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GENOME SEQUENCES

Complete Genome Sequence of *Escherichia coli* Phage vB_EcoM Sa157lw, Isolated from Surface Water Collected in Salinas, California

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ABSTRACT Here, we report the complete genome sequence of a new member of Vi1-like phages, *Escherichia coli* phage vB_EcoM Sa157lw, isolated from surface water collected near a produce-growing area in California. This phage does not harbor *stx* or other lysogeny-associated genes and therefore may have biocontrol application potential.

Shiga toxin-producing *Escherichia coli* (STEC), particularly *E. coli* O157:H7, has been recognized as the leading cause of hemolytic-uremic syndrome and high mortality among immunocompromised populations from various foodborne outbreaks (1). Bacteriophages have demonstrated their potential as an alternative to antibiotics for improving food safety and treating bacterial infection (2, 3). Due to the emergence of antimicrobial-resistant STEC strains, it is crucial to characterize newly isolated lytic bacteriophages to facilitate the selection of potential biocontrol agents. In this report, *Escherichia coli* phage vB_EcoM Sa157lw (or Sa157lw) was isolated from surface water collected in a produce-growing area (4). Briefly, the water sample was enriched with a cocktail of STEC O157 strains, the top 6 non-O157 strains, and three nonpathogenic *E. coli* strains, ATCC 13706, ATCC 43888, and DH5α, in tryptic soy broth (TSB) at 37°C for 48 h, as previously described (4). The enrichment was centrifuged and filtered through a 0.22-μm membrane filter. Phage Sa157lw was then isolated after spot tests against all pathogenic and nonpathogenic strains and purified with 3 runs of single-plaque purification (4). The host range of the purified phage was determined against 7 serogroups of STEC and *Salmonella enterica* subsp. *enterica* serovar Typhimurium using the spot test.

Phage DNA was extracted using a phage DNA isolation kit (Norgen Biotek, Ontario, Canada). The phage DNA library was prepared using a TruSeq Nano DNA library prep kit (Illumina, San Diego, CA) and was subsequently sequenced on an Illumina MiSeq sequencer. A total of 1,578,346 2 $\times$ 250-bp paired-end raw sequences were obtained, followed by trimming of poor reads using Trimmomatic, with the setting of average quality Q30, on Galaxy server (version 1.12.0; https://usegalaxy.org/). Genome assembly was performed using a BLAST-based *de novo* assembler, Geneious v10.2.3, with k-mers of 29, 53, 95, and 115, and was validated using Unicycler version 0.4.1 (SPAdes) on the Galaxy server, with the default parameters. The open reading frames (ORFs) of the final contig were annotated using the prokaryotic genome annotation algorithm (Prokka version 1.12.0) on the Galaxy server (5). PhageTerm (https://galaxy.pasteur.fr/) was used to determine bacteriophage termini and packaging modes (6). Comparative genomics was assessed using BLASTn against the nonredundant NCBI database.

Phage Sa157lw, lytic against STEC O157, ATCC 43888, and *Salmonella* Typhimu-

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rium, contained a genome of 155,887 bp in length with an average G+C content of 45%. The BLASTn results indicated that Sa157lw shared 99%, 97%, and 92% average nucleotide identity (ANI) with 93% coverage of *Salmonella* phage Vi01 (GenBank accession number FQ312032), 95% coverage of *Escherichia* phage ECML-4 (JX128257), and 92% coverage of *Escherichia* virus CBA120 (JN593240), respectively. Moreover, PhageTerm predicted that this phage might possess a novel packaging mechanism with redundant termini. The findings suggest that phage Sa157lw likely belongs to a newly proposed genus, *Vi1virus*, under the family *Ackermannviridae* (7, 8).

The phage Sa157lw was predicted to possess 198 ORFs and 4 tRNAs. There were 59 ORFs with known protein functions, from which 4 encoded cell lysis-associated proteins, 25 encoded phage structural proteins, and 30 encoded proteins related to DNA packaging and replication. The protein encoded by ORF84 showed 100% identity to the amino acid sequence of peptidoglycan binding protein of *Salmonella* phage vB-_SalM_SJ2 (NCBI RefSeq accession number YP_009021289), associated with bacterial cell wall degradation (9). Additionally, ORF93 was annotated as baseplate central spike complex protein Gp5, which shared 100% amino acid sequence identity to the counterpart in *Salmonella* phage Vi01 and was essential for the localized hydrolysis bacterial cell wall (10). The results confirmed the lytic activity of Sa157lw against *Salmonella* Typhimurium. As it does not harbor *stx* or other lysogeny-associated genes, phage Sa157lw has the potential to control STEC and *Salmonella* strains.

Data availability. The genome sequence of the phage vB_EcoM Sa157lw has been deposited in GenBank under the accession number MH427377. The sequencing reads have been deposited under the accession number PRJNA473230. The version of the phage genome described in this paper is the first version.

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