Draft Genome Sequence of *Burkholderia* sp. Strain WAC0059, a Bacterium Isolated from the Medicinal Fungus *Antrodia cinnamomea*

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ABSTRACT *Burkholderia* sp. strain WAC0059 was isolated from a fruiting body of the medicinal fungus *Antrodia cinnamomea* collected in Taiwan. Here, we report the draft genome sequence of this bacterium to facilitate the investigation of its biology.

The fungal species *Antrodia cinnamomea* (1), synonyms *Antrodia camphorata* (2) and *Taiwanofungus camphoratus* (3), is a popular medicinal mushroom in Taiwan that is noted for its protective effects against liver injury (4). The bacterial strain *Burkholderia* sp. WAC0059 was isolated from the fruiting body of an *A. cinnamomea* specimen wild-collected by C.-L.C. and T.-F.W. in 2013. To facilitate future investigation into the biology of this bacterium, and of its possible interactions with the fungal host, we report here a draft genome assembly of this bacterium.

The procedures for whole-genome shotgun sequencing and genome assembly were based on those described in our previous studies (5–7). Briefly, we utilized the Illumina MiSeq platform to obtain 301-bp sequencing reads from one paired-end library with approximately 1,273-fold coverage. The initial *de novo* assembly was performed using Velvet version 1.2.10 (8). Subsequently, an iterative process was used to improve the assembly. For each iteration, all raw reads were mapped to the assembly using the Burrows-Wheeler Alignment (BWA) tool version 0.7.12 (9), programmatically checked using the MPILEUP program in the SAMtools package version 1.2 (10), and visually inspected using Integrative Genomics Viewer (IGV) version 2.3.57 (11). Regions that involved possible misassembly were removed, and polymorphic sites were corrected based on the mapped reads. The annotation was performed using the Prokaryotic Genome Annotation Pipeline (PGAP) provided by the National Center for Biotechnology Information (NCBI) (12).

The first version of this draft genome contains 61 contigs with a combined size of 5,349,796 bp; the average G+C content is 66.8%. The annotation includes 4 rRNA genes, 49 tRNA genes, and 4,575 protein-coding genes.

Accession number(s). This whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number PNEO00000000. The version described in this paper is the first version, PNEO01000000.

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