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:	***2016.009a-fB***	(to be completed by ICTV officers)

Short title: To create one (1) new genus, *Cp1virus*, including one (1) new species in the family *Podoviridae*.
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)					
	1 ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☒	**9** ☐	**10** ☒

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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 Bacterial and Archaeal Viruses Subcommittee

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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	***2016.009aB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Cp1virus* (new)**
Subfamily:	***Picovirinae***
Family:	***Podoviridae***
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Streptococcus virus Cp7	Streptococcus phage Cp-7	LK392619

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.009bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Picovirinae***
Family:	***Podoviridae***
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	***2016.009cB***	(assigned by ICTV officers)

To name the new genus: *Cp1virus*

Assigning the type species and other species to a new genus

Code	***2016.009dB***	(assigned by ICTV officers)

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

Streptococcus virus Cp1

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:**

2

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 representative isolate of this genus, Streptococcus phage Cp-1, is not the same isolate as isolate Cp-1 from the Félix d'Hérelle Reference Center for Bacterial Viruses, which was re-named SOCP after genome variations were found. These isolates share 99% of their DNA sequence and belong subsequently to the same species, *Streptococcus virus Cp1*.

Phage SOCP belongs to the *Podoviridae* family and has a hexagonal capsid of 65.8 nm (top to bottom) and 42.1 nm in width (Fig. 1). This phage has a short non-contractile tail, 19.3 nm in length and 7.5 nm in width [4]. Phage CP-1-related viruses (Cp-7, SOCP) infect both *Streptococcus pneumoniae* and *S. mitis*. The genomes of these viruses have imperfect inverted terminal repeats of 347 bp, and carry at the 5'-end a covalently bound replication protein.

BLASTN, CoreGenes (Table 1) [2], progressiveMauve alignment (Fig. 2) [1] and phylogenetic analyses (Fig. 3) [3] all indicate that the proposed genus, *Cp1virus*, is cohesive and distinct from other genera. On average the genomes of members of this genus are 19.54 kb in length (38.6 mol% G+C), and encode 26.5 proteins and 0 tRNAs.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus. TaxoProp 2008.061-062B classified *Streptococcus* phage Cp-1 as an unassigned species in the subfamily *Picovirinae*, family *Podoviridae*.

Reasons to justify the choice of type species:

The first sequenced member of this genus.

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. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2016.009eB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Streptococcus virus Cp1

The present taxonomic position of these taxon/taxa:

Genus:	***Unassigned***
Subfamily:	***Picovirinae***
Family:	***Podoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Streptococcus virus Cp1 was an unassigned species and will now be the type species of a new genus.

Part (b) re-assign to a higher taxon

Code	***2016.009fB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Cp1virus*** **(new)**
Subfamily:	***Picovirinae***
Family:	***Podoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Streptococcus virus Cp1 was an unassigned species and will now be the type species of a new genus.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.

2. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013; 6:140. doi: 10.1186/1756-0500-6-140.

3. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008; 36(Web Server issue):W465-9.

4. Ouennane S, Leprohon P, Moineau S. Diverse virulent pneumophages infect *Streptococcus mitis*. PLoS One. 2015;10(2):e0118807. [SOCP]

5. Martín AC, López R, García P. Analysis of the complete nucleotide sequence and functional organization of the genome of *Streptococcus pneumoniae* bacteriophage Cp-1. J Virol. 1996;70(6):3678-87.

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.

Fig. 1. Electron micrographs of negatively stained (2% Uranyl acetate) Streptococcus phage Cp-1 (provided by Denise Tremblay, Département de biochimie, de microbiologie et de bio-informatique, Faculté des sciences et de genie, Université Laval, Québec, QC, Canada).

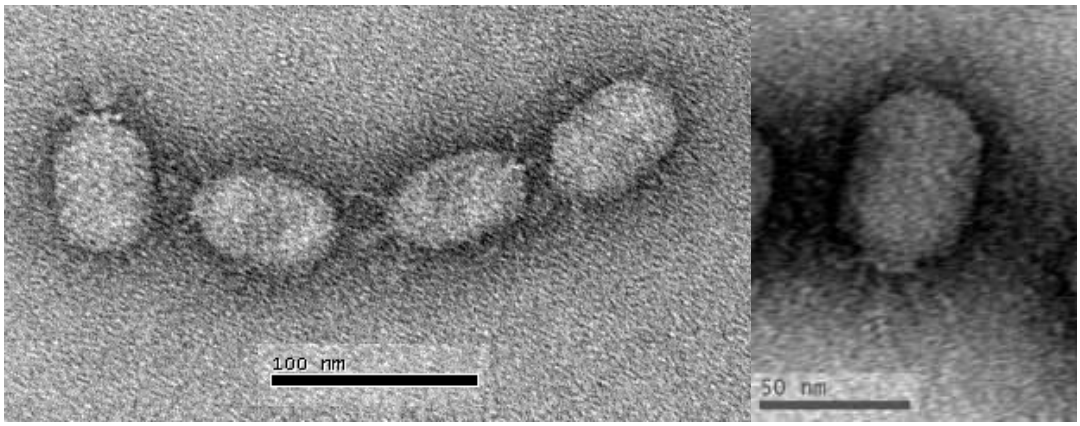


Table 1. Properties of the two phages belonging to the genus *Cp1virus*.

Streptococcus Phage	RefSeq No.	GenBank Accession No.	Genome size (kb)	Genome (mol%G+C)	No. CDS	DNA (% sequence identity)*	% Homologous proteins **
Cp-1	NC_001825.1	Z47794.1	19.34	38.8	25	100	100
Cp-7		LK392619	19.74	38.5	28	82	78.6
***SOCP		KJ617393	19.35	38.8	27	99	85.7

* Determined using BLASTN; ** Determined using CoreGenes [2] N.B. questionable annotation of Streptococcus phage Cp-1 has affected the results; *** Streptococccus phage SOCP (KJ617393) should be considered a strain of Streptococcus phage Cp-1 though the accuracy of the sequence analysis is probably greater than that for Streptococcus phage Cp-1 which was sequenced in 2008.

Fig. 2. progressiveMauve alignment [1] of the annotated genomes of members of the *Cp1virus* genus – from top to bottom: Streptococcus phages Cp-1, Cp-7, and SOCP. 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 (Aaron Darling, personal communication).

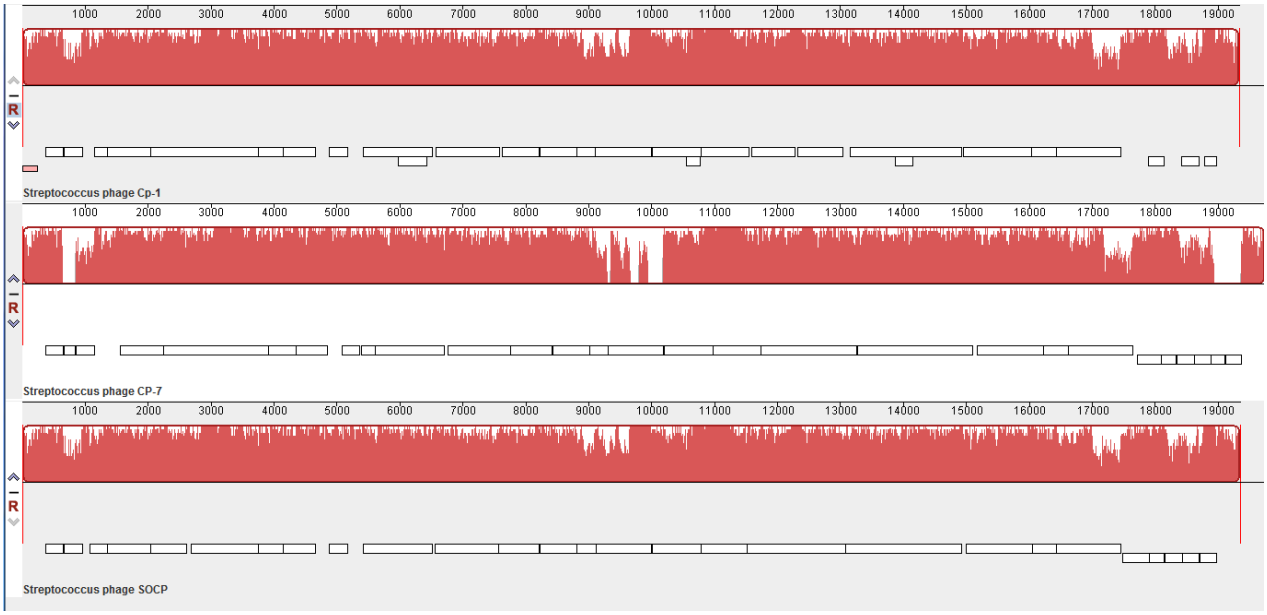
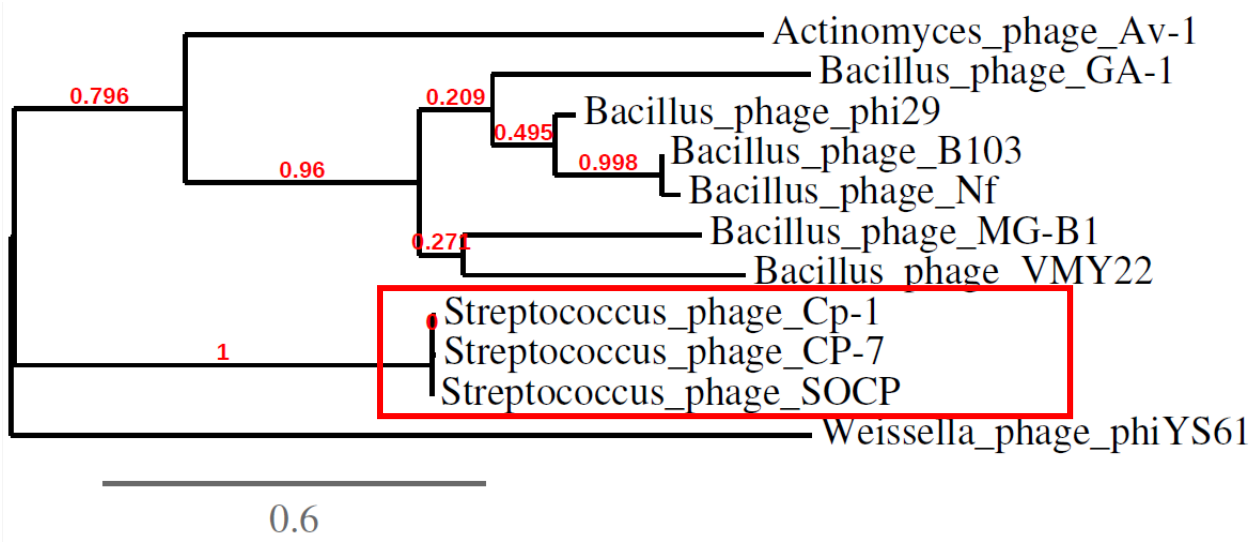


Fig. 3. Phylogenetic analysis of the major capsid proteins of Streptococcus phage Cp1-like viruses and homologous proteins from a variety of other phages constructed using “one click” at phylogeny.fr [3]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative (Syst Biol. 2006;55(4):539-52.) for details."


Actinomyces_phage_Av-1
Bacillus_phage_GA-1
Bacillus_phage_phi29
Bacillus_phage_B103
Bacillus_phage_Nf
Bacillus_phage_MG-B1
Bacillus_phage_VMY22
Streptococcus_phage_Cp-1
Streptococcus_phage_CP-7
Streptococcus_phage_SOCP
Weissella_phage_phiYS61
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0.209
0.495
0.998
0.96
0.271
1
0
0.6