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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Serratia plymuthica* Bacteriophage ϕMAM1

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A virulent bacteriophage (ϕMAM1) that infects *Serratia plymuthica* was isolated from the natural environment and characterized. Genomic sequence analysis revealed a circular double-stranded DNA sequence of 157,834 bp, encoding 198 proteins and 3 tRNAs. The ϕMAM1 genome shows high homology to previously reported ViI-like enterobacterial bacteriophage genomes.

Serratia plymuthica strains are Gram-negative ubiquitous plant-associated bacteria that produce a wide range of secondary metabolites, including a variety of antimicrobial compounds (4). These characteristics have made several *Serratia plymuthica* strains attractive organisms for biological control purposes (4). *Serratia plymuthica* A153 was isolated from the rhizosphere of wheat (2), and it produces the halogenated macrolide oocydin A (13), which is very active against plant-pathogenic fungi and oomycetes (9, 13). While screening for a series of bacteriophages infecting clinical and environmental isolates of *Serratia*, we isolated the new lytic phage ϕMAM1, which infected *S. plymuthica* strain A153. To our knowledge, this is first published genome sequence of any *Serratia plymuthica*-infecting phage.

Phage ϕMAM1 was isolated from treated sewage effluent collected from the sewage treatment plant at Milton (Cambridge, United Kingdom). The phage DNA was isolated using the Lambda DNA extraction protocol from the Phase Lock gel kit by 5 Prime (Hamburg, Germany). Genomic DNA sequencing was performed at the DNA Sequencing Facility, Department of Biochemistry, University of Cambridge (Cambridge, United Kingdom), using 454 DNA pyrosequencing technology on a Pico titer plate for a Roche genome sequencer FLX system. The shotgun assemblies were carried out using 454 GS *De Novo* Assembler software (Newbler v2.6). Traditional Sanger sequencing across the junctions was used to close the gaps between contigs.

The genome of phage ϕMAM1 consists of a circular double-stranded DNA of 157,834 bp with a G+C content of 51.9%, which is slightly lower than the 55.9% G+C content of *S. plymuthica* A153 (M. A. Matilla and G. P. C. Salmond, unpublished data). The genome was scanned for open reading frames (ORFs) longer than 100 bp using Glimmer 3.0 (3) and resulted in 198 predicted genes with lengths ranging between 135 and 4,848 nucleotides. Translated ORFs were manually annotated based on PSI-BLAST, the NCBI Conserved Domains Database (8), and the Pfam database (12). Three tRNAs were also identified using ARAGORN (7). Within the identified ORFs, 40.4% had a predicted function, whereas 32.3% encoded hypothetical proteins and 27.3% were unique. Based on the similarities and the presence of conserved domains, structural proteins encoded in the ϕMAM1 genome included baseplate, tail fiber, capsid, neck, and tail tube proteins. Genes encoding nonstructural proteins, such as a DNA polymerase, DNA helicase, DNA ligase, DNA topoisomerase, deoxyribonucleotidase, ribonucleoside-diphosphate reductase, deaminase, and hydrolase, were also identified.

The analysis of the complete genomic sequence revealed that ϕMAM1 shows high homology to genomes of the previously reported ViI-like enterobacterial bacteriophages ϕSboM-AG3 (1), Vi01 (11), SFP10 (10), ϕSH19 (5), and vB_EcoM_CBA120 (6).

Nucleotide sequence accession number. The complete genome sequence of *Serratia plymuthica* phage ϕMAM1 has been submitted to the NCBI database under accession no. JX878496.

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