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Draft Genome Sequence of the Chemolithoheterotrophic, Halophilic Methylotroph *Methylophaga thiooxydans* DMS010▽

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***Methylophaga thiooxydans* is a mesophilic, obligately halophilic bacterium that is capable of methylotrophic growth on a range of one-carbon compounds as well as chemolithoheterotrophic growth at the expense of thiosulfate. Here we present the draft genome sequence of *Methylophaga thiooxydans* DMS010 (DSM 22068^T, VKM B2586^T), the type strain of the species, which has allowed prediction of the genes involved in one-carbon metabolism, nitrogen metabolism, and other aspects of central metabolism.**

Methylophaga thiooxydans (1, 3, 11) is one of seven recognized species within the genus *Methylophaga*, which includes *M. alcalica* (6), *M. aminisulfidivorans* (10), *M. marina* (type species [11]), *M. muralis* (2, 8), *M. sulfidovorans* (4), and *M. thalassica* (9). Two species without validly published names have also been described: "*M. limanica*" (5) and "*M. natronica*" (7). All were isolated from environments with low water activity, including seawater and salt lakes. All members of the genus can grow on one-carbon (C_1) compounds, such as methanol and methylated sulfur compounds, and an apparently narrow range of multicarbon substrates (3). C_1 compounds are dissimilated to formaldehyde, which is then assimilated via the 2-keto-3-deoxy-6-phosphogluconate aldolase (KDPG) variant of the ribulose monophosphate (RuMP) pathway (3).

Methylophaga species are relatively poorly characterized in terms of physiology, biochemistry, and genetics. *M. thiooxydans* is the best characterized to date and can grow chemolithoheterotrophically on dimethylsulfide, oxidizing the sulfur to thiosulfate and then to tetrathionate, using this final oxidation step to drive ATP synthesis (3). Oxidation of exogenous thiosulfate to tetrathionate for energy occurs during growth on methanol. This results in an increased maximum yield in continuous culture, with obvious competitive advantages (3).

The draft genome (about 3 Mbp) of the type strain of *M. thiooxydans*, DMS010 (DSM 22068^T, VKM B2586^T), was determined by a whole-genome shotgun approach and included 43 contigs of greater than 20 Sanger reads, united into 26 scaffolds. The mean GC content of the sequence was 45 mol%, in agreement with experimental data (45.9 mol% [5]). Autoannotation was performed, predicting coding sequences based on comparison to public databases. Synthetic pathways for tRNAs of 19 structural amino acids were accounted for. Genes for 21 putative cytochromes, the bc_1 complex, and one terminal oxidase (cbb_3) were found.

All genes for Krebs' cycle were predicted. The E2 component of 2-oxoglutarate dehydrogenase—absent in some chemolithoautotrophs (12)—was predicted. Most of the genes of the Emden-Meyerhof-Parnas and KDPG-variant RuMP pathways could be predicted, though fructose bisphosphate aldolase could not, consistent with enzyme assay data (3). All genes for the tetrahydromethanopterin and tetrahydrofolate system of assimilation were predicted. The *mxaFJGIRSACKLDEK* cluster, encoding methanol dehydrogenase, was predicted, along with the cluster *pqqBCDE*, for biosynthesis of the cofactor pyrroloquinoline quinone. Genes for RubisCO were not found, consistent with a lack of enzyme activity (3).

Genes for ammonia transport were predicted, along with those for the glutamate synthase pathway, glutamine synthetase, glutamate dehydrogenase, alanine dehydrogenase, urease, nitrate reductase (*narHGI*), and the *nirK* dissimilatory nitrite reductase. Genes for sulfate assimilation were predicted.

The information provided in the draft genome sequence of *M. thiooxydans* DMS010 reported here will enable further studies into the metabolism of this and other chemolithoheterotrophic organisms. These data also provide the first overview of the metabolic diversity of the genus *Methylophaga*.

Nucleotide sequence accession number. The nucleotide sequence for the draft genome sequence was deposited in DDBJ/EMBL/GenBank as ABXT00000000.

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