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:	***2013.034a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *Sfi1unalikevirus*, 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	***2013.034aB***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Sfi1unalikevirus* (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:
Streptococcus phage Sfi11	AF158600
Streptococcus phage O1205	U88974
Streptococcus phage 2972	AY699705
Streptococcus phage Alq132	FJ226752
Streptococcus phage 858	EF529515

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 *Streptococcus* 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	***2013.034bB***	(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	***2013.034cB***	(assigned by ICTV officers)

To name the new genus: *Sfi1unalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.034dB***	(assigned by ICTV officers)

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

Streptococcus phage Sfi11

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

Phages belonging to this genus have small, isometric heads, and long non-contractile tails. Phages share a comparable genome size and GC content, and a common packaging mechanism with *pac* sites [1–6] (Table 1).
We propose 40% shared proteins with the type phage for new phages to be included in the new genus, as calculated with CoreGenes [7–9].

Origin of the new genus name:

Streptococcus phage sf11

Reasons to justify the choice of type species:

One of the first isolates of this group, a well-characterized phage.

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, with the two most related phages ALQ13.2 and 2972 sharing 71.5% DNA identity.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Stanley E, Fitzgerald GF, Le Marrec C, Fayard B, van Sinderen D (1997) Sequence analysis and characterization of phi O1205, a temperate bacteriophage infecting *Streptococcus thermophilus* CNRZ1205. Microbiology 143: 3417–3429.

2. Guglielmotti DM, Deveau H, Binetti AG, Reinheimer JA, Moineau S, et al. (2009) Genome analysis of two virulent *Streptococcus thermophilus* phages isolated in Argentina. Int J Food Microbiol 136: 101–109. doi:10.1016/j.ijfoodmicro.2009.09.005.

3. Deveau H, Barrangou R, Garneau JE, Labonté J, Fremaux C, et al. (2008) Phage response to CRISPR-encoded resistance in *Streptococcus thermophilus*. J Bacteriol 190: 1390–1400. doi:10.1128/JB.01412-07.

4. Proux C, van Sinderen D, Suarez J, Garcia P, Ladero V, et al. (2002) The dilemma of phage taxonomy illustrated by comparative genomics of Sfi21-like *Siphoviridae* in lactic acid bacteria. J Bacteriol 184: 6026–6036. doi:10.1128/JB.184.21.6026-6036.2002.

5. Lucchini S, Desiere F, Brüssow H (1999) Comparative genomics of *Streptococcus thermophilus* phage species supports a modular evolution theory. J Virol 73: 8647–8656.

6. Lévesque C, Duplessis M, Labonté J, Labrie S, Fremaux C, et al. (2005) Genomic organization and molecular analysis of virulent bacteriophage 2972 infecting an exopolysaccharide-producing *Streptococcus thermophilus* strain. Appl Environ Microbiol 71: 4057–4068. doi:10.1128/AEM.71.7.4057-4068.2005.

7. 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 Res Notes 2: 168. doi:10.1186/1756-0500-2-168.

8. Mahadevan P, King JF, Seto (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: 100–114.

9. 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.

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

References:

doi:10.1371/journal.pone.0011147.

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	Accession No.	Size (bp)	Mol%G+C	Packaging – termini	% DNA sequence relatedness (a)	% Protein relatedness (b)
Sfi11	AF158600	39807	39	*pac* site	100	100
O1205	U88974	43075	38	*pac* site	ND	92.2
2972	AY699705	34704	40	*pac* site	67.6	70.6
Alq13.2	FJ226752	35525	39	*pac* site	66.0	66.7
858	EF529515	35543	40	*pac* site	65.8	74.5

(a) EMBOSS Stretcher values relative to the type phage Sfi11 could not be calculated for O1205 due to different origins of the sequences in GenBank

(b) CoreGenes 3.5 (relative to Sfi11)

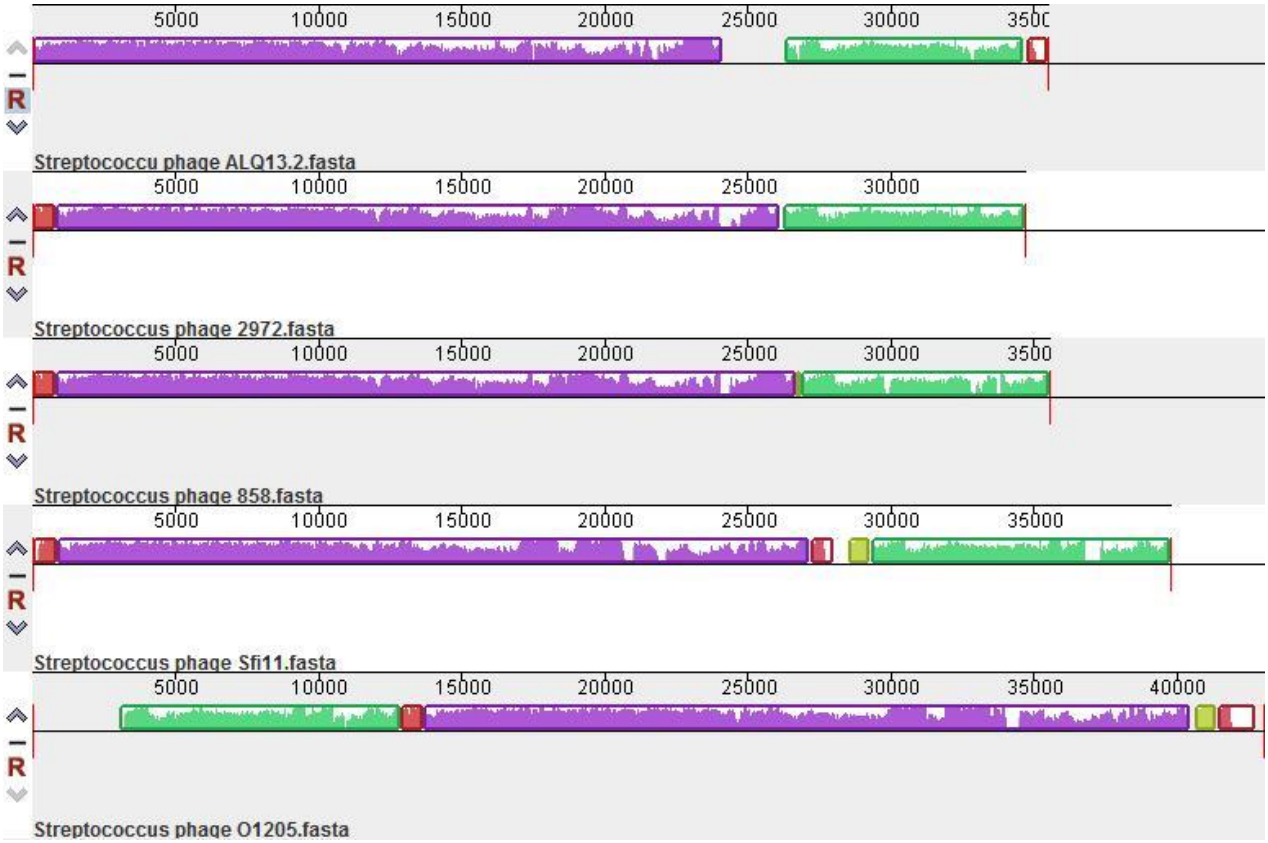

Figure 1. progressiveMauve alignment of the genomes of the these *Streptococcus* phages indicates that they are very similar [10]. The sequence of phage O1205 was deposited in GenBank with a different starting point from the others. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement 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.

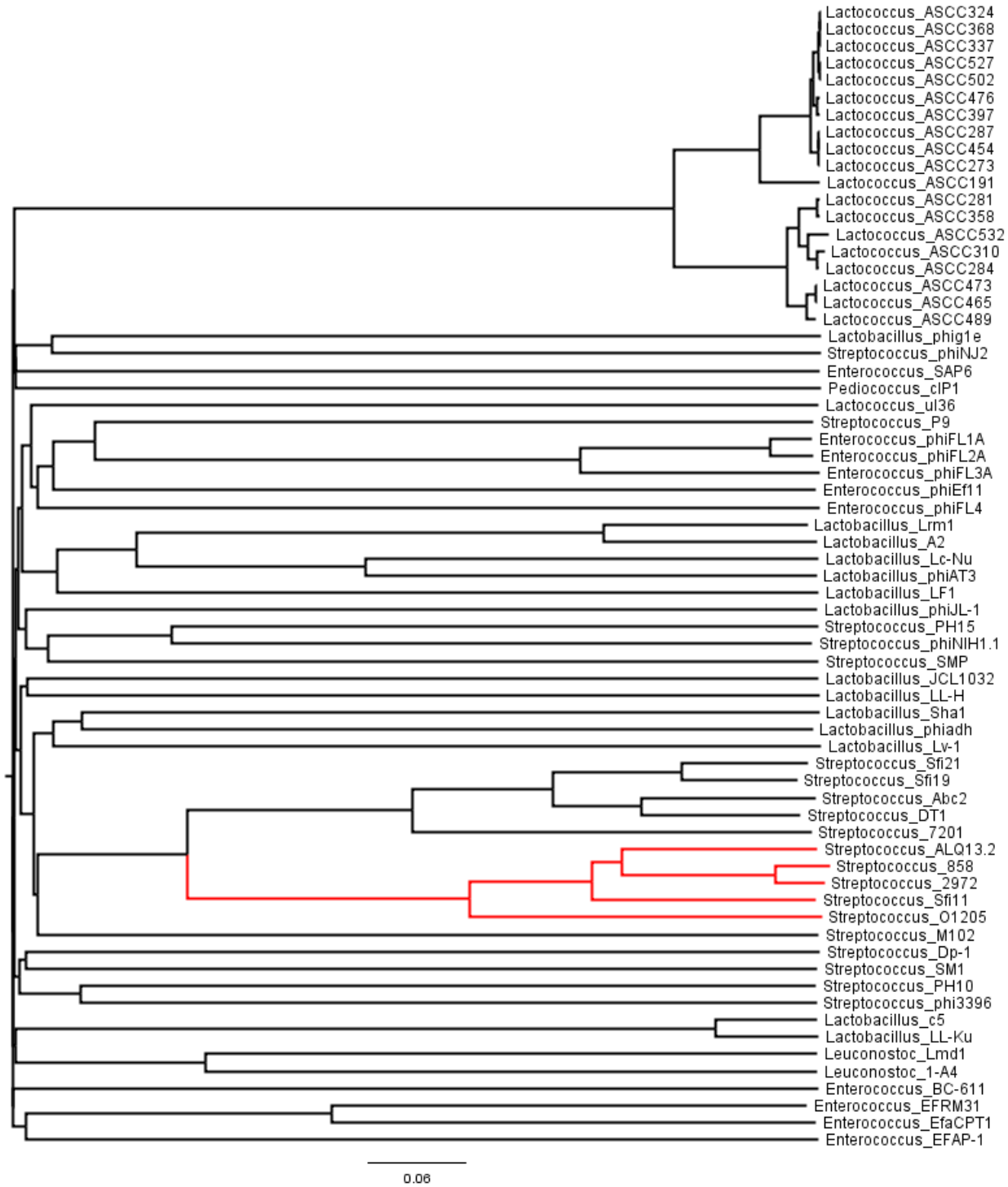

Figure 2: Whole genome phylogenetic tree of selected low GC content *Siphoviridae* phages in the NCBI database in November 2012. Genome sequences were aligned and the tree (NJ) was created with ClustalW 2.0 and visualized with FigTree. The newly proposed genus is colored in red.