



This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either Part 3 for proposals to create new taxa or change existing taxa
or Part 2 for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic_Proposals_Help_2019.

Part 1: TITLE, AUTHORS, etc

Code assigned:	2019.059B
Short title: Create one new family (<i>Halspiviridae</i>), move one unassigned genus (<i>Salterprovirus</i>) to the family and rename the type species	

Author(s) and email address(es):

List authors in a single line <i>Archives of Virology</i> citation format (e.g. Smith AB, Huang C-L, Santos, F)	Provide email address for each author in a single line separated by semi-colons
Krupovic M, Oksanen HM, Prangishvili D, Dyall-Smith ML	mart.krupovic@pasteur.fr ; hanna.oksanen@helsinki.fi ; david.prangishvili@pasteur.fr ; mike.dyallsmith@gmail.com

Author(s) institutional address(es) (optional):

Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL])
Institut Pasteur [MK, DP] University of Helsinki [HMO] University of Melbourne [MLD-S]

Corresponding author

Mart Krupovic (mart.krupovic@pasteur.fr)
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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal)	Bacterial and Archaeal Viruses Subcommittee
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ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:**Part 2: NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

Text of proposal:**Part 3: PROPOSED TAXONOMY**

Name of accompanying Excel module: 2019.059B.A.v2.Halspiviridae_1fam.xlsx

The taxonomic changes you are proposing should be presented on an accompanying Excel module, [2019_TP_Template_Excel_module](#). Please enter the file name of the completed module in this box.

Supporting material:

Viruses His1 and His2 have linear double-stranded DNA genomes and infect the halophilic archaeon *Haloarcula hispanica* (phylum Euryarchaeota). His1 was classified into an unassigned genus *Salterprovirus* (Bath et al., 2006), and His2 was a tentative species of the same genus. However, subsequent research has shown that the similarity between His1 and His2 is restricted to the shared protein-primed family B DNA polymerases (pPolB), whereas the modules responsible for virion formation are unrelated (Figure 1). Whereas His1 forms spindle-shaped virions (Bath and Dyll-Smith, 1998; Hong et al., 2015), His2 virions are pleomorphic (Bath et al., 2006; Pietilä et al., 2016). Consequently, His2 has been removed from the genus *Salterprovirus* and assigned to a genus *Gammaleolipovirus* in the family *Pleolipoviridae* (Pietilä et al., 2016).

The major capsid protein of His1 is homologous to that of other spindle-shaped viruses infecting hyperthermophilic archaea (phylum Crenarchaeota) and classified into the family *Fuselloviridae* (Pietilä et al., 2013; Krupovic et al., 2014). However, unlike His1, fuselloviruses have circular dsDNA genomes and do not encode pPolB. Because His1 is sufficiently distinct from all other known viruses, we suggest to assign the genus *Salterprovirus* to a separate new family, which we propose to name "*Halspiviridae*" (*hal-* for halophilic, *spi-* for spindle-shaped).

The species including His1 is currently called *His 1 virus*. We propose to rename the species to *Salterprovirus His1*.

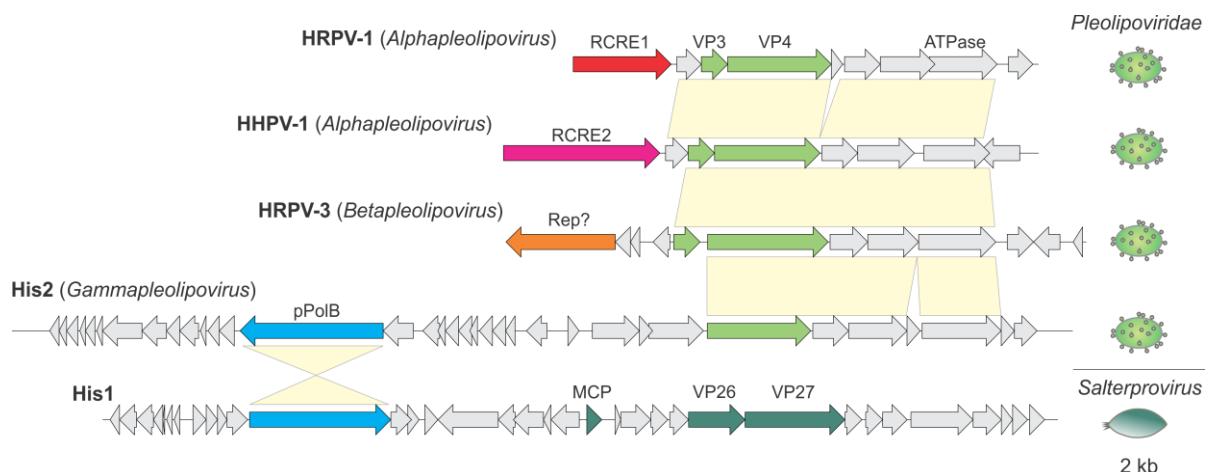


Figure 1. Genome comparison of pleolipoviruses and salterprovirus His1. The genome schematics are drawn roughly to scale (shown at the bottom of the figure). The genes are shown by block arrows indicating the direction of transcription. The genes encoding for genome replication-associated proteins and virion proteins are color coded: structural proteins of pleolipoviruses and salterproviruses are shown in light and dark green, respectively; two families of rolling circle replication initiation endonucleases (RCRE1 and RCRE2) are colored red and magenta, respectively; uncharacterized Rep is shown in orange; protein-primed family B DNA polymerase (pPolB), light blue. Genes shared between viruses are indicated by yellow shading. Morphologies of the corresponding viruses are shown on the right of the figure. MCP, major capsid protein. Genome accession numbers: HRPV-1, FJ685651; HHPV-1, GU321093; HRPV-3, JN882265; His2, AF191797; His1, AF191796. The figure is adapted from Krupovic et al., 2018.

References:

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