



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:	2019.105B
Short title: Create seven new species in the genus <i>Betapleolipovirus</i> , 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
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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])
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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 virus subcommittee

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:

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: 2019.105B.A.v1.Betapleolipovirus_7sp.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:

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

additional material in support of this proposal

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.

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.

A cluster of five to six genes and open reading frames (ORF) is conserved among the members of the family (Figure 1, see HRPV-1 in the genus *Alphapleolipovirus*, HHPV3 in the genus *Betapleolipovirus*, and His2 in the genus *Gammapleolipovirus*). The shared clusters include genes encoding spike proteins and internal membrane proteins as well as ORFs encoding a putative NTPase (Figure 1). Betapleolipoviruses share two additional putative ORFs, the products of which display high amino acid sequence identity (Figure 1; HHPV3 ORF7 and ORF11). The ORFs encode proteins of unknown functions, and one of these proteins contains a C-terminal winged helix-turn-helix (wHTH) domain, suggesting that it has a role linked to the interaction with DNA (Senčilo et al., 2012).

Seven new halophilic archaeal pleomorphic virus isolates, namely, HHPV3, HHPV4, HRPV9, HRPV10, HRPV11, HRPV12, and SNJ2 have been described (Atanasova et al., 2018a; Atanasova et al., 2018b; Demina et al., 2016; Liu et al., 2015; Mizuno et al., 2019). HHPV3 and HHPV4 viruses infect *Haloarcula hispanica*, whereas HRPV9, HRPV10, HRPV11, and HRPV12 are viruses of *Halorubrum* species. SNJ2 has been induced from *Natrinema* sp. J7-1, where it exists as a provirus integrated into the host tRNA(Met) gene (SNJ2 genome sequence: *Natrinema* sp. J7-1 Contig 004: AJVG01000023, nt coordinates 19792-36797). In addition to SNJ2, HHPV4 and HRPV9 also have genes encoding integrases and phiH1-like repressors (Figure 1).

All seven new viruses have dsDNA genomes and share the conserved cluster of genes and ORFs with the members of the family *Pleolipoviridae* (Figure 1). Their genomes are collinear, having less than 92% nucleotide identity. These viruses have two signature ORFs specific for members of the genus *Betapleolipovirus* (Figure 1 asterisks). We propose to have 95% nucleotide sequence identity as the criterion for demarcation of species in the genera of the family *Pleolipoviridae* and thus to assign these seven viruses as seven new species of the genus *Betapleolipovirus*.

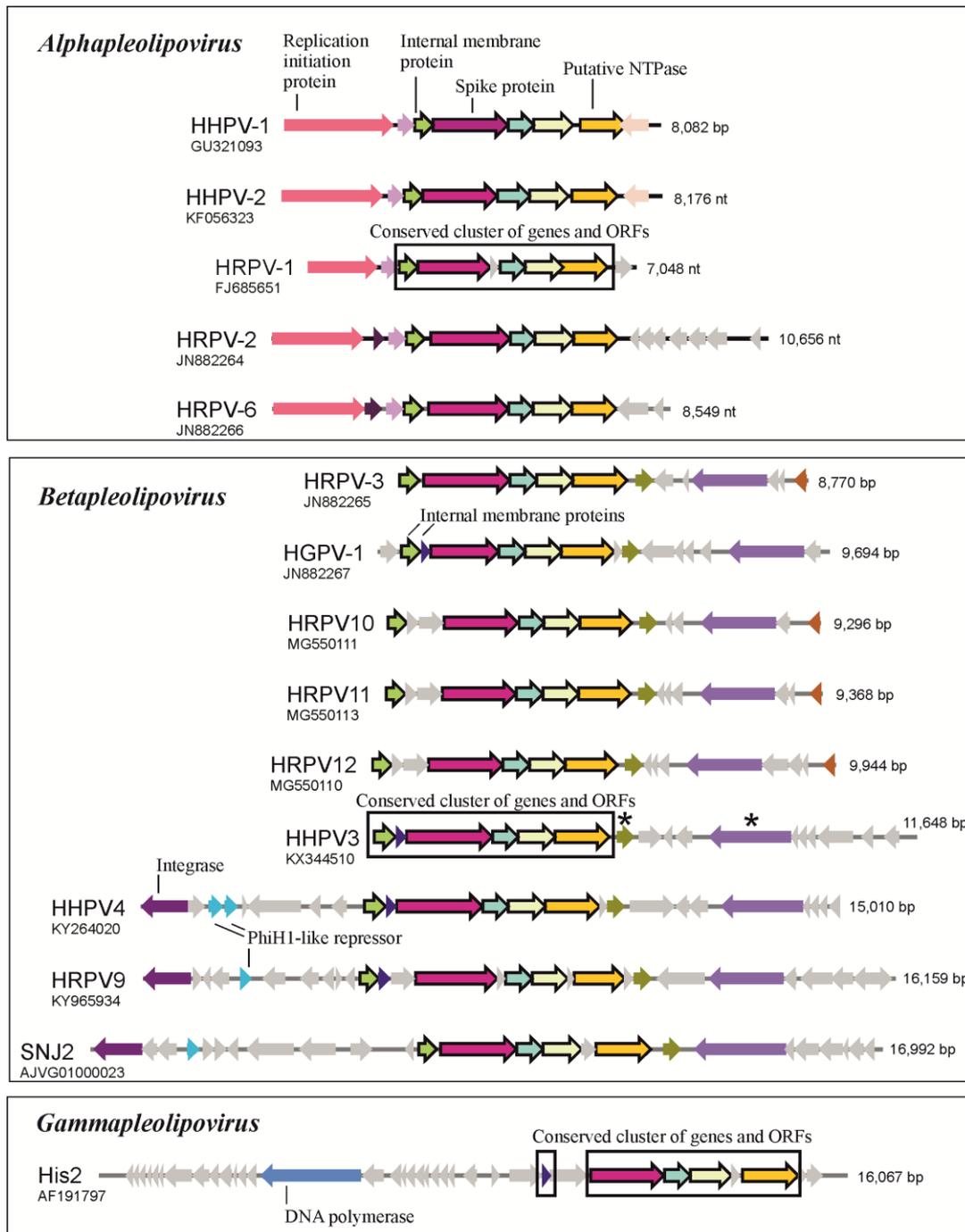


Figure 1. The family *Pleolipoviridae*. A linear representation of the pleolipovirus genomes. The genomes are circular, except for the genome of His2, which is linear. The genes and ORFs are shown by arrows indicating the direction of transcription, and similar ones are highlighted with the same colours. Boxes in HRPV-1, HHPV3, and His2 show the conserved blocks of pleolipoviral genes and ORFs. The conserved betapleolipoviral ORFs are marked by asterisks in HHPV3. Image generated with Easyfig version 2.2.3 (Sullivan et al., 2011).

References:

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