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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Methylocystis* sp. Strain SC2, an Aerobic Methanotroph with High-Affinity Methane Oxidation Potential

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***Methylocystis* sp. strain SC2 is an aerobic type II methanotroph isolated from a highly polluted aquifer in Germany. A specific trait of the SC2 strain is the expression of two isozymes of particulate methane monooxygenase with different methane oxidation kinetics. Here we report the complete genome sequence of this methanotroph that contains not only a circular chromosome but also two large plasmids.**

Methylocystis spp. are among the most ecologically relevant methanotrophic bacteria in terrestrial environments (3, 6, 9, 11, 13, 16). Apart from their ability to oxidize methane, several strains have been reported to possess additional metabolic capabilities. These include their facultative nature (2, 10), ability to utilize different nitrogen sources (14, 15), and anaerobic fermentation of poly-β-hydroxybutyrate (18). *Methylocystis* sp. strain SC2 expresses two particulate methane monooxygenases (pMMO) (1). While the conventional pMMO1 promotes its growth under high methane concentrations, pMMO2 allows this bacterium to live in low-methane (<600 ppm) environments. This makes *Methylocystis* sp. strain SC2 unique and calls for complete characterization of its genetic information.

The genome of *Methylocystis* sp. strain SC2 was obtained by whole-genome shotgun sequencing using a 454 GS-FLX Titanium platform, resulting in 0.5 million reads, with an average read length of 380 bp. In addition, 4,000 fosmid inserts were end-sequenced using the Sanger platform. Reads were assembled by MIRA (4). Contigs were finished by primer walking and manually curated in Consed (8). Potential coding sequences (CDS) were predicted using GLIMMER 2.1 (7). *Methylocystis* sp. strain SC2 contains a circular chromosome of 3,773,444 bp and two plasmids of 229,614 bp (pBSC2-1) and 143,536 bp (pBSC2-2), with an average GC content of 63, 61, and 60%, respectively. The chromosome contains a single rRNA operon, a full complement of 47 tRNA genes and 3,666 CDS, with a coding density of 90%.

All genes required for a methanotrophic lifestyle were identified. The presence of two nearly identical copies of *pmoCAB1* and one copy of *pmoCAB2* was validated (1, 17). In addition, we could detect three singleton *pmoC* paralogs, with one present in the plasmid pBSC2-2 (5). The absence of genes encoding the soluble methane monooxygenase was confirmed. Genes encoding methanol dehydrogenase, pyrroloquinoline quinone cofactor biosynthesis proteins, tetrahydromethanopterin-linked and tetrahydrofolate-mediated pathways, NAD-linked formate dehydrogenase, and serine cycle enzymes for formaldehyde assimilation were found.

A homolog of the gene encoding the precursor peptide of methanobactin in *Methylosinus trichosporium* strain OB3b could not be identified (12). However, the chromosome and the plasmids of *Methylocystis* sp. strain SC2 encode several copper homeostasis systems, including two *copCD* operons and several copies of copper-transporting P-type ATPases. A large repertoire of genes involved in nitrogen metabolism was detected. This includes genes whose products are involved in transport and assimilation of ammonia, hydroxylamine detoxification, nitrogen fixation, and denitrification. Detoxification presumably involves the activity of both hydroxylamine oxidoreductase (HAO) and hydroxylamine reductase (hybrid cluster protein; HCP). While HAO oxidizes hydroxylamine to nitrite, HCP detoxifies hydroxylamine by reducing it to ammonia. Genes encoding nitric oxide reductase and nitrous oxide reductase are present in the plasmids (5). The genome sequence of *Methylocystis* sp. strain SC2 provides a blueprint for its ability to thrive in environments with varying methane or nitrogen availability.

Nucleotide sequence accession numbers. The nucleotide sequences of the *Methylocystis* sp. strain SC2 chromosome and the two plasmids have been submitted to the EMBL, GenBank, and DDBJ databases under the accession numbers HE956757, FO000001, and FO000002, respectively.

ACKNOWLEDGMENTS

This project was funded by the LOEWE Research Center for Synthetic Microbiology (SYNMIKRO) and the Max Planck Society.

B.D. is grateful to the Alexander von Humboldt Foundation for his fellowship. S.D. is a postdoctoral fellow of the Max Planck Institute for Terrestrial Microbiology.

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Received 10 August 2012 Accepted 24 August 2012

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doi:10.1128/JB.01446-12

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