This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

## MODULE 1: TITLE, AUTHORS, etc

**Code assigned:** ***2009.004a-gB*** (to be completed by ICTV officers)

**Short title:** Create new genus named *Hap1likevirus* in the family *Myoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

| | | | | | |
|---|---|---|---|---|---|
| **Modules attached**<br>(modules 1 and 9 are required) | **1** ☒ | **2** ☒ | **3** ☒ | **4** ☐ | **5** ☐ |
| | **6** ☐ | **7** ☐ | **8** ☐ | **9** ☒ | |

**Author(s) with e-mail address(es) of the proposer:**

Rob Lavigne rob.lavigne@biw.kuleuven.be
Andrew Kropinski kropinsk@queensu.ca
Pieter-Jan Ceyssens pieterjan.ceyssens@biw.kuleuven.be

| | |
|---|---|
| Has this proposal has been seen and agreed by the relevant study group(s)?<br>Please select answer in the box on the right | **Yes** |

**ICTV-EC or Study Group comments and response of the proposer:**

[previous (EC41) decision: inconsistent with naming rules.]

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

MODULE 2: **NEW SPECIES**

**Part (a)** to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

| | | |
|---|---|---|
| Code | ***2009.004aB*** | (assigned by ICTV officers) |

**To create 2 new species with the name(s):**

*Halomonas phage phiHAP-1*
*Vibrio phage VP882*

---

**Part (b)** assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

| | | |
|---|---|---|
| Code | ***2009.004bB*** | (assigned by ICTV officers) |

**To assign the species listed in section 2(a) as follows:**

| | |
|---|---|
| Genus: | ***Hap1likevirus*** (new) |
| Subfamily: | |
| Family: | ***Myoviridae*** |
| Order: | ***Caudovirales*** |

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

**Reasons to justify the creation and assignment of the new species:**

- Explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

*Vibrio parahaemolyticus* phage VP882 (NC_009016) and *Halomonas aquamarina* phage φHAP-1 are temperate viruses possessing 38-43 kb genomes which lack integrase genes.

The ΦHAP-1 genome shares synteny and gene similarity with coliphage N15 and vibriophages VP882 and VHML, suggesting an evolutionary heritage from an N15-like linear plasmid prophage ancestor. While our proteomic analysis (Figure 1-3), and the literature suggests that *Vibrio harveyi* phage VHML should be included in this genus, there is no evidence that this phage can be propagated: it is only produced after induction, does not plaque, and must be considered a defective prophage. The data presented by Mobberley et al. show that φHAP-1 exists as a linear prophage in lysogens and possesses a protelomerase (ORF34, YP_001686770.1) and a partitioning protein (ParA homolog, ORF33, YP_001686769.1) which are homologous to proteins encoded by VHML and VP882. While these viruses share some homology with the coliphage P2, it is largely restricted to the genes associated with tail morphogenesis V (gp*V, W, J, I, H, G*) and F operons (gp*FI, FII, E, T, U, D*).

MODULE 3: **NEW GENUS**

creating and naming a new genus

| | | |
|---|---|---|
| Code | ***2009.004cB*** | (assigned by ICTV officers) |

**To create a new genus to contain the species listed below**

| | | |
|---|---|---|
| Code | ***2009.004dB*** | (assigned by ICTV officers) |

**To name the new genus: *Hap1likevirus***

assigning a new genus to higher taxa

| | | |
|---|---|---|
| Code | ***2009.004eB*** | (assigned by ICTV officers) |

**To assign the new genus as follows:** Ideally, a genus should be placed within a higher taxon, but if not, write "**unassigned**" in the box below.

| | |
|---|---|
| Subfamily: | |
| Family: | ***Myoviridae*** |
| Order: | ***Caudovirales*** |

If any of these taxa has yet to be created (in module 4, 5 or 6) please write "**(new)**" after its proposed name.

assigning type species and other species to a new genus

| | | |
|---|---|---|
| Code | ***2009.004fB*** | (assigned by ICTV officers) |

**To designate the following as the type species of the new genus**

*Halomonas phage phiHAP-1*

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

| | | |
|---|---|---|
| Code | ***2009.004gB*** | (assigned by ICTV officers) |

**To assign the following as additional species of the new genus:**

*Halomonas phage phiHAP-1*
*Vibrio phage VP882*

**Reasons to justify the creation of a new genus:**

Additional material in support of this proposal may be presented in the Appendix, Module 9

Based on proteomic comparison (Figure 1)

**Origin of the new genus name:**

Named after type species ΦHAP-1

**Reasons to justify the choice of type species:**

ΦHAP-1 was the first sequenced phage within this genus. ΦHAP-1, was induced with mitomycin C from a *Halomonas aquamarina* strain isolated from surface waters in the Gulf of Mexico (Figure 2).

**Species demarcation criteria in the new genus:**

- If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

See module 2

## MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

### References:

Mobberley JM, Authement RN, Segall AM, Paul JH: The temperate marine phage fHAP-1 of Halomonas aquamarina possesses a linear plasmid-like prophage genome. J Virol 2008, 82: 6618-6630.

Oakey HJ, Cullen BR, Owens L, Oakey HJ, Cullen BR, Owens L: The complete nucleotide sequence of the Vibrio harveyi bacteriophage VHML. Journal of Applied Microbiology 2002, 93: 1089-1098.

Oakey HJ, Owens L, Oakey HJ, Owens L: A new bacteriophage, VHML, isolated from a toxin-producing strain of Vibrio harveyi in tropical Australia. Journal of Applied Microbiology 2000, 89: 702-709.

Mobberley JM, Authement RN, Segall AM, Paul JH: The temperate marine phage phiHAP-1 of Halomonas aquamarina possesses a linear plasmid-like prophage genome. Journal of Virology 2008, 82: 6618-6630.

### Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.

The use of Figures and Tables is strongly recommended.

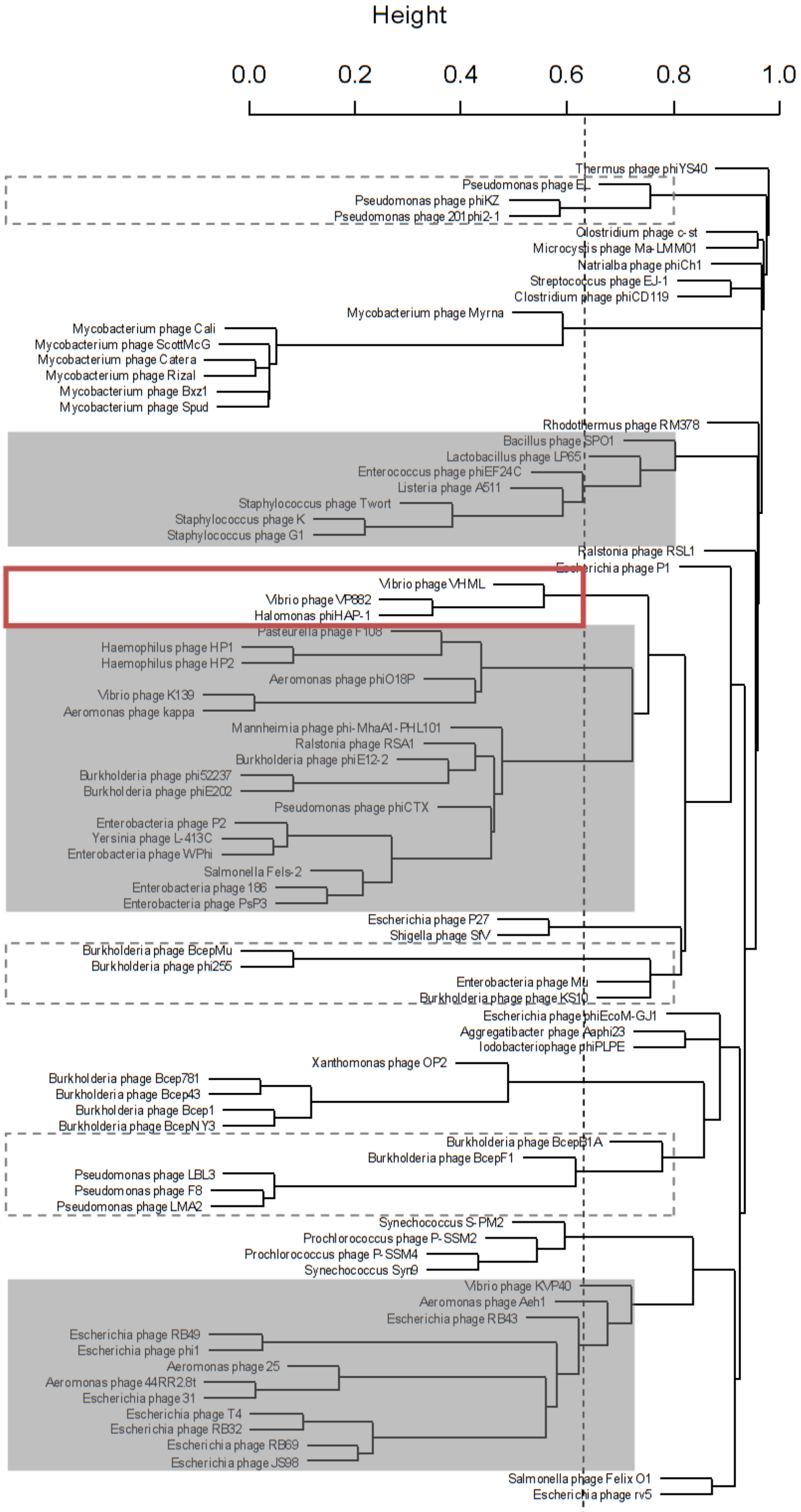

Figure 1: Hierarchical cluster dendrogram of the *Myoviridae*

The relative dissimilarity between the phage proteomes (between 0.0 and 1.0) forms the basis for the proposed groupings. The dotted lines reflects the cut-off value used for the establishement of genera, used consistently for all *Myoviridae* and the previously defined *Podoviridae* (Lavigne et al., 2008). Subfamily and tentative subfamily groupings are indicated in the grey and dotted boxes, respectively. The members of the genus *Hap1likevirus* are highlighted in the red box. Note the relationship with prophage VHML, which is clearly present, but does not produce stable, independent virions.

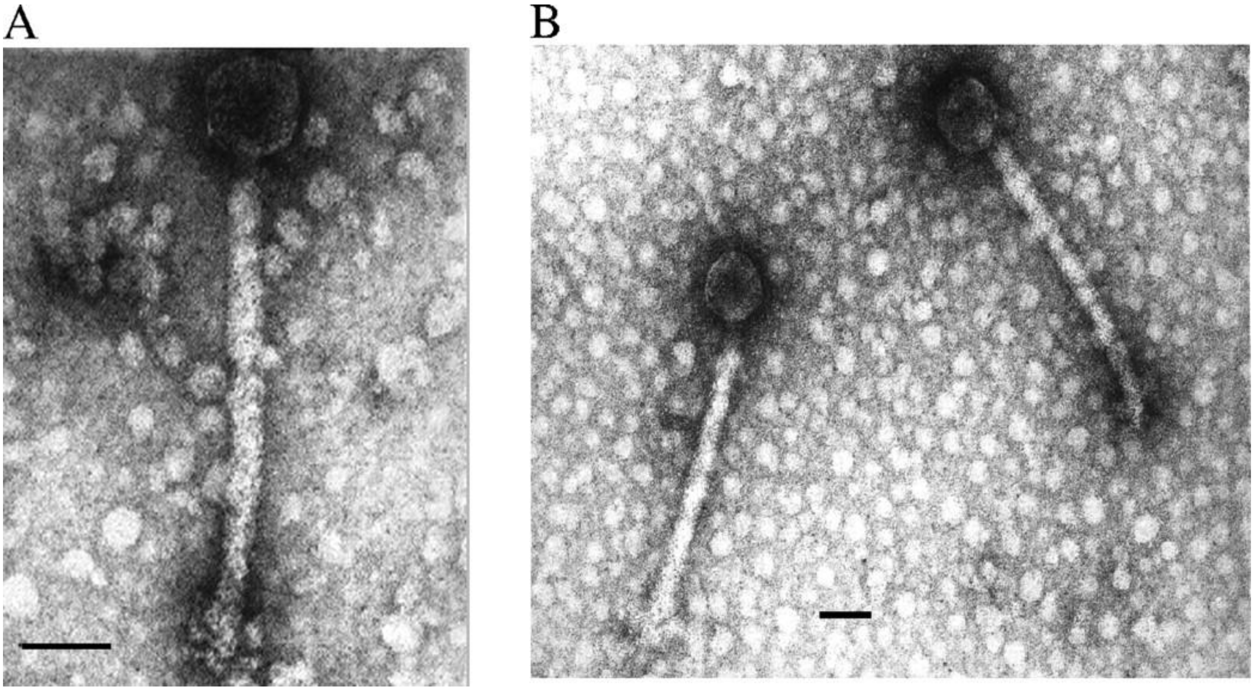

Figure 2. Transmission electron micrographs of ΦHAP-1 particles. Black scale bars represent 50 nm.

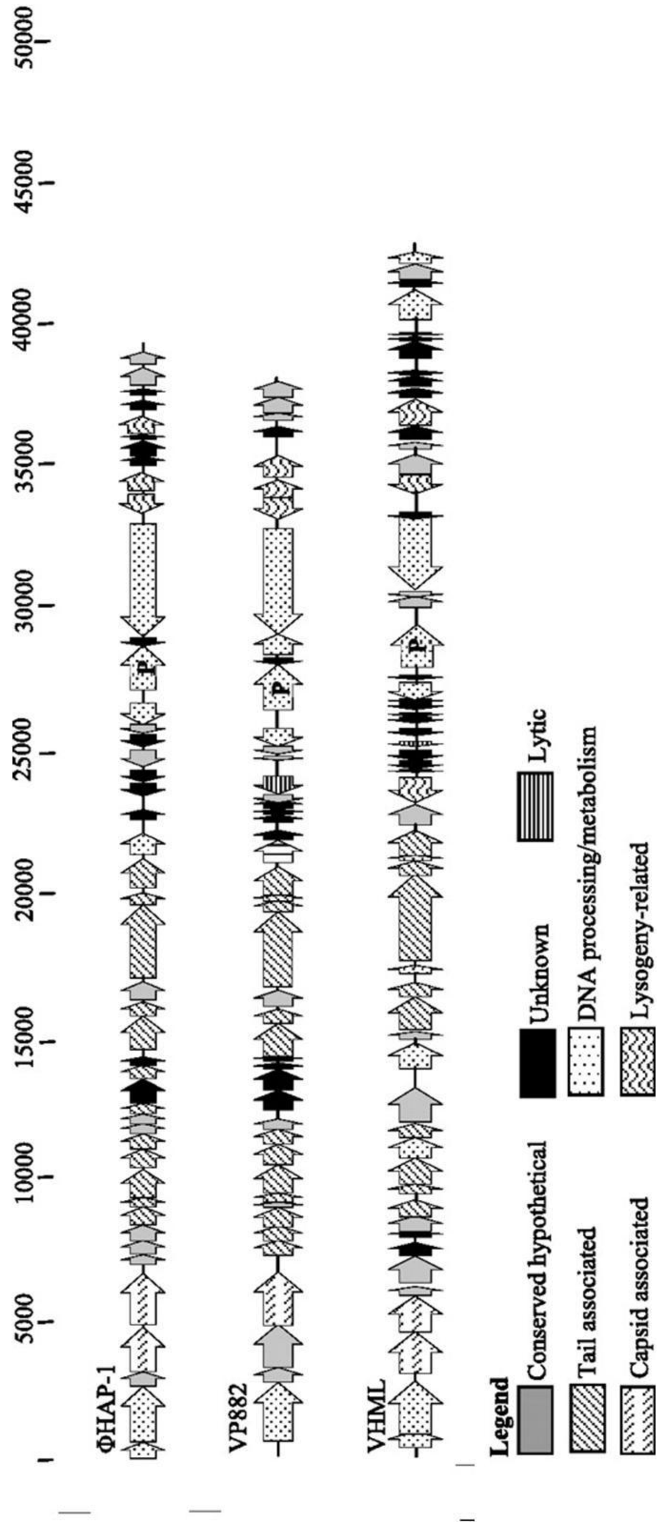

Figure 3: Genomic comparisons of completed phage genomes that contained a protelomerase gene. The location of the protelomerase gene in each genome is denoted by a "P." Patterns were assigned based on functional assignment of the ORFs as indicated in the key.