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Genome Sequence of *Janthinobacterium* sp. Strain PAMC 25724, Isolated from Alpine Glacier Cryoconite

Su Jin Kim,^a Seung Chul Shin,^b Soon Gyu Hong,^b Yung Mi Lee,^b Hyoungseok Lee,^b Jungeun Lee,^b In-Geol Choi,^a and Hyun Park^b

College of Life Sciences and Biotechnology, Korea University, Seongbuk-gu, Seoul, South Korea,^a and Korea Polar Research Institute, Yeosu-gu, Incheon, South Korea^b

The draft genome of *Janthinobacterium* sp. strain PAMC 25724, which is a violacein-producing psychrotolerant bacterium, was determined. The strain was isolated from glacier cryoconite of the Alps mountain permafrost region. The sequence will allow identification and characterization of the genetic determination of its cold-adaptive properties.

The genus *Janthinobacterium* includes violacein-producing, Gram-negative, motile, rod-shaped bacteria that are commonly isolated from the microbiota of soils and water of rivers, lakes, and springs, including permafrost regions, such as Antarctic soil (4, 7). *Janthinobacterium* sp. is one of the most common purple-pigmented species that produces the water-insoluble pigment violacein (6), and it is suggested that the inhibitory effects of the antifungal symbionts are due to secondary bacterial metabolites as opposed to resource competition (2). *Janthinobacterium* sp. strain PAMC 25724 was isolated from glacier cryoconite of the Alps mountain range, Austria (47°04'N, 12°41'E).

The genome of *Janthinobacterium* sp. PAMC 25724 was analyzed using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (111,434 reads) and the Illumina GAIIX (San Diego, CA) with a 500-bp paired-end library (10,757,494 reads). The 454 GS FLX sequencing achieved about 8.7-fold coverage, while 208-fold read coverage was achieved by Illumina paired-end sequencing. The reads generated by the Illumina GAIIX and the 454 GS FLX Titanium were assembled using Celera assembler 6.1 (5). Gene prediction and annotation were carried out using Glimmer3 (3), the rapid annotations using subsystems technology (RAST) server (1), and the NCBI COG database (8). The draft genome sequence of *Janthinobacterium* sp. PAMC 25724 includes 4,985,247 bases and comprises 4,339 predicted coding sequences. It consists of 48 contigs (N_{50} contig size was approximately 245 kb), which can be assembled into 4 scaffolds (N_{50} scaffold size was approximately 4,183 kb). The G+C content was 59.5%. Additionally, 72 tRNA genes, two 5S rRNA genes, one 23S rRNA gene, and one 16S rRNA gene were predicted in the draft genome. Approximately 84.9% of nucleotides were predicted as protein-coding regions, and 73.7% (3,197) of the open reading frames were annotated with known proteins. Comparison with genome sequences available in the RAST server showed that *Janthinobacterium* sp. Marseille (score, 537), *Herminiimonas arsenicoxydans* (score, 422), and *Oxalobacter formigenes* OXCC13 (score, 351) were the closest neighbors of strain PAMC 25724.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AHHB000000000](http://www.ncbi.nlm.nih.gov/nuccore/AHHB000000000). The version described in this paper is the first version, AHHB01000000.

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Address correspondence to Hyun Park, hpark@kopri.re.kr, or In-Geol Choi, igchoi@korea.ac.kr.

S.J.K. and S.C.S. contributed equally to this publication.

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