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# Genome Sequence of a Novel Member of the Genus *Psychrobacter* Isolated from Antarctic Soil

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*Psychrobacter* spp. have shown characteristics indicating remarkable capabilities at subzero temperatures that identify them as potential model organisms for the study of low-temperature adaptations. Here we present the draft genome sequence of *Psychrobacter* sp. PAMC 21119, which was isolated from permafrost soil of Antarctica; this information could provide insight into adaptation and evolution strategies under extreme environmental conditions.

Antarctica is an extreme environment that has exerted low-temperature, desiccation, and starvation stresses on bacteria over thousands to millions of years. The genus *Psychrobacter* comprises psychrophilic microorganisms that are Gram negative, spherical to rod shaped, strictly aerobic, chemoheterotrophic, nonmotile, cold adapted, and osmotolerant. *Psychrobacter* species are capable of growth at temperatures between  $-10^{\circ}\text{C}$  and  $42^{\circ}\text{C}$ , and they have frequently been isolated from various cold environments, including Antarctic sea ice, sediments, deep seawater, and permafrost (2, 4, 6, 8). The *Psychrobacter* genus contains a widespread and evolutionarily successful group of bacteria, the biology of which may provide important insights into environmental adaptation and survival in extreme environments. *Psychrobacter* sp. PAMC 21119 was isolated from permafrost soil on Barton Peninsula, King George Island, Antarctica ( $62^{\circ}13'S$ ,  $58^{\circ}47'W$ ).

The genome of *Psychrobacter* sp. PAMC 21119 was analyzed by using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (114,846 reads) and the Illumina GAIIX system (San Diego, CA) with a 500-bp paired-end library (2,279,614 reads). The 454 GS FLX sequencing achieved about 5.9-fold coverage, while 67.5-fold read coverage was achieved with the Illumina paired-end sequencing. The reads generated by the Illumina GAIIX and the 454 GS FLX Titanium systems were assembled using Celera Assembler 7.0 (5). Gene predictions and annotations were carried out using Glimmer3 (3), the RAST annotation server (1), and the NCBI COG database (7). The draft genome sequence of *Psychrobacter* sp. PAMC 21119 includes 3,512,050 bases and comprises 3,016 predicted coding sequences. It consists of 42 contigs (N50 contig size, approximately 118 kb), which can be assembled into 13 scaffolds (N50 scaffold size, approximately 454 kb). The G + C content is 43.4%. Additionally, 47 tRNA-encoding genes, 4 5S rRNA genes, 3 23S rRNA genes, and 3 16S rRNA genes were predicted in the draft genome. Approximately 83.3% of nucleotides were predicted as protein-coding regions, and 70.5% (2, 127) of the open reading frames were annotated as known proteins. Comparison with genome sequences available with RAST showed that *Psychrobacter arcticus* 273-4 (score, 546) and *Psychrobacter cryohalolentis* K5 (score, 532), followed by *Psychrobacter* sp. PRwf-1 (score, 506), were the closest neighbors of *Psychrobacter* sp. strain PAMC 21119.

The availability of the genome sequence of *Psychrobacter* sp.

PAMC 21119 will allow further analysis and understanding of adaptation and evolution strategies under extreme environmental conditions.

**Nucleotide sequence accession numbers.** The data obtained in this whole-genome shotgun project have been deposited with DDBJ/EMBL/GenBank under accession number [AHVZ00000000](http://www.ncbi.nlm.nih.gov/nuccore/AHVZ00000000). The version described in this paper is the first version, AHVZ01000000.

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