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ICTV Virus Taxonomy Profile: Finnlakeviridae

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Abstract

Finnlakeviridae is a family of icosahedral, internal membrane-containing bacterial viruses with circular, single-stranded DNA genomes. The family includes the genus, Finnlakevirus, with the species, Flavobacterium virus FLiP. Flavobacterium phage FLiP was isolated with its Gram-negative host bacterium from a boreal freshwater habitat in Central Finland in 2010. It is the first described single-stranded DNA virus with an internal membrane and shares minimal sequence similarity with other known viruses. The virion organization (pseudo $T=21$ dextro) and major capsid protein fold (double-$\beta$-barrel) resemble those of Pseudoalteromonas phage PM2 (family Corticoviridae), which has a double-stranded DNA genome. A similar major capsid protein fold is also found in other double-stranded DNA viruses in the kingdom Bamfordvirae. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) report on the family Finnlakeviridae, which is available at ictv.global/report/finnlakeviridae.

Table 1. Characteristics of members of the family Finnlakeviridae

<table>
<thead>
<tr>
<th>Typical member:</th>
<th>Flavobacterium phage FLiP (MF361639), species Flavobacterium virus FLiP, genus Finnlakevirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virion</td>
<td>Icosahedral, internal membrane-containing virions, approximately 59 nm in diameter. Spikes protrude from the virion surface</td>
</tr>
<tr>
<td>Genome</td>
<td>9.2 kb of circular, single-stranded DNA</td>
</tr>
<tr>
<td>Replication</td>
<td>Possibly rolling circle replication</td>
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<tr>
<td>Translation</td>
<td>By the host translation machinery</td>
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<tr>
<td>Host range</td>
<td>Gram-negative bacteria from the genus Flavobacterium</td>
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<tr>
<td>Taxonomy</td>
<td>The genus Finnlakevirus includes the species Flavobacterium virus FLiP</td>
</tr>
</tbody>
</table>

VIRION

The virion of Flavobacterium phage FLiP consists of an icosahedral protein shell and an internal membrane, uniquely combined with a circular ssDNA genome [1] (Table 1, Fig. 1). The diameter of the virion is about 59 nm (vertex-to-vertex). Pentameric spike complexes protrude about 12 nm from the protein shell surface at the fivefold vertices. The inner surface of the icosahedral protein capsid is covered by a lipid bilayer membrane (5 nm thick), enclosing the single-stranded DNA genome. The major capsid proteins (MCPs) forming the outer protein shell follow a pseudo $T=21$ dextro icosahedral capsid organization, previously described only for the marine double-stranded DNA Pseudoalteromonas phage PM2 [2]. The Flavobacterium phage FLiP MCPs consist of two $\beta$-barrels with jellyroll topology and arrange into trimers to form pseudohexameric molecules [1]. A similar major capsid protein fold has also been described for members of the kingdom Bamfordvirae [3], such as Enterobacteria phage PRD1 (family Tectiviridae) [4].

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Abbreviations: CDS, coding sequence; MCP, major capsid protein; $T$, triangulation number.

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GENOME
Virions contain a single copy of a circular single-stranded DNA of 9174 nucleotides with a GC content of 34% [1]. 16 predicted coding sequences (CDS), all in the same orientation (Fig. 2), show limited similarity with other known sequences. Five CDSs have been shown to encode structural proteins (CDS7–9, 11, 14). There are sequence similarities between CDS14 and several lytic transglycosylases and between CDS15 and rolling circle replication proteins [1, 5].

REPLICATION
Flavobacterium phage FLiP is a virulent virus that induces host-cell lysis at the end of the viral reproduction cycle [1]. CDS14 is predicted to encode a virion-associated lytic protein likely assisting in the penetration of the host peptidoglycan layer during entry. Flavobacterium phage FLiP does not encode any identifiable DNA or RNA polymerase. However, the sequence resemblance of CDS15 to rolling circle replication proteins suggests a replication mechanism typical of single-stranded DNA viruses [1, 5]. The absence of a putative packaging ATPase implies that a viral-encoded ATPase is not required for the encapsidation of the genome [5].

TAXONOMY
Current taxonomy: ictv.global/report/finnlakeviridae. The family Finnlakeviridae contains the genus Finnlakevirus with the species Flavobacterium virus FLiP. Based on phylogenetic analysis of MCP sequences, Flavobacterium phage FLiP forms its own group among the tailless prokaryotic DNA viruses and proviruses with double-β-barrel MCPs [5].

RESOURCES
Current ICTV Report on the family Finnlakeviridae: ictv.global/report/finnlakeviridae

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Conflicts of interest
The authors declare that there are no conflicts of interest.

References

Fig. 1. Flavobacterium phage FLiP virion structure. (a) Cryo-electron microscopic reconstruction [1]. (b) virions negatively-stained with 2% phosphotungstic acid (pH 8.5) and visualized under transmission electron microscopy. Scale bar represents 100 nm.

Fig. 2. Genome organization of Flavobacterium phage FLiP. Arrows show the direction of transcription of predicted CDSs, with light blue indicating those encoding the structural proteins P7–9, P11 and P14. The unique EcoRII restriction site is at nucleotide position 1.