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Draft Genome Sequence of Arctic Marine Bacterium *Pseudoalteromonas issachenkonii* PAMC 22718

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The psychrotolerant *Pseudoalteromonas issachenkonii* PAMC 22718 was isolated for its higher chitinase and protease activities from cold seawater in the Kara Sea, Arctic. Here, we present the draft genome sequence of PAMC 22718 to provide further information for the ecological function of the genus *Pseudoalteromonas* in a cold marine environment.

Chitin and proteins and their constituent amino acids are the most abundant natural substances in cold marine systems and serve as nutrient sources for marine microbes (3, 5). Thus, many cold-adapted chitinolytic and proteolytic bacteria have been isolated from various marine habitats (2, 6). Marine heterotrophic bacteria of the genus *Pseudoalteromonas*, comprising one of the most abundant groups of *Proteobacteria*, are widely distributed in the marine environment. Current evidence suggests that psychrophilic and/or psychrotolerant *Pseudoalteromonas* bacteria are believed to play a critical role in the carbon and nitrogen recycling process due to their cold-active enzymes.

The genome of *Pseudoalteromonas issachenkonii* PAMC 22718 was analyzed using a 150-bp paired-end library (5,495,145 reads) with the Illumina Genome Analyzer II× (Illumina, San Diego, CA). The genome assembly was performed using Celera assembler 7.0 (4). Gene prediction and annotation were performed using the RAST server (1). The draft genome sequence of *P. issachenkonii* PAMC 22718 was approximately 4.2 Mb long and comprised 56 contigs with an average G+C content of 39.91%. The resulting N_{50} size of contigs was 127,821 bp and the total coverage over the genome was 131-fold. A total of 3,944 open reading frames (ORFs), 76 tRNA genes, and 7 rRNA genes were predicted in the draft genome. Approximately 84.84% of nucleotides were predicted as ORFs, and 3,182 (79.67%) ORFs were annotated with known proteins.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession number [AJTK000000000](http://www.ncbi.nlm.nih.gov/nuccore/AJTK000000000). The version described in this paper is the first version, AJTK01000000.

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