Complete Genome Sequence of *Salmonella enterica* Serovar Typhimurium Bacteriophage SPN1S

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To understand the interaction between the host of pathogenic *Salmonella enterica* serovar Typhimurium and its bacteriophage, we isolated the bacteriophage SPN1S. It is a lysogenic phage in the *Podoviridae* family and uses the O-antigen of lipopolysaccharides (LPS) as a host receptor. Comparative genomic analysis of phage SPN1S and the *S. enterica* serovar Anatum-specific phage ϵ 15 revealed different host specificities, probably due to the low homology of host specificity-related genes. Here we report the complete circular genome sequence of *S. Typhimurium*-specific bacteriophage SPN1S and show the results of our analysis.

Salmonella infection is one of the most common food-borne illnesses (representing more than 30% of all bacterial food-borne poisoning) (4, 5). More than 1.4 million cases of food-borne *Salmonella* infection have been reported every year in the United States, and the number of cases has increased by 10% in recent years (4, 9, 13). Moreover, the emergence of multidrug-resistant *Salmonella* strains, such as *Salmonella enterica* serovar Typhimurium DT104, has been getting more problematic (7, 14). To control these drug-resistant *Salmonella* strains, applications of *Salmonella*-specific bacteriophages have been proposed (8, 15). Therefore, it is important to understand the infection mechanism between the *Salmonella* host and *Salmonella*-specific phages. To increase our knowledge of this interaction, we isolated *S. Typhimurium*-specific phage SPN1S from environmental water and completely sequenced its genome.

The genomic DNA of phage SPN1S was isolated using an alkaline lysis method (16) and sequenced using Genome Sequencer FLX Titanium (GS-FLX Titanium) technology at Macrogen (Korea) with 130 times coverage. Sequence assembly of quality filtered reads was performed using a 454 Newbler 2.3 assembler. From the complete genome sequence of phage SPN1S, open reading frames (ORFs) were predicted using the GAMOLA automatic annotation program (1) and confirmed using GeneMarkS (3), Glimmer 3.02 (6), and FgenesV (SoftBerry). Conserved protein domain analysis was conducted using BLASTP (2), InterProScan (17), and the NCBI Conserved Domain database (CDD) (12). Prediction of tRNAs was carried out using the tRNAscan-SE program (11).

Bacteriophage SPN1S has a circular genome consisting of 38,684 bp with a GC content of 50.16% and 52 ORFs but no tRNA. The annotation of this genome revealed genes related to phage packaging (terminase small and large subunits), morphogenesis (a phage head-to-tail connector protein, an endoprotease, a major capsid protein, and a minor structural protein), host specificity (a tail spike protein), conversion of host lipopolysaccharide (LPS) (a GtrA and two copies of lipopolysaccharide modification acyltransferase), host lysis (a holin, an endolysin, an Rz-like protein, and an Rz1), DNA replication/modification (a DNA replication protein, an integrase, an exonuclease VIII/RecE-like protein, and an adenine methylase), and transcription regulation (a transcriptional activator and transcriptional regulators).

Comparative genome analysis of phage SPN1S and *S. enterica* serovar Anatum-specific phage ϵ 15 (GenBank accession number

AY150271) revealed that while these two phages are closely related at the DNA level, their host specificity-related genes encoding tail spike/tail fiber proteins are quite different. In addition, the receptor study of phage SPN1S showed that the tail spike protein (SPN1S_0022) interacts with the O-antigen of LPS in *S. Typhimurium*, suggesting that this phage infects the host strain via LPS as a host receptor (data not shown). Interestingly, Rz1 and Rz-like protein collaborate with the endolysin for host lysis. Expression of the endolysin gene alone using the *Escherichia coli* gene expression system does not lyse the host strain, but coexpression of the genes encoding endolysin, Rz1, and Rz-like protein does (10). The genome study of phage SPN1S would increase our knowledge of the interaction between the *S. Typhimurium* host and its bacteriophages.

Nucleotide sequence accession number. The complete genome sequence of *S. Typhimurium* phage SPN1S is available in GenBank under accession number [JN391180](#).

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