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GENOME SEQUENCES

Complete Genome Sequence of *Escherichia* Phage vB_EcoM-Pr121LW, Isolated from Soil in an Organic Farm

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ABSTRACT Here, we report a new member of rV5-like phages, *Escherichia* phage vB_EcoM-Pr121LW, isolated from soil samples and lytic against different serogroups of Shiga toxin-producing *Escherichia coli* (STEC) strains. With molecular properties that contain no antibiotic resistance, virulence, or lysogenic genes, this phage is a potential biocontrol agent against STEC.

Shiga toxin-producing *Escherichia coli* (STEC) strains have been recently associated with the increasing number of produce outbreaks (1, 2). Bacteriophages have shown their potential as alternative biocontrol agents to replace antibiotics or preservatives against these pathogens (3). In the current study, the complete genome sequence of *Escherichia* phage vB_EcoM-Pr121LW, which is lytic against various STEC strains, is described.

Escherichia phage vB_EcoM-Pr121LW (or Pr121LW) was isolated from a soil sample collected in an organic farm by enriching with STEC O121 strains in tryptic soy broth with 10% calcium chloride solution and incubating at 37°C overnight, followed by the purification process described previously, with subtle modification (4). The phage DNA was extracted using a phage DNA isolation kit (Norgen Biotek, Ontario, Canada), and the libraries were prepared as previously described (5). Briefly, a TruSeq Nano DNA library prep kit (Illumina) was used for the library preparation, with quantification performed using an Agilent 2100 Bioanalyzer. Approximately 2.5 million 2 × 250-bp paired-end sequence reads were generated using a MiSeq sequencer, according to the manufacturer's instruction. The raw sequence reads were subjected to FastQC for quality check, followed by sequence trimming using Trimmomatic, with default settings. The resultant quality reads were assembled to a single contig using Unicycler version 0.4.1 (SPAdes) on the Galaxy server (https://usegalaxy.org/). The open reading frames (ORFs) of the final contig were predicted using Geneious (version 11.0.4) with a reference genome and confirmed with the BLASTp results. The phage packaging mechanisms and genome termini were predicted using PhageTerm (6). tRNA was detected using the tRNAscan-SE search server (7). Antibiotic resistance genes were examined on the ResFinder (version 3.0) database (8).

Pr121LW contained a 134,575-bp double-stranded DNA (224-fold coverage), with an average G+C content of 43.6%, and was classified as a novel rV5-like virus, with 96% sequence identity over 96% coverage of the phage rV5 (GenBank accession number DQ832317), under subfamily *Vequintavirinae* within *Myoviridae*, according to NCBI BLASTn analysis. Genome annotation predicted 220 open reading frames (ORFs), of which 50 encoded functional proteins, including those for DNA replication and metabolism, cell lysis, and structural integrity. No antibiotic resistance genes, lysogenic genes, or virulence genes, such as *stx* and *eaeA*, were found. Pr121LW also shared 98% sequence identity with approximately 98% of an rV5-like phage genome, that of

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Escherichia phage Murica (GenBank accession number KT001917). However, a 423-bp noncoding region interrupted a large terminase in Pr121LW, unlike the complete terminase sequence in phage Murica. Additionally, Pr121LW had 5 tRNA genes, whereas Murica had 7 (9). PhageTerm predicted that the packaging mechanism of Pr121LW was headful with a *pac* site, without terminal cohesive ends (10).

Most rV5-like phages, including Murica, were categorized in a cluster of lytic phages, Lytic22, among 337 fully sequenced tail phages based on comparative genomic analyses (11). Furthermore, three tail fiber proteins of Pr121LW (ORF_117, ORF_122, and ORF_131) show 99% identity to the amino acid sequences of another rV5-like phage, vB_EcoM_FFH2 (GenBank accession number NC_024134), which had a wide host range against STEC strains (12). The genomic analyses were consistent with the wide host range of Pr121LW.

The findings of this study demonstrate that Pr121LW may be a new member of rV5-like phages isolated from a nonfecal environment. Additionally, the genomic features provide valuable insights into the use of a potential biocontrol agent against STEC strains.

Data availability. The complete genome sequence of *Escherichia* phage vB_EcoM-Pr121LW has been deposited in GenBank under the accession number MH752840. The sequencing reads have been deposited under the accession number SRP159220. The version of the phage genome described in this paper is the first version.

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