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GENOME ANNOUNCEMENT

Complete Genome Sequences of *Methylophaga* sp. Strain JAM1 and *Methylophaga* sp. Strain JAM7

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***Methylophaga* sp. strains JAM1 and JAM7 have been isolated from a denitrification system. Strain JAM1 was the first *Methylophaga* strain reported to be able to grow under denitrifying conditions. Here, we report the complete genome sequences of the two strains, which allowed prediction of gene clusters involved in denitrification in strain JAM1.**

Members of the genus *Methylophaga* (gammaproteobacteria) are methane-utilizing methylotrophs, typically isolated from marine environments or brackish waters (1, 5–8, 11, 12). Genome sequences have been reported for *M. thiooxydans* (strain DMS010T) (4) and *M. aminisulfidivorans* (strain MP^T) (10). *Methylophaga* sp. strains JAM1 and JAM7 have been isolated from a methanol-fed denitrification system treating seawater at the Montreal Biodome (2). Strain JAM1 has the particularity among *Methylophaga* species to grow under denitrifying conditions in the presence of nitrate and methanol.

The genome sequences of strain JAM1 (586,834 reads, 35× coverage) and strain JAM7 (546,596 reads, 35× coverage) consist of one chromosome (3,137,192 bp) for strain JAM1 and one chromosome (2,697,465 bp) and one plasmid (47,825 bp, 63× coverage) for strain JAM7. The sequences were determined using the Roche Genome Sequencer FLX system and titanium chemistry (paired ends with an insert size of 2.7 kb). Primary assembly of the sequencing reads was carried out with Newbler gsAssembler version 2.5.3 (Roche) to generate scaffolds from a 454 paired-end library. After multiple rounds of gap-closing steps using CONSED version 20.0 (9) and synteny with *M. aminosulfidivorans* (AFIG00000000), a single contig representing the chromosome was obtained for each strain. The genome sequencing and assembly were performed at the Plateforme d'Analyses Génomiques from the Institut de Biologie Intégrative et des Systèmes (IBIS-Université Laval, Québec, Canada). The genome sequences were uploaded into Integrated Microbial Genomes Expert Review (IMG/ER) (https://img.jgi.doe.gov/cgi-bin/er/main.cgi) to be annotated.

The chromosome of strain JAM1 harbors 3,043 predicted coding open reading frames (ORFs), of which 2,476 have a predicted function. There are 3 rRNA operons (5S, 16S, 23S) and 44 tRNAs corresponding to 20 structural amino acids. The chromosome of strain JAM7 harbors 2,698 ORFs, of which 2,194 have a predicted function, 3 rRNA operons, and 41 tRNAs corresponding to 20 structural amino acids, whereas 56 ORFs were found in the plasmid. For both strains, the *mxaDEFJGIRACKL* gene cluster, encoding the methanol dehydrogenase, was predicted. Both genomes predict to encode all the genes of the Emden-Meyerhof-Parnas (glycolysis) pathway and of the Entner-Doudoroff variant of the ribulose monophosphate (RuMP) pathway. The latter pathway is the one used by the other *Methylophaga* species to assimilate one-carbon substrate (3).

Growth of strain JAM1 under denitrifying conditions by reducing nitrate into nitrite was shown to be correlated with the presence of two nitrate reductase *narG* genes (2). The strain JAM1 genome sequence confirmed the presence of two *nar* operons but, interestingly, also two *nor* operons (nitric oxide reductase) and one *nos* operon (nitrous oxide reductase). In addition, an *nirK* sequence encoding an 82-amino-acid truncated nitrate reductase was found, which could explain that strain JAM1 can reduce only nitrate into nitrite. No genes involved in denitrification were predicted for strain JAM7.

Nucleotide sequence accession numbers. The genome sequences and annotations of *Methylophaga* strains JAM1 and JAM7 have been deposited in GenBank under accession number CP003390 for the strain JAM1 chromosome, CP003380 for the strain JAM7 chromosome, and CP003381 for the strain JAM7 plasmid.

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