ICTV Virus Taxonomy Profile: *Pleolipoviridae*

Dennis H. Bamford,¹,* Maija K. Pietilä,² Elina Roine,¹ Nina S. Atanasova,¹ Ana Dienstbier,³ Hanna M. Oksanen¹,* and ICTV Report Consortium

**Abstract**

Members of the family *Pleolipoviridae* (termed pleolipoviruses) are pseudo-spherical and pleomorphic archaeal viruses. The enveloped virion is a simple membrane vesicle, which encloses different types of DNA genomes of approximately 7–16 kbp (or kilonucleotides). Typically, virions contain a single type of transmembrane (spike) protein at the envelope and a single type of membrane protein, which is embedded in the envelope and located in the internal side of the membrane. All viruses infect extremely halophilic archaea in the class Halobacteria (phylum Euryarchaeota). Pleolipoviruses have a narrow host range and a persistent, non-lytic life cycle. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of the *Pleolipoviridae* which is available at www.ictv.global/report/pleolipoviridae.

---

**Table 1. Characteristics of the family Pleolipoviridae**

<table>
<thead>
<tr>
<th>Typical member</th>
<th>Halorubrum pleomorphic virus 1 (FJ685651), species Halorubrum virus HRPV1, genus Alphapleolipovirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virion</td>
<td>Enveloped, pseudo-spherical and pleomorphic virions (diameters 40–70 nm), typically with a single type of spike protein at the envelope and a single type of internal membrane protein embedded in the envelope</td>
</tr>
<tr>
<td>Genome</td>
<td>Circular ssDNA, circular dsDNA or linear dsDNA, approximately 7–16 kilonucleotides or kbp</td>
</tr>
<tr>
<td>Replication</td>
<td>Possibly rolling-circle replication for circular molecules; protein-primed replication for linear molecules</td>
</tr>
<tr>
<td>Translation</td>
<td>Prokaryotic translation using viral mRNA and host ribosomes</td>
</tr>
<tr>
<td>Host range</td>
<td>Archaea, euryarchaeal Halorubrum, Haloarcha or Haloarcheum strains</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Three genera Alphapleolipovirus, Betapleolipovirus and Gammapleolipovirus</td>
</tr>
</tbody>
</table>

---

**VIRION**

Virions are enveloped pleomorphic membrane vesicles of 40–70 nm diameter (Table 1, Fig. 1a, b) with one or two types of major proteins forming spikes and one or two as internal membrane proteins (Fig. 1c). The spike and internal membrane proteins of Halorubrum pleomorphic virus 1 are VP4 and VP3 respectively. Virions lack a capsid or nucleocapsid.

**GENOME**

Virus genomes are circular ssDNA of 7.0–10.7 kilonucleotides (Fig. 2), circular dsDNA of 8.1–9.7 kbp, or linear dsDNA of 16 kbp [1]. Members of the genus *Alphapleolipovirus* have circular ssDNA or dsDNA genomes, members of the genus *Betapleolipovirus* have circular dsDNA genomes with single-stranded discontinuities, and the only member of the genus *Gammapleolipovirus* has a linear dsDNA genome. A cluster of five genes/ORFs is conserved among the members of the family (Halorubrum pleomorphic virus 1 genes 3, 4 and 8, ORFs 6 and 7). The cluster includes genes encoding a spike and an internal membrane protein as well as an ORF encoding a putative NTPase. The only member of the genus *Gammapleolipovirus* is predicted to encode a putative type B DNA-dependent DNA polymerase. The genome ends bear terminal proteins.

**REPLICATION**

Pleolipoviruses are non-lytic and most likely enter cells by membrane fusion. Either rolling-circle or protein-primed replication may be used; transcription has not been studied. Progeny virions exit host cells continuously retarding host growth with concurrent unselective lipid acquisition implying that virions bud through the cell membrane.

Received 5 September 2017; Accepted 26 October 2017

**Author affiliations:** ¹Department of Biosciences, University of Helsinki, Viikinkaari 9B, FI-00014, Helsinki, Finland; ²Department of Food and Environmental Sciences, University of Helsinki, Viikinkaari 9B, FI00014, Helsinki, Finland; ³Institute of Microbiology of the CAS, v.v.i., Vídenska 1083, Prague, Czech Republic.

*Correspondence:* Dennis H. Bamford, dennis.bamford@helsinki.fi; Hanna M. Oksanen, hanna.oksanen@helsinki.fi

**Abbreviations:** Rep, replication initiation protein; NTPase, nucleoside triphosphate hydrolase.
Fig. 1. Morphology of pleolipovirus virions. (a) Electron micrograph of negatively stained Halorubrum pleomorphic virus 1 particles. (b) A close-up of one Halorubrum pleomorphic virus 1 virion. The arrows point to the spike structures covering the particle surface. Reproduced with permission from Pietilä et al. [5]. Scale bars in (a) and (b), 50 nm (c) Schematic presentation of the pleolipovirus virion.

TAXONOMY

Alphapleolipovirus

The genus includes the species Haloarcvirus HHPV1, Haloarcvirus HHPV2, Halorubrum virus HRPV1, Halorubrum virus HRPV2 and Halorubrum virus HRPV6. The genomes of alphapleolipoviruses contain 8–15 ORFs, and besides the conserved gene/ORF cluster, an ORF encoding a putative rolling-circle replication protein and one ORF with unknown function [2–4]. Virions contain a single spike and internal membrane protein. Additionally, Halorubrum pleomorphic virus 1 virions contain one minor structural protein predicted to be an NTPase; tomographic reconstruction shows that the glycosylated spikes [5] form irregular arrays on the virion surface [6].

Betapleolipovirus

The genus includes the species Halogeometricum virus HGPV1 and Halorubrum virus HRPV3. The betapleolipovirus genomes contain 12 or 15 ORFs. In addition to the cluster of five genes/ORFs, genomes share two ORFs encoding proteins with unknown function [4]. Virions contain one type of spike protein and one or two types of internal membrane proteins. The spike protein of Halogeometricum pleomorphic virus 1 is lipid-modified [6].

Gammapleolipovirus

Haloarcvirus His2 is the only species of this genus. The member has a genome with 35 ORFs [7] and a virion consisting of one type of internal membrane protein and two types of spike protein as well as one minor structural protein [6]. One of the spike proteins is lipid-modified.

RESOURCES


Funding information
Production of this summary, the online chapter and associated resources was funded by a grant from the Academy of Finland (127474/ M.K.P) and by a grant from the Wellcome Trust (WT108418AIA). H. M. O. was supported by University of Helsinki funding for Instruct-FI research infrastructure Virus and Macromolecular Complex Production (ICVIR).

Acknowledgements
Members of the ICTV Report Consortium are Elliot J. Lefkowitz, Andrew J. Davison, Stuart G. Siddell, Peter Simmonds, Sead Sabanadzovic, Donald B. Smith, Richard J. Orton and Andrew M. Kropinski.

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

References