Abstract
Members of the family Sphaerolipoviridae have non-enveloped tailless icosahedral virions with a protein-rich internal lipid membrane. The genome is a linear double-stranded DNA of about 30 kbp with inverted terminal repeats and terminal proteins. The capsid has a pseudo triangulation $T=28$ dextro symmetry and is built of two major capsid protein types. Spike complexes decorate fivefold vertices. Sphaerolipoviruses have a narrow host range and a lytic life cycle, infecting haloarchaea in the class Halobacteria (phylum Euryarchaeota). This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family Sphaerolipoviridae, which is available at ictv.global/report/sphaerolipoviridae.

Table 1. Characteristics of members of the family Sphaerolipoviridae

<table>
<thead>
<tr>
<th>Example</th>
<th>Haloarcula californica icosahedral virus 1 (KT809302), species Alphasphaerolipovirus HCIV1, genus Alphasphaerolipovirus</th>
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<tr>
<td>Virion</td>
<td>Non-enveloped, tailless icosahedral virion with an internal lipid membrane, diameter 80 nm, capsid is pseudo $T=28$ dextro, two types of major capsid protein, horn-shaped or propeller-shaped fivefold vertex spike complexes, membrane-associated proteins</td>
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<tr>
<td>Genome</td>
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<td>Taxonomy</td>
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</tbody>
</table>

VIRION
Sphaerolipoviruses have tailless icosahedral virions with an internal protein-rich membrane vesicle (Table 1; Fig. 1) [1–5]. The virion is typically about 80 nm in diameter with major and minor capsid proteins, internal membrane proteins and vertex complex proteins (Fig. 1). The capsid has a pseudo $T=28$ dextro triangulation number [4]. The two major capsid proteins (MCPs) VP4 and VP7 have a vertical single jelly-roll fold. The capsid lattice is built of pseudohexameric capsomers with either two or three towers (Fig. 1) made of VP4-VP4 homodimers and VP4-VP7 heterodimers [4]. The vertices are occupied by penton proteins forming the binding position for the spike complex. Vertex complexes are either horn-shaped or propeller-shaped [4]. MCPs, the major membrane protein, and the putative packaging
ATPase are the most conserved structural proteins among sphaerolipoviruses [3, 4]. The lipids of the internal membrane vesicle are selectively acquired from host-cell membranes. Membrane vesicles are rich in virus-specific proteins. Major phospholipid species are phosphatidylglycerol, phosphatidylglycerophosphate methyl ester and phosphatidylglycerosulfate [3].

**GENOME**

Members of the family *Sphaerolipoviridae* have a linear double-stranded DNA genome of 28–31 kbp with a GC content of 67–68% and inverted terminal repeats of about 300bp with terminal proteins attached [2, 3, 5]. Genomes contain about 50 predicted genes, arranged in a conserved synteny (Fig. 2) [2, 3, 5]. The overall nucleotide identity between sphaerolipovirus genomes is 56–76% [6].

**REPLICATION**

Replication is probably protein-primed [5], but the genome does not encode a canonical DNA polymerase. The genome of SH1 virus has genes organized in seven major transcripts, some of which overlap [5]. Six early transcripts encode structural genes, while one late transcript encodes proteins of unknown function. Sphaerolipoviruses originate from hypersaline environments, and their host range is limited to a few haloarchaeal strains belonging to the genera *Haloarcula* and *Halorubrum* [6]. Sphaerolipoviruses bind to their hosts most probably by spike complexes at the virion vertices. Adsorption is relatively slow and the infection cycle is lytic, lasting 6–12 h [1–3]. Several putative proviral regions related to sphaerolipoviruses are found in the chromosomes of halophilic archaea [6].

**TAXONOMY**

Current taxonomy: ictv.global/taxonomy . The family *Sphaerolipoviridae* together with the families *Matsushitaviridae* (species *Hukuchivirus P2377* and *Hukuchivirus IN93*) and *Simuloviridae* (species *Yingchengvirus SNJ1*, *Yingchengvirus NVIV1* and *Yingchengvirus HJIV1*) are assigned to the order *Halopanivirales*.

**RESOURCES**


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References