

Genome Sequence of the Psychrophilic Deep-Sea Bacterium *Moritella marina* MP-1 (ATCC 15381)

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***Moritella marina* MP-1 is a bacterial species known for its production of docosahexaenoic acid. We present the draft genome sequence of the type strain *Moritella marina* MP-1 (ATCC 15381), having 4,636,778 bp with a G+C content of 40.5% and consisting of 83 contigs.**

Polyunsaturated fatty acids (PUFA), such as docosahexaenoic acid [DHA, 22:6(*n*-3)], have beneficial effects on human health through their effect on membrane fluidity and contribute to many aspects of health (6, 7, 13, 15). Twenty-five years ago, a marine bacterium originally designated *Vibrio marinus* (3) and later renamed *Moritella marina* MP-1 (14) was reported to produce high levels of DHA (18% of the total fatty acids) (4). Such high levels of DHA presumably provide this bacterium with the ability to maintain appropriate membrane fluidity in the low temperatures and high pressures of its marine environment. Indeed, it has been proposed that such marine microbes are the source of omega-3 fatty acids in the marine food web (10). A comparison of marine bacteria showed that MP-1 produced more than twice as much DHA as 9 other species (9). The PUFA biosynthesis pathway used by marine bacteria, such as MP-1, is distinct from the plant and microalgae pathways (5, 8, 10).

MP-1 is a Gram-negative facultative anaerobe with curved or straight rods that is motile by polar flagella, convex, opaque, cream colored, a halophile, and nonpigmented and that grows in low temperatures. Acid is produced fermentatively from D-glucose and D-galactose, but no gas is produced (14).

There is no genome sequence yet available for MP-1 in the Genome OnLine Database (GOLD) (11). Only 84 proteins and 79 nucleotide sequences were reported in NCBI (12) or characterized at the time we started genome sequencing. MP-1 was grown under standard conditions in marine broth 2216 at 15°C (Difco, BD Bioscience) and 200 rpm. The genomic DNA was extracted by the use of the alkaline lysis method with the QIAamp DNA blood minikit (Qiagen Inc.). We then sequenced the genome of MP-1 by Illumina (San Diego, CA) next-generation sequence technology at the Iowa State University DNA facility.

Here we report the draft genome sequence of MP-1, obtained using 49.18 million bases of paired-end (410-bp insert size) sequencing data with 100-bp reads. A contig N_{50} of 147,059 bp was used to assist genome assembly. Sequence data were assembled using CLC bio's Genomics Workbench 5.1 (CLC bio, Aarhus, Denmark); 83 contigs larger than 200 bp were generated. The draft genome was annotated using rapid annotations using subsystems technology (RAST 4.0) (2) and BLAST (1) using a closely related sequence of *Moritella* sp. PE36 as a reference organism (GOLD database number Gi00854).

The uncompleted genome includes 4,636,778 bp and 4,121 predicted coding DNA sequences (CDSs) with a G+C content of 40.5%. There are 34 predicted RNAs, one predicted copy of 16S rRNA, and four predicted copies of 23S rRNA. The draft genome

has 482 subsystems (related functional roles) predicted by the RAST server for the construction of metabolic networks.

The availability of the genome sequence of *Moritella marina* MP-1 will allow deeper comparative genomic studies and track the potential pathway involved in long-chain polyunsaturated fatty acids by the polyketide pathway.

Nucleotide sequence accession number. The whole-genome draft sequence of *Moritella marina* MP-1 has been deposited in GenBank under the accession number [ALOE000000000](http://www.ncbi.nlm.nih.gov/nuccore/ALOE000000000).

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