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:	***2013.026a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *Sap6likevirus*, 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	***2013.026aB***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Sap6likevirus* (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:
Enterococcus phage SAP6	JF731128
Enterococcus phage BC611	AB712291
Enterococcus phage IMEEF1	KF192053
Streptococcus phage SPQS1	HE962497
Enterococcus phage VD13	KJ094032

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 five enterobacterial 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	***2013.026bB***	(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	***2013.026cB***	(assigned by ICTV officers)

To name the new genus: *Sap6likevirus*

Assigning the type species and other species to a new genus

Code	***2013.026dB***	(assigned by ICTV officers)

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

Enterococcus phage SAP6

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

BLASTN analyses reveal that these *Enterococcus/Streptococcus* phages are related and distinct from any other phage. These are all lytic viruses with genomes of 54-59 kb (ca. 40 mol%G+C) (1-4).

Origin of the new genus name:

Enterococcus phage SAP6

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: Lee,Y.D. and Park,J.H. 2012. Complete Genome Sequence of Enterococcal Bacteriophage SAP6. J. Virol. 86 (9), 5

2: Horiuchi,T., Sakka,M., Hayashi,A., Shimada,T., Kimura,T. and Sakka,K. 2012. Complete Genome Sequence of Bacteriophage BC-611 Specifically Infecting Enterococcus faecalis Strain NP-10011. J. Virol. 86 (17), 9538-9539.

3: Denes T, Vongkamjan K, Ackermann HW, Moreno Switt AI, Wiedmann M, den Bakker HC. Comparative genomic and morphological analysis of *Listeria* phages isolated from farm environments. Appl Environ Microbiol. 2014 May 16. pii: AEM.00720-14.

4: Zhang W, Mi Z, Yin X, Fan H, An X, Zhang Z, Chen J, Tong Y. Characterization of *Enterococcus faecalis* phage IME-EF1 and its endolysin. PLoS One. 2013 Nov 13;8(11):e80435.

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

6: Bao Y., Kapustin Y. & Tatusova T. (2008). Virus Classification by Pairwise Sequence Comparison (PASC). Encyclopedia of Virology, 5 vols. (B.W.J. Mahy and M.H.V. Van Regenmortel, Editors). Oxford: Elsevier. Vol. 5, 342-348.

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 *Sap6likevirus*.

Phage	GenBank Accession No.	Genome size (bp)	Mol%G+C tRNA	% DNA relatedness (a)	% Shared proteins (b)
Enterococcus phage SAP6	JF731128	58,619	40.00	100%	100%
Enterococcus	AB712291	53,996	40.45	81%	84.1

phage BC-611					
Enterococcus phage IME-EF1	KF192053	57,081	40.04	86%	95.4
Streptococcus phage SP-QS1	HE962497	58,305	39.87	79%	93.2
Enterococcus phage VD-13	KJ094032	55,113	40.01	74%	90.9

(a) DNA-DNA relatedness was determined by a modification of PASC (PAirwise Sequence Comparison) which is a well-accepted nucleotide comparator (6) used in taxonomy. The products of the % coverage and % identity were multiplied to get the % DNA relatedness reported here.

(b) Calculated using CoreGenes 3.0

Figure 1. progressiveMauve alignment of the phage genomes belonging to the proposed genus (full genome represented by its annotated ORFs in white blocks) (6). 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.

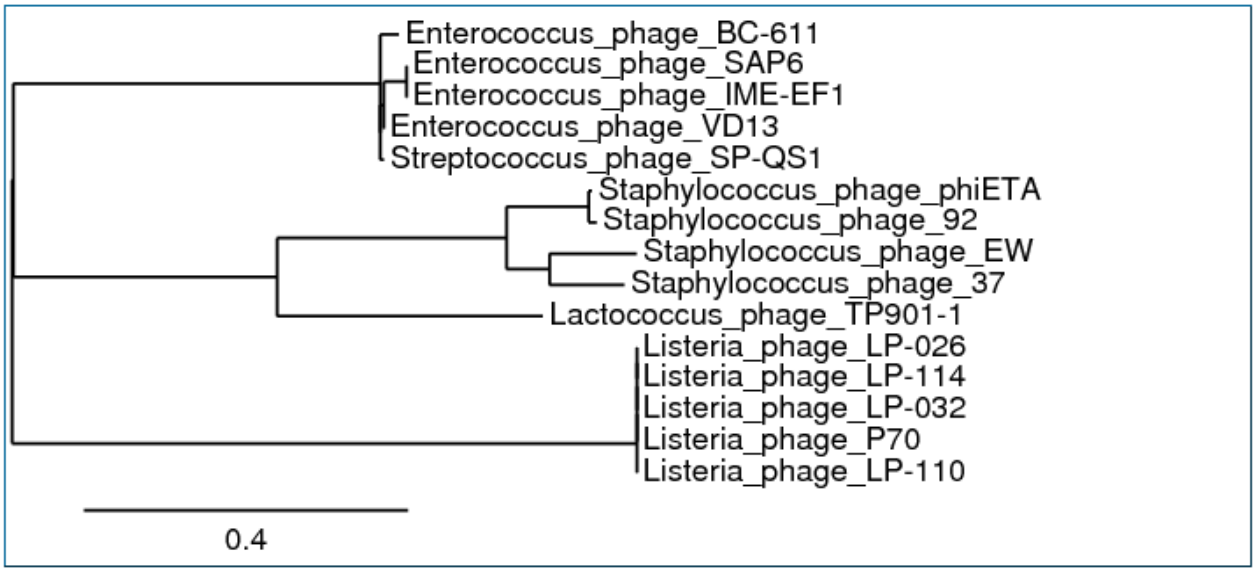

Figure 2. Phylogenetic tree of major capsid protein produced using “one click” phylogeny.fr.