

# Genome Sequence of *Sphingomonas* sp. Strain PAMC 26605, Isolated from Arctic Lichen (*Ochrolechia* sp.)

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**The endosymbiotic bacterium *Sphingomonas* sp. strain PAMC 26605 was isolated from Arctic lichens (*Ochrolechia* sp.) on the Svalbard Islands. Here we report the draft genome sequence of this strain, which could provide further insights into the symbiotic mechanism of lichens in extreme environments.**

The genus *Sphingomonas* accommodates strictly aerobic, chemoheterotrophic, Gram-negative, rod-shaped, usually yellow-pigmented bacteria that suggest this genus is well adapted for the degradation of high-molecular-weight polycyclic aromatic hydrocarbons and other aromatic contaminants (5, 6, 11). They have been widely isolated from anthropogenically polluted river water and sediments, the surfaces of various plants, and also extreme environments, such as Arctic and Antarctic soil (2, 3, 7, 8). The *Sphingomonas* sp. strain PAMC 26605 was isolated from Arctic lichens (*Ochrolechia* sp.) that grow on rocks (lat 78.54.72, long 11.57.09).

The genome of *Sphingomonas* sp. PAMC 26605 was analyzed using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (115,616 reads) and the Illumina GAIx (San Diego, CA) with a 500-bp paired-end library (16,989,710 reads). The 454 GS FLX sequencing achieved about 9.3-fold coverage, while 303.4-fold read coverage was achieved by Illumina paired-end sequencing. The reads generated by Illumina GAIx 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 by 454 GS FLX into contigs, GS Assembler v2.5.3 (Roche) software was used. Gene prediction and annotation were carried out using Glimmer3 (4), the rapid annotations using subsystems technology (RAST) annotation server (1), and the NCBI clusters of orthologous groups (COG) database (10). The draft genome of *Sphingomonas* sp. PAMC 26605 (about 4.8 Mb) contains 166 contigs ( $N_{50}$  contig size was approximately 53.3 kb), which can be assembled into 23 scaffolds ( $N_{50}$  scaffold size was approximately 4.0 Mb). The G+C content was 66.0%. A total of 4,661 protein-encoding genes, 45 tRNA genes, and 1 rRNA operon were predicted in the draft genome. Approximately 88.2% of nucleotides were predicted as protein-coding regions, and 3,103 (66.5%) of the protein-coding sequences were annotated with known proteins. Comparison with genome sequences available in the RAST server showed that *Sphingopyxis alaskensis* RB2256 (score, 515), *Sphingomonas wittichii* RW1 (score, 510), and *Sphingobium japonicum* UT26S (score, 457) were the closest neighbors of *Sphingomonas* sp. PAMC 26605. A more detailed analysis of this genome and a comparative analysis with other *Sphingomonas* sp. genomes may provide further insights into the symbiotic mechanism of lichens.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AHIS000000000](https://www.ncbi.nlm.nih.gov/nuclink/AHIS000000000). The version described in this paper is the first version, AHIS01000000.

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