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Genome Sequence of the Mercury-Methylating and Pleomorphic *Desulfovibrio africanus* Strain Walvis Bay▽

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***Desulfovibrio africanus* strain Walvis Bay is an anaerobic sulfate-reducing bacterium capable of producing methylmercury (MeHg), a potent human neurotoxin. The mechanism of methylation by this and other organisms is unknown. We present the 4.2-Mb genome sequence to provide further insight into microbial mercury methylation and sulfate-reducing bacteria.**

Methylmercury (MeHg) is a potent human neurotoxin that bioaccumulates in aquatic and terrestrial food webs. This contaminant is known to be produced by bacteria that reduce sulfate or iron (SRB or IRB, respectively) (13, 16, 19, 22), but not all such strains are able to produce MeHg and relatively few methylating bacteria have been identified (17).

The mechanism(s) for microbial Hg methylation is presently unknown, and while considerable insight was gained from *Desulfovibrio desulfuricans* LS (2, 11, 12), this strain was lost. *Desulfovibrio desulfuricans* ND132 has metabolic similarity to *D. desulfuricans* strain LS: both have high rates of Hg methylation (21). We recently determined the genome sequence for *D. desulfuricans* ND132 (3) and described its physiological characteristics (17). *Desulfovibrio africanus* produces MeHg (14) and has different morphotypes associated with a cell cycle (8–10, 18). Its genome sequence was determined and is summarized here to facilitate future analyses into SRBs, mercury methylation, and cell cycle differentiation and regulation.

D. africanus strain Walvis Bay was originally isolated from a marine sediment sample from Walvis Bay, Republic of Namibia (formerly South-West Africa), and has been deposited in the American Type Culture Collection (ATCC 19997) (4). *D. africanus* DSM2603T was been reported as plasmid-free, while others, such as *D. africanus* subsp. *uniflagellum*, which was isolated from uranium(VI)- and sulfate-containing sediments, has a small plasmid (5). *D. africanus* SR-1 has a 8,568-bp mobilizable plasmid, pNC1, which has been characterized for genetic manipulation of *D. africanus* (6).

The genome of *D. africanus* strain Walvis Bay was generated using a combination of Illumina (1) and 454 (20) technologies. All aspects of the DNA sequencing and genome finishing for this project have been described previously (15). The genome size is 4,200,509 bp, and the final assembly is based on ~85 Mb of 454 draft data, which provide an average of ~20-fold coverage of the genome, and ~5,363 Mb of Illumina draft data, which provide an average of 1,247-fold coverage of the genome. The genome is defined as finished, noncontiguous (7). One region has 100 nucleotides in the sequence that are not identified. The order and arrangement of known sequences are correct based on paired-end sequence data and the finishing process, as described earlier (15). Plasmid DNA was not detected in this strain.

A total of 3,725 candidate protein-encoding gene models were predicted, and the genome had 61.4% G+C DNA content, which is similar to the 60.2% G+C content measured from buoyant density measurements in cesium chloride for this strain (4) and the 62.4% G+C content measured for *D. africanus* subsp. *uniflagellum* (6). We identified three separate and identical rRNA operons, each containing a 23S, 16S, and 5S rRNA gene. The 16S rRNA gene sequence is 99% similar to the *D. africanus* (GenBank accession no. EU659693.1), uncultured *Desulfovibrio* sp. clone BH11 (GU565246.1), and *D. africanus* strain DSM 2603 (NR_026351.1) sequences and 88% similar to the *D. desulfuricans* ND132 gene sequence (3). The *D. africanus* genome sequence will facilitate further studies with this genus and species.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AFHE00000000. The version described in this paper is the first version, AFHE00000000.

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