coverage) with the Illumina HiSeq 2000 (Illumina, San Diego, CA). The 38 contigs were generated using the CLC Genomics Workbench 5.1 (CLC bio, Denmark). The functional annotation of the predicted genes was performed using the RAST server [5] and the COG database [6]. The draft genome sequence is 2,885,101 bp in length and contains 2,892 open reading frames (ORFs). Eleven rRNA genes and 68 tRNA genes were also identified. The G+C content of the genome is 45.26 mol%. Using comparative genomics for the various *L. brevis* strains with different characteristics, i.e., regarding their roles as symbionts or pathobionts within the *Drosophila* gut, it is now feasible to dissect the molecular principles governing gut-microbe symbiosis and pathogenesis.

Nucleotide sequence accession numbers. The result of this whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AUTD00000000. The version described in this paper is the first version, AUTD01000000.

REFERENCES

1. **Makarova K, Slesarev A, Wolf Y, Sorokin A, Mirkin B, Koonin E, Pavlov A, Pavlova N, Karamychev V, Polouchine N, Shakhova V, Grigoriev I, Lou Y, Rohksar D, Lucas S, Huang K, Goodstein DM, Hawkins T, Plengvidhya V, Welker D, Hughes J, Goh Y, Benson A, Baldwin K, Lee JH, Díaz-Muñiz I, Dosti B, Smeianov V, Wechter W, Barabote R, Lorca G, Altermann E, Barrangou R, Ganesan B, Xie Y, Rawsthorne H, Tamir D, Parker C, Breidt F, Broadbent J, Hutkins R, O'Sullivan D, Steele J, Unlu G, Saier M, Klaenhammer T, Richardson P, Kozyavkin S, Weimer B, Mills D.** 2006. Comparative genomics of the lactic acid bacteria. Proc. Natl. Acad. Sci. U. S. A. **103**:15611–15616.
2. **Fukao M, Oshima K, Morita H, Toh H, Suda W, Kim SW, Suzuki S, Yakabe T, Hattori M, Yajima N.** 2013. Genomic analysis by deep sequencing of the probiotic *Lactobacillus brevis* KB290 harboring nine plasmids reveals genomic stability. PLoS One **8**:e60521. doi:10.1371/journal.pone.0060521.
3. **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.
4. **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.
5. **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, 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**:75. doi:10.1186/1471-2164-9-75.
6. **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.