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:	***2012.003a-dB***	(to be completed by ICTV officers)

Short title: To create eight new species in a new genus, *D3112likevirus*, within the family *Siphoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (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:

Andrew M. Kropinski kropinsk@queensu.ca
Rob Lavigne rob.lavigne@biw.kuleuven.be
Evelien Adriaenssens evelien.adriaenssens@gmail.com

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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	

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

Date first submitted to ICTV:	2012
Date of this revision (if different to above):	July 2014

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2012.003aB***	(assigned by ICTV officers)

To create 8 new species within:

Genus:	***D3112likevirus* (new)**
Subfamily:	
Family:	***Siphoviridae***
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.

And name the new species: *D3112likevirus*	**GenBank sequence accession number(s) of reference isolate:**
Pseudomonas phage D3112	AY394005
Pseudomonas phage DMS3	DQ631426
Pseudomonas phage FHA0480	JN808773
Pseudomonas phage LPB1	HE584812
Pseudomonas phage MP22	DQ873690
Pseudomonas phage MP29	EU272036
Pseudomonas phage MP38	EU272037
Pseudomonas phage PA1phi	HM624080

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2012.003bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Siphoviridae***
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2012.003cB***	(assigned by ICTV officers)

To name the new genus: *D3112likevirus*

Assigning the type species and other species to a new genus

Code	***2012.003dB***	(assigned by ICTV officers)

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

Pseudomonas phage D3112

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

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

8

Reasons to justify the creation of a new genus:

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

Pseudomonas aeruginosa phage D3112 (AY394005) and its associated species are all temperate transposable viruses possessing 34.6-37.8 kb genomes sharing DNA identities over 75% and have a shared protein content of over 80% (Table 1) (1,2,3,5). Originally mistakenly considered to be members of the "Mu-like virus", along with *Pseudomonas* phage B3 genus whole genome proteomic analyses reveals that Mu and D3112 share only 11 homologs (20%), while B3 (4) and D3112 share 19 homologs (34.5%). These values are too low for these phages to be considered part of the same genus. In addition, Mu is a member of the *Myoviridae*, while the other phages are members of the *Siphoviridae*. Phylogenetic analysis of the large subunit terminase (Fig 3) also indicates that Mu and B3 are distant from the *D3112likevirus* group. A number of proteins unique to this group of phages has been discovered (Table 2).

Origin of the new genus name:

Named after the well characterized transposable *Pseudomonas* phage D3112

Reasons to justify the choice of type species:

First member of this proposed genus to be full sequenced

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.

We have chosen 95% DNA identity as species demarcation criterion.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Kim S, Rahman M, Kim J. Complete genome sequence of *Pseudomonas aeruginosa* lytic bacteriophage PA1O which resembles temperate bacteriophage D3112. J Virol. 2012.86(6):3400-1.

2. Zegans ME, Wagner JC, Cady KC, Murphy DM, Hammond JH, O'Toole GA. Interaction between bacteriophage DMS3 and host CRISPR region inhibits group behaviors of *Pseudomonas aeruginosa*. J Bacteriol. 2009. 191(1):210-9.

3. Heo YJ, Chung IY, Choi KB, Lau GW, Cho YH. Genome sequence comparison and superinfection between two related *Pseudomonas aeruginosa* phages, D3112 and MP22. Microbiology. 2007. 153(Pt 9):2885-95.

4. Braid MD, Silhavy JL, Kitts CL, Cano RJ, Howe MM. Complete genomic sequence of bacteriophage B3, a Mu-like phage of *Pseudomonas aeruginosa*. J Bacteriol. 2004. 186(19):6560-74.

5. Wang PW, Chu L, Guttman DS. Complete sequence and evolutionary genomic analysis of the *Pseudomonas aeruginosa* transposable bacteriophage D3112. J Bacteriol. 2004.186(2):400-10.

6. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147

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 but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

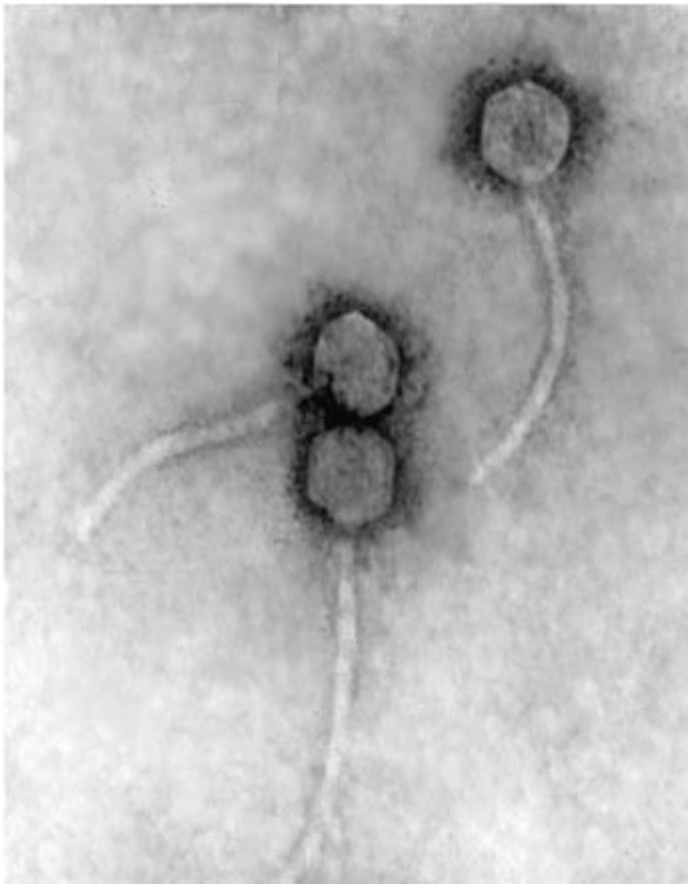

Fig. 1. Electron micrograph of phage D3112 (http://jb.asm.org/content/186/2/400/F1.expansion)

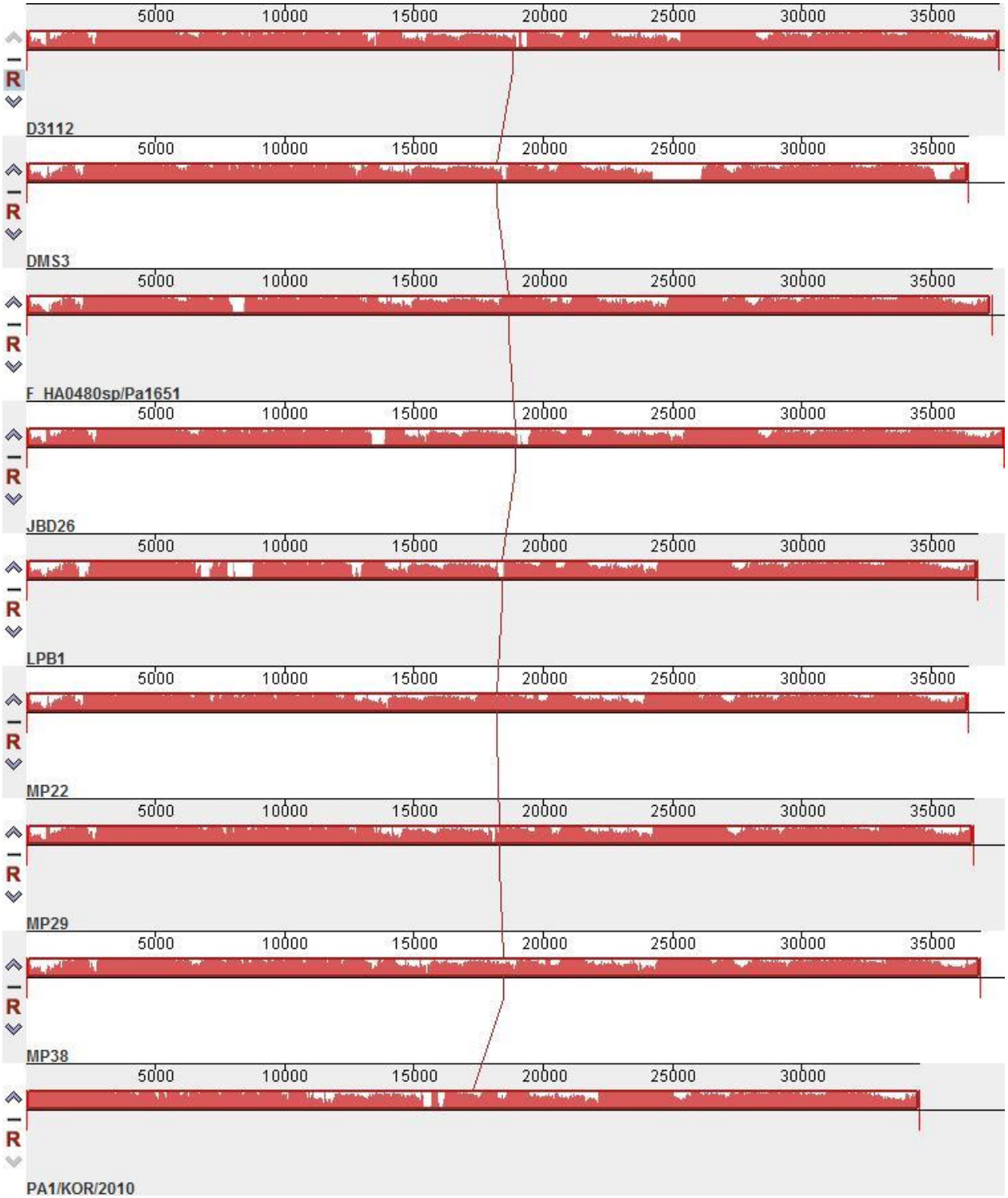

Fig 2. progressiveMauve (6) alignment of the phage genomes belonging to the proposed genus (Darling et al, 2010). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

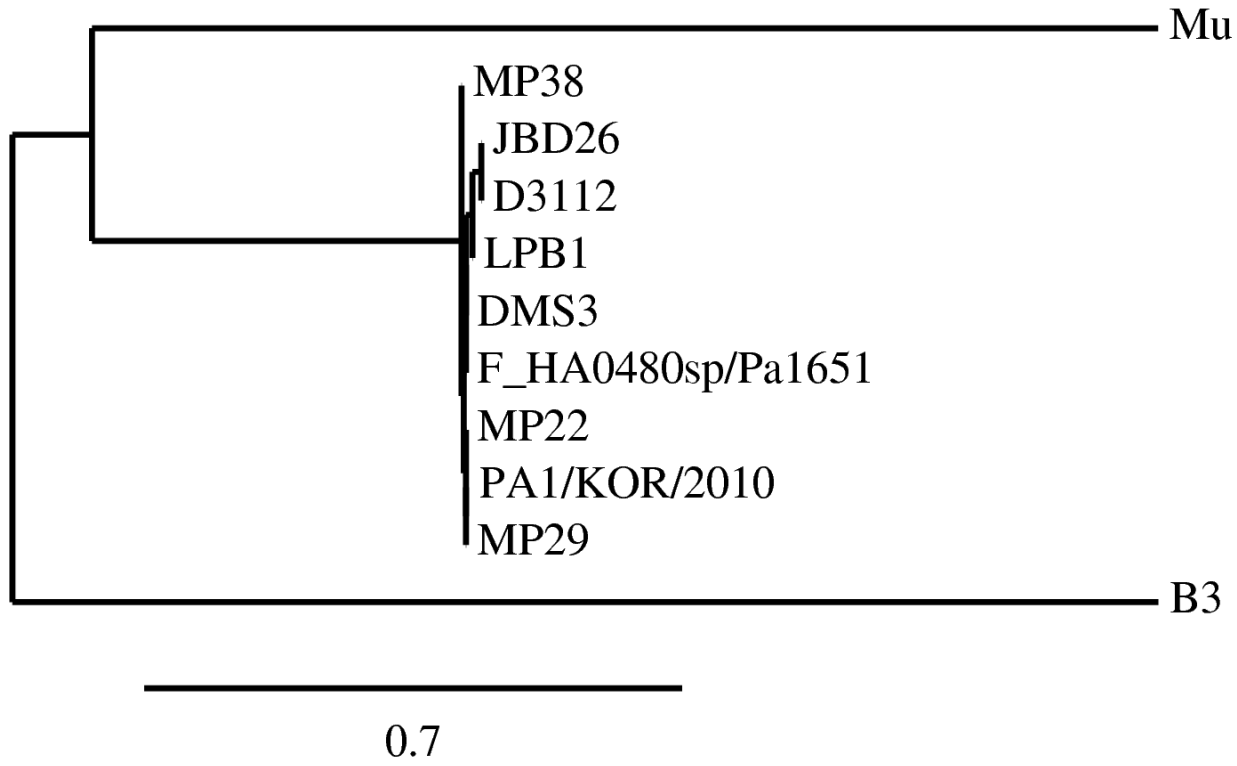

Fig. 3. “One Click” phylogenetic analysis at phylogeny.fr of D3112likevirus large subunit transposases together with similar proteins from Enterobacteria phage Mu and *Pseudomonas* phage B3.

Table 1. Phage genomes belonging to the proposed genus *D3112likevirus*. Phage JBD26 is considered as an isolate of D3112 with a DNA identity over 95%.

	Genome length (kb)	% shared proteins[a]	% DNA similarity[b]
Pseudomonas phage D3112	37.6	100.0	100.0
Pseudomonas phage JBD26 (JN811560)	37.8	90.9	95.4
Pseudomonas phage DMS3	36.4	85.5	81.2
Pseudomonas phage FHA0480	37.4	80.0	76.3
Pseudomonas phage LPB1	36.8	83.6	87.7
Pseudomonas phage MP22	36.4	83.6	75.1
Pseudomonas phage MP29	36.6	89.1	89.9
Pseudomonas phage MP38	36.9	87.3	80.2
Pseudomonas phage PA1phi	34.6	80.0	82.1

a) Calculated using CoreGenes 3.5
b) Calculated using EMBOSS Stretcher
c) The high degree of sequence identity to D3112 precludes its classification as a species