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Draft Genome Sequence for *Desulfovibrio africanus* Strain PCS

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***Desulfovibrio africanus* strain PCS is an anaerobic sulfate-reducing bacterium (SRB) isolated from sediment from Paleta Creek, San Diego, CA. Strain PCS is capable of reducing metals such as Fe(III) and Cr(VI), has a cell cycle, and is predicted to produce methylmercury. We present the *D. africanus* PCS genome sequence.**

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Sulfate-reducing bacteria (SRB) are anaerobic microorganisms that play important roles in sulfur and carbon cycles in diverse environments (see reviews [1–3]). *Desulfovibrio africanus* strain PCS was isolated from a lactate/sulfate enrichment culture inoculated with sediment samples obtained from Paleta Creek, San Diego, CA. The isolated strain was Gram negative, motile, nonsporulating, and 99% similar by 16S rRNA gene sequencing to *Desulfovibrio africanus* subsp. *uniflagellum* (GenBank accession number EU659693) and *D. africanus* strain Walvis Bay (CP003221.1) (4), which is consistent with the species definition (5). *D. africanus* strains, including PCS, have different morphotypes associated with a cell cycle (6–10), and PCS incompletely oxidizes lactate, accumulating acetate as an end product.

D. africanus strains have been shown to methylate inorganic mercury [Hg(II)] to methylmercury (MeHg), a potent human neurotoxin (10–12). The capability to produce MeHg is found only in a subset of SRB and Fe(III)-reducing bacteria (IRB) (11–16). A 4.2-Mb complete genome sequence for *D. africanus* strain Walvis Bay (4, 17), which produces MeHg, has been reported (10, 12). Recently, genetic studies have shown that a two-gene cluster encoding a putative corrinoid-containing CO dehydrogenase/acetyl coenzyme A (acetyl-CoA) synthase, HgcA, and a 2[4Fe-4S] ferredoxin, HgcB, is required to produce MeHg in SRB and IRB (18). HgcA and HgcB are predicted to have roles as a methyl carrier and an electron donor, respectively. To date, strain PCS has not been tested for its ability to generate MeHg.

The genome sequence for strain PCS was generated using Illumina data, as described previously (19). Briefly, CLC Genomics Workbench (version 5.5) was used to trim 100-bp reads from a paired-end library for quality sequence data, and these were then assembled using Velvet (version 1.2.01) (20). The resulting assembly generated 45 DNA contigs for an estimated genome size of ~3.9 Mb. The maximum contig size was 609,036 bp, the average contig size was 87,322 bp, and the N_{50} was 140,584 bp. The average read depth was approximately 560× the estimated genome size. The draft genome sequence was annotated as previously described (21) and 3,561 candidate protein coding genes were predicted.

The PCS genome had a G+C content of 61.2%, which is similar to the 61.4% G+C content reported for strain Walvis Bay (4). Strain PCS shows 95% average nucleotide identity to strain Walvis Bay when the two genome sequences are compared using the JSpecies program (22). Strain PCS contains putative *hgcA* (PCS_01240) and *hgcB* (PCS_01242) genes that are ~97% and 98% identical, respectively, to their Walvis Bay counterparts at the nucleotide level. In both strains, a gene encoding a predicted radical *S*-adenosylmethionine (SAM) superfamily or Fe-S oxidoreductase protein is in a 3′ position relative to *hgcA* and 5′ relative to *hgcB*, a genetic organization that differs from those of other MeHg-producing bacteria like *D. desulfuricans* strain ND132 (16, 18). The *D. africanus* PCS genome sequence will facilitate further studies with this bacterium.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AOSV00000000. The version described in this paper is the first version, AOSV01000000.

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