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:	***2013.040a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *F116likevirus* within the family *Podoviridae*
(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:

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

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

Date first submitted to ICTV:	June 2013
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	***2013.040aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***F116likevirus (new)***
Subfamily:	
Family:	***Podoviridae***
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:	**GenBank sequence accession number(s) of reference isolate:**
Pseudomonas phage F116 *Pseudomonas phage H66*	AY625898 KC262634

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus.

MODULE 3: NEW GENUS

creating a new genus

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

Code	**2013.040bB**	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Podoviridae***
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	**2013.040cB**	(assigned by ICTV officers)

To name the new genus: *F116likevirus*

Assigning the type species and other species to a new genus

Code	**2013.040dB**	(assigned by ICTV officers)

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

Pseudomonas phage F116	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:**

2

Reasons to justify the creation of a new genus:

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

F116 was isolated from a lysogenic a clinical strain of *Pseudomonas aeruginosa* by B.W. Holloway (1). It has been a frequently used generalized transducing phage for this genus (2). While initial EM studies classified it as a member of the *Siphoviridae*, further EM investigations determined that the appearance of long tails in most micrographs are artifacts resulting from the tail fibres being tightly packed together. F116 can digest alginate and penetrate *P. aeruginosa* exopolysaccharides killing established biofilms (3) where it binds to the sides of type IV pili of its host.

While it possesses an integrase it exists as a plasmid in the lysogenic state (4). Its genome sequence was determined by Byrne & Kropinski (5), while the nature of the termini had been previously shown to be circularly permuted and terminally redundant (6).

Uniquely this virus, and its relative H66, possess a protein containing PRK00378 (nucleoid-associated protein NdpA), pfam04245 (37-kD nucleoid-associated bacterial protein) & COG3081 (Nucleoid-associated protein) motifs.

EMBOSS Stretcher analysis shows that these phages share 82.3% DNA sequence identity; while CoreGenes 2.0 (7,8) reveals that they share 72.9% homologous proteins.

Previously recognized by ICTV as an unassigned member of the *Podoviridae*: 02.054.0.00.024.

Origin of the new genus name:

Pseudomonas phage *F116*

Reasons to justify the choice of type species:

The genus *F116likevirus* is named after the first isolated and sequenced phage of this group, *Pseudomonas* phage F116.

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 sequence identity as the criterion for demarcation of species in this new genus.

MODULE 9: APPENDIX: supporting material

additional material in support of this proposal

References:

1. Holloway,B.W., Egan, J.B., & Monk, M. 1960. Lysogeny in Pseudomonas aeruginosa. Aust. J. Exp. Biol. 38:321–330

2: Morrison WD, Miller RV, Sayler GS. 1978. Frequency of F116-mediated transduction of Pseudomonas aeruginosa in a freshwater environment. Appl Environ Microbiol. 36(5):724-30.

3. Hanlon,G.W., S.P. Denyer, C.J. Olliff, L.J. Ibrahim. 2001. Reduction in exopolysaccharide viscosity as an aid to bacteriophage penetration through Pseudomonas aeruginosa biofilms. Appl. Environ. Microbiol. 67:2746–2753

4. Miller, R.V., J.M. Pemberton, A.J. Clark. 1977. Prophage F116: evidence for extrachromosomal location in Pseudomonas aeruginosa strain PAO. J. Virol. 22: 844–847

5. Byrne M, Kropinski AM. 2005. The genome of the Pseudomonas aeruginosa generalized transducing bacteriophage F116. Gene 346: 187-94.

6. Caruso,M. & Shapiro, J.A. 1982. Interactions of Tn7 and temperate phage F116L of Pseudomonas aeruginosa. Mol. Gen. Genet. 188: 292–298

7. Mahadevan P, King JF, Seto D. 2009. Data mining pathogen genomes using GeneOrder and CoreGenes and CGUG: gene order, synteny and *in silico* proteomes. Int J Comput Biol Drug Des. 2(1):100-14.
8. Kropinski AM, Borodovsky M, Carver TJ, Cerdeño-Tárraga AM, Darling A, Lomsadze A, Mahadevan P, Stothard P, Seto D, Van Domselaar G, Wishart DS. 2009. *In silico* identification of genes in bacteriophage DNA. Methods Mol Biol. 502:57-89.

References:

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

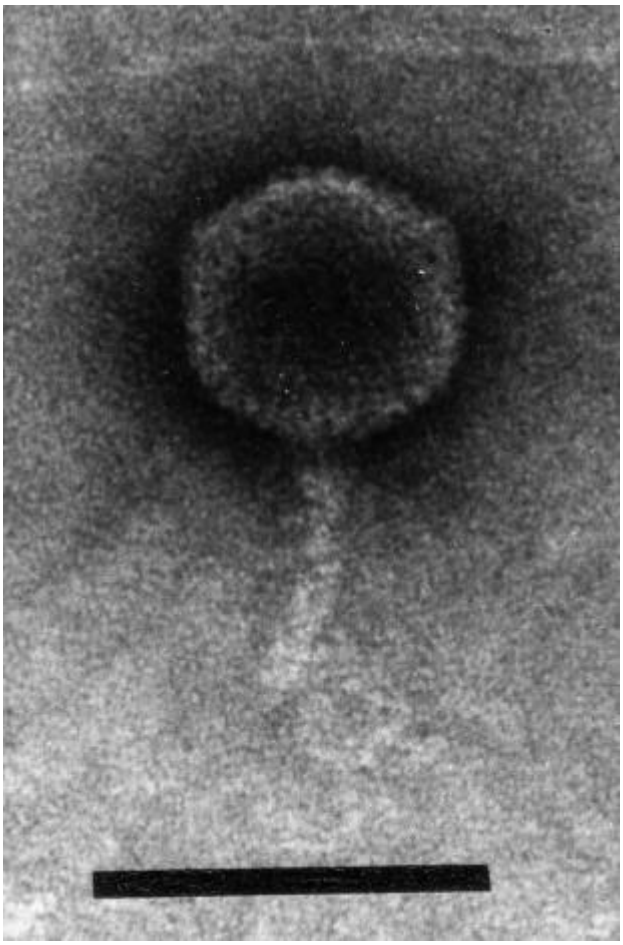

Figure 1. Electron micrograph of 2% (wt/vol) uranyl acetate-stained preparation of phage F116. Bar, 100 nm. While initial EM studies classified it as a member of the *Siphoviridae*, further EM investigations determined that the appearance of “tails” in most micrographs are artifacts resulting from the tail fibres being tightly packed together.

Table 1. Phage genomes

Phage	GenBank Accession No.	Genome size (bp)	Mol%G+C	Termini	% DNA sequence identity (a)	% Shared proteins (b)
Pseudomonas phage F116	AY625898	65,195	63.17	Terminally redundant & circularly permutted	100	100
Pseudomonas phage H66	KC262634	65,270	62.63	unknown	82.3	72.9

(a) EMBOSS Stretcher (relative to F116)
(b) CoreGenes 2.0 (7,8)

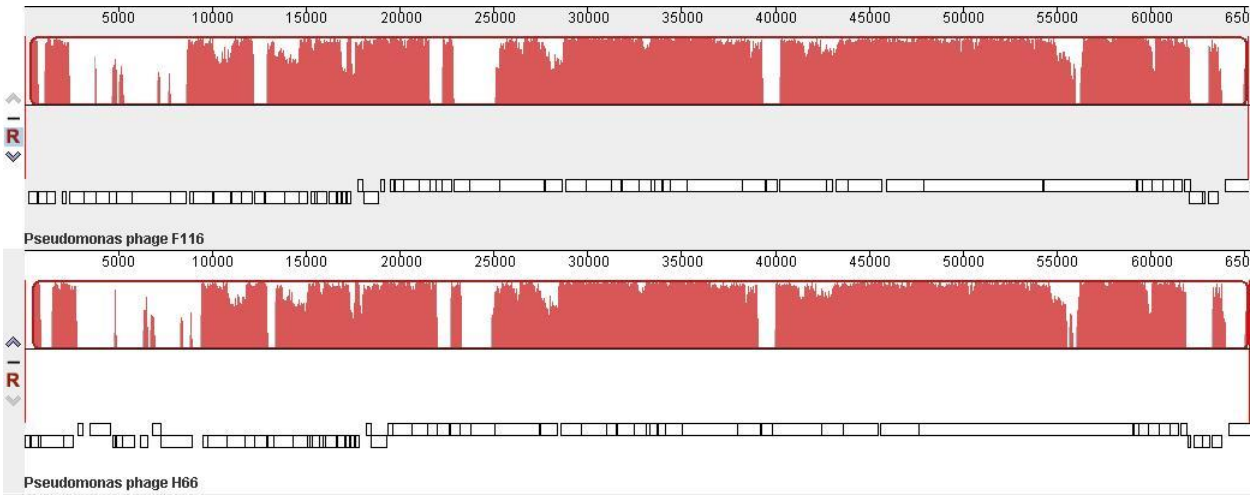

Figure 2. progressiveMauve alignment (9) of the genomes of the proposed genus Bcep22likevirus (full genome represented by its annotated ORFs in white blocks. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence 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.

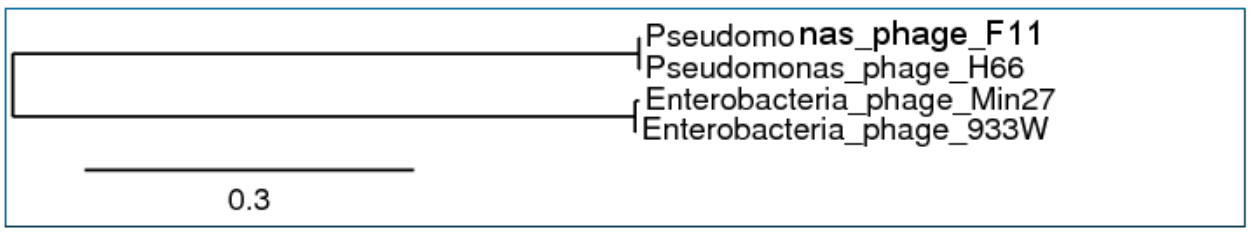

Figure 2. Phylogeny of capsid proteins from members of the *F116likevirus* and relatives constructed using “one click” at phylogeny.fr. Phages Min27 and 933W are also members of the *Podoviridae*.