Whole-Genome Sequence of *Cupriavidus* sp. Strain BIS7, a Heavy-Metal-Resistant Bacterium

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*Cupriavidus* is a member of the *Burkholderiaceae*, which is well known for its heavy-metal resistance (7, 12) and diverse metabolic capabilities. *Cupriavidus* spp. inhabit diverse niches, including root nodule (2), soil (5), organic-chemical-contaminated soils (13), heavy-metal-contaminated water (10), and immunocompromised individuals (1). Here we present the genome of *Cupriavidus* sp. strain BIS7, isolated from a Malaysian tropical soil sample. We sequenced the complete genome of *Cupriavidus* sp. strain BIS7 as a step toward understanding its heavy-metal resistance.

Genomic DNA of *Cupriavidus* sp. strain BIS7 was isolated using a QIAGEN DNA minikit (Qiagen, Germany) according to the manufacturer’s instructions. The quality of DNA was examined using a NanoDrop spectrophotometer (Thermo Scientific) and Qubit 2.0 fluorometer (Life Technologies). Whole-genome sequencing of *Cupriavidus* sp. strain BIS7 was performed using an Illumina MiSeq personal sequencer (Illumina, Inc., CA). This resulted in 1,916,808 filtered reads, with approximately 108.25-fold coverage. The filtered reads were assembled *de novo* with CLC Genomics Workbench version 5.1 (CLC Bio, Denmark), which yielded 139 contigs, with a quality measurement of N50 of 104,523 bp. The resulting draft genome of *Cupriavidus* sp. strain BIS7 contains a total of 5,871,951 bp, and the GC content of this genome is 63.9%. Gene prediction was performed using Prodigal (version 2.60), and a total of 5,322 open reading frames (ORFs) were predicted with an accuracy of 63.9%. Gene prediction was performed using Prodigal (version 2.60), and a total of 5,322 open reading frames (ORFs) were predicted with an accuracy of 63.9%. Gene prediction was performed using Prodigal (version 2.60), and a total of 5,322 open reading frames (ORFs) were predicted with an accuracy of 63.9%. Gene prediction was performed using Prodigal (version 2.60), and a total of 5,322 open reading frames (ORFs) were predicted with an accuracy of 63.9%.

From the BLAST results, *Cupriavidus* sp. strain BIS7 possesses a number of proteins involved in heavy-metal resistance, such as ZntA [P-type ATPase involved in Zn(II), Cd(II), Tl(I), and Pb(II) resistance] (11). There are several putative proteins believed to contribute to the heavy-metal resistance of this bacterium. *Cupriavidus* sp. strain BIS7 possesses a unique mechanism of heavy-metal resistance; therefore, this bacterium has a great biotechnological potential in bioremediation of an area contaminated with heavy metals.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALOU00000000. The version described in this paper is the first version, ALOU01000000.

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**REFERENCES**