Salmonella enterica serovar Enteritidis is one of the most common causes of salmonellosis worldwide. S. Enteritidis is typically transmitted by food-products derived from the poultry industry. Since phage prophylaxis can reduce the use of antibiotics, we isolated the bacteriophage f18SE from poultry sewage (1). This phage has a broad host range infecting S. Enteritidis Pts, Salmonella Pullorum, and Salmonella Typhimurium serovars (1). The morphology of the viral particles is similar to that of phage λ. It has an icosahedral head of 30 × 24 nm, a tail of 95 × 5 nm, and basal spikes. Although, the genome annotation included fibers, they could not be visualized by transmission electron microscopy.

f18SE consists of double stranded DNA with a characteristic EcoRI digestion profile (1). According to its characteristics, the phage f18SE belongs to the family Siphoviridae, subfamily Jerseyvirinae (2). f18SE has been successfully evaluated as prophylactic agent in polysaccharide

Bacteriophage f18SE was isolated from poultry sewage in Olmue, Chile, and lytic activity was demonstrated against Salmonella enterica serovar Enteritidis and serovar Pullorum strains. This bacteriophage has a 41,868-bp double-stranded DNA (ds-DNA) genome encoding 53 coding sequences (CDSs) and belongs to the family Siphoviridae, subfamily Jerseyvirinae.

Based on the predictions, this phage genome contains genes for phage replication, structure, and lysis. Open reading frames (ORFs) were found for putative homing endonuclease, helicase, and DNA polymerase. The ORFs for terminase, head morphogenesis protein, putative tail protein, and tail fiber protein were found. No lysogenization genes, such as site-specific integrases and repressors, were identified. The ORFs for holin and endolysin were also found. Alignment and molecular phylogenetic analysis by maximum likelihood method (8–10) shown that three phages closely related to f18SE are Salmonella phages L13 (GenBank accession no. KC832325), wksI3 (GenBank accession no. JX202565), and SS3e (GenBank accession no. AY730274).

Nucleotide sequence accession number. The complete genome of the Salmonella Enteritidis f18SE has been deposited in GenBank under the accession no. KR270151.

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