

# Genome Sequence of the Broad-Host-Range *Pseudomonas* Phage $\Phi$ -S1

Sanna Sillankorva,<sup>a</sup> Andrew M. Kropinski,<sup>b</sup> and Joana Azeredo<sup>a</sup>

Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, University of Minho, Campus de Gualtar, Braga, Portugal,<sup>a</sup> and Public Health Agency of Canada, Laboratory for Foodborne Zoonoses, and University of Guelph, Department of Molecular and Cellular Biology, Guelph, Ontario, Canada<sup>b</sup>

**The broad-host-range lytic *Pseudomonas* phage  $\Phi$ -S1 possess a 40,192 bp double-stranded DNA (dsDNA) genome of 47 open reading frames (ORFs) and belongs to the family *Podoviridae*, subfamily *Autographivirinae*, genus *T7likevirus*.**

The lytic phage  $\Phi$ -S1 was isolated from the Greater Vancouver Sewage Processing plant using *Pseudomonas fluorescens* PW. This virus lysed most of the fluorescent *Pseudomonas* species tested and one strain of *Pseudomonas stutzeri*. Morphologically it is a member of the *Podoviridae*, with an icosahedral head 60 nm in diameter and short (30-nm) tails (4). The host, *P. fluorescens* Migula ATCC 27663, and virus (27663-B1) were purchased from the American Type Culture Collection. We have shown that  $\Phi$ -S1 is effective in killing planktonic cultures, adherent cells, and young and mature biofilms (11–13).

Phage  $\Phi$ -S1 was amplified and the DNA extracted as described previously (10). The genome was sequenced using Roche/454 recommended procedures at the Plateforme d'analyses génomiques of the Institut de Biologie Intégrative et des Systèmes (Laval University, Canada). Shotgun reads were assembled using the gsAssembler module of Newbler v2.5.3. Potential open reading frames (ORFs) were initially annotated using myRAST (1) and manually checked using KODON (Applied Maths, Austin, TX). Translated ORFs were compared with known protein sequences using BLASTP against the nonredundant protein GenBank database. Promoter sequences were found using MEME/MAST (2), terminators were predicted using ARNold (7) and TransTerm (3), and tRNAscan-SE (8) and ARAGORN (6) were used for tRNA detection.

The genome of phage  $\Phi$ -S1 consists of linear double-stranded DNA of 40,192 bp with a G+C content of 56.2%. The genome was scanned for open reading frames (ORFs) of 100 bp or longer, and the search resulted in 47 predicted genes with lengths varying from 123 to 3,996 nt. The initiation codon of 96% of the protein-coding genes is ATG, and only the RNA polymerase and endonuclease start with GTG. Of the ORFs, 25 (53.2%) possessed defined functions, 20 (42.6%) were conserved hypothetical proteins, and two were unique. Furthermore, this phage lacks a frameshifting site at the end of the capsid gene (T7 gp10 homolog). Four putative early host-dependent promoters were identified upstream of the first hypothetical protein (ORF1) and 10 phage-specific promoters with the consensus sequence TAAAAMCMCTCACCMAAACA GGA were also discovered. The genome has three rho-independent terminators and no tRNAs.

The closest relative of phage  $\Phi$ -S1 is phage phiIBB-PF7A, isolated from raw sewage using a dairy *Pseudomonas fluorescens* isolate with which it shares 42 homologs (80.8% homology) (9). Relative to *Pseudomonas putida* phages gh-1 (5) and phi15 (NC\_015208),  $\Phi$ -S1 possesses 34 (81.0% homology) and 40 homologs (80%), respectively. All of these viruses belong to the order

*Caudovirales*, family *Podoviridae*, subfamily *Autographivirinae*, genus *T7likevirus*.

**Nucleotide sequence accession number.** The sequence of *Pseudomonas* phage  $\Phi$ -S1 has been submitted to the NCBI database under the accession number [JX173487](http://www.ncbi.nlm.nih.gov/nucl/173487).

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Address correspondence to Sanna Sillankorva, [s.sillankorva@deb.uminho.pt](mailto:s.sillankorva@deb.uminho.pt).

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