



# Complete Genome Sequence of *Escherichia coli* Phage vB\_EcoS Sa179lw, Isolated from Surface Water in a Produce-Growing Area in Northern California

Yen-Te Liao,<sup>a</sup> Fang Liu,<sup>a,e</sup> Xincheng Sun,<sup>a,c,d</sup> Robert W. Li,<sup>b</sup>  Vivian C. H. Wu<sup>a</sup>

<sup>a</sup>Produce Safety and Microbiology Research Unit, U.S. Department of Agriculture, Agricultural Research Service, Western Regional Research Center, Albany, California, USA

<sup>b</sup>Animal Genomics and Improvement Laboratory, U.S. Department of Agriculture, Agricultural Research Service, Beltsville, Maryland, USA

<sup>c</sup>College of Food and Biological Engineering, Zhengzhou University of Light Industry, Zhengzhou, China

<sup>d</sup>Collaborative Innovation Center of Food Production and Safety, Zhengzhou, China

<sup>e</sup>College of Food Science and Engineering, Ocean University of China, Qingdao, China

**ABSTRACT** We report here the whole-genome sequence of a novel *Escherichia coli* phage, vB\_EcoS Sa179lw, isolated from surface water collected in a produce-growing area. With the presence of a putative *eae*-like gene that was associated with previous non-O157 Shiga toxin-producing *E. coli* outbreaks, this phage is a candidate for the study of virulence gene transfer.

Non-O157 Shiga toxin-producing *Escherichia coli* (STEC) strains can cause foodborne illness as severe as O157 STEC strains and have been associated with produce outbreaks in Europe and the United States. A previous study indicated that bacteriophages carrying virulence genes, such as *stx* genes, were associated with virulence gene transfer among bacteria (1). Here, a complete genome sequence of a novel phage—*E. coli* phage vB\_EcoS Sa179lw—is reported. This phage was isolated from surface water collected in a produce-growing area in Salinas Valley, California, USA (2).

Phage DNA was extracted using a phage DNA extraction kit from Norgen Biotek (Canada). The DNA library was prepared using a TruSeq Nano DNA library prep kit (Illumina, USA). Approximately 6 million paired-end ( $2 \times 250$ -bp) sequence reads were generated using a MiSeq sequencer (Illumina). The quality of the raw sequence reads was first checked using FastQC. The Metagenomics RAST (MG-RAST) server was used to obtain taxonomic information (3). In addition, *de novo* assembly was performed using the SPAdes algorithm with default settings in KBase (4) and further validated using the BLAST-based *de novo* assembler Geneious version 11.0.4. Annotation was performed using Prokka with default settings (5) and further confirmed using a BLASTn search to determine the sequence similarity. The phage termini and possible packaging mechanism were determined using PhageTerm (6).

Phage vB\_EcoS Sa179lw, belonging to the family *Siphoviridae*, has double-stranded DNA with a genome size of 46,833 bp and a G+C content of 46%. Annotation of phage vB\_EcoS Sa179lw predicted 86 genes, including 28 with a known protein function. The packaging mechanism was predicted to be associated with phage P1, that is, headful packaging with a *pac* site (7). *Shigella* phage Sf11 (GenBank accession number MF158038)—an unclassified phage at the species level—shared the highest genetic similarity, with a 91% identity to phage vB\_EcoS Sa179lw in approximately 68% of the genome. Although *stx* genes were not detected, the phage genome harbored a putative phage *eae* gene with 95% homology to the phage *eae* gene in the *E. coli* O145:H28 strain linked to a previous lettuce outbreak in the United States (8). The

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results reveal that the genome of the novel phage vB\_EcoS Sa179lw should provide valuable insights into the diversity of those coliphages and could be used for the study of virulence gene transfer among bacteria.

**Accession number(s).** The complete genome sequence of *E. coli* phage vB\_EcoS Sa179lw has been deposited in GenBank under the accession number [MH023293](https://doi.org/10.1093/genome/10.1101/096354).

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