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:	***2013.035a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *Skunalikevirus*, 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** ☒	

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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	***2013.035aB***	(assigned by ICTV officers)

To create 17 new species within:

Genus:	***Skunalikevirus* (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:
Lactococcus phage SK1	AF011378
Lactococcus phage bil170	AF009630
Lactococcus phage jj50	DQ227764
Lactococcus phage 712	DQ227763
Lactococcus phage P008	DQ054536
Lactococcus phage Sl4	FJ848881
Lactococcus phage CB13	FJ848882
Lactococcus phage CB14	FJ848883
Lactococcus phage CB19	FJ848884
Lactococcus phage CB20	FJ848885
Lactococcus phage Bibb29	EU221285
Lactococcus phage P2	GQ979703
Lactococcus phage Ascc273	JQ740788
Lactococcus phage Ascc191	JQ740813
Lactococcus phage Ascc281	JQ740787
Lactococcus phage Ascc532	JQ740789
Lactococcus phage Ascc465	JQ740804

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 *Lactococcus* 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	***2013.035bB***	(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	***2013.035cB***	(assigned by ICTV officers)

To name the new genus: *Skunalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.035dB***	(assigned by ICTV officers)

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

Lactococcus phage SK1

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:**

17

Reasons to justify the creation of a new genus:

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

This genus is derived from the 936-like phage group of dairy phages infecting *Lactococcus lactis*, a grouping currently without taxonomic status. It is named after *Lactococcus* phage sk1, the type species and first fully sequenced isolate of the group [1], since unfortunately phage 936 has not been sequenced in full. This genus also comprises a large group of Australian dairy phages [2] which have been grouped into five species, with isolates belonging to the same species sharing over 95% DNA identity.

Origin of the new genus name:

Lactococcus phage SK1

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. 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. Chandry PS, Moore SC, Boyce JD, Davidson BE, Hillier AJ (1997) Analysis of the DNA sequence, gene expression, origin of replication and modular structure of the *Lactococcus lactis* lytic bacteriophage sk1. Mol Microbiol 26: 49–64. doi:10.1046/j.1365-2958.1997.5491926.x.

2. Castro-Nallar E, Chen H, Gladman S, Moore SC, Seemann T, et al. (2012) Population genomics and phylogeography of an Australian dairy factory derived lytic bacteriophage. Genome Biol Evol 4: 382–393. doi:10.1093/gbe/evs017.

3. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147. doi:10.1371/journal.pone.0011147.

4. Rohwer F, Edwards R (2002) The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol 184: 4529–4535. doi:10.1128/JB.184.16.4529.

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.

Phage	GenBank Accession No.	Genome size (bp)	% DNA sequence identity (a)	% Shared proteins (b)
Lactococcus phage Sk1	AF011378	28,451	100	100
Lactococcus phage bIL170	AF009630	31,754	70.6	83.3
Lactococcus phage jj50	DQ227764	27,453	93.9	88.9
Lactococcus phage 712	DQ227763	30,510	75.9	79.6
Lactococcus phage P008	DQ054536	28,538	75.3	77.8
Lactococcus phage Sl4	FJ848881	28,144	74.1	75.9
Lactococcus phage CB13	FJ848882	32,182	67.1	79.6
Lactococcus phage CB14	FJ848883	29,459	73.2	79.6
Lactococcus phage CB19	FJ848884	28,643	71.6	75.9
Lactococcus phage CB20	FJ848885	28,625	71.7	75.9

Lactococcus phage Bibb29	EU221285	29,305	71.7	79.6
Lactococcus phage P2	GQ979703	27,595	94.5	87.0
Lactococcus phage Ascc273	JQ740788	32,582	70.6	75.9
Lactococcus phage Ascc532	JQ740813	32,384	69.4	79.6
Lactococcus phage Ascc191	JQ740787	32,414	67.9	79.6
Lactococcus phage Ascc281	JQ740789	32,023	71.2	85.2
Lactococcus phage Ascc465	JQ740804	31,772	70.4	79.6

(a) Calculated using EMBOSS Stretcher (relative to SK1)
(b) Calculated CoreGenes 2.0

Table 2. Related phages

Species	**Similar phage**
Lactococcus phage Ascc273	*Lactococcus* phages ASCC287, ASCC324, ASCC337, ASCC368, ASCC397, ASCC476, ASCC502, ASCC527, ASCC544
Lactococcus phage Ascc532	*Lactococcus* phages ASCC284, ASCC310
Lactococcus phage Ascc281	*Lactococcus* phage ASCC358
Lactococcus phage Ascc465	ASCC473, ASCC489

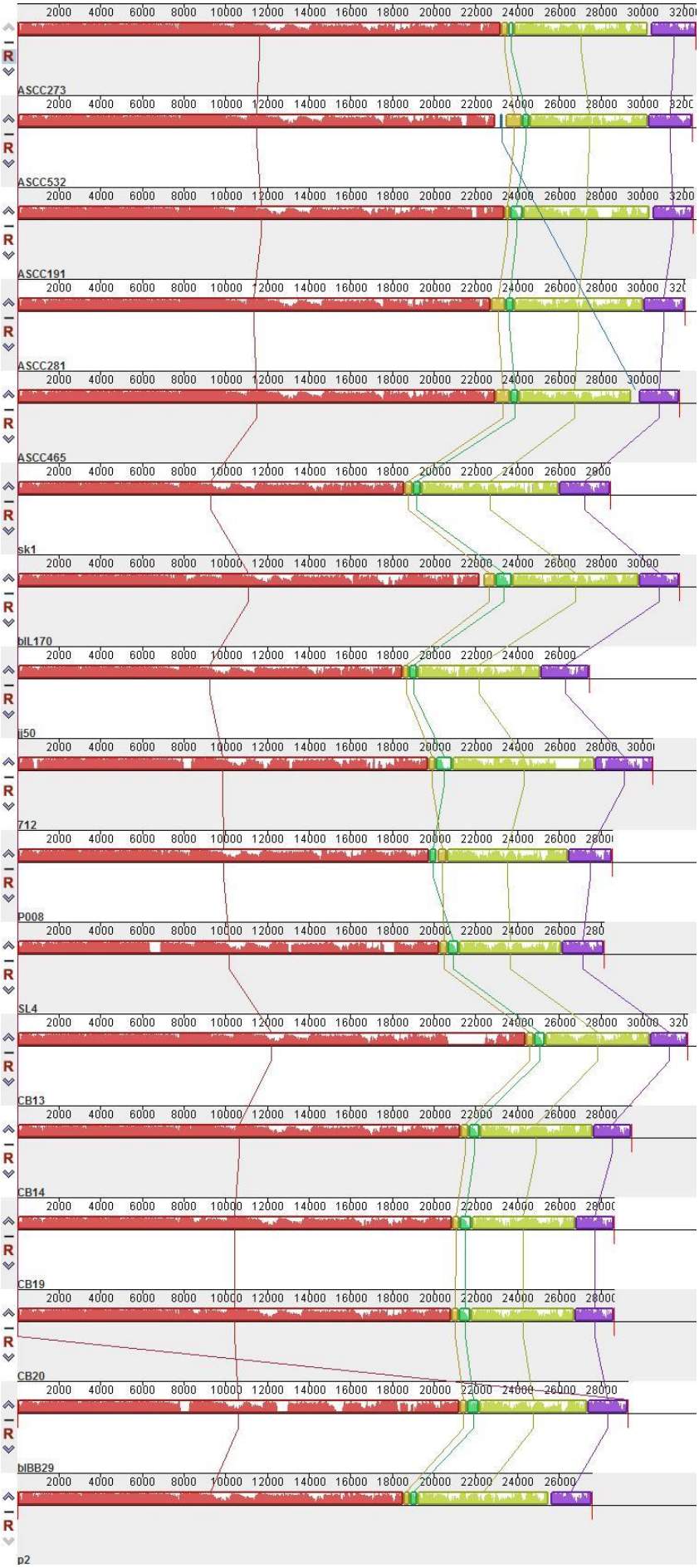
ASCC273
ASCC532
ASCC191
ASCC281
ASCC465
sk1
bIL170
ji50
712
P008
SL4
CB13
CB14
CB19
CB20
bIBB29
p2

Figure 1. progressiveMauve alignment of the phage genomes belonging to the proposed genus [3]. 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: Phage Proteomic Tree (Rohwer & Edwards, 2002) 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 [4]. The

tree was generated using FITCH. The proposed genus is in red. The scale bar represents protein distances of 2.0.

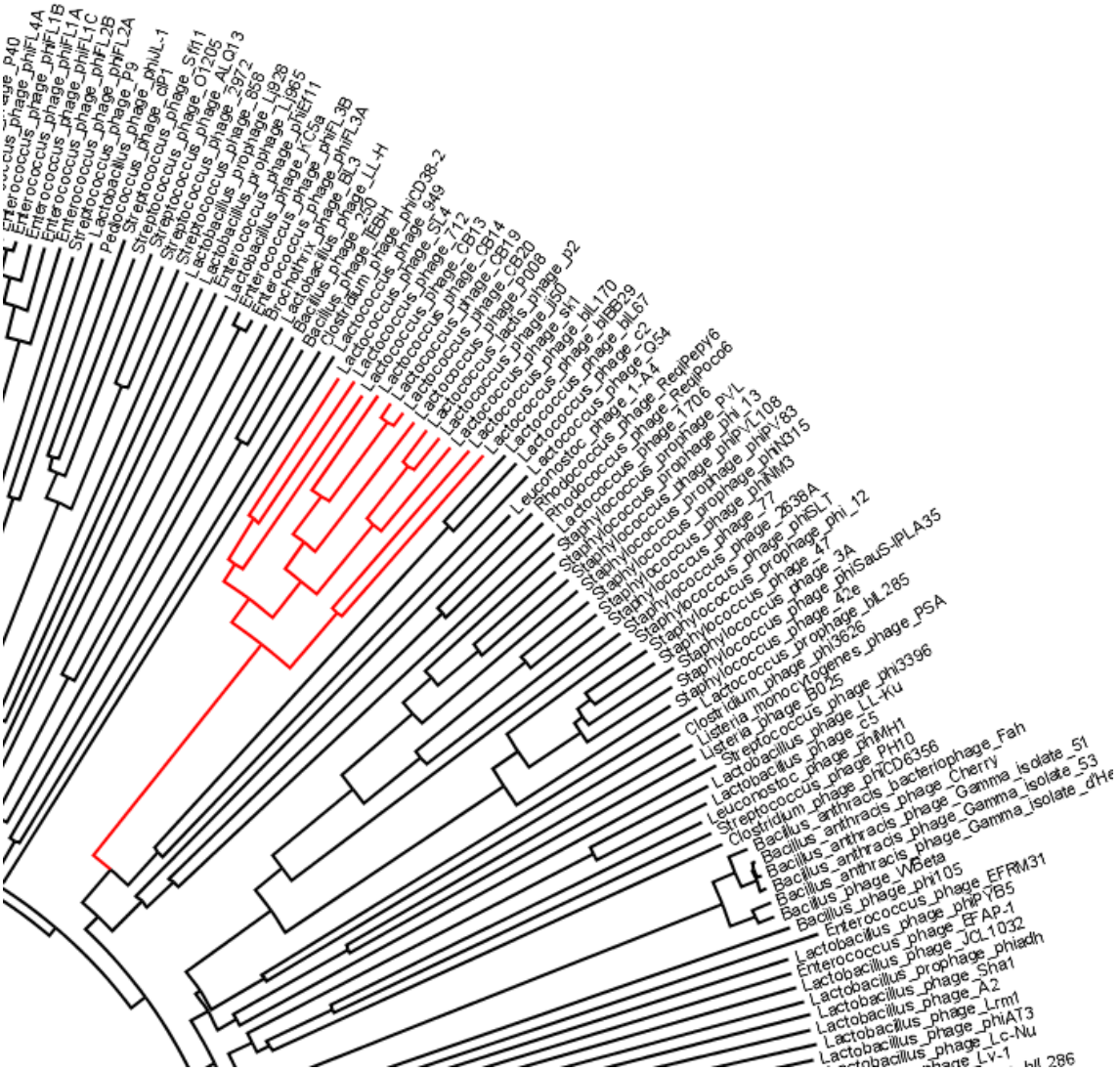

Figure 3: Fragment of the phylogenetic tree of Figure 2, zoomed in on the proposed genus. The ASCC phages were not included in this tree, but the mauve alignment of Figure 1 shows that they are sufficiently similar to be included in this genus.