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GENOME SEQUENCES

Draft Genome Sequence of *Cupriavidus basilensis* SRS, a Bacterium Isolated from Stream Sediments

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ABSTRACT *Cupriavidus basilensis* SRS was isolated from stream sediments from the Savannah River Site in South Carolina. Here, we report the draft genome sequence and annotation of *Cupriavidus basilensis* SRS. The genome contains 8,918,236 bp and 7,916 predicted protein-coding genes, with a total G+C content of 65.2%.

Cupriavidus species (formerly known as *Wautersia* or *Ralstonia*) are Gram-negative betaproteobacteria that are known for their diverse metabolic capabilities (1–4). In addition, heavy metal resistance is a typical characteristic of *Cupriavidus* strains. Previously sequenced *Cupriavidus* strains, such as *Cupriavidus metallidurans*, *Cupriavidus taiwanensis*, *Cupriavidus basilensis*, *Cupriavidus* sp. strain BIS7, and *Cupriavidus* sp. strain HMR-1, encode a number of putative proteins involved in heavy metal resistance and biodegradation activities (5–11).

Cupriavidus basilensis SRS was isolated from sediments from Tims Branch Creek (33.330008N, 81.689198W) at the Savannah River Site (Aiken, SC), which is well known to be contaminated with heavy metals and radionuclides (12–14). Briefly, sandy loam soil samples from the surface to 6 inches below the surface were collected with a stainless-steel auger and handled aseptically for subsequent analysis. The auger was cleaned and rinsed with 70% ethanol between samplings. The soil samples were transferred to sterile 50-mL centrifuge tubes (Thermo Fisher Scientific) and transported to the laboratory for immediate microbiological processing. The bacteria were grown on Difco nutrient agar (BD Biosciences, Franklin Lakes, NJ) for 3 days at 25°C. A single colony was inoculated into Reasoner's 2A (R2A) medium (Teknova, Hollister, CA) and incubated overnight at 25°C. Then, 2 mL of the culture was centrifuged (4,000 $\times$ *g* for 5 min), and the pellet was used for DNA extraction with the Qiagen DNA blood and tissue kit. A sample of DNA (approximately 2.5 μg) was sent to GENEWIZ (South Plainfield, NJ, USA) for library preparation using the NEBNext Ultra DNA library preparation kit (New England Biolabs, Ipswich, MA) and whole-genome sequencing (2 $\times$ 150-bp paired-end sequencing) using an Illumina MiSeq instrument. A total of 25,239,038 reads were generated, with a mean quality score of 36.3. The subsequent data processing and analysis were performed in KBase (https://www.kbase.us) (15). Default parameters were used for all software unless otherwise specified. Trimmomatic (v0.36) was used to trim the raw reads (16). A total of 24,980,570 trimmed reads with a mean quality score of 36.4 were used by SPAdes (v3.15.3) for *de novo* assembly (17). The quality of the draft genome was assessed using CheckM (v1.0.18) (18).

The taxonomy of *Cupriavidus basilensis* SRS was classified using the Genome Taxonomy Database (GTDB) (v1.1.0) (19). FastANI (v0.1.3) was used to calculate the average nucleotide identity (ANI) (20). We found that *Cupriavidus basilensis* SRS shared 97.3% ANI with the type strain of *Cupriavidus basilensis* (DSM 11853 = CCUG 49340 = RK1) (RefSeq accession number GCF_008801925.2) (4), indicating that these two bacteria belong to the same species (21, 22).

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TABLE 1 General features of the draft genome of *Cupriavidus basilensis* SRS

Parameter	Finding
Size	8.92 Mb
G+C content (%)	65.2
No. of contigs	176
N_{50} (bp)	123,203
Coverage (×)	411
CheckM completeness (%)	99.94
CheckM contamination (%)	2.68

We annotated the *Cupriavidus basilensis* SRS genome using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (v6.1) (23–25). The genome contains 8,918,236 bp and 7,916 predicted protein-coding genes, with a total G+C content of 65.2% (Table 1). The genome annotation reveals numerous putative proteins responsible for metal acquisition and homeostasis, including 10 TonB-dependent siderophore transporters, 3 TonB proteins, 3 ExbB/ExbD proteins, 2 ferric iron ABC transporters, 4 magnesium and cobalt transport proteins, 8 extracytoplasmic function (ECF) sigma factors, and 7 heavy metal efflux pumps (lead-, cadmium-, zinc-, and mercury-transporting ATPases/copper-transporting P-type ATPases). The presence of these putative metal uptake- and metal efflux-related proteins in *Cupriavidus* make this organism relevant for bioremediation and bioextraction studies.

Data availability. The whole-genome sequence of *Cupriavidus basilensis* SRS has been deposited in DDBJ/ENA/GenBank under the accession number JAMBNM000000000. The version described in this paper is the first version. The BioProject accession number is PRJNA833476, the BioSample accession number is SAMN27996175, and the SRA accession number is SRR19544536.

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