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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Sphingomonas echinoides* ATCC 14820

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***Sphingomonas* is a Gram-negative, yellow-pigmented, chemoheterotrophic, strictly aerobic bacterium. The bacterium is known to be metabolically versatile and can utilize a wide range of natural compounds as well as some types of environmental contaminants, such as creosote, polychlorinated biphenyls, etc. Here, we report the draft genome sequence of *Sphingomonas echinoides* ATCC 14820, which will provide additional information to enhance our understanding of metabolic versatility of *Sphingomonas*.**

Sphingomonas echinoides ATCC 14820 was first isolated as a plate contaminant, and defined as *Pseudomonas echinoides* (5). However, subsequent studies of DNA-rRNA hybridization showed that this strain did not belong to the genus *Pseudomonas*, but the genus *Sphingomonas* (4). This strain was identified as a Gram-negative, non-spore-forming, motile, yellow-pigmented, polar-flagellated, slightly curved rod-shaped bacterium, and the yellow pigment of this species was identified as the carotenoid nostoxanthin (3, 6). This strain had also been determined to possess ubiquinone 10 as the major respiratory quinone and sphingoglycolipids in their cell envelopes like those of other *Sphingomonas* strains (7).

The genome of *Sphingomonas echinoides* ATCC 14820 was analyzed using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (110,779 reads), and the Illumina GAIIx (San Diego, CA) with a 500-bp paired-end library (18,021,882 reads). The 454 GS FLX sequencing achieved about 10.1-fold coverage, while 374.4-fold read coverage was achieved by Illumina paired-end sequencing. The reads generated by Illumina GAIIx were assembled using ABySS 1.3.1 (8), 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 (2), the RAST annotation server (1), and the NCBI COG database (9). The draft genome of *Sphingomonas echinoides* ATCC 14820 (about 4.2 Mb) contains 65 contigs (N_{50} contig size was approximately 134.9 kb), which can be assembled into 6 scaffolds (N_{50} scaffold size was approximately 4.0 Mb). The G+C content was 64.7%. A total of 4,047 protein-encoding genes, 45 tRNA-encoding genes, and 1 rRNA operon were predicted in the draft genome. Approximately 90.5% of nucleotides were predicted as protein-coding regions, and 2,781 (68.7%) of protein coding sequences were annotated with known proteins. Comparison with genome sequences available at RAST showed that *Sphingomonas* sp. strain SKA58 (score, 514), *Sphingobium japonicum* UT26S (score, 513), and *Sphingomonas wittichii* RW1 (score, 476) are the closest neighbors of *Sphingomonas echinoides* ATCC 14820.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AHIR00000000. The version described in this paper is the first version, AHIR01000000.

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