

Whole-Genome Sequence of *Serratia symbiotica* Strain CWBI-2.3^T, a Free-Living Symbiont of the Black Bean Aphid *Aphis fabae*

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The gammaproteobacterium *Serratia symbiotica* is one of the major secondary symbionts found in aphids. Here, we report the draft genome sequence of *S. symbiotica* strain CWBI-2.3^T, previously isolated from the black bean aphid *Aphis fabae*. The 3.58-Mb genome sequence might provide new insights to understand the evolution of insect-microbe symbiosis.

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The bacterium *Serratia symbiotica* is described as a mutualistic inherited endosymbiont found in many aphid species (1). Two different phylogenetic clades have been reported for this species (2). On the one hand, clade A is composed of facultative endosymbionts infecting several aphid families. In the pea aphid *Acyrtosiphon pisum*, this facultative endosymbiont is associated with heat stress tolerance and parasite resistance (3, 4). On the other hand, the clade B members are restricted to aphids of the subfamily *Lachinae* and correspond to primary-like endosymbionts implicated in the synthesis of amino acids, like in the aphid *Cinara cedri* (5). Recently, *S. symbiotica* strain CWBI-2.3^T was isolated from *Aphis fabae* and cultivated on artificial rich medium (6), constituting the first symbiotic bacterium of aphids with a free-living capacity.

The complete genome of *S. symbiotica* strain CWBI-2.3^T was sequenced using the Pacific Biosciences RS sequencing technology (Pacific Biosciences, Menlo Park, CA, USA). A 10-kb library was prepared from sheared genomic DNA using a 10-kb template library preparation workflow. The library was sequenced on two single-molecule real-time (SMRT) cells, yielding >40× average genome coverage, with 64,305 reads with a mean read length of 3,187 bp. Assembly of the reads was done with the HGAP2 version 2.1 *de novo* assembly pipeline. Coding sequence prediction and automatic functional annotation were performed using the MicroScope platform (7).

The draft genome of *S. symbiotica* strain CWBI-2.3^T consists of 32 contigs, corresponding to 3,584,847 bp, with a G+C content of 52.08%. The genome contains 3,664 predicted protein-coding sequences, 74 tRNA genes, and 32 rRNAs (10 16S rRNAs, 12 23S rRNAs, and 10 5S rRNAs). It also includes the 203 single-copy genes conserved among gammaproteobacterial genomes (8).

The CWBI-2.3^T strain belongs to *S. symbiotica* clade A and is phylogenetically close to the *S. symbiotica* strain Tucson of the pea

aphid *A. pisum*, based on a high nucleic acid identity for the 16S rRNA genes (99%). However, the CWBI-2.3^T strain has a different overall genomic structure and composition than those of the previously sequenced *S. symbiotica* strains. The total genome size of *S. symbiotica* strain CWBI-2.3^T is 0.80 and 1.82 Mb larger than the genomes of *S. symbiotica* strains Tucson and strain “*Cinara cedri*,” respectively. Furthermore, the CWBI-2.3^T strain conserved a larger repertoire of genes related to metabolism than did the two other strains. These results are consistent with the genomic erosion of host-dependent bacteria (9).

Most of facultative insect symbionts are uncultivable, precluding the development of genetic techniques used to understand host-symbiont interactions (10, 11). The genome of *S. symbiotica* strain CWBI-2.3^T reported here is the first genome of a symbiotic bacterium of aphids that is able to grow outside its host. It represents a missing link in the evolution of free living toward host-dependent mutualistic bacteria and provides the opportunity to carry on unique genomic comparative analyses and genetic modification experiments to investigate the bacterial symbiotic relationships in aphids.

Nucleotide sequence accession numbers. The complete genome sequences of *S. symbiotica* strain CWBI-2.3^T have been deposited in DDBJ/ENA/GenBank under accession numbers [CCES01000001](https://www.ncbi.nlm.nih.gov/nuccore/CCES01000001) to [CCES01000032](https://www.ncbi.nlm.nih.gov/nuccore/CCES01000032).

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