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GENOME ANNOUNCEMENT

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

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***Cupriavidus* sp. strain BIS7 is a Malaysian tropical soil bacterium that exhibits broad heavy-metal resistance [Co(II), Zn(II), Ni(II), Se(IV), Cu(II), chromate, Co(III), Fe(II), and Fe(III)]. It is particularly resistant to Fe(II), Fe(III), and Zn(II). Here we present the assembly and annotation of its genome.**

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 QIAamp 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 N_{50} 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 (6). ORFs were further annotated by comparison with NCBI-NR and Blast2GO (3, 4). A total of 54 tRNA genes were predicted using tRNAscan-SE (version 1.21) (9). The draft genome contains 1 rRNA operon, 1 copy of 5S rRNA gene, 23S rRNA, and 16S rRNA gene each, as identified by using RNAmmer (8).

From the BLAST results, *Cupriavidus* sp. strain BIS7 possesses a number of proteins involved in heavy-metal resistance, such as CzcE [involved in Cd(II), Zn(II), and Co(III) resistance] (14) and 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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