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GENOME ANNOUNCEMENT

Genome Sequence of *Sphingomonas* sp. Strain PAMC 26621, an Arctic-Lichen-Associated Bacterium Isolated from a *Cetraria* sp.

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The lichen-associated bacterial strain *Sphingomonas* sp. PAMC 26621 was isolated from an Arctic lichen *Cetraria* sp. on Svalbard Islands. Here we report the draft genome sequence of this strain, which could provide novel insights into the molecular principles of lichen-microbe interactions.

Recently, a few studies have characterized the bacterial communities of lichens by culture-independent methods like next-generation sequence (NGS) analysis (4, 7, 8), suggesting the importance of the symbiotic relationship between lichen and lichen-associated microbes. *Sphingomonas* was identified as one of the dominant Gram-negative taxa inside several lichen species (4). Members of the genus *Sphingomonas* are traditionally known as degraders well adapted for the bioremediation of polycyclic aromatic hydrocarbons (3, 6, 10), and *Sphingomonas* has some oligotrophic strains isolated from extreme environments such as Antarctic soil (2, 10). In this study, the genome sequence of *Sphingomonas* sp. strain PAMC 26621, which was isolated from an Arctic lichen *Cetraria* sp. that grows on rocks (78°54′73″N, 11°57′78″E), was determined to provide novel insight into the molecular principles of lichen-microbe interactions.

The genome of *Sphingomonas* sp. PAMC 26621 was analyzed using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (90,068 reads) and the Illumina GAIIx (San Diego, CA) with a 500-bp paired-end library (15,486,626 reads). The 454 GS FLX sequencing achieved about 3.5-fold coverage, while 290.2-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 7.0 (9). Gene prediction and annotation were carried out using Glimmer3 (5), the RAST annotation server (1), and the NCBI COG database (11). The draft genome sequence of *Sphingomonas* sp. PAMC 26621 includes 4,769,913 bases and comprises 4,817 predicted coding sequences. It consists of 68 contigs (N_{50} contig size was approximately 210 kb), which can be assembled into eight scaffolds (N_{50} scaffold size was approximately 2,722 kb). The G+C content was 65.3%. Additionally, 47 tRNA-encoding genes, 2 23S rRNA genes, and 2 16S rRNA genes were predicted in the draft genome. Approximately 87.7% of nucleotides were predicted as protein-coding regions, and 67.4% (3,246) of the open reading frames were annotated with known proteins. Comparison with genome sequences available at RAST showed that *Sphingomonas* sp. strain SKA58 (score, 542), *Sphingopyxis alaskensis* RB2256 (score, 540), and *Sphingobium japonicum* UT26S (score, 496) were the closest neighbors of *Sphingomonas* sp. strain PAMC 26621.

By determining the genome sequence of *Sphingomonas* sp. PAMC 26621, it is now possible to perform various comparative genomic analyses with other bacteria, which should provide clues regarding the functional roles of this microbe within the lichen symbiosis.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AIDW00000000. The version described in this paper is the first version, AIDW01000000.

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