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:	***2013.010a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *Phijlunalikevirus*, 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:

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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	***2013.010aB***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Phijlunalikevirus (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.

	GenBank sequence accession number(s) of reference isolate:
Lactobacillus phage phijl1	AY236756
Pediococcus phage clp1	JN051154
Lactobacillus phage ATCC8014	JX486087

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

BLASTN analyses reveal that these three phages are related and distinct from any other phage. We have chosen 95% DNA sequence identity as the criterion for demarcation of species.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.010bB***	(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	***2013.010cB***	(assigned by ICTV officers)

To name the new genus: *Phijlunalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.010dB***	(assigned by ICTV officers)

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

Lactobacillus phage phijl1

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:**

3

Reasons to justify the creation of a new genus:

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

BLASTN analyses reveal that these three phages are related and distinct from any other phages.
This genus, named after *Lactobacillus* phage phiJL-1, contains two other phages, *Lactobacillus* phage ATCC 8014-B1 and *Pediococcus* phage clP1 (1,2,3,4). The latter show a very high degree of DNA identity (92.7%) and shared protein content (96.5%), but are clearly distinct species based on their host range. Both phages share 63.0% of protein identity with phiJL-1. Morphology of the type phage is an isometric head of about 59 nm diameter and a non-contractile tail of 182 nm long and 11 nm wide (1). "The baseplate appears somewhat complex, with spikes or fibers" (4).

Origin of the new genus name:

Lactobacillus phage phiJL-1 The number '1' in the name was replaced with the word 'una' to avoid confusion with the letter 'l' following in the genus name, and the hyphen was removed.

Reasons to justify the choice of type species:

The original isolate of this group.

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, as well as a difference in host range. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the EMBOSS Stretcher algorithm.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1: Lu Z, Breidt F, Fleming HP, Altermann E & Klaenhammer TR (2003) Isolation and characterization of a Lactobacillus plantarum bacteriophage, phiJL-1, from a cucumber fermentation. International Journal of Food Microbiology 84: 225–235

2: Lu Z, Altermann E, Breidt F, Predki P, Fleming HP & Klaenhammer TR (2005) Sequence analysis of the Lactobacillus plantarum bacteriophage PhiJL-1. Gene 348: 45–54

3: Kelly,D., O'Sullivan,O., Mills,S., McAuliffe,O., Ross,R.P., Neve,H. and Coffey,A. 2012. Genome sequence of the phage clP1, which infects the beer spoilage bacterium *Pediococcus damnosus*. Gene 504 (1), 53-63.

4: Briggiler Marco,M., Garneau,J.E., Tremblay,D., Quiberoni,A. and Moineau,S. 2012. Characterization of Two Virulent Phages of *Lactobacillus plantarum*. Appl. Environ. Microbiol. 78 (24), 8719-8734.

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

6: Rohwer F, Edwards RE (2002) The Phage Proteomic Tree: a genome-based taxonomy for phage. Journal of Bacteriology 184: 4529-4535

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.

Table 1. Phage genomes

Phage	**GenBank Accession No.**	**Genome size (bp)**	**Mol%G+C tRNA**	**Termini/ packaging**	**% DNA sequence identity (a)**	**% Shared proteins (b)**
Lactobacillus phage phiJL-1	AY236756	36674	39.4	*pac*-type	100	100
Pediococcus phage clP1	JN051154	38013	47.6	ND**(c)**	47.0	63.0
Lactobacillus	JX486087	38002	47.6	*pac*-type	47.9	63.0

phage ATCC 8014-B1						

(a) EMBOSS Stretcher (relative to φJL-1)
(b) CoreGenes 2.0
(c) ND = not determined

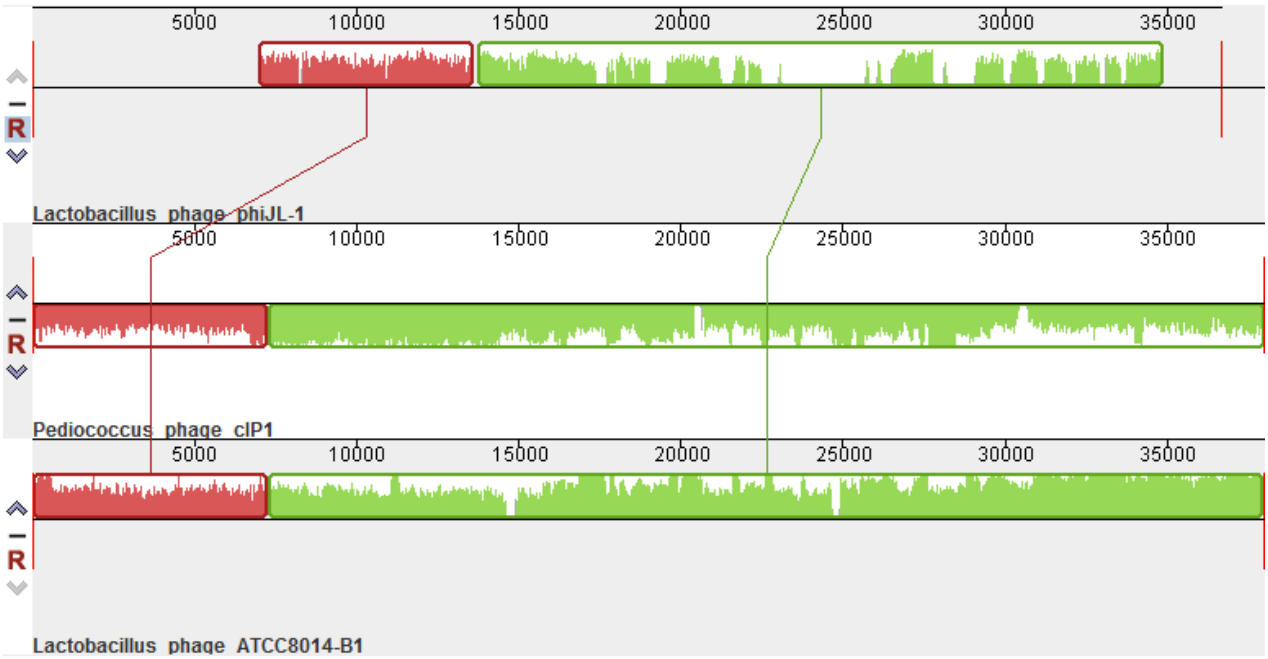

Figure 1. progressiveMauve alignment of the phage genomes (5). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

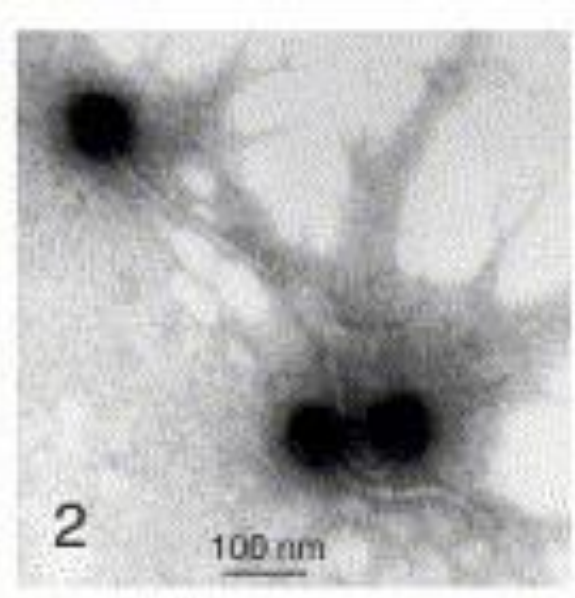

Figure 2. TEM image of *Lactobacillus* phage phiJL-1 (picture taken from 2).

Figure 3 Phage Proteomic Tree (6) of all the *Siphoviridae* phages in the NCBI database November 2012. Briefly, all predicted proteins sequences are compared with all others and a length-corrected protein distance matrix was calculated based on CLUSTALW alignment of sequences with a BLASTP e value < 0.001, with missing protein penalties of 10 and gap extension penalties of 0.20 (6). The tree was generated using FITCH. The proposed genus is highlighted. The scale bar represents protein distances of 2.0.

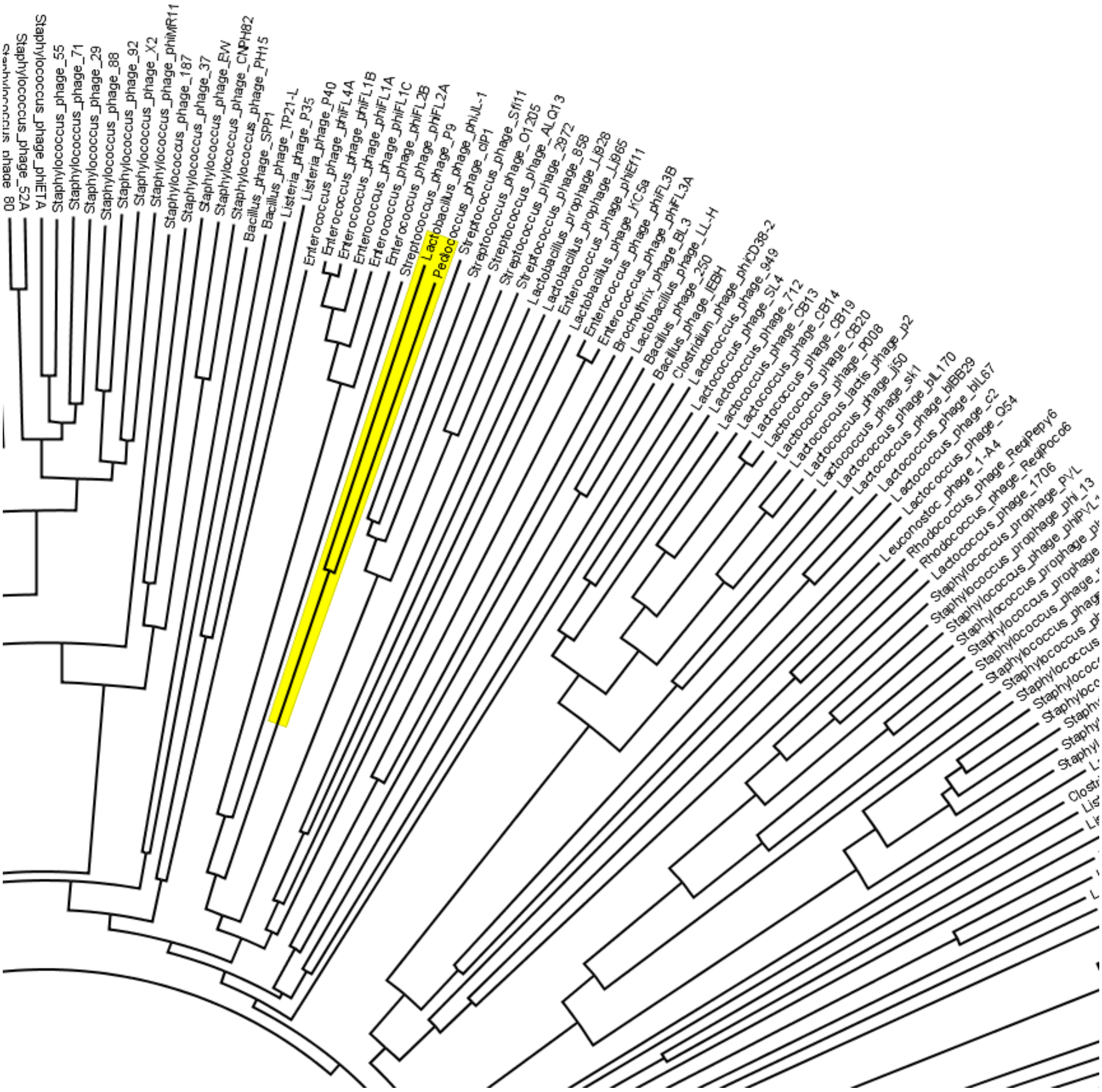

Figure 4: Fragment of the phylogenetic tree of Figure 3, zoomed in on the proposed genus. Phage ATCC 8014-b1 was not included in this tree, but since it shares 96.5% of its proteins with clP1, it would cluster in the same clade.