Whole-Genome Sequence of *Serratia symbiotica* Strain CWBI-2.3T, 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-2.3T, 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.

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 *Acrithosiphon pismus*, 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 *Lachninae* 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-2.3T 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-2.3T 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 Mi-Scrope platform (7).

The draft genome of *S. symbiotica* strain CWBI-2.3T 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-2.3T strain belongs to *S. symbiotica* clade A and is phylogenetically close to the *S. symbiotica* strain Tucson of the pea aphid *A. pismus*, based on a high nucleic acid identity for the 16S rRNA genes (99%). However, the CWBI-2.3T 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-2.3T is 0.80 and 1.82 Mb larger than the genomes of *S. symbiotica* strains Tucson and strain “*Cinara cedri*,” respectively. Furthermore, the CWBI-2.3T 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-2.3T 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-2.3T have been deposited in DDBJ/ENA/GenBank under accession numbers CCES01000001 to CCES01000032.

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