Draft Genome Sequences of *Methanoculleus horonobensis* Strain JCM 15517, *Methanoculleus thermophilus* Strain DSM 2373, and *Methanofollis ethanolicus* Strain JCM 15103, Hydrogenotrophic Methanogens Belonging to the Family *Methanomicrobiaceae*

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The family *Methanomicrobiaceae* comprises hydrogen- and formate-utilizing methanogens. Genome sequencing of nine species of *Methanomicrobiaceae* has been conducted so far. Here, we report three additional draft genome sequences of *Methanomicrobiaceae*, those of *Methanoculleus horonobensis* JCM 15517 (=T10^T), *Methanoculleus thermophilus* DSM 2373 (=CR-1^T), and *Methanofollis ethanolicus* JCM 15103 (=HASU^T).

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Members of the family *Methanomicrobiaceae* in the phylum *Euryarchaeota* are known to contain hydrogen- and formate-utilizing methane-producing archaea (1). Some of the known species of this family can also use a secondary alcohol (such as ethanol, 1-propanol, and 1-butanol) as a methanogenic substrate. Currently, complete or draft genome sequences are available for nine species of *Methanomicrobiaceae* (2–6). To compare the genomic features of *Methanomicrobiaceae* species, we additionally sequenced three genomes, those of *Methanoculleus horonobensis* strain JCM 15517 ^{T} (=strain T10^T), *Methanoculleus thermophilus* strain DSM 2373 (=CR-1^T), and *Methanofollis ethanolicus* strain JCM 15103^T (=HASU^T). These strains were isolated from a variety of methanogenic ecosystems: strain T10^T was isolated from a groundwater sample collected from a deep diatomaceous shale formation (7), strain CR-1^T was isolated from coastal sediment underlying high-temperature effluent from nucleic power plants (8), and strain HASU^T was isolated from a mud sample from a lotus field (9). Such ecological diversification may affect the genomic features involved in methanogenesis and interaction with syntrophic metabolizers (syntrophs).

Strains T10^T and HASU^T were provided by the RIKEN BRC through the National Bio-Resource Project of the MEXT, Japan. Strain CR-1^T was provided by Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), Germany. Whole-genome shotgun sequencing was conducted using the Illumina MiSeq platform (Illumina, San Diego, CA, USA) at the Fasmac Co., Ltd. (Atsugi, Japan). We constructed and sequenced paired-end libraries (4,506,900, 5,396,179, and 9,926,795 bp for T10^T, CR-1^T, and HASU^T, respectively) on the MiSeq. Assembly of the output reads was performed using a SPAdes software version 3.5.0 (10), and the assembled data provide >1,000× coverage of each genome. The draft genome sequences of strains T10^T, CR-1^T, and HASU^T are composed of a total of 15, 24, and 3 scaffolds, have a G+C content of 62.0, 59.3, and 60.3%, estimated genome sizes of 2.49, 2.22, and 2.75 Mb, and 2,430, 2,249, and 2,651 protein-coding genes with function prediction annotated by the Prokka pipeline (11), respectively. Further attempts to identify hydrogenotrophic methanogenesis pathways and energy conservation systems for comparison with the genomes of other *Methanomicrobiaceae* methanogens are now in progress.

Nucleotide sequence accession numbers. This draft genome sequence has been deposited at DDBJ/GenBank/EMBL under the accession numbers BCNY01000001 to BCNY01000015 for *M. horonobensis* strain JCM 15517, BCNX01000001 to BCNX01000023 for *M. thermophilus* strain DSM 2373, and BCNW01000001 to BCNW01000003 for *M. ethanolicus* strain JCM 15103.

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