Draft Genome Sequence of the Methane-Oxidizing Bacterium Methylococcus capsulatus (Texas)

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Methanotrophic bacteria perform major roles in global carbon cycles via their unique enzymatic activities that enable the oxidation of one-carbon compounds, most notably methane. Here we describe the annotated draft genome sequence of the aerobic methanotroph Methylococcus capsulatus (Texas), a type strain originally isolated from sewer sludge.

The ability of methanotrophic bacteria to metabolize the potent greenhouse gas methane as their sole carbon and energy source has generated significant interest in conjunction with their bioremediation potential (2) and commercial bioprotein applications (7). Methanotrophs initially oxidize methane to methanol, which is then converted into formaldehyde and ultimately assimilated into cellular biomass or oxidized further to formate and carbon dioxide for energy production. Methylococcus capsulatus is characterized as a type I methanotroph, depicted by its affiliation to the Gammaproteobacteria and utilization of the ribulose monophosphate pathway (RuMP) for formaldehyde assimilation. Several strains of M. capsulatus have been isolated and studied, including M. capsulatus (Bath), for which a genome sequence is available (8). Here we report the draft genome sequence representative of the type strain M. capsulatus (Texas) (4), which was sequenced as part of a larger project to compare different M. capsulatus strains and their effects in mammalian cellular systems.

The genome of M. capsulatus (Texas) (NCIMB 11853) was sequenced using Illumina-MiSeq technology, which produced a total of 6,106,323 reads (51 bp; coverage, ~94×) subsequently used for assembly with SOAPdenovo v1.05 (6). A total of 114 contigs of >500 bp were constructed, with an N50 of 46.8 kb and an average length of 28.6 kb; the largest contig assembled measured 271.3 kb. The DNA sequence (3,259,715 bp) was annotated by the rapid annotation using subsystem technology (RAST) system (version 4.0) (1). The G+C content of the draft genome is 63.4%, and the genome contains 3,036 complete open reading frames (ORFs) (61 structural RNAs). Genome alignment against the M. capsulatus (Bath) strain using NCmer (3) determined that 93.9% of M. capsulatus (Texas) was shared, with an average percent identity of 97.01%. Moreover, comparisons in RAST determined that 340 ORFs (∼11%) contained within the M. capsulatus (Texas) genome sequence had no homologs in M. capsulatus (Bath).

Genes encoding both particulate membrane-bound and soluble methane monoxygenases (pMMO and sMMO, respectively) were verified; however, unlike the M. capsulatus (Bath) genome, duplicate copies of the pMMO subunits were not identified. Two clusters containing methanol dehydrogenase genes (mxaF) (11022) were found, as well as genes necessary for formaldehyde oxidation via the RuMP pathway and the tetrahydromethanopterin-linked and tetrahydrofolate pathways. A contiguous region of the genome was identified to contain genes utilized in nitrogen fixation (nitrogenase), including structural genes (nifH, nifD, and nifK) and synthesis genes for the iron-molybdenum cofactor (nifE, nifN, and nifX). Interestingly, a complete tricarboxylic acid (TCA) cycle was observed, including putative 2-oxoglutarate dehydrogenases, which is contradictory to earlier reports that have reported their absence in type I methanotrophs (5). Additional comparative analysis of methanotroph genomes from diverse habitats will provide a greater understanding of their ecological contributions and biotechnological potential and specifically present clues toward delineating immunomodulatory properties among different M. capsulatus strains.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AMCE00000000. The version described in this paper is the first version, AMCE01000000.

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