

The Draft Genome Sequence of *Sphingomonas paucimobilis* Strain HER1398 (*Proteobacteria*), Host to the Giant PAU Phage, Indicates That It Is a Member of the Genus *Sphingobacterium* (*Bacteroidetes*)

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The draft genome sequence of *Sphingomonas paucimobilis* host index number (HER) 1398, host of the giant PAU phage isolated from silk moths (*Bombyx mori*), indicates that this isolate belongs within the genus *Sphingobacterium*. We suggest that *Sphingomonas paucimobilis* strain HER1398 be reclassified as *Sphingobacterium paucimobilis* strain HER1398.

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Sphingomonas paucimobilis host index number (HER) 1398 was obtained from the Félix D'Hérelle Reference Center for Bacterial Viruses at the University of Laval, Quebec City, Canada. It was isolated by S. Basavarajappa and C. Savanurmah from a homogenate of diseased silkworms (*Bombyx mori*) collected from various areas within Karnataka State, India, and is a host for the giant phage, PAU (1). The isolate was originally classified as *Pseudomonas paucimobilis* (1), but it was reclassified as *Sphingomonas paucimobilis* strain HER1398 by the Félix D'Hérelle Reference Center.

The draft genome sequence indicates that *Sphingomonas paucimobilis* HER1398 is a member of the genus *Sphingobacterium*. BLAST analysis indicates 94 to 96% identity of the 16S rRNA genes to other members of this genus, including *Sphingobacterium bambusae* and *Sphingobacterium composti* (2, 3). Moreover, *Sphingomonas* spp. and *Sphingobacterium* are members of different phyla, *Proteobacteria* and *Bacteroidetes*, respectively.

High-quality DNA was extracted using Qiagen QiaAMP followed by MinElute Cleanup columns. The Illumina library was constructed using Lucigen's NxSeq library prep kit without final PCR enrichment. Quality control of the resulting library was completed using Agilent high-sensitivity DNA chips and digital droplet PCR (4).

Whole-genome shotgun sequencing was completed using Illumina MiSeq and HiSeq in the 250-bp and 100-bp paired-read formats, respectively. A partial flow cell of HiSeq/MiSeq obtained 2.86 million raw paired reads and 626,550,788 bp of raw sequence. The reads were merged using FLASH (version 1.2.5) screened for phiX using Bowtie2 (version 2.1.0), then filtered using Picard tools (version 1.90) (<http://picard.sourceforge.net/>) (5, 6). Reads were assembled using Ray assembler (version 2.2.0), yielding 23 contigs summing to 5,126,359 bp, with an average contig length of 222,885 bp, with the largest contig being 1,001,915 bp, (N_{50} length, 416,944 bp; N_{90} length, 132,253 bp; G+C content, 40.86%) (7, 8).

Annotation of the draft genome was conducted on the RAST annotation server using the Glimmer-3 option FigFam database version-59 (9). The genome annotation contains 4,475 predicted protein-coding genes, including 79 noncoding RNAs and 371 predicted SEED subsystem features. Given its role as the host for phage PAU, the genome was screened for evidence of phages, prophages, gene-transfer agents (GTAs), CRISPR arrays, and other phage-resistance elements (such as exopolysaccharide [EPS]) or abortive infection systems (10); none were found. However, type I and type III restriction-modification systems were predicted, which could help avoid phage infection (10). In addition, there are predicted genes for antibiotic resistance to aminoglycosides, fluoroquinolones, and beta-lactams. The resistance to these antibiotics could be due to predicted aminoglycoside adenylyltransferases, beta-lactamases, and DNA gyrases. We found *S. paucimobilis* HER1398 to be resistant to tobramycin (10 µg), an aminoglycoside, and penicillin (10 IU), a beta-lactam. Fluoroquinolone resistance has not been tested.

Based on analysis of the full-length 16S rRNA gene sequence and whole-genome shotgun sequencing, it is clear that *Sphingomonas paucimobilis* HER1398 has been incorrectly classified. Based on sequence comparison it should be classified as *Sphingobacterium paucimobilis* HER1398, a member of a different phylum. This is the fourth *Sphingobacterium* genome sequenced, but the first isolated from an insect.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [ATDL00000000](https://www.ncbi.nlm.nih.gov/nuccore/ATDL00000000). The version described in this paper is version ATDL01000000.

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