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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Commensalibacter intestini* A911^T, a Symbiotic Bacterium Isolated from *Drosophila melanogaster* Intestine

Eun-Kyoung Kim, Sung-Hee Kim, Hyuck-Jin Nam, Myoung Kwon Choi, Kyung-Ah Lee, Seung-Hoon Choi, You Yeong Seo, Hyejin You, Boram Kim, and Won-Jae Lee

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

***Commensalibacter intestini* A911^T, a predominant symbiotic bacterium capable of stably colonizing gut epithelia, was isolated from the fruit fly, *Drosophila melanogaster*. Here we report the draft genome sequence of *Commensalibacter intestini* A911^T.**

All metazoan guts harbor a diverse range of symbiotic microorganisms. Although the exact molecular mechanism of this symbiotic relationship is still unknown, commensal bacteria are known to be involved in the homeostasis of host physiology, such as immunity, metabolism, and growth (2, 7–9, 12). Due to the complexity of gut-microbe interactions, there is an increasing demand for genetically tractable animal model hosts that can be used to perform a simultaneous genetic analysis of both host and microbe *in vivo*. In recent studies, *Drosophila melanogaster* has been established as an emerging model for the analysis of gut-microbe interactions (3, 5, 6, 11, 12). *Commensalibacter intestini* A911^T was reported to be a dominant member of gut commensal bacteria found in both wild-caught and laboratory-reared *Drosophila* (4, 11). The colonization of *C. intestini* A911^T has been shown to be important to antagonize the dominance of a potentially pathogenic gut bacterium, thereby contributing to gut homeostasis and host fitness (11). *C. intestini* A911^T was shown to be an aerobic Gram-negative bacterium belonging to the novel genus *Commensalibacter* in the family *Acetobacteraceae* (10). In this study, genome information of *C. intestini* A911^T, which was critical to determine its symbiotic role in the *Drosophila* gut, is presented.

The genome sequence of *Commensalibacter intestini* A911^T was analyzed using a 3-kb paired-end library (309,233 reads, ~58.9 Mb) with a Genome Sequencer FLX system (Roche Diagnostics, Branford, CT) and a 100-bp paired-end library (43,376,566 reads, ~4,381 Mb) with Genome Analyzer IIx (Illumina, San Diego, CA). The sequence reads were assembled into 26 contigs using the GS Assembler 2.3 (Roche Diagnostics, Branford, CT) and CLC Genomics Workbench 4.5.1 (CLC bio, Denmark). The total coverage over the whole genome reached ~1,812-fold. The functional annotation of predicted genes was performed using the RAST server (1) and COG (13) database. The genome of *C. intestini* A911^T was estimated to be 2,454,778 bp, and 2,210 open reading frames (ORFs) were identified, which included 3 rRNA genes and 43 tRNA genes. Among the 2,210 ORFs, only 1,104 (49.9%) were identified as having predicted functions based on homology to previously known proteins. The G+C content of the genome was 36.85%. By determining the genome sequence of *C. intestini* A911^T, it is now possible to perform various genetic analyses of this bacterium as well as comparative genomics analysis with other bacteria, which should provide novel insight into the molecular principles of gut-microbe interactions.

Nucleotide sequence accession numbers. The result of this whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AGFR00000000. The version described in this paper is the first version, AGFR01000000.

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

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