



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

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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 (2×250 -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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