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:	***2013.028a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *Xp10likevirus*, 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	***2013.028aB***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Xp10likevirus* (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:
Xanthomonas phage Xp10	AY299121
Xanthomonas phage OP1	AP008979
Xanthomonas phage Xop411	DQ777876
Xanthomonas phage phil7	EU717894
Xanthomonas phage CP1	AB720063

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 *Xanthomonas oryzae* 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	***2013.028bB***	(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	***2013.028cB***	(assigned by ICTV officers)

To name the new genus: *Xp10likevirus*

Assigning the type species and other species to a new genus

Code	***2013.028dB***	(assigned by ICTV officers)

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

Xanthomonas phage Xp10

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:**

5

Reasons to justify the creation of a new genus:

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

The members of this genus of *Xanthomonas*-infecting phages, like the members of the *Autographivirinae,* encode a single-subunit DNA-dependent RNA polymerase. The type phage Xp10 possesses an isometric head of 53 nm diameter and a long, non-contractile, flexible tail (173 nm). "The distal end of the tail is poorly defined, and has discernible threads with unusual and possibly not well preserved spherical and triangular-shaped objects attached" (1). It contains multiple HNH endonucleases. Another unusual feature of Xp10 is that the major capsid subunit proteins are cross-linked creating oligomers.
A ClustalW analysis of the complete genomes of this genus with all other phages belonging to the *Siphoviridae* reveals that this genus is a clearly separate group (Figures 2 and 3).
We propose a shared protein content of at least 40% with the type phage, *Xanthomonas phage Xp10*. We performed a CoreGenes 3.5 analysis (5-7) with the five phages of this genus (Table 1).

Origin of the new genus name:

Xanthomonas oryzae phage Xp10

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.

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

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Yuzenkova J, Nechaev S, Berlin J, Rogulja D, Kuznedelov K, Inman R, Mushegian A, Severinov K. Genome of *Xanthomonas oryzae* bacteriophage Xp10: an odd T-odd phage. J Mol Biol. 2003 Jul 18;330(4):735-48. PubMed PMID: 12850143.

2. Inoue,Y., Matsuura,T., Ohara,T. and Azegami,K. 2006. Bacteriophage OP1, lytic for *Xanthomonas oryzae* pv. oryzae, changes its host range by duplication and deletion of the small domain in the deduced tail fiber gene. J. Gen. Plant Pathol. 72: 111-118

3. Lee CN, Hu RM, Chow TY, Lin JW, Chen HY, Tseng YH, Weng SF. Comparison of genomes of three *Xanthomonas oryzae* bacteriophages. BMC Genomics. 2007 Nov 29;8:442. PubMed PMID: 18045507; PubMed Central PMCID: PMC2248197.

4. Lee C-N, Lin J-W, Weng S-F & Tseng Y-H (2009) Genomic characterization of the intron-containing T7-like phage phiL7 of *Xanthomonas campestris*. Applied and Environmental Microbiology 75: 7828–7837

5. Mahadevan P, King JF, Seto (2009) Data mining pathogen genomes using GeneOrder and CoreGenes and CGUG: gene order, synteny and in silico proteomes. International Journal of Computational Biology and Drug Design 2: 100–114.
6. Mahadevan P, King JF, Seto D (2009) CGUG: in silico proteome and genome parsing tool for the determination of "core" and unique genes in the analysis of genomes up to ca. 1.9 Mb. BMC research notes 2: 168. doi:10.1186/1756-0500-2-168.
7. Zafar N, Mazumder R, Seto D (2002) CoreGenes: A computational tool for identifying and cataloging "core" genes in a set of small genomes. BMC Bioinformatics 3: 12. doi:10.1186/1471-2105-3-12.
8. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147
9. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35.

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 belonging to the proposed genus *Xp10likevirus*

Phage	GenBank Accession No.	Genome size (kbp)	Termini	Mol%G+C	% DNA sequence identity (a)	% Shared proteins (b)
Xanthomonas phage Xp10	AY299121	44.3	9-bp 3'-overhangs 5'-GGACAGTCT-3'	52.04	100	100
Xanthomonas phage OP1	AP008979	43.8	blunt	51.07	76.9	85.0
Xanthomonas phage Xop411	DQ777876	44.5	9-bp 3'-overhangs 5'-GGACAGTCT-3'	51.90	79.5	85.0
Xanthomonas phage Phil7	EU717894	44.6		55.6	51.1	58.3
Xanthomonas phage CP1	AB720063	43.9		53.3	51.0	61.7

(a) Calculated using EMBOSS Stretcher (relative to Xp10)
(b) Calculated using CoreGenes 3.5

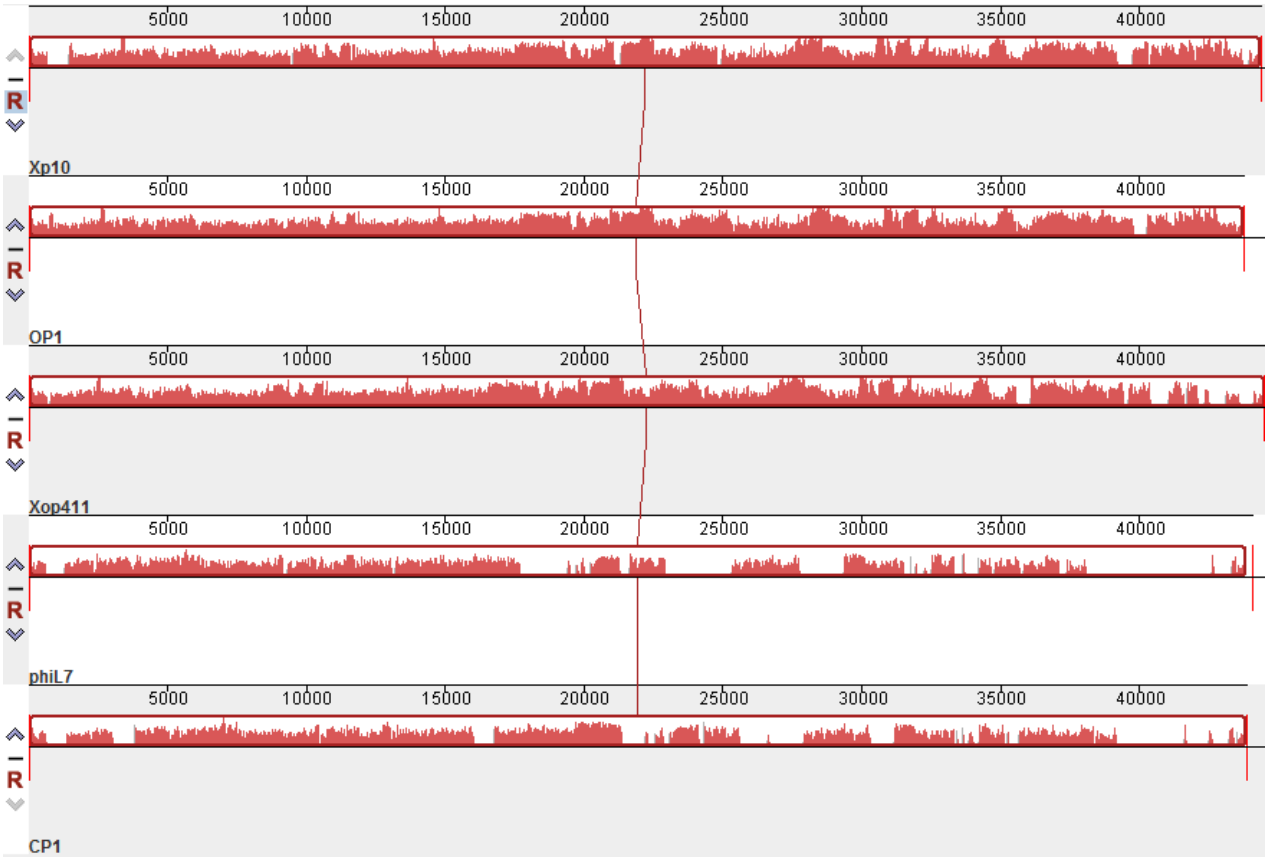

Figure 1. progressiveMauve alignment of the phage genomes belonging to the proposed genus (8). Colored blocks indicate the regions of 1 to 1 best alignment with

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.

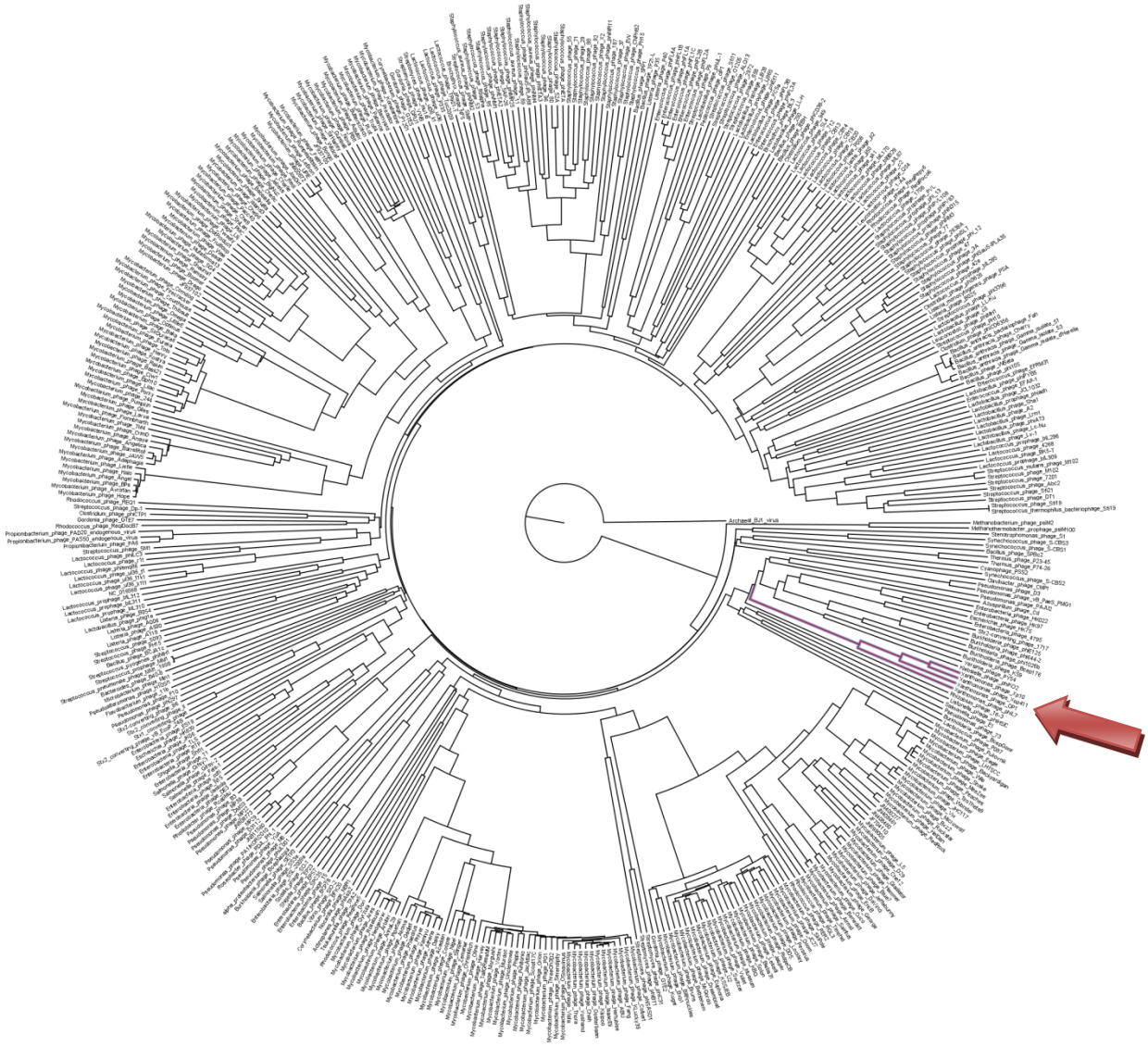

Figure 3: Phage Proteomic Tree (9) of all the *Siphoviridae* phages in the NCBI database November 2012. Briefly, all predicted proteins sequences are compared with all others and a length-corrected protein distance matrix was calculated based on CLUSTALW alignment of sequences with a BLASTP e value < 0.001, with missing protein penalties of 10 and gap extension penalties of 0.20 (9). The tree was generated using FITCH. The proposed genus is in red (red arrow). The scale bar represents protein distances of 2.0.

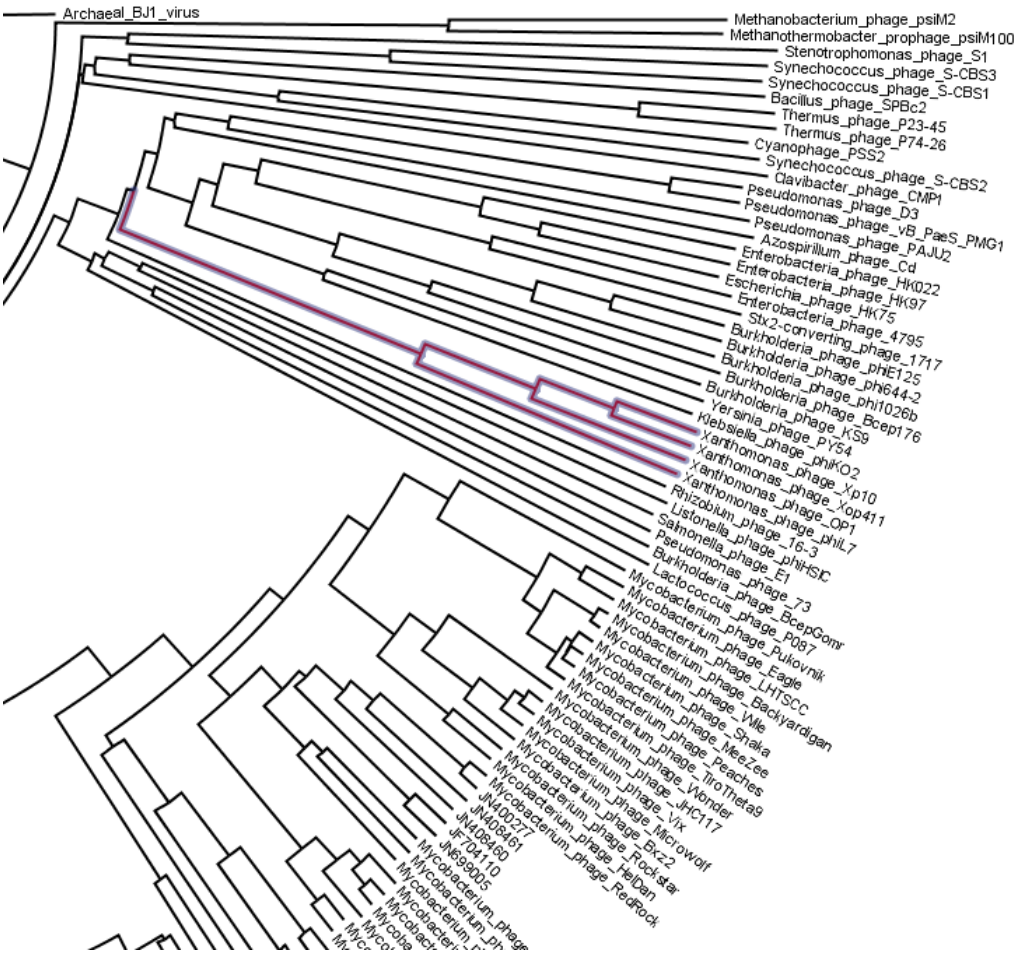

Figure 4: Fragment of the phylogenetic tree of Figure 3, zoomed in on the proposed genus.