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

Cristopher Segovia, Ignacio Vasquez, Vinicius Maracaja-Coutinho, James Robeson, Javier Santander

Microbial Pathogenesis and Vaccinology Laboratory, Faculty of Sciences, Universidad Mayor, Huechuraba, Chile; Integrative Genomics PhD program, Faculty of Sciences, Universidad Mayor, Huechuraba, Chile; School of Biotechnology, Universidad Mayor, Huechuraba, Chile; Laboratory of Integrative Bioinformatics, Center for Genomics and Bioinformatics, Faculty of Sciences, Universidad Mayor, Huechuraba, Chile; Instituto Vandiquest, João Pessoa, Brazil; Microbiology Laboratory, Institute of Biology, Pontificia Universidad Católica de Valparaíso, Valparaíso, Chile; School of Life Sciences, Arizona State University, Tempe, Arizona, USA.

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 *Jerservirinae*.

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) showed that three phages closely related to f18SE are *Salmonella* phages L13 (GenBank accession no. K8232325), wks13 (GenBank accession no. JX202565), and S33e (GenBank accession no. AT730274).

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

ACKNOWLEDGMENTS

This work was supported by the CONICYT/CONDECyC Regular competition 1140330, FIC-BIP 30170275-0, and COPEC-UC 2014.J0.71. We thank Carolina Sanchez (Center for Genomics and Bioinformatics, Universidad Mayor) and Mario Moreno (Center for Genomics and Bioinformatics, Universidad Mayor) for their assistance at the sequencing facility, and to Maria Ignacia Diaz for logistic support.

REFERENCES


