Genome Sequence of Deep-Sea Manganese-Oxidizing Bacterium
Marinobacter manganoxydans MnI7-9

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Here we report the draft genome of Marinobacter manganoxydans MnI7-9, isolated from a deep-sea hydrothermal vent in the Indian Ocean and capable of oxidizing manganese even when there is a very high concentration of Mn²⁺. The strain also displayed high resistance and adsorption ability toward many metal(loid)s.

Bacteria of the genus Marinobacter (Gammaproteobacteria) are Gram-negative, motile, halophilic or halotolerant, and ubiquitous in various marine environments (8). All known strains have the ability to use petroleum hydrocarbons as sole carbon sources and interact with marine algae and plankton (1, 6). Marinobacter manganoxydans MnI7-9 was isolated from a heavy-metal-rich sediment sample collected from a deep-sea hydrothermal vent in the Indian Ocean (lat 25.32, long 70.04; depth, 2,474 m). It was assigned to the Marinobacter genus based on its 16S rRNA sequence and fatty acid analyses. M. manganoxydans MnI7-9 can tolerate high levels of metal(loid)s, oxidize manganese [Mn(II)] to Mn(III)/Mn(IV), even under 10 mM MnCl₂ conditions, and adsorb many metal(loid)s. So far, the complete genome sequences of 4 Marinobacter species, M. adhaerens HP15 (GenBank accession numbers CP001978 to CP001980), M. algicola DGG93 (GenBank accession number ABCP00000000), M. aquaeolei VT8 (GenBank accession numbers CP000514 to CP000516), and Marinobacter sp. EL17 (GenBank accession number AAXY00000000), have been published; however, a genome sequence for a highly metal-resistant and Mn(II)-oxidizing Marinobacter species from a deep-sea environment has not been reported.

Genome sequencing was performed using the 454 GS FLX sequencer (9), producing 314,378 random shotgun reads with an average length of 373 bp. The approximate genome coverage was 24-fold. The sequence reads were assembled into 88 contigs with a total of 4,549,590 bp using the GS De Novo Assembler, version 2.5.3. The rapid annotations using subsystems technology (RAST) server was used to annotate the assembled contigs (3). A total of 4,171 protein-coding genes (CdGs) and 3,128 RNA sequences were annotated, and 2,562 proteins have orthologs with M. adhaerens HP15 and M. aquaeolei VT8 in RAST (identities of >60%). A total of 3,128 proteins could be assigned to cluster of orthologous groups (COG) families. The GC content was 57.3% when analyzed using CLC Main Workbench 5 (http://www.clcbio.com). The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) was employed for the gene annotation that was submitted to GenBank (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

We particularly analyzed genes possibly responsible for Mn(II) oxidation, such as the multicopper oxidase genes mofA, mnxA, and mnxG (4, 10). We found 5 genes encoding multicopper oxidases, 3 annotated as copA, 1 annotated as a twin-arginine translocation pathway signal gene, and 1 of unknown function, but none of them had significant homology with mofA, mnxA, and mnxG. In addition, genes encoding cytochrome c synthetase, tryptophan biosynthesis, parts of the tricarboxylic acid (TCA) cycle, and the secretory pathway (7) with a possible accessory role in Mn(II) oxidation were found in the genome of MnI7-9. However, the genes encoding heme-binding peroxidase (2) and sensor kinases (MnxS1 and MnxS2) (7) with a possible involvement in Mn(II) oxidation were not found.

We also found genes encoding proteins associated with resistance to metal(loid)s based on the high tolerance of M. manganoxydans MnI7-9 to many metal(loid)s. We identified genes putatively involved in nickel, mercury, copper, chromate, arsenic, zinc, cobalt, and cadmium resistance. In addition, genes important for degradation of aliphatic and polycyclic aromatic hydrocarbons were found in the genome (5, 12). The draft genome sequence of M. manganoxydans MnI7-9 from a metal-rich, deep-sea hydrothermal vent might aid in understanding evolutionary processes in different Marinobacter species to adapt to variable marine environments (11).

Nucleotide sequence accession numbers. The genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession number AGTR00000000. The version described in this paper is the first version, accession number AGTR00000000.

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