Draft Genome Sequence of *Syntrophomonas wolfei* subsp. *methylbutyratica* Strain 4J5T (JCM 14075), a Mesophilic Butyrate- and 2-Methylbutyrate-Degrading Syntroph

Takashi Narihiro,a,b Masaru K. Nobu,b Hideyuki Tamaki,a Yoichi Kamagata,a Wen-Tso Liuab

National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Ibaraki, Japan; Department of Civil and Environmental Engineering, University of Illinois at Urbana-Champaign, Urbana, Illinois, USAa

*Syntrophomonas wolfei* subsp. *methylbutyratica* strain 4J5T (=JCM 14075T) is a mesophilic bacterium capable of degrading butyrate and 2-methylbutyrate through syntrophic cooperation with a partner methanogen. The draft genome sequence is 3.2 Mb, with a G+C content of 45.5%.

**REFERENCES**


This work, including the efforts of Takashi Narihiro, was funded by JSPS KAKENHI (26630250 and 15H05331). This work, including the efforts of Hideyuki Tamaki, was funded by JSPS KAKENHI (26710012).

### FUNDING INFORMATION

This work, including the efforts of Takashi Narihiro, was funded by JSPS KAKENHI (26630250 and 15H05331). This work, including the efforts of Hideyuki Tamaki, was funded by JSPS KAKENHI (26710012).

**SYNOPSIS**

*Syntrophomonas wolfei* subsp. *methylbutyratica* strain 4J5T (=JCM 14075T) is one of a few isolated bacteria capable of volatile fatty acid (VFA) degradation through syntrophic association with a partner hydrogenotrophic methanogen (1–3). Strain 4J5T was isolated from rice field mud in Jiangxi Province, China, and tentatively assigned to the genus *Syntrophomonas* (4). Known *Syntrophomonas* species all catabolize butyrate, and some also catabolize long-chain fatty acids in coculture with a partner methanogen (1) and play an important role in anaerobic ecosystems, such as sludge digestion (5, 6) and rice paddy fields (7). Of these *Syntrophomonas*-related syntrophs, strain 4J5T is unique for its ability to degrade 2-methylbutyrate (4), suggesting that strain 4J5T likely contributes to methanogenic degradation of organic compounds.

Strain JCM 14075T was provided by the RIKEN BioResource Center (BRC) through the National Bio-Resource Project of the Ministry of Education, Culture, Sports, Science, and Technology (MEXT), Japan. Whole-genome shotgun sequencing was performed using the Illumina MiSeq platform (Illumina, San Diego, CA, USA) at the FASMAC Co., Ltd. (Atsugi, Japan). We constructed and sequenced a paired-end library (3,810,689 pairs; 2.26 Gb) and performed assembly using SPAdes (version 3.1.1) (8). The final assembly implemented 300 Mb of MiSeq paired-end reads (500,000 pairs), which provided 714.5× coverage of the draft genome. The JCM 14075T draft genome is 3.2 Mb, contains a total of 89 scaffolds, and has a G+C content of 45.5%, Prokka (version 1.80) annotated 2,964 protein-coding genes, of which 2,186 have predicted functions, and 778 are hypothetical proteins (9). This pipeline also predicted 59 RNA genes, consisting of genes encoding 11 rRNAs (partial) and 43 tRNAs. We are currently exploring this genome to identify butyrate and 2-methylbutyrate degradation genes and pathways for further comparison with fatty-acid-degrading syntrophs.

**Nucleotide sequence accession numbers**. This draft genome sequence has been deposited at DDBJ/GenBank/EMBL under accession numbers BBQT01000001 to BBQT01000092.