Draft Genome Sequence of *Microbacterium profundi* Shh49T, an Actinobacterium Isolated from Deep-Sea Sediment of a Polymetallic Nodule Environment

Yue-Hong Wu, a Peng Zhou, a Hong Cheng, a,b Chun-Sheng Wang, a Min Wu, b Xue-Wei Xu a

Laboratory of Marine Ecosystem and Biogeochemistry, Second Institute of Oceanography, State Oceanic Administration, Hangzhou, China; College of Life Sciences, Zhejiang University, Hangzhou, China

*Microbacterium profundi* strain Shh49T was isolated from deep-sea sediment from a polymetallic nodule area located in the East Pacific Ocean. Strain Shh49T contains genes related to the reduction/oxidation of metals. It has potential application in the bioremediation of heavy-metal-contaminated environments.

Ocean polymetallic nodules are widely distributed in the deep-sea floor and are a potential source of metals, such as Fe, Mn, Ni, Cu, and Co (1). Microbes participate in the formation of polymetallic nodules (2). *Microbacterium profundi* Shh49T belongs to the class *Actinobacteria*. It was isolated from deep-sea sediment of a polymetallic nodule environment (8°22′38″N 145°23′56″W) at a depth of 5,280 m (3). To understand the ecological function of strain Shh49T and its potential role in the formation of nodules, the genome of strain Shh49T was sequenced and analyzed.

Genomic DNA sequencing was performed using Solexa paired-end sequencing technology (HiSeq 2000 system; Illumina, Inc., USA) (4) by a whole-genome shotgun (WGS) strategy, with a 500-bp paired-end library (333 Mb available reads, 100-fold genome coverage) and a 2,000-bp paired-end library (140 Mb available reads, 42-fold genome coverage). All clean reads were assembled using SOAPdenovo version 1.05 (5, 6). The quality of the sequencing read data was estimated by G+C content and sequencing depth correlation analysis. The tRNAs and rRNAs were identified using tRNAscan-SE (7), RNAmmer (8), and the Rfam database (9). The open reading frames (ORFs) and the functional annotation of translated ORFs were predicted and achieved using the RAST server online (10). The classification of some predicted genes and pathways was analyzed using the KEGG databases (11–13).

The draft genome sequence of strain Shh49T revealed a genome size of 3,369,357 bp (scaffold length) and was assembled into 12 contigs. The G+C content was 66.54%. These scaffolds contain 3,269 coding sequences (CDSs), 44 tRNAs, and one copy of 16S-23S-5.8 rRNA gene operons. Among the protein-coding genes, 2,355 were assigned to putative functions, and the remaining were annotated as hypothetical proteins.

To study the ecological function of strain Shh49T in the metal cycle, the reductase/oxidase relationship to metal reduction/oxidation, including Fe, Mn, Cu, and Hg, was analyzed. Four multicopper oxidases (MCOs), a family of enzymes known to be involved in Fe (14), Cu (15, 16), and Mn oxidation (17), were detected. Strain Shh49T may have potential ability to oxidize iron from ferrous to ferric iron on the basis of the detection of two ferroxidases. Further experiments need to be performed to confirm its function. Strain Shh49T encodes one mercuric ion reductase and one flavin adenine dinucleotide (FAD)-dependent NAD(P)-disulfide oxidoreductase, both of which participate in the reduction of Hg(II) to Hg. The genome of strain Shh49T may further help us investigate the cycles of metals in deep-sea polymetallic nodules. Strain Shh49T also has potential application in the bioremediation of heavy metal-contaminated environments.

Nucleotide sequence accession number. The draft genome sequence of strain Shh49T is available in GenBank under the accession no. JPSY00000000.

ACKNOWLEDGMENTS

This work was supported by grants from China Ocean Mineral Resources R & D Association (COMRA) Special Foundation (DY125-14-E-02), the National Natural Science Foundation of China (grants 41406174 and 41276173), and the Zhejiang Provincial Natural Science Foundation of China (grant LY14D060006).

REFERENCES


