

Genome Sequence of a *Salinibacterium* sp. Isolated from Antarctic Soil

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The draft genome of *Salinibacterium* sp. PAMC 21357, isolated from permafrost soil of Antarctica, was determined. Here we present a 3.1-Mb draft genome sequence of *Salinibacterium* sp. that could provide further insight into the genetic determination of its cold-adaptive properties.

The genus *Salinibacterium* accommodates Gram-positive, aerobic, high-G+C content, nonmotile, non-spore-forming, irregular rods; the genus was first assigned by Han et al. (3) This genus, which has been mainly isolated from seawater samples taken from the East Sea and frozen soil from a glacier, was proposed as a psychrotolerant bacterium (3, 6). *Salinibacterium* sp. PAMC 21357 was isolated from the seashore soil on Barton Peninsula, King George Island, Antarctica (62°13'S, 58°47'W).

The genome of *Salinibacterium* sp. PAMC 21357 was analyzed using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT), with an 8-kb paired-end library (123,242 reads), and the Illumina GAIIX system (San Diego, CA), with a 500-bp paired-end library (5,344,240 reads). The 454 GS FLX sequencing achieved about 8.3-fold coverage, while 167.6-fold read coverage was achieved by 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 (4). Gene prediction and annotation were carried out using Glimmer3 (2), the RAST annotation server (1), and the NCBI COG database (5). The draft genome sequence of *Salinibacterium* sp. PAMC 21357 includes 3,109,262 bases and comprises 3,137 predicted coding sequences. It consists of 6 contigs (N50 contig size, approximately 679 kb), which can be assembled into 3 scaffolds (N50 scaffold size, approximately 2,104 kb). The G+C content is 60.1%. Additionally, 45 tRNA-encoding genes, 2 5S rRNA genes, 2 23S rRNA genes, and 2 16S rRNA genes were predicted in the draft genome. Approximately 92.0% of nucleotides were predicted as protein-coding regions, and 70.7% (3,197) of the open reading frames were annotated as known proteins. Comparison with genome sequences available at RAST showed that the unclassified *Actinobacteria* marine actinobacterium PHSC20C1 (score, 548) and *Clavibacter michiganensis* subsp. *michiganensis* NCPPB 382 (score, 496), followed by *Clavibacter michiganensis* subsp. *sepedonicus* (score, 441), were the closest neighbors of *Salinibacterium* sp. PAMC 21357.

This represents the first genome sequence report for *Salinibacterium* sp. and may provide further insight into the genetic determination of its cold-adaptive and evolutionary strategy under extreme environmental conditions, such as those of Antarctica.

Nucleotide sequence accession numbers. The results from this whole-genome shotgun project have been deposited with DDBJ/EMBL/GenBank under the accession number [AHWA00000000](https://www.ncbi.nlm.nih.gov/nuclink/AHWA00000000). The version described in this paper is the first version, AHWA01000000.

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