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PROKARYOTES

Draft Genome Sequence of *Mariprofundus micogutta* Strain ET2

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ABSTRACT *Mariprofundus micogutta* strain ET2 was isolated in 2014 from a deep-sea hydrothermal field on the Bayonnaise Knoll of the Izu-Ogasawara arc. Here, we report its draft genome, which comprises 2,497,805 bp and contains 2,417 predicted coding sequences.

Mariprofundus micogutta ET2 (=KCTC15556^T=JCM30585^T) is a microaerophilic and chemolithoautotrophic mesophile that grows by oxidizing ferrous iron. The stalk-forming type strain *M. ferrooxydans* PV-1 and the non-stalk-forming strain *M. ferrooxydans* JV-1 were the first reported isolates belonging to the genus *Mariprofundus* (1). Since that initial isolation, strains belonging to the class "*Candidatus* (*Ca.*) Zetaproteobacteria" have been discovered throughout the Pacific and Atlantic oceans, mainly from deep-sea hydrothermal fields (2). Recently, *M. ferrooxydans* strains were successfully isolated from a salt marsh of the Great Salt Bay, Newcastle, Maine (3), and the Spillway Area of the Loihi Seamount (4). Here, we report the genetic features of *M. micogutta* strain ET2, which were determined using draft genome sequencing.

Strain ET2 was isolated from sediment of a 772-m-deep hydrothermal field on the Bayonnaise Knoll, Izu-Ogasawara Arc. A pure culture was obtained by a dilution-to-extinction series with artificial seawater (ASW) medium, as previously described (5). Strain ET2 was grown in ASW medium at 25°C with filament formation. Genomic DNA was extracted from cell pellets using a PowerMax Soil DNA isolation kit (Mo Bio, Carlsbad, CA, USA). A sequencing library was prepared with a Nextera DNA prep kit (Illumina, Inc., San Diego, CA, USA) and subsequently sequenced using an Illumina MiSeq version 3 reagent kit (600 cycles) with 300-bp paired-end reads on the Illumina MiSeq platform. A total of 17.6 million reads were produced, yielding 7.5 Gb of data. Read quality was assessed with FastQC (https://www.bioinformatics.babraham.ac.uk/projects/fastqc). Quality-controlled reads were used to assemble the draft genome with SPAdes version 3.5.0 (6), resulting in 59 contigs with an N_{50} value of 105,204 bp (the largest contig was 249,769 bp); the assembled draft genome was 2,497,805 bp in size with a G+C content of 48.75%. Annotation was carried out using Prokka version 1.11 (7), with 2,417 coding sequences (CDSs), 6 rRNAs, and 49 tRNAs being identified. Average nucleotide identity (ANI) comparisons with other *M. ferrooxydans* genomes, including strains PV-1 and M34, revealed ANIs of 95.89% and 95.8%, respectively. This confirms the placement of *M. micogutta* strain ET2 in the genus *Mariprofundus* of the class "*Ca.* Zetaproteobacteria." Similar to strains PV-1 and M34, strain ET2 encodes genes for growth by chemoautotrophy and motility via a flagellum, although motility was not observed in laboratory experiments and observations (5). A complete set of CDSs for carrying out carbon fixation using the Calvin-Benson-Bassham cycle was identified. Unlike other members of the class "*Ca.* Zetaproteobacteria", *M. micogutta* strain ET2 has both *aa3*- and *cbb3*-type oxidase genes. The genome includes eight

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chemotaxis (*che*) genes and four methyl-accepting chemotaxis proteins, which were previously shown to play important roles in adaptation to deep-sea vent environments (8). Moreover, since the cobalt-zinc-cadmium resistance protein (*czc*) is present, it is considered to exhibit heavy-metal tolerance (9). The outer membrane cytochrome Cyc2 (10), a possible key gene for catalyzing iron oxidation, was detected. Genes for the putative outer membrane Fe oxidase MtoA (11, 12) were not found in the ET2 genome, like other *Mariprofundus* species.

Accession number(s). The whole-genome shotgun project reported here was deposited at DDBJ/EMBL/GenBank under the accession number BDFD00000000, and the 59 contigs generated were deposited under the accession numbers BDFD01000001 to BDFD01000059.

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