

Draft Genome Sequence of *Methanoculleus sediminis* S3Fa^T, a Hydrogenotrophic Methanogen Isolated from a Submarine Mud Volcano in Taiwan

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Here, we announce the genome sequence of *Methanoculleus sediminis* S3Fa^T (DSM 29354^T), a strict anaerobic methanoeocyte, which was isolated from sediments near the submarine mud volcano MV4 located offshore in southwestern Taiwan. The 2.49-Mb genome consists of 2,459 predicted genes, 3 rRNAs, 48 tRNAs, and 1 ncRNA. The sequence of this novel strain may provide more information for species delineation and the roles that this strain plays in the unique marine mud volcano habitat.

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Methanoculleus sediminis S3Fa^T, a mesophilic and hydrogenotrophic methanogen, was isolated from sediments near the submarine mud volcano MV4 located offshore in southwestern Taiwan and described as a novel species within the genus *Methanoculleus* (1). The genus *Methanoculleus* currently comprises 11 characterized and valid species: *M. marisnigri* JR1^T (2), *M. submarinus* Nankai-1^T (3), *M. chikugoensis* MG62^T (4), *M. thermophiles* CR-1^T (5), *M. palmolei* INSLUZ^T (6), *M. bourgensis* MS2^T (7), *M. receptaculi* ZC-2^T (8), *M. hydrogenitrophicus* HC^T (9), *M. horonobensis* T10^T (10), *M. taiwanensis* CYW4^T (11), and *M. sediminis* S3Fa^T (1). The sources of these *Methanoculleus* spp. are truly diverse, including marine sediments, wastewater plants, wetlands, oil fields, and paddy fields. Here, we provide the draft genome sequence of *M. sediminis* S3Fa^T as a basis for future comparative studies and understanding the ecological roles of this genus.

Whole-genome shotgun sequencing was performed using the Illumina MiSeq platform with 2 × 300-bp reads. The reads were quality-filtered, trimmed, and assembled into contigs using the *de novo* assembler CLC Genomic Workbench version 7.5. The draft genome comprises 15 contigs with total length of ~2.49-Mb and a G+C content of 62.3%. Gene annotations were performed by using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP); 2,459 predicted genes, 3 rRNAs, 48 tRNAs, and 1 ncRNA were obtained.

The genome contains the genes of formate dehydrogenase, which is essential for formate utilization for methane production and growth of *Methanoculleus sediminis* S3Fa^T. Three clusters of regularly interspaced short palindromic repeat (CRISPR)-associated *cas* genes were identified. Furthermore, this genome contains three coding genes for trehalose synthases, which convert ADP-glucose to trehalose. This genome also comprises complete gene sets of heat shock proteins, including DnaK, DnaJ, GrpE, GroEL, GroES, prefoldin subunits, and small heat shock proteins. The genetic and physiological characteristics of strain S3Fa^T will be unveiled by comparative genomic analyses with *Methanoculleus* spp. and methanogens within other taxa.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JXOJ00000000](https://doi.org/10.1101/000000). The version described in this paper is the first version, JXOJ01000000.

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