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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Vibrio vulnificus* Bacteriophage SSP002

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***Vibrio vulnificus* phages are abundant in coastal marine environments, shellfish, clams, and oysters. SSP002, a *V. vulnificus*-specific bacteriophage, was isolated from oysters from the west coast of South Korea. In this study, the complete genome of SSP002 was sequenced and analyzed for the first time among the *V. vulnificus*-specific bacteriophages.**

The marine bacterium *Vibrio vulnificus* is the causative agent of food-borne diseases such as gastroenteritis and (possibly life-threatening) septicemia in individuals with underlying predisposing conditions (5). The Centers for Disease Control and Prevention has estimated that about 100 persons in the United States per year are infected with *V. vulnificus* and that approximately half of them die (10). Recently, the application of bacteriophages has come to be considered one of the most promising therapeutic methods for bacterial infection, owing to the increase in antibiotic resistance among bacteria (2).

Although several *V. vulnificus* phages have been isolated and characterized previously (4, 6), their complete genome sequences have not yet been reported. In this study, *V. vulnificus* phage SSP002 was isolated and its complete genome was sequenced. The genomic DNA of phage SSP002 was extracted (11) and sequenced (55 times coverage) using Genome Sequencer FLX Titanium technology at Macrogen in South Korea. Assembly of the quality-filtered reads was executed for the complete genome sequence using a 454 Newbler 2.3 assembler. Open reading frames (ORFs) of the genome sequence of SSP002 were predicted using the CLC Genomics Workbench program (version 4.7; CLCbio) and confirmed with GeneMark.hmm (8) and Glimmer 3.02 (3). The conserved protein domain was analyzed for the annotation of the predicted ORFs with BLASTP (1), InterProScan (12), and the NCBI Conserved Domain database (9). Sequences for tRNAs were predicted using the tRNAscan-SE program (7).

Sequencing revealed that the complete genome of SSP002 is a linear and double-stranded DNA sequence. It is 76,350 nt in length with a G+C content of 48.78% and 102 ORFs but no tRNA. The average gene length is 673 bp, and the gene density is 1.336/kb. While 79 ORFs were shown to encode hypothetical proteins, only 23 ORFs were annotated as functional genes. Functional categories of the annotated genes are related to the phage structure and packaging (a terminase large subunit, structural proteins, and a head morphogenesis domain), a tail structure for interaction with the host (a tail tape measure protein and a tail assembly protein), host lysis (an endolysin), DNA replication/modification (a DNA ligase, an HNH endonuclease, DNA exonucleases, DNA helicases, a RecA protein, and DNA polymerases I and III), transcription regulation (a transcriptional regulator), and additional functions (an Ist ATP-binding domain containing protein, a thymidylate synthase, and a thymidylate kinase).

Almost half of the annotated genes are related to DNA replication/modification, which may allow the efficient replication of SSP002 during infection. Interestingly, the thymidylate synthase of SSP002 revealed a high level of homology (85% identity in amino acid sequences) to that of *V. vulnificus*. The thymidylate synthase of SSP002 presumably originates from *V. vulnificus*, suggesting that SSP002 may be able to transfer gene elements through transduction. This complete genome analysis of SSP002 can lay the groundwork for understanding the interaction between SSP002 and *V. vulnificus* and further contribute to the development of a biological control practice for the fulminating pathogen.

Nucleotide sequence accession number. The complete genome sequence of SSP002 is available in GenBank under accession number JQ692107.

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