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GENOME ANNOUNCEMENT

Genome Sequence of *Pseudomonas* sp. Strain PAMC 25886, Isolated from Alpine Glacial Cryoconite

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***Pseudomonas* spp. have shown characteristics of efficiently metabolizing environmental pollutants and also producing exopolysaccharides known as biofilms. Here we present the draft genome sequence of *Pseudomonas* sp. strain PAMC 25886, which was isolated from glacier cryoconite in the Alps mountain permafrost region and which may provide further insight into biodegradative and/or biofilm-producing mechanisms in a cold environment.**

The genus *Pseudomonas* contains strictly aerobic, Gram-negative, rod-shaped, and motile (by means of a single polar flagellum) bacteria and is commonly found in soil and water. Some species of the genus *Pseudomonas* are able to metabolize chemical pollutants in the environment and, as a result, can be used for bioremediation (5–7), and a number of cells can also produce exopolysaccharides known as biofilms (3). This bacterium is an opportunistic pathogen, meaning that it exploits some break in the host defenses to initiate an infection (9). *Pseudomonas* sp. strain PAMC 25886 was isolated from glacier cryoconite in the Alps mountain range in Austria (47°04′N, 12°41′E).

The genome of *Pseudomonas* sp. PAMC 25886 was analyzed using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (203,820 reads) and the Illumina GAIIx (San Diego, CA) with a 500-bp paired-end library (2,300,862 reads). The 454 GS FLX sequencing achieved about 12.1-fold coverage, while 30.6-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 (4). Gene prediction and annotation were carried out using Glimmer3 (2), the rapid annotations using subsystems technology (RAST) annotation server (1), and the NCBI clusters of orthologous groups (COG) database (8). The draft genome sequence of *Pseudomonas* sp. PAMC 25886 was approximately 7.02 Mb long and comprised 7 scaffolds containing 95 contigs. The N_{50} contig size was approximately 245 kb, and the N_{50} scaffold size was 4,183 kb. The G+C content was 59.9%. A total of 5,830 protein-encoding genes, 50 tRNA-encoding genes, and 1 rRNA operon were predicted in the draft genome. Approximately 85.2% of nucleotides were predicted as protein-coding regions, and 4,731 bp (81.1%) of the open reading frames were annotated with known proteins. Comparison with genome sequences available in the RAST server showed that *Pseudomonas fluorescens* SBW25 (score, 527), *P. fluorescens* PfO-1 (score, 501), and *P. fluorescens* Pf-5 (score, 477) were the closest neighbors of strain PAMC 25886. The availability of the genome sequence of *Pseudomonas* sp. PAMC 25886 will allow further analysis and understanding of biodegradative and/or biofilm-producing mechanisms in a cold environment.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AHHC00000000. The version described in this paper is the first version, AHHC01000000.

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