

<https://helda.helsinki.fi>

ICTV Virus Taxonomy Profile: Pleolipoviridae 2022

Liu, Ying

2022

Liu , Y , Dyall-Smith , M & Oksanen , H M 2022 , ' ICTV Virus Taxonomy Profile:
Pleolipoviridae 2022 ' , Journal of General Virology , vol. 103 , no. 11 . <https://doi.org/10.1099/jgv.0.001793>

<http://hdl.handle.net/10138/351365>
<https://doi.org/10.1099/jgv.0.001793>

cc_by
publishedVersion

Downloaded from Helda, University of Helsinki institutional repository.

This is an electronic reprint of the original article.

This reprint may differ from the original in pagination and typographic detail.

Please cite the original version.



ICTV Virus Taxonomy Profile: *Pleolipoviridae* 2022

Ying Liu¹, Mike Dyal-Smith^{2,3}, Hanna M. Oksanen^{4,*} and ICTV Report Consortium

Abstract

Members of the family *Pleolipoviridae* are pseudo-spherical and pleomorphic archaeal viruses composed of a membrane vesicle, which encloses a DNA genome. The genome is either circular ssDNA or dsDNA, or linear dsDNA molecules of approximately 7 to 17 kilonucleotides or kbp. 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. Some viruses are temperate and can integrate into the host chromosome. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Pleolipoviridae*, which is available at ictv.global/report/pleolipoviridae.

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

Example	Halorubrum pleomorphic virus 1 (HRPV-1; FJ685651), species <i>Alphapleolipovirus</i> HRPV1, genus <i>Alphapleolipovirus</i>
Virion	Enveloped, pseudo-spherical and pleomorphic virions (diameter 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
Genome	Circular ssDNA, circular dsDNA or linear dsDNA, 7–17 kilonucleotides or kbp
Replication	Possibly rolling-circle replication for circular molecules; protein-primed replication for linear molecules
Translation	Prokaryotic translation using viral mRNA and host ribosomes
Host range	Archaea; euryarchaeal <i>Halorubrum</i> , <i>Haloarcula</i> , <i>Halogeometricum</i> or <i>Natrinema</i> strains
Taxonomy	Realm <i>Monodnaviria</i> , kingdom <i>Trapavirae</i> , phylum <i>Saleviricota</i> , class <i>Huolimaviricetes</i> , order <i>Haloruvirales</i> : three genera <i>Alphapleolipovirus</i> , <i>Betapleolipovirus</i> and <i>Gammapleolipovirus</i>

VIRION

Virions are enveloped pleomorphic membrane vesicles of 40–70 nm diameter (Table 1, Fig. 1a) with one or two types of major proteins forming spikes and one or two as internal membrane proteins (Fig. 1b) [1, 2]. The fusion-inducing spike protein has a unique V-shaped fold and belongs to a new structural class of fusion proteins [3]. Virions lack a capsid or nucleocapsid.

GENOME

Virus genomes are circular ssDNA of 7–11 kilonucleotides (Fig. 2), circular dsDNA of 8–17 kbp or linear dsDNA of 16 kbp. 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 members of the genus *Gammapleolipovirus* have linear dsDNA genomes [4–7]. A

Received 16 August 2022; Accepted 21 August 2022; Published 14 November 2022

Author affiliations: ¹Archaeal Virology Unit, Institut Pasteur, Université Paris Cité, CNRS UMR6047, Paris, France; ²Computational Biology Group, Max Planck Institute of Biochemistry, Martinsried, Germany; ³Veterinary Biosciences, Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, Australia; ⁴Molecular and Integrative Biosciences Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki, Finland.

*Correspondence: Hanna M. Oksanen, hanna.oksanen@helsinki.fi

Keywords: ICTV Report; *Pleolipoviridae*; taxonomy; archaeal virus.

001793 © 2022 The Authors



This is an open-access article distributed under the terms of the Creative Commons Attribution License.

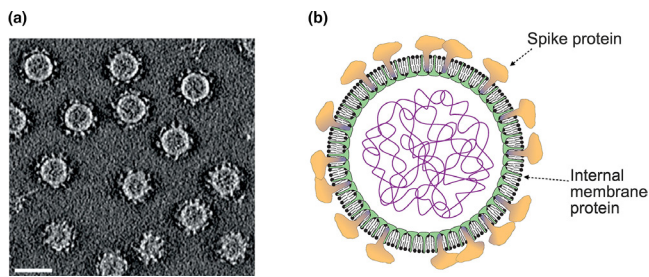


Fig. 1. Morphology of pleolipovirus virions. (a) A slice through a three-dimensional cryo-electron microscopy tomogram of Halorubrum pleomorphic virus 6 reconstructed from tilt series data. Reproduced with permission from [3] under Creative commons license 4.0. Bar, 40 nm. (b) Schematic of the pleolipovirus virion.

cluster of five genes/ORFs is conserved among 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 (Fig. 2). Members of the genus *Gammappleolipovirus* are predicted to encode a putative type B DNA-dependent DNA polymerase [6]. The genome ends bear terminal proteins.

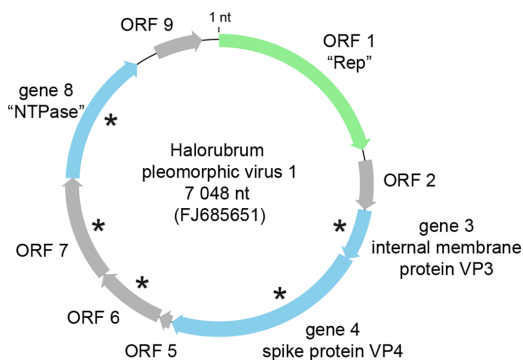


Fig. 2. Genome organization of Halorubrum pleomorphic virus 1. Blue - structural proteins (NTPase - nucleoside triphosphate hydrolase); green - ORF1 encoding a putative replication initiation protein (Rep); Grey - other ORFs; asterisk - core gene.

References

- Demina TA, Oksanen HM. Pleomorphic archaeal viruses: the family *Pleolipoviridae* is expanding by seven new species. *Arch Virol* 2020;165:2723–2731.
- Pietilä MK, Atanasova NS, Manole V, Liljeroos L, Butcher SJ, et al. Virion architecture unifies globally distributed pleolipoviruses infecting halophilic archaea. *J Virol* 2012;86:5067–5079.
- El Omari K, Li S, Kotecha A, Walter TS, Bignon EA, et al. The structure of a prokaryotic viral envelope protein expands the landscape of membrane fusion proteins. *Nat Commun* 2019;10:846.
- Pietilä MK, Roine E, Paulin L, Kalkkinen N, Bamford DH. An ssDNA virus infecting archaea: a new lineage of viruses with a membrane envelope. *Mol Microbiol* 2009;72:307–319.

REPLICATION

Pleolipoviruses are non-lytic and most likely enter cells by membrane fusion [3]. Either rolling-circle or protein-primed genome replication may be used. The transcription of His2 virus has been reported using a microarray approach [8]. Progeny virions exit host cells continuously, retarding host growth with concurrent unselective lipid acquisition, indicating that virions bud through the cell membrane [2]. Some viruses are temperate and can integrate in the host chromosome [7].

TAXONOMY

Current taxonomy: ictv.global/taxonomy. The family *Pleolipoviridae* includes three genera: *Alphappleolipovirus*, *Betappleolipovirus* and *Gammappleolipovirus* [1]. The genera are identified by gene content and well-supported monophyletic groups based on phylogenomic analysis of whole-genome sequences. Members of the genus *Alphappleolipovirus* share an ORF encoding a rolling circle replication initiation protein (RCR Rep). Betappleolipoviruses share two ORFs encoding proteins of unknown function (e.g. Halorubrum pleomorphic virus 3 ORFs 6 and 9). Gammappleolipovirus genomes have a gene encoding a putative type B DNA polymerase [7]. Viruses with genomes that differ by more than 5% in nucleotide sequence are assigned to different species.

RESOURCES

Full ICTV Report on the family *Pleolipoviridae*: www.ictv.global/report/pleolipoviridae.

Funding information

Production of this Profile, the ICTV Report and associated resources was supported by the Microbiology Society. H. M. O. was supported by the University of Helsinki and Academy of Finland funding for FINStruct, part of Biocenter Finland and Instruct-ERIC.

Acknowledgements

Members of the ICTV (10th) Report Consortium are Stuart G. Siddell, Elliot J. Lefkowitz, Peter Simmonds, Sead Sabanadzovic, F. Murilo Zerbini, Donald B. Smith and Mart Krupovic.

Conflicts of interest

The authors declare that there are no conflicts of interest.