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GENOME SEQUENCES

Draft Genome Sequence of the Phenol-Degrading Bacterium *Cupriavidus* sp. Strain P-10, Isolated from Trichloroethene-Contaminated Aquifer Soil

Kenshi Suzuki,[a] Fatma A. A. Aziz,[b] Masahiro Honjo,[c] Tomoka Nishimura,[c] Kensei Masuda,[c] Ayaka Minoura,[c] Yuki Kudo,[c] Ryota Moriuchi,[d] Hideo Dohra,[d,e] Yosuke Tashiro,[c] Hiroyuki Futamata[a,c,d]

[a]Graduate School of Science and Technology, Shizuoka University, Shizuoka, Japan
[b]Laboratory of Food Crops, Institute of Tropical Agriculture, Universiti Putra Malaysia, Seri Kembangan, Malaysia
[c]Graduate School of Integrated Science and Technology, Shizuoka University, Shizuoka, Japan
[d]Research Institute of Green Science and Technology, Shizuoka University, Shizuoka, Japan
[e]Department of Biological Science, Graduate School of Integrated Science and Technology, Shizuoka University, Shizuoka, Japan

ABSTRACT A batch culture was enriched on phenol with trichloroethene-contaminated aquifer soil as an inoculum. *Cupriavidus* sp. strain P-10 was isolated from the culture using a diluted plating method. Here, we report the draft genome sequence and annotation of strain P-10, which provides insights into the metabolic processes of phenol degradation.

Members of the *Cupriavidus* genus have been studied as model organisms of heavy metal resistance, synthesis of polyhydroxyalkanoates, and degradation of aromatic compounds for biotechnology applications (1–3). Phenol is a common constituent of effluents derived from various industrial processes, such as polymeric resin production, petroleum refining, and pharmaceutical manufacturing. Since phenol is highly toxic and easily dissolved in water, phenol contamination is a serious problem for human life. The biodegradation of phenol is commonly used to clean up polluted environments; hence, sequencing the genomes of environmental microbes to unveil the metabolic processes of phenol degradation will assist in the construction of effective biodegradation systems (4, 5). Here, we present the genome sequence of *Cupriavidus* sp. strain P-10, identified as *Ralstonia* sp. strain P-10 in our previous work, which was isolated from a batch enrichment culture grown on phenol with trichloroethene-contaminated aquifer soil as the inoculum (6).

The genomic DNA of strain P-10 was extracted by a method reported previously (7) and was fragmented using the Covaris acoustic solubilizer. A paired-end library was constructed with the TruSeq DNA PCR-free library preparation kit and was sequenced using the Illumina MiSeq platform (300-bp paired ends) at the Instrumental Research Support Office of the Research Institute of Green Science and Technology at Shizuoka University. The raw read sequences were cleaned up using Trimmomatic v. 0.36 (8) by trimming adapter sequences, low-quality ends, which were defined as having a quality score of less than 15, the last 300 bases, and reads less than 150 bp. The quality-controlled reads were assembled using SPAdes v. 3.10.0 (9), with a default set of k-mer sizes and options (–careful, –only-assembler, and –cov-cutoff auto), and contigs less than 200 bp and less than 10-fold coverage were eliminated. Through this process, 1,801,979 high-quality reads totaling 490 Mb, which corresponds to an approximately 54-fold coverage of the genome, were assembled. The draft genome sequence of strain P-10 has a total length of 8,983,816 bp, including 174 contigs, with an estimated G+C content of 65.3% and an N_{50} value of 227,897 bp.

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Address correspondence to Kenshi Suzuki, suzuki.kenshi.15@shizuoka.ac.jp, or Hiroyuki Futamata, futamata.hiroyuki@shizuoka.ac.jp.

The draft genome was annotated by Rapid Annotations using Subsystem Technology (RAST) (10) and the Microbial Genome Annotation Pipeline (MiGAP) (11). The annotated genome includes 8,184 coding sequences and 66 tRNA sequences. A Southern blot hybridization targeting 16S rRNA genes was conducted to identify the number of 5S-16S-23S rRNA clusters, and five clusters were obtained. The relatedness of *Cupriavidus* sp. P-10 with other *Cupriavidus* spp. was assessed by calculating the average nucleotide identity (ANI) using JSpecies (12). The highest ANI at 92% was with *Cupriavidus oxalaticus* NBRC 13593 (13).

Genes encoding for a multicomponent-type phenol hydroxylase, which is one of the major enzymes related to phenol degradation found in natural environments (14), were found in the genome of strain P-10, as in our previous study (7). The complete set of *meta*-cleavage and *ortho*-cleavage metabolic pathways for catechol via catechol 2,3-dioxygenase and catechol 1,2-dioxygenase (3), respectively, were also found. The gene encoding biphenyl 2,3-dioxygenase, which also converts catechol to 2-hydroxymuconate semialdehyde, was found as part of the benzoate-degrading process (3). This genome information of strain P-10 suggests the presence of multiple phenol metabolic pathways, via *meta*-cleavage or *ortho*-cleavage, which may be exploitable for designing an effective biodegradation system for phenol or other phenolic compounds.

Data availability. The raw read sequences have been deposited at DDBJ under the accession no. DRA007291. The draft genome of *Cupriavidus* sp. P-10 has been deposited at DDBJ/GenBank under the accession no. BGPQ01000001 to BGPQ01000174.

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