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## Taxonomy proposal 2019 : Rename the species in the family Pleolipoviridae

Oksanen, Hanna M

International Committee on Taxonomy of Viruses (ICTV)  
2020

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Oksanen , H M & Krupovic , M 2020 , Taxonomy proposal 2019 : Rename the species in the family Pleolipoviridae . in ICTV Online: International Committee on Taxonomy of Viruses (ICTV) . International Committee on Taxonomy of Viruses (ICTV) . <  
[https://talk.ictvonline.org/files/ictv\\_official\\_taxonomy\\_updates\\_since\\_the\\_8th\\_report/m/all-proposals/9600](https://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/all-proposals/9600)  
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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

<b>Code assigned:</b>	<b>2019.104B</b>
<b>Short title:</b> Rename eight species in the family <i>Pleolipoviridae</i>	

### 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
Oksanen HM, Krupovic M	<u>mart.krupovic@pasteur.fr;</u> <u>hanna.oksanen@helsinki.fi</u>

### 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])
Molecular and Integrative Biosciences Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Finland [HMO] Department of Microbiology, Institut Pasteur, France [MK]

### Corresponding author

Hanna M. Oksanen

### List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at <a href="http://www.ictvonline.org/subcommittees.asp">http://www.ictvonline.org/subcommittees.asp</a> . 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)	<b>Bacterial and archaeal virus subcommittee</b>
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**ICTV Study Group comments (if any) and response of the proposer:**

Date first submitted to ICTV:

June 19, 2019

Date of this revision (if different to above):

**ICTV-EC comments and response of the proposer:**

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**Part 2: NON-STANDARD**

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

**Text of proposal:**

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**Part 3: PROPOSED TAXONOMY**

<b>Name of accompanying Excel module:</b> 2019.104B.A.v1.Pleolipoviridae_ren8sp.xlsx
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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:**

additional material in support of this proposal

Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:

- **Species demarcation criteria:** Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteria have previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
- **Higher taxa:**
  - There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
  - Please indicate the **origin of names** assigned to new taxa at genus level and above.
  - For each new genus a **type species** must be designated to represent it. Please explain your choice.
- **Supporting evidence:** The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).

Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information.

additional material in support of this proposal

The family *Pleolipoviridae* contains archaeal pleomorphic viruses with either circular dsDNA or ssDNA, or linear dsDNA genomes of approximately 7–17 kb (or knt) (Bamford et al., 2017; Pietilä et al., 2016). The enveloped virion is a membrane vesicle, which contains two transmembrane proteins, one of which forms a spike protruding to the outside of the virion and the other one is located on the internal side of the membrane. All virus isolates of this group infect extremely halophilic archaea in the class Halobacteria (phylum Euryarchaeota). Pleolipoviruses have a narrow host range and a persistent, non-lytic life cycle.

Currently the family contains eight species in three genera *Alphapleolipovirus*, *Betapleolipovirus*, and *Gammapleolipovirus*. We have submitted a TaxoProp (2019) to assigned seven new virus species in the genus *Betapleolipovirus* (by Demina T, Krupovic M, Oksanen HM), where the new species were proposed to have binomial names consisting of the genus name and the specific epithet e.g. *Betapleolipovirus HHPV3*.

To have uniform names for all virus species in the family, we propose to rename the species in the family *Pleolipoviridae* by using the binomial species names.

#### References:

- Bamford DH, Pietilä MK, Roine E, Atanasova NS, Dienstbier A, Oksanen HM, ICTV Report Consortium. 2017 ICTV Virus Taxonomy Profile: *Pleolipoviridae*. J Gen Virol. 98:2916-2917.
- Pietilä MK, Roine E, Sencilo A, Bamford DH, Oksanen HM. 2016. *Pleolipoviridae*, a newly proposed family comprising archaeal pleomorphic viruses with single-stranded or double-stranded DNA genomes. Arch Virol. 161:249-256.