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Draft Genome Sequence of *Moritella dasanensis* Strain ArB 0140, a Psychrophilic Bacterium Isolated from the Arctic Ocean

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The psychrophilic bacterium *Moritella dasanensis* strain ArB 0140 was isolated near a glacier in Kongsfjorden, Svalbard Archipelago, Norway. Here we report a 4.89-Mb draft genome sequence of *Moritella dasanensis* ArB 0140, which could provide comprehensive information on a psychrophilic mechanism in extreme environments.

The genus *Moritella* is composed of aerobic, motile, Gram-negative, rod-shaped psychrophilic and/or halophilic bacteria. Most of the strains in this genus have been found in seawater, fish farms, and marine sediments, including the deep sea (2, 5, 7, 8, 15, 16), where any living bacterium could be psychrophilic and/or piezophilic (16). Our previous study showed that culture media of *Moritella dasanensis* strain ArB 0140, isolated from the Arctic Ocean, exhibited ice-pitting and hexagonal ice crystal formation activities (5). Moreover, this strain is the only *Moritella* species that possesses ice-modifying activity. It was suggested that this strain would produce ice-active substances (IAS), which affect the shape of ice crystals by binding to the ice crystal growth (11–13). *M. dasanensis* ArB 0140 was isolated from seawater collected near a glacier in Kongsfjorden, Svalbard Archipelago, Norway (78°55'N, 11°56'E) (5).

The genome of *M. dasanensis* ArB 0140 was analyzed using the Illumina HiSeq 2000 (San Diego, CA) with a 300-bp paired-end library (49,752,114 reads). The Illumina HiSeq 2000 sequencing achieved a coverage of about 1,027.7-fold. The reads generated by Illumina HiSeq 2000 were assembled using CLC genomics workbench v5.0 (CLC bio), and the resulting contigs were curated by CodonCode Aligner v3.7 (CodonCode Co.). Gene prediction and annotation were carried out using Glimmer3, tRNA-Scan, EzTaxon-e with hidden Markov model searching, NCBI reference sequences, and several open databases (3, 4, 6, 9, 10, 14, 17). The draft genome of *M. dasanensis* ArB 0140 (about 4,889,582 bp) contains 61 contigs (N_{50} contig size was approximately 179.3 kb). The G+C content was 40.82%. A total of 4,293 protein-encoding genes and 91 tRNA genes were annotated in the draft genome, and 10 rRNA operons were predicted based on the sequence coverage value. Approximately 85.9% of nucleotides were predicted as protein-coding regions, and 2,898 (62.9%) of the protein-coding sequences were annotated with known proteins. A comparison of genome sequences available from the rapid annotations using a subsystems technology (RAST) server (1) shows that *Moritella* sp. strain PE36 (score, 543) and *Shewanella violacea* strain DSS12 (score, 209) are the closest neighbors of strain ArB 0140. Further analysis of the *M. dasanensis* ArB 0140 genome will be conducted to identify the genes involved in the cold adaptation mechanism and the ecological roles of this organism in the Arctic Ocean.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank un-

der the accession number [AKXQ0000000](http://dx.doi.org/10.1093/bioinformatics/btu000). The version described in this paper is the first version, AKXQ01000000.

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