Complete Genome Sequence of *Salmonella enterica* Serovar Enteritidis Bacteriophage f18SE, Isolated in Chile

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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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**REFERENCES**


