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GENOME SEQUENCES

Complete Genome Sequence of *Methanofollis formosanus* DSM 15483^T, Isolated from an Aquaculture Fish Pond

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ABSTRACT The hydrogenotrophic strain *Methanofollis formosanus* DSM 15483^T (= ML15^T = OCM 798^T) was isolated from an aquaculture fish pond near Wang-gong, Taiwan. The genome of strain DSM 15483^T was selected for sequencing in order to provide further information about the species delineation and its unique habitat.

At present, a total of 6 *Methanofollis* species have been characterized and validly described: *Methanofollis tationis* (1, 2), *M. liminatans* (2, 3), *M. aquaemaris* (4), *M. formosanus* (5), *M. ethanolicus* (6), and *M. fontis* (7). Isolates of the genus *Methanofollis* are widespread in various anaerobic environments, such as solfataric fields, wastewater reactors, aquaculture fish ponds, lotus fields, and cold seep sediments (1, 3–7). Moreover, *Methanofollis*-related sequences have been found in acetate-rich gas-petroleum reservoir surface facilities (8), municipal solid waste landfill leachates (9), a long-duration gas injection oil reservoir in the south of Iran (10), a crust formed on SS400 carbon steel during corrosion (11), and biogas reactors (12, 13). Here, we report the complete genome sequence of *M. formosanus* DSM 15483^T to further understand the microbial adaptation to various environments.

M. formosanus DSM 15483^T (= ML15^T = OCM 789^T) was obtained from the Leibniz Institute DSMZ, grown in anaerobic MB/W medium with 100 mM sodium formate and 5 mM sodium acetate, and incubated at 37°C, according to the method used in our previous studies (5, 14, 15). Genomic DNA from strain DSM 15483^T was isolated using a modification of the methods of Jarrell et al. (16) and Johnson (17). Briefly, cells from 500 mL of culture were lysed with sodium dodecyl sulfate (SDS) (1%, wt/vol). After phenol-chloroform extraction and ethanol precipitation, the quantity and quality of the dissolved DNA samples were examined using a UV-visible (UV-Vis) spectrophotometer.

The genome was sequenced at the Genomics BioSci and Tech Co., Ltd. (Taiwan), using the Illumina MiSeq platform. The genomic DNA was sheared randomly, and a paired-end DNA library of 300-bp reads was constructed using the TruSeq Nano DNA high-throughput (HT) library prep kit and the TruSeq DNA kit with 96 CD indexes (Illumina). The constructed DNA library was sequenced using the MiSeq reagent kit v3 (600 cycle) on the MiSeq platform (Illumina), and 300-bp paired-end reads (~1.79 Gb) were generated by the Genomics BioSci and Tech Co. All generated reads were quality trimmed to obtain high-quality reads using Trimmomatic (18). These reads were *de novo* assembled using SPAdes v3.10.1 (19), and the quality of the assembled genome was evaluated using QUAST v4.5 (20). The sequencing protocol generated 337× mean coverage of the genome. The longest contig obtained comprised an N_{50} value of 2,966,023 bp and was circularized by aligning both ends of the contig sequences (~300 bp) and

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deleting the overlapping sequences from one end. The genes of the genome were identified using the Prokaryotic Genome Annotation Pipeline (PGAP) at the website of the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov) (21).

The complete genome of strain DSM 15483^T comprised a total of 2,965,921 bp and an average G+C content of 60.32%. No plasmids were identified. The genome was predicted to harbor 2,676 genes, of which 2,568 were protein coding. The genome contains 4 rRNA genes and 51 tRNA genes. Two clustered regularly interspaced short palindromic repeats (CRISPRs) with a high evidence level were found in the genome using CRISPRCasFinder (22). Default parameters were used for all bioinformatics analyses.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under accession number CP037968.1. The version described in this paper is the first version. The BioProject accession number is PRJNA527005. The raw sequence reads have been deposited in the Sequence Read Archive (SRA) under accession number SRR17713754.

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