A novel temperate phage, vB_AbaS_TRS1, was isolated from cultures ofAcinetobacter baumannii strain A118 that had been exposed to mitomycin C. Phage TRS1 belongs to the Siphoviridae family of bacteriophages and encapsulates a 40,749-bp genome encoding 70 coding sequences and a single tRNA. 

Multidrug-resistant strains of Acinetobacter baumannii have emerged as prominent causative agents of nosocomial and community-acquired infections. To date, the complete genome sequences of 38 bacteriophages infecting the genus Acinetobacter have been deposited in the international nucleotide sequence databases comprising members of the Myoviridae, Siphoviridae, Podoviridae, and Leviridae families. Many strains of A. baumannii are polylysogenic, harboring multiple integrated prophages (1), yet the influence of these upon host fitness and virulence is little understood.

Acinetobacter baumannii strain A118 was originally isolated from a blood culture in Buenos Aires, Argentina. Distinguishing features of this strain include a broad susceptibility to antibiotics and natural competence (2,3). A draft genome sequence of A118 is available (whole-genome shotgun project AEOW01) (4). Phage TRS1 was induced from cultures of A. baumannii A118 by culturing in the presence of 1 μg·ml⁻¹ mitomycin C and purified by CsCl density gradient centrifugation (5). Transmission electron microscopy revealed that TRS1 belongs to the family Siphoviridae. The virion particles possess an isometric head of 56-nm diameter and a noncontractile tail of 142-nm length that terminates in a tail tip and side tailspikes. Phage genomic DNA was sequenced using an Illumina HiSeq at the Genomic Services and Development Unit (Public Health England) with 100-bp paired-end reads and an average insert size of 338 bp. The genome was assembled using SPAdes version 3.5.0 (6) and resulted in a single circular contig. The TRS1 genome is organized into discrete modules comprising genes involved in DNA packaging, virion morphogenesis, lysis, integration, transcriptional regulation, and replication. The putative attP site was identified as a 29-bp sequence (TTATAAATAGTGGTGCGTCGGC GGG) located upstream of a tyrosine family integrase. This sequence was also identified at the boundaries of putative prophages in the A. baumannii strains A1, SDF, LAC-4, and AB030. Alignment with the assembly data available for A118 revealed that the TRS1 genome sequence mapped across 11 contigs (GenBank no. AEOW01001344-55), and gap-fills between these contigs represented approximately 660 bp.

Genomic comparisons at the nucleotide level revealed little sequence identity between TRS1 and other phages. Greater nucleotide and protein similarity was observed among Acinetobacter spp. with sequenced genomes and consisted of limited regions of sequence similarity interspersed by nonhomologous regions, suggesting that TRS1 is highly mosaic.

Accession number(s). This whole-genome shotgun project has been deposited in GenBank under the accession number KX268652. The version described in this paper is the first version, KX268652.1.

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REFERENCES


