This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.061-062B***	(to be completed by ICTV officers)

Short title: Move species Streptococcus Cp-1 from genus Phi29-like viruses to be unassigned in the subfamily Picovirinae, family Podoviridae

(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☐	**5** ☐
	6 ☒	**7** ☐			

Author(s) with e-mail address(es) of the proposer:

ICTV-EC or Study Group comments and response of the proposer:

MODULE 6: **REMOVE and MOVE**

- To remove an existing taxon entirely, complete section (a)
- To remove a taxon from one position and re-assign it elsewhere (e.g. to move an existing species from its current position into a genus THAT ALREADY EXISTS) complete BOTH sections (a) and (b). Please note that if an existing species is being moved into a NEW genus (or family) then you should complete only section (a) in this module but ALSO module 4 (for a new genus) or module 2 (for a new family)

SECTION (a)

Code	***2008.061B***	(assigned by ICTV officers)

To remove (abolish) the following taxon(s):

Species *Streptococcus* phage Cp-1

Old and new composition of the higher taxon that will be depleted by the removal:

Previous list of species in the genus *Phi29-like viruses* (subfamily *Picovirinae*, family *Podoviridae*, order *Caudovirales*):

Bacillus phage φ29
Kurthia phage 6
Streptococcus phage Cp-1

New list of species in genus:

Bacillus phage φ29
Kurthia phage 6
In addition, 2 new species, *Bacillus phage B103*, and *Bacillus phage GA-1*, are currently being proposed in 2008.032B.01 and 2008.039B.01, respectively

Argument to justify the removal:

See section 2, below

SECTION (b)

Code	***2008.062B***	(assigned by ICTV officers)

To re-assign the following taxon(s):

Species *Streptococcus* phage Cp-1

Proposed new position of these taxon(s):

Unassigned in the subfamily *Picovirinae*, family *Podoviridae*, order *Caudovirales*

Argument to justify the re-assignment:

If it is proposed to re-assign species to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

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The existing genus of the φ29-like viruses includes virions characterized by very small size, elongated heads, a collar, and 12 collar appendages. The DNA has a terminal protein covalently linked to its 5' ends and codes for a type B (*E. coli* Pol II) DNA polymerase. Based on our analysis, we propose to retain the current "φ29-like viruses" group which consists of *Bacillus* phages φ29, GA-1 (Salas et al., 2006) and B103 (Pecenkova et al., 1997). These phages have a genome size ranging between 18.6 and 21.1 kb and share 56% common gene products. Unfortunately, the genome sequence of the type species, φ29, consists of several contigs in GenBank, which contain numerous regions of sequence difference upon assembly. For this phage, sequence verification needs to be addressed. While phage Cp-1 shows a significant correlation to this group (~30%), it falls below the threshold for its inclusion in the genus. Despite a clear genomic relationship with φ29, Cp-1 is excluded from this genus because of its different genome anatomy. This phage has the same protein priming mechanism and DNA polymerase as other φ29-like viruses, but differs from it significantly in transcriptional organization (Martin et al., 1996). Cp-1 transcribes almost exclusively from left to right, whereas the φ29 early transcript is inverted. The role of specific short RNA in the packaging process during phage assembly of φ29 (Guo et al., 1987) seems also conserved in Cp-1, although it is encoded elsewhere on the genome. All *Bacillus* phages above are closely related and have short inverted terminal repeats (ITRs) of 6-7 bp; only phage Cp-1 stands apart by its long inverted terminal repeats (236 bp) and less than 40% genome homology with the others (NC_001825). Cp-1 may be considered as a representative of a separate genus within the *Picovirinae* and is therefore removed from this taxon.

References:

** Salas, M. (2006) Phage ϕ29 and its relatives. In: The Bacteriophages (Calendar, R., Ed.), pp. 315-330. Oxford University Press, New York.

** Pecenková, T., Benes, V., Paces, J., Vlcek, C. and Paces, V. (1997) Bacteriophage B103: complete DNA sequence of its genome and relationship to other *Bacillus* phages. Gene 199, 157-163.

** Martin, A.C., López, R. and Garcia, P. (1996) Analysis of the complete nucleotide sequence and functional organization of the genome of *Streptococcus pneumoniae* bacteriophage Cp-1. Journal of Virology 70, 3678-3687.

** Guo, P., Erickson, S. and Anderson, D. (1987) A small viral RNA is required for the *in vitro* packaging of bacteriophage ϕ29. Science 236, 690-694.

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.