Complete genome sequence of the salmonella enterica serovar enteritidis bacteriophages fSE1C and fSE4C isolated from food matrices

Javier Santander 1,2,4*, Jose I. Vasquez 2, Cristopher Segovia 2, Leonardo Santos 2, Gabriel Turra 3, Karen Huber 3 and James Robeson 3

Abstract

Salmonella enterica serovar Enteritidis is one of the most common causes of Salmonellosis worldwide. Utilization of bacteriophages as prophylactic agents is a practical solution to prevent Salmonellosis in ready-to-eat products. Shelf stability is one of the desirable properties for prophylactic bacteriophages. Here, we describe the phenotype, genome, and phylogeny of fSE1C and fSE4S Salmonella bacteriophages. fSE1C and fSE4S were previously isolated from pickle sauce and ground beef respectively and selected for their significant shelf stability. fSE1C and fSE4S showed a broad S. enterica serovar range, infecting several Salmonella serovars. The viral particles showed an icosahedral head structure and flexible tail, a typical morphology of the Siphoviridae family. fSE1C and fSE4C genomes consists of dsDNA of 41,720 bp and 41,768 bp with 49.73% and 49.78% G + C, respectively. Comparative genomic analysis reveals a mosaic relationship between S. enterica serovar Enteritidis phages isolated from Valparaiso, Chile.

Keywords: Salmonella enterica serovar Enteritidis, Bacteriophages fSE1C and fSE4C, Shelf stability, Phage prophylaxis, Food security

Introduction

The current methodologies to inactivate bacterial pathogens in ready-to-eat products are not infallible. Foodborne diseases caused by non-typhoid Salmonella still have an enormous impact on public health [1, 2]. Salmonella enterica serotype Enteritidis is one of the most common causes of non-typhoid Salmonellosis with contaminated food [3–5]. The increasing cases of Salmonellosis together with the emergence of antibiotic resistant strains have led to efforts searching for new methods to control Salmonella colonization in ready-to-eat products. Traditional methods to reduce bacterial contamination (U.V., steam, and dry heat) face the problems of food organoleptic properties deterioration and lack of prophylactic protection once the product is contaminated. Also, some of these approaches used in the food industry to reduce contamination by food borne pathogens cannot be directly applied to fresh fruits, vegetables, and raw meat [6]. Despite technical advances to avoid transmission of bacterial pathogens throughout the food chain, novel strategies are still required to fulfill consumer demands to minimize chemical preservatives in fresh food products. Bacteriophage-based biocontrol has a great potential to enhance microbiological safety based on their long history of safe use, relatively easy handling, high and specific antimicrobial activity and public acceptance [7].

Shelf stability is one of the desirable characteristics that a bacteriophage must have for its effective utilization in fresh food [6]. Previously, we isolated the bacteriophages fSE1C and fSE4S from pickle sauce and ground beef respectively [8]. These bacteriophages have a significant stability in shelf conditions and in food matrices with respect to other Salmonella bacteriophages [8], making
fSE1C and fSE4S excellent candidates to be used in ready-to-eat products. Here, we report the phenotypic characteristics, genome sequence, and phylogeny of fSE1C and fSE4S bacteriophages isolated from food matrices in Valparaiso, Chile.

Organism information

Classification and features

The bacteriophages fSE1C and fSE4S were isolated from pickle sauce and ground beef respectively, from samples obtained at the Central Market of Valparaiso, Chile, during 2013. Routine enrichment techniques [9] and the host, S. enterica serovar Enteritidis PT4 [8] were utilized for the isolation process. The two phages isolated formed clear plaques on the host bacterial lawn after 18 h of incubation at 37 °C. The diameters of plaques were 1 mm for both phages (Fig. 1a and b). fSE1C and fSE4S showed a productive lytic infection in different S. enterica serovars including S. enterica serovar Enteritidis (control), S. enterica serovar Infantis, S. enterica serovar Heidelberg, S. enterica serovar Typhi, S. enterica serovar Typhimurium, S. enterica serovar Paratyphi B and S. enterica serovar Pullorum. The bacteriophages have a different host range. fSE4S can have a productive lytic infection in S. enterica serovar Derby and S. enterica serovar Hadar in contrast to fSE1C [10]. The transmission electron microscopy showed that these bacteriophages have a typical morphology of the Siphoviridae family consisting of an icosahedral head (~50 nm), flexible long non-contractile tail (~150 nm) and base (Fig. 1b and d). The extracted nucleic acids from phage particles were treated with EcoRI, HindIII and HaeIII restriction enzymes. The genomic material of both phages was digested by these enzymes, revealing that their genomic material is dsDNA (Fig. 1e). The restriction enzyme patterns were similar for both phages (Fig. 1e). Together, these results indicated these phages belong to the Siphoviridae family [11]. Phylogenetic analysis, using the
complete bacteriophage genomes, showed that these phages are close related to f18SE [12], SSe and wksl3 Salmonella phages (Fig. 1f). The bacteriophage SSe, wksl3 and f18SE are members of the proposed subfamily Jersyvirinae [12], genera Jersylikekvirus [13]. However, our phylogenetic analysis, which includes the most recently sequenced Salmonella Siphoviridae bacteriophages, revealed that fSE1C, fSE4S, f18SE, SSe and wksl3 are distant members from the Jersylikekvirus genera (Fig. 1f).

Genes encoding DNA polymerase, helicase, the major tail protein, portal protein, the terminase large subunit and the major capsidase, were predicted from the genomes of both phages and used for phylogenetic analysis (Fig. 1g and h). DNA polymerase, helicase and the major tail protein are closely related to the bacteriophage f18SE [12] (Fig. 2). On the other hand, the portal protein and the terminase large subunit are closely related between both phages, but not related to the f18SE bacteriophage (Fig. 2). The major capsid subunit of the

![Phylogenetic analysis of conserved genes of Siphoviridae bacteriophages](image-url)

**Fig. 2** Phylogenetic analysis of conserved genes of Siphoviridae bacteriophages. Phylogenetic tree of conserved gene on bacteriophages of Siphoviridae family, and fSE1C and fSE4S. The evolutionary history was inferred using the Neighbor-Joining method [23]. DNA Polymerase, helicase, major tail, portal protein, terminase, and major capsid gene sequences were selected. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [24]. The evolutionary distances were computed using the p-distance method [25] and are in the units of the number of base differences per site. Evolutionary analyses were conducted in MEGA6 [26].
phage fSE1C is closely related to f18SE, in contrast to fSE4S, which is closely related to the SETP3 phage (Fig. 2). Mosaicism is known to be prevalent in the family Siphoviridae, which is reflected in our results. However, the DNA polymerase, and helicase proteins presented similar phylogenetic relationships, analogous to the complete bacteriophage genome phylogenetic relationships (Fig. 1f). Information on the isolation, classification, and general features of the phages fSE1C and fSE4S are presented in Table 1.

Genome sequencing information
Genome project history
Genome sequencing of the bacteriophages fSE1C and fSE4S was performed as a part of a research project that aimed to sequence effective bacteriophages for use in anti-Salmonella prophylactic cocktails for ready-to-eat products. Previously, we reported the genome sequence of the Salmonella bacteriophage f18SE isolated from the poultry industry in Valparaiso, Chile, during 2001, which has been tested successfully in vivo and in processed foods [14–16] as part of this project.

Genome sequencing of fSE1C and fSE4S was performed using the NGS Illumina MiSeq at Universidad Mayor, Center for Genomics and Bioinformatics (Huechuraba, Chile). The sequences were assembled using CLC Genomics Workbench 8.5.1 (Qiagen), resulting in single contigs. The assembled sequences were annotated by the PHASTER server [17, 18] and the NCBI-PGAAP. The complete genome sequences and annotation information of both bacteriophages were submitted to GenBank under the accession numbers KT962832 (fSE1C) and KT881477 (fSE4S) (Table 2).

Growth conditions and genomic DNA preparation
The bacteriophages fSE1C and fSE4S were isolated from pickle sauce and ground beef respectively using S. enterica serovar Enteritidis PT4 as host [8]. Isolation and propagation methods were those used routinely [9, 19]. Briefly, the bacteriophages were enriched using a S. Santander et al. Standards in Genomic Sciences (2017) 12:1

Table 1 Classification and general features of Salmonella enterica bacteriophages fSE1C and fSE4S

| MIGS ID | Property                        | Term fSE1C and fSE4S                | Evidence codea |
|---------|---------------------------------|------------------------------------|----------------|
|         | Classification                  | Domain Akamara                     | TAS [34]       |
|         |                                 | Kingdom Viruses                    | TAS [34]       |
|         |                                 | Class dsDNA viruses, no RNA stage  | IDA            |
|         |                                 | Order Caudovirales                 | TAS [34]       |
|         |                                 | Family Siphoviridae                | TAS [34]       |
|         |                                 | Genus Jerseyvirus                  | TAS [34]       |
|         |                                 | Species Salmonella phage           | TAS [34]       |
|         |                                 | Strains: fSE1C, fSE4S              | TAS [34]       |
|         | Gram stain                      | Not applicable                     | TAS [34]       |
|         | Particle shape                  | Icosahedral head with a flexible long non-contractile tail | IDA |
|         | Motility                        | none                               | TAS [34]       |
|         | Sporulation                     | none                               | NAS            |
|         | Temperature range               | −80 °C – 45 °C                     | TAS [34]       |
|         | Optimum temperature             | 37 °C                              | TAS [34]       |
|         | pH range; Optimum               | 3.5–6.5; 7.0                       | TAS [34]       |
|         | Carbon source                   | Not applicable                     | TAS [34]       |
| MIGS-6  | Habitat                         | Contaminated food or waste water   | IDA            |
| MIGS-15 | Biotic relationship             | intracellular parasite of Salmonella enterica | IDA |
| MIGS-14 | Pathogenicity                   | virulent phage of Salmonella enterica | IDA |
| MIGS-4  | Geographic location             | Mercado Cardonal, Valparaiso, Chile | IDA            |
| MIGS-5  | Sample collection               | 2013                               | IDA            |
| MIGS-4.1| Latitude                        | 33°20’S                           | IDA            |
| MIGS-4.2| Longitude                       | 71°40’W                           | IDA            |
| MIGS-4.4| Altitude                        | 0 m                                | IDA            |

aEvidence codes – IDA Inferred from Direct Assay, TAS Traceable Author Statement, NAS Non-traceable Author Statement. These evidence codes are from Gene Ontology project [35]
*enterica* serovar Enteritidis PT4 Rif⁻, Na⁺ derivative. Lysis plaques were obtained by under streaking using the same bacterial host. Individual plaques were purified twice to establish the final bacteriophage culture typified by the formation of clear, haloed round plaques of about 1 mm in diameter. Both phages showed similar plaque morphology. The two phages formed clear plaques on *S. enterica* serovar Enteritidis lawn after 18 h incubation at 37 °C. Genomic DNA from concentrated lysates were purified according to the method described by Kaiser et al. [20].

Genome sequencing and assembly

The purified bacteriophage DNA was used to prepare the libraries (one library for each phage) with the Nextera kit (Illumina, San Diego, CA). High-throughput sequencing of the libraries was performed using a MiSeq (Illumina) with a 2x300bp paired-end run, with the reagent kit version 3 (600 cycles) at the Center for Genomics and Bioinformatics, Universidad Mayor, Chile. In total, about 127 and 317 million pairs of reads were obtained for *f*SE1C and *f*SE4S, respectively. Raw reads were assembled by using CLC Genomics Workbench 8.5.1. Coverage was calculated from the sequencing statistics, and final contig sizes were 2874X and 7590X for *f*SE1C and *f*SE4S, respectively (Table 2).

**Table 2** Project information of *Salmonella enterica* bacteriophages *f*SE1C and *f*SE4S

| MIGS ID | Property          | Term *f*SE1C                        | Term *f*SE4S                        |
|---------|-------------------|-------------------------------------|-------------------------------------|
| MIGS 31 | Finishing quality | Finished                            | Finished                            |
| MIGS 28 | Libraries used    | 1                                   | 1                                   |
| MIGS 29 | Sequencing platforms | One paired-end Illumina library, MiSeq | One paired-end Illumina library, MiSeq |
| MIGS 31.2 | Fold coverage    | 2874X                               | 7590X                               |
| MIGS 30 | Assemblers        | CLC Genome Workbench 8.5.1          | CLC Genome Workbench 8.5.1          |
| MIGS 32 | Gene calling method | RAST version 2.0, GeneMark.hmm, and GLIMMER | RAST version 2.0, GeneMark.hmm, and GLIMMER |
|         | Locus Tag         | *f*SE1C                             | *f*SE4S                             |
|         | Genbank ID        | KT962832                            | KT881477                            |
|         | GenBank Date of Release | 18-NOV-2015                           | 31-JUL-2016                           |
|         | GOLD ID           | 952094059                           | 952094006                           |
|         | BIOPROJECT        | PRJNA291403                          | PRJNA291403                          |
| MIGS 13 | Source Material Identifier | NA⁺                                 | NA⁺                                 |
|         | Project relevance | Phage prophylaxis in ready-to-eat products | Phage prophylaxis in ready-to-eat products |

*Viruses have not been deposited yet*

Genome properties

The complete genomes of both phages were assembled into single circular contigs. Bacteriophage *f*SE1C contains 41,720 bp and has a G + C content of 49.73%. The bacteriophage *f*SE4S contains 41,768 bp and has a G + C content of 49.78%. The genome of *f*SE1C contains 53 predicted genes and *f*SE4S contains 52 predicted genes, with a total gene length between 186–3099 bp. We found in *f*SE1C genome 17 genes with rightward orientation, while 36 were leftward oriented, and in *f*SE4S genome 35 genes with rightward orientation and 17 were leftward (Fig. 1g and h) (Table 3). Both phage genomes contain genes for replication, structure, and lysis. Open reading frames (ORFs) were found for putative homing endonuclease, helicase, and DNA polymerase. The ORFs for terminase (large and small subunit), head morphogenesis protein, major capsid protein, putative tail transmembrane helices were predicted by the Phobius software [22]. BLASTp searches against the NCBI nr database were also performed. The CRISPRs were predicted base on structure using the web base software Structure RNA finder.

The evolutionary history was inferred using the Neighbor-Joining method [23]. The trees were drawn to scale. The percentage of replicate trees for the conserved proteins in the bootstrap test (1000 replicates) are shown next to the branches [24] (Fig. 2). The evolutionary distances were computed using the *p*-distance method [25] and are in the units of the number of base differences per site. The ambiguous positions were removed for each sequence pair. Evolutionary analyses were conducted in MEGA6 [26].
### Table 3: Genome statistics

| Attribute                | Value /SE1C | % of Total /SE1C | Value /SE4S | % of Total /SE4S |
|--------------------------|-------------|------------------|-------------|------------------|
| Genome size (bp)         | 41,720      | 100.00           | 41,768      | 100.00           |
| DNA coding (bp)          | 36,813      | 88.24            | 37,032      | 88.66            |
| DNA G + C (bp)           | 20,747      | 49.73            | 20,926      | 49.78            |
| DNA scaffolds             | 1           | 100.00           | 1           | 100.00           |
| Total genes              | 53          | 88.24            | 52          | 88.66            |
| Protein coding genes     | 53          | 88.24            | 52          | 88.66            |
| RNA genes                | 0           | 0.00             | 0           | 0.00             |
| Pseudo genes             | 0           | 0.00             | 0           | 0.00             |
| Genes in internal clusters | 0         | 0.00             | 0           | 0.00             |
| Genes with function prediction | 22       | 36.62            | 18          | 30.69            |
| Genes assigned to COGs   | 10          | 19.98            | 26          | 20.46            |
| Genes with Pfam domains  | 31          | 36.36            | 33          | 52.26            |
| Genes with signal peptides | 0        | 0.00             | 0           | 0.00             |
| Genes with transmembrane helices | 0   | 0.00             | 0           | 0.00             |
| CRISPR direct repeats    | 2           | 0.24             | 2           | 0.24             |

The total is based on the size of the genome in base pairs.

### Table 4: Number of genes associated with general COG functional categories

| Code | /SE1C Value | %age | /SE4S Value | %age | Description                                                                 |
|------|-------------|------|-------------|------|------------------------------------------------------------------------------|
| J    | 1           | 1.89 | 1           | 1.92 | Translation, ribosomal structure and biogenesis                               |
| A    | 0           | 0.00 | 0           | 0.00 | RNA processing and modification                                               |
| K    | 2           | 3.78 | 11          | 21.12| Transcription                                                                |
| L    | 5           | 9.45 | 19          | 36.48| Replication, recombination and repair                                         |
| B    | 0           | 0.00 | 0           | 0.00 | Chromatin structure and dynamics                                              |
| D    | 0           | 0.00 | 0           | 0.00 | Cell cycle control, Cell division, chromosome partitioning                   |
| V    | 1           | 1.89 | 1           | 1.92 | Defense mechanisms                                                           |
| T    | 0           | 0.00 | 0           | 0.00 | Signal transduction mechanisms                                               |
| M    | 0           | 0.00 | 0           | 0.00 | Cell wall/membrane biogenesis                                                |
| N    | 0           | 0.00 | 0           | 0.00 | Cell motility                                                                |
| U    | 0           | 0.00 | 0           | 0.00 | Intracellular trafficking and secretion                                       |
| O    | 0           | 0.00 | 1           | 1.92 | Posttranslational modification, protein turnover, chaperones                 |
| C    | 0           | 0.00 | 0           | 0.00 | Energy production and conversion                                              |
| G    | 0           | 0.00 | 0           | 0.00 | Carbohydrate transport and metabolism                                         |
| E    | 0           | 0.00 | 0           | 0.00 | Amino acid transport and metabolism                                           |
| F    | 0           | 0.00 | 0           | 0.00 | Nucleotide transport and metabolism                                          |
| H    | 0           | 0.00 | 0           | 0.00 | Coenzyme transport and metabolism                                            |
| I    | 0           | 0.00 | 0           | 0.00 | Lipid transport and metabolism                                               |
| P    | 0           | 0.00 | 1           | 1.92 | Inorganic ion transport and metabolism                                        |
| Q    | 0           | 0.00 | 5           | 9.6  | Secondary metabolites biosynthesis, transport and catabolism                 |
| R    | 0           | 0.00 | 2           | 3.84 | General function prediction only                                              |
| S    | 3           | 4.67 | 10          | 19.2 | Function unknown                                                             |
| -    | 43          | 81.27| 23          | 44.16| Not in COGs                                                                  |

The total is based on the total number of protein coding genes in the genome.
protein, and tail fiber protein and a portal protein were found. Also, a lysozyme, holing-like classes I and putative endolysins were also found. Lysogeny related genes, like C2 of P22 [27], CI and Cro of λ [28], and others are absent from both phage genomes.

The phage genomes closely related to fSE1C and fSE4S were Salmonella phages f18SE (GenBank accession no. KR270151), SSe3 (GenBank accession no. AY730274), and ws1k13 (GenBank accession no. JX202565). Comparative analysis between both phages showed that their genomes are 43.09% similar and all 52 genes of fSE4S have orthologous in the fSE1C genome. These orthologous proteins have a similarity between 73.58 and 100%. The only gene different in the fSE1C genome encodes for a hypothetical protein (GI:952094085) of 108 aa with no ortholog in fSE4S, but present in f18SE and other lytic Salmonella bacteriophages.

Non-coding RNA prediction was similar in both bacteriophages, presenting the CRISPR-DR41 and CRISPR-DR23 single direct repeat. This prediction was coincident with the COGs analyses (Table 4), which detected the Cas4 protein family (cl00641) in both bacteriophages. Functional CRISPRs have been described in V. cholerae bacteriophages [29], however, the CRISPRs predicted for fSE1C and fSE4S seem not a completed CRISPR system.

Conclusions
The ORFs involved in structure, replication, host specificity (i.e., tail fibers and tailspikes) and DNA metabolism were found to be conserved in these two phages compared to other Salmonella enterica bacteriophages. However, the major capsid protein showed some diversity (Fig. 2) that might be related to the high shelf stability presented by fSE1C and fSE4S phages [8].

The Jersyvirine subfamily consists of three genera, “Jerseyvirus”, “Sp3unavirus” and “Klgvirus” [13]. The Jersyvirine subfamily include a distinct morphotype, genomes of 40–44 kb (49.6-51.4 mol % G + C), a syntenic genome organization, high degree of nucleotide sequence identity, and strictly lytic cycle [30]. As mentioned previously, the Siphoviridae family presents considerable mosaicism [31, 32] and although we distinguished a possible new genus for the subfamily Jersyvirinae (Fig. 1f), we considered that a high number of sequenced Jersyvirinae phages are required to propose a new genus.

Abbreviations
CDD: Conserved domain database; CRISPRs: Clustered regularly interspaced short palindromic repeats; DR: Direct repeats; MEGAs: Molecular evolutionary genetics analysis; NGS: Next generation sequencer; PGAAP: Prokaryotic genomes automatic annotation pipeline; PHASTER: PHAge search tool enhanced release; TEM: Transmission electron microscopy.

Acknowledgements
We thank Dr. 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 Mª Ignacia Diaz (FONDECYT 1140330) for its logistic support.

Funding
This work was supported by the CONICYT/FONDECYT Regular Competition 1140330 and COPE-UC 2014.J0.71 grants.

Authors’ contributions
KH, JR and GT isolated the two bacteriophages and their genomes. JS, CS, NV and LS performed the laboratory work related to genome sequencing, genome analysis and drafted the manuscript. JS wrote the manuscript. All authors read and approved the final manuscript.

Competing interests
The authors declare that they have no competing interests.

Author details
1Department of Ocean Sciences, Memorial University of Newfoundland, St. John’s, Canada. 2University Mayor, Faculty of Sciences, Huechuraba, Chile. 3Pontificia Universidad Católica de Valparaíso, Institute of Biology, Valparaíso, Chile. 4Memorial University of Newfoundland, Faculty of Sciences, Ocean Science Centre, Marine Microbial Pathogenesis and Vaccinology Laboratory, AX3005, 0 Marine Lab Rd, Logy Bay, NL A1K 3E6, Canada.

Received: 20 August 2016 Accepted: 7 December 2016
Published online: 05 January 2017

References
1. DuPont HL. The growing threat of foodborne bacterial enteropathogens of animal origin. Clin Infect Dis. 2007;45:1353–61.
2. Center for Disease Control Prevention (CDC). Estimates of Foodborne Illness in the United States (updated 15 April 2011). Atlanta: CDC; 2011. https://www.cdc.gov/foodborneburden/PDFs/pathogens-complete-list-01-12.pdf.
3. Fisher IS. Dramatic shift in the epidemiology of Salmonella enterica serotype Enteritidis phage types in western Europe, 1998-2003—results from the Enter-net international Salmonella database. Euro Surveill. 2004;94:5–3.
4. Velge P, Cloeckaert A, Barrow P. Emergence of Salmonella epidemics: the problems related to Salmonella enterica serotype Enteritidis and multiple antibiotic resistance in other major serotypes. Vet Res. 2005;36:267–88.
5. Poirier E, Water L, Espie E, Well FX, De Valk H, Desenclos JC. Evaluation of the impact on human salmonellosis of control measures targeted to Salmonella Enteritidis and Typhimurium in poultry breeding using time-series analysis and intervention models in France. Epidemiol Infect. 2008;136:1217–24.
6. Garcia P, Martinez B, Obeso JM, Rodriguez A. Bacteriophages and their application in food safety. Lett Appl Microbiol. 2008;47:879–85.
7. Hagens S, Loesner MJ. Application of bacteriophages for detection and control of foodborne pathogens. Appl Microbiol Biotechnol. 2007;76:513–9.
8. Robeson J, Turra G, Huber K, Borie C. A note on stability in food matrices of Salmonella enterica serovar Enteritidis-controlling bacteriophages. Electron J Biotechnol. 2014;17:189–91.
9. Adams MH. Bacteriophages. New York: Interscience; 1959.
10. Galarce N, Escobar B, Rojas V, Navarro C, Turra G, Robeson J, Borie C. Application of a virulent bacteriophage cocktail leads to reduction of Salmonella enterica serovar Enteritidis counts in processed meat products. Biocontrol Sci Technol. 2016;26:462–72.
11. Ackermann HW, Prangishvili D. Prokaryote viruses studied by electron microscopy. Arch Virol. 2012;157:1843–9.
12. Segovia C, Vasquez I, Maracaja-Coutinho V, Robeson J, Santander J. Complete genome sequence of Salmonella enterica serovar Enteritidis bacteriophage f18SE, isolated in Chile. Genome Ann. 2015;3:e00600–15.
13. Anany H, Switt AI, De Lappe N, Ackermann HW, Reynolds DM, Kropinski AM, et al. A proposed new bacteriophage subfamily: “Jerseyviraenae”. Arch Virol. 2015;160:1021–33.
14. Borie C, Sanchez ML, Navarro C, Ramírez S, Morales MA, Retamales J, et al. Aerosol spray treatment with bacteriophages and competitive exclusion reduces Salmonella enteritidis infection in chickens. Avian Dis. 2009;53:250–4.
15. Galarce NE, Bravo JL, Robeson JP, Borie CF. Bacteriophage cocktail reduces Salmonella enterica serovar Enteritidis counts in raw and smoked salmon tissues. Rev Argent Microbiol. 2014;46:333–7.
16. Santander J, Robeson J. Phage prophylaxis against Salmonella enteritidis using C. elegans as an assay system. Electron J Biotechnol. 2004;7:11–4.
17. Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, et al. PHASTER: a better, faster version of the PHAST phage search tool. Nucleic Acids Res. 2016;44: W16–21.
18. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. PHAST: a fast phage search tool. Nucleic Acids Res. 2011;39:W347–52.
19. Borne C, Albala I, Sanchez P, Sanchez ML, Ramirez S, Navarro C, et al. Bacteriophage treatment reduces Salmonella colonization of infected chickens. Avian Dis. 2008;52:64–7.
20. Kaiser K, Murray N, Whittaker P. Construction of representative genomic DNA libraries using phages lambda replacement vectors. In: Glover D, Hames B, editors. DNA cloning 1: a practical approach. New York: Oxford University Press; 1995. p. 37–83.
21. Marchler-Bauer A, Zheng C, Chitsaz F, Derbyshire MK, Geer LY, Geer RC, et al. CDD: conserved domains and protein three-dimensional structure. Nucleic Acids Res. 2013;41:D348–52.
22. Kall L, Krogh A, Sonnhammer EL. A combined transmembrane topology and signal peptide prediction method. J Mol Biol. 2004;338:1027–36.
23. Saitou N, Nei M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol. 1987;4:406–25.
24. Felsenstein J. Confidence limits on phylogenies: an approach using the bootstrap. Evolution. 1985;39:783–91.
25. Nei M, Kumar S. Molecular evolution and phylogenetics. Oxford; New York: Oxford University Press; 2000.
26. Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Mol Biol Evol. 2013;30:2725–9.
27. Watkins D, Hsiao C, Woods KK, Kouldeika GB, Williams LD. P22 c2 repressor-operator complex: mechanisms of direct and indirect readout. Biochemistry. 2008;47:2325–38.
28. Oppenheim AB, Kobiler O, Savrans J, Court DL, Adhya S. Switches in bacteriophage lambda development. Annu Rev Genet. 2005;39:409–29.
29. Seed KD, Lazinski DW, Caldenwood SB, Camilli A. A bacteriophage encodes its own CRISPR/Cas adaptive response to evade host innate immunity. Nature. 2013;494:889–91.
30. Ackermann HW, Gershman M. Morphology of phages of a general Salmonella typing set. Res Virol. 1992;143:303–10.
31. Adriaenssens EM, Edwards R, Nazh JH, Mahadevan P, Seto D, Ackermann HW, et al. Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. Virology. 2015;477:144–54.
32. Hendrix RW. Bacteriophages: evolution of the majority. Theor Popul Biol. 2002;61:471–80.
33. Carver T, Thomson N, Bleasby A, Berriman M, Parkhill J. DNAPlotter: circular and linear interactive genome visualization. Bioinformatics. 2009;25:119–20.
34. King AM, Adams MJ, Cartens EB, Lefkowitz EJ. Virus taxonomy: ninth report of the international committee on taxonomy of viruses. San Diego: Elsevier; 2012.
35. Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, et al. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. Nat Genet. 2000;25:25–9.