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GENOME ANNOUNCEMENT

Complete Genomic Sequence of *Salmonella enterica* Serovar Enteritidis Phage SE2

Birendra R. Tiwari, Shukho Kim, and Jungmin Kim

Department of Microbiology, School of Medicine, Kyungpook National University, Daegu, Republic of Korea

***Salmonella enterica* serovar Enteritidis has remained a major food-borne pathogen in humans. We isolated a virulent *S. enterica* serovar Enteritidis bacteriophage, SE2, which belongs to the family *Siphoviridae*. Phage SE2 could lyse *S. enterica* serovar Enteritidis PT-4, and its virulence was maintained even at ambient temperature. The genomic sequence of phage SE2 was composed of 43,221 bp with close similarity to those of *Salmonella* phage SETP3 and *Salmonella* phage SS3e. The strong and stable lytic activity of this phage might enable its use as a therapeutic or biocontrol agent against *S. enterica* serovar Enteritidis.**

Salmonella enterica serovar Enteritidis has remained a major food-borne pathogen in humans (5, 7). Bacteriophage had been found to be useful in reducing *S. enterica* serovar Enteritidis *in vivo* and *in vitro* (1). We report here a new virulent *S. enterica* serovar Enteritidis bacteriophage, SE2, that was isolated from sewage samples from poultry farms in South Korea. Phage amplification and purification were carried out by the agar overlay method using *S. enterica* serovar Enteritidis PT-4 as the propagating host. Morphological analysis showed that phage SE2 belongs to the family *Siphoviridae*. Phage SE2 could lyse planktonic and biofilm cells of *S. enterica* serovar Enteritidis PT-4. Furthermore, its virulence was maintained at ambient temperature and even at 4°C (data not shown). The genomic DNA of phage SE2 was extracted and purified by using the Qiagen Lambda midi kit (Qiagen, Hilden, Germany) according to the protocol supplied. A shotgun library was created and sequenced (ABI PRISM 3730XL; Applied Biosystems, Foster City, CA) with 10-fold coverage of the phage genome. Open reading frame (ORF) prediction was done by using Glimmer version 3.0 (3), and sequence annotations were performed by database homology searching of the GenBank (2), Swiss-Prot (4), and PIR protein databases (6). The genomic sequence of phage SE2 was composed of 43,221 bp with a G+C content of 49.6%. The genome showed 61 ORFs, and 50 ORFs were annotated as hypothetical proteins. Only 11 ORFs were found to have significant annotated functions, which were identified as small- and large-subunit DNA polymerase, terminase, structural protein, amidase, tail protein, putative head protein, putative tail protein, putative DNA binding protein, DNA methylase N-4/N-6 domain protein, and tailspike protein. Similarity searching revealed that the phage SE2 genome was highly homologous to those of *Salmonella* phage SETP3 (GenBank accession number EF177456) and *Salmonella* phage SS3e (GenBank accession number AY730274). Phage SE2 differed from phage SETP3 in that it lacks a holin-encoding gene upstream of the amidase gene, suggesting that it may use a holin-independent lytic mechanism. Phage SE2 has two DNA polymerases (small and large subunits); the small subunit is very homologous to the DNA polymerase of phage SETP3, whereas the large subunit shows only 95% similarity. The DNA methylase N-4/N-6 domain protein of the phage SE2 genome is absent from the SETP3 phage genome. The genome sequence of phage SE2 was very similar to that of phage SS3e, except for some amino acid sequence changes in the C-terminal domain of the tail spike protein-encoding gene.

In conclusion, this study analyzed the complete genome sequence of newly isolated virulent *S. enterica* serovar Enteritidis phage SE2. The strong and stable lytic activity of this phage might enable its use as a therapeutic agent against *S. enterica* serovar Enteritidis and as a biocontrol agent for preventing contamination of food by *S. enterica* serovar Enteritidis.

Nucleotide sequence accession number. The complete genome of phage SE2 has been submitted to GenBank and assigned accession number JQ007353.

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Address correspondence to Jungmin Kim, minkim@knu.ac.kr.

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