Draft genome sequence of *Methylophaga aminisulfidivorans MP*<sup>T</sup>

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Methylophaga aminisulfidivorans MP¹ is a restricted facultatively marine methylotrophic bacterium that grows on methanol, methylated amines, dimethylsulfide and DMSO. Here we present the high-quality draft genome sequence of *M. aminisulfidivorans* MP¹ (KCTC 12909T = JCM 14647T) consisting of a chromosome (3,092,085-bp) and a plasmid (16,875-bp).

The genus *Methylophaga* is a unique group of aerobic, halophilic, and non-methane-utilizing methylotrophs (6). Members of this genus have been isolated from various marine sediments and soda lakes, and play an important role in the coastal environments participating in biogeochemical cycling of one-carbon substrates containing nitrogen, sulfur or halogens (1,7). They use the ribulose monophosphate (RuMP) pathway for one-carbon compound assimilation. The genus *Methylophaga* currently has seven species with validly published names while only the genome sequence of *M. thiooxydans* (strain DMS010T) is reported (3).

*Methylophaga aminisulfidivorans* MP¹ (KCTC 12909T = JCM14647T) was isolated from the seawater at Mokpo, South Korea (7). The strain is aerobic, neutrophilic, halophilic, and grows well on methanol, methylated amines, dimethylsulfide and DMSO. Only fructose is utilized as a multi-carbon source.

The high coverage genome sequence of *M. aminisulfidivorans* MP¹ was determined using a combination of Illumina Genome Analyzer IIx (150 bp single end shotgun sequencing; 33,762,341 sequencing reads; 1365× fold coverage) and Roche Genome Sequencer FLX system (paired-end with an insert size of 3 Kb; 909,213 reads; 60× fold coverage). The assembly of Illumina sequencing reads was carried out the CLC genomics wb4 (CLCbio) whereas Newbler assembler 2.3 (Roche) was used to generate scaffolds from a 454 paired-end library. Two assemblies were merged into single assembly using the CodonCode Aligner software (CodonCode Co.).

After multiple rounds of gap-closing steps based on standard PCR and Sanger sequencing, 2 contigs (2,266,798 and 825,287 bp, respectively; G+C mol%=43.5) representing a chromosome and one circular plasmid (169,875 bp; G+C mol%=41.20). The resultant genome sequence was uploaded into the RAST server (2) to predict the open reading frames, tRNAs and rRNAs. The predicted ORFs were annotated by searching against clusters of orthologous group (8) and SEED databases (5).

The chromosome of *M. aminisulfidivorans* MP¹ harbors 2,984 protein coding genes, 3 rRNA operons, and 31 tRNAs whereas 190 coding genes and 9 rRNAs were found in the plasmid. The gene clusters responsible for methanol oxidation (*mxaFJGIRSACKL*) and for synthesis of the cofactor pyrroloquinoline quinone (*pqqBCDE*)...
were identified from the draft genome sequence. Five types of cytochromes and one cytochrome c oxidase (cbb₃) were also predicted. A gene encoding a novel bacterial flavin-containing monooxygenase (MAMP_00532), which catalyzes nitrogen-containing compounds or indole by use of oxygen through an NADPH-dependent pathway (4) was identified. At least four different gene clusters potentially encoding restriction modification (RM) systems, which include type I and type II, were predicted. Very low transformation efficiency of *M. aminisulfidivorans* MPT may result from these multiple RM systems. The information provided in the whole genome sequence of *M. aminisulfidivorans* MPT here should facilitate future studies of the metabolic diversity of the genus *Methylophaga*.

**Nucleotide sequence accession number.**
The genome sequence and annotation of *M. aminisulfidivorans* MPT has been deposited in GenBank under accession number AFIG00000000.

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**REFERENCES**


