

# Draft Genome Sequence of a *Sphingomonas* sp., an Endosymbiotic Bacterium Isolated from an Arctic Lichen *Umbilicaria* sp.

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***Sphingomonas* sp. strain PAMC 26617 has been isolated from an Arctic lichen *Umbilicaria* sp. on the Svalbard Islands. Here we present the draft genome sequence of this strain, which represents a valuable resource for understanding the symbiotic mechanisms between endosymbiotic bacteria and lichens surviving in extreme environments.**

The genus *Sphingomonas* is a group of aerobic, Gram-negative, chemoheterotrophic, rod-shaped, yellow-pigmented bacteria that belongs to the *Alphaproteobacteria* (10, 12). The genus has been a focus of studies for bioremediation of environmental contaminants because it has a remarkable biodegradative activity and catalysis for refractory pollutants, such as polycyclic aromatic hydrocarbons and other aromatic contaminants (5, 6, 8, 13). They have been isolated under various environmental conditions, such as terrestrial subsurfaces, anthropogenically polluted waters and sediments, the surfaces of various plants, and Antarctic soil (2, 3, 7). *Sphingomonas* sp. strain PAMC 26617 was isolated from an Arctic lichen *Umbilicaria* sp. that grows on rocks (78.54.72N, 11.57.09E).

The genome of *Sphingomonas* sp. PAMC 26617 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 (117,628 reads) and the Illumina GAIIX system (San Diego, CA) with a 500-bp paired-end library (6,336,970 reads). The 454 GS FLX sequencing achieved about 9.7-fold coverage, while 145-fold read coverage was achieved with Illumina paired-end sequencing. The reads generated by Illumina GAIIX were assembled using ABySS 1.3.1 (9), and the resulting contigs were shredded into 1.5-kb overlapped fake reads. To merge these fake reads with the reads generated with 454 GS FLX into contigs, GS Assembler software v. 2.5.3 (Roche) was used. Gene prediction and annotation were carried out using Glimmer3 (4), the RAST annotation server (1), and the NCBI COG database (11). The draft genome of *Sphingomonas* sp. PAMC 26617 (about 4.67 Mb) contains 110 contigs (N50 contig size, approximately 165 kb) that can be assembled into 11 scaffolds (N50 scaffold size, approximately 4,215 kb). The G+C content was 65.7%. A total of 4,503 protein-encoding genes, 45 tRNA-encoding genes, and 1 rRNA operon were predicted in the draft genome. Approximately 87.5% of nucleotides were predicted as protein-coding regions, and 3,056 bp (67.9%) of the protein-coding sequences were annotated with known proteins. Comparison with genome sequences available with RAST showed that *Novosphingobium aromaticivorans* DSM 12444 (score, 500) and *Sphingopyxis alaskensis* RB2256 (score, 495), followed by *Sphingobium japonicum* UT26S (score, 491), were the closest neighbors of *Sphingomonas* sp. PAMC 26617.

A more detailed analysis of this genome and a comparative

analysis with other *Sphingomonas* sp. genomes could expand our understanding of the symbiotic mechanisms of lichens.

**Nucleotide sequence accession numbers.** The results of this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under accession number [AHHA00000000](https://www.ncbi.nlm.nih.gov/nuccore/AHHA00000000). The version described in this paper is the first version, [AHHA01000000](https://www.ncbi.nlm.nih.gov/nuccore/AHHA01000000).

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