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:	***2008.011a-gB.U***	(to be completed by ICTV officers)

Short title: create the subfamily Picovirinae in the 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:

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

MODULE 3: **NEW SUBFAMILY**

(if more than one subfamily is to be created, please complete additional copies of this module)

Code	***2008.011aB.U***	(assigned by ICTV officers)

To create a new Subfamily assigned as follows:

Family:	***Podoviridae***	If there is no Order, put "unassigned" here.
Order:	***Caudovirales***	

Code	***2008.011bB.U***	(assigned by ICTV officers)

To name the new Subfamily: *Picovirinae*

Code	***2008.011cB.U***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:

- **"Phi29-like viruses"** (modified; module 7)
- **"AHJD-like viruses"** (proposed in 2008.006-009B)

Code	***2008.011dB.U***	(assigned by ICTV officers)

To assign the following species to be unassigned in the new subfamily (i.e. within the subfamily but not assigned to any genus):

Actinomyces phage Av-1 (new; module 5)
Streptococcus phage Cp-1 (moved; module 7)

Argument to justify the creation of a new Subfamily:

Background (Lavigne et al., 2008):
The proposed taxonomic classification is based on available proteomic data. Using developed programs (CoreExtractor & CoreGenes) and careful review of available literature data, phages can be grouped. These programs parse-out/quantify the relationship between two phages into a single correlation score (= the relative number of homologous proteins between two sequenced phages).

Analysis and biological interpretation of the molecular correlations among all tailed phages (Caudovirales) with known genome sequence, shows this approach supports the current ICTV classification and proves that horizontal gene transfer does not mask the evolutionary relationship between phages.
Using a cut-off score of 40% homologous proteins between two phages, phages cluster correctly within existing genera.
In addition, we observe higher level relationships (20% correlation) that warrant the introduction of subfamilies. Subfamilies emphasize commonalities between related genera, prevent excessive subdivision during classification and solve classification difficulties with

Argument to justify the creation of a new Subfamily:

cross-family correlations.

The *Picovirinae*

The virus group is considered by the ICTV to include *Bacillus* phages φ29 and GA-1, *Streptococcus* phage Cp-1, and tentatively *Bacillus* phage B103. This is partially corroborated by our analyses. All these phages share unique properties, which differentiate them from other *Podoviridae*: which include a similar, special tail structure, their relatively small size and genome (with DNA with inverted terminal repeats or ITRs), a similar gene number (20-29), a protein-primed DNA polymerase which, among phages, is found elsewhere only in the *Tectiviridae* family (Fauquet et al., 2005). Several genomic relationships to φ29 shown by the CoreExtractor/CoreGenes analysis have previously been observed for phages 44AJHD, P68 and C1. These relatives of the φ29-like phages are listed in the VIIIth ICTV Report. We propose that φ29 and its relatives are upgraded from a genus to a subfamily with two genera: the “phi29-like viruses” and the “AHJD-like viruses”.

The evolutionary link to the φ29-like phages is clearly present, both morphologically and molecularly, since all these phages also contain a type B polymerase, apart from other similar gene products and overall genome size. From this perspective, phages *Actinomyces* phage Av-1 (NC_006953), *Streptococcus* phage Cp-1 (NC_001825) could be included within this subfamily, although the current classification of Cp-1 within the “phi29-like viruses” is not substantiated based on the proteomic correlation to this genus.

Mycoplasma phage P1 occupies a distinct and unclear position. The genome of the latter phage has 11 structural genes, the same type of DNA polymerase as the other φ29-like viruses, and a genome size of only 11,660 kb (Tu et al., 2001). This needs confirmation since we may be observing a case of genome size reduction (as shown by *Mycoplasma* hosts themselves). Therefore, we propose to tentatively exclude this phage from the subfamily.

Origin of the new Subfamily name:

This name refers to the small (*Pico*-) virion and genome sizes of the viruses within this subfamily (virinae), which represent the smallest tailed phages known

References:

** Fauquet, C.M., Mayo, M.A., Maniloff, J., Desselberger, U. and Ball, A. (2005) Virus Taxonomy. In: VIIIth Report of the International Committee on Taxonomy of Viruses (Fauquet, C.M., Mayo, M.A., Maniloff, J., Desselberger, U. and Ball, A., Eds.), pp. 35-85. Elsevier Academic Press, New York, NY.

Lavigne, R., Seto, D., Mahadevan, P., Ackermann, H-W. en Kropinski, A.M. (2008) Use of BLASTP-tools to develop a rational classification system for the *Podoviridae*. **Research in Microbiology in press (see appended proof).

** Tu, A.H., Voelker, L.L., Shen, X. and Dybvig, K. (2001) Complete nucleotide sequence of the mycoplasma virus P1 genome. **Plasmid** 45, 122-126.

MODULE 5: **NEW SPECIES**

Code	*2008.011eB.U*	(assigned by ICTV officers)

To create new species assigned as follows:

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

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Actinomyces phage Av-1

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Actinomyces phage Av-1, has a fully sequenced genome (NC_009643) of 17,171 bp and contains 22 predicted protein coding genes (as well as a single tRNA gene). Comparative genome analysis to the genera within the Picovirinae, shows that Av-1 contains a majority of non-similar proteins (74%) and has no genome-wide DNA homology with members within this subfamily.

References:

Delisle AL, Barcak GJ, Guo M.
Isolation and expression of the lysis genes of Actinomyces naeslundii phage Av-1.
Appl Environ Microbiol. 2006 Feb;72(2):1110-7.

Annexes:

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	***2008.011fB.U***	(assigned by ICTV officers)

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

Streptococcus phage Cp-1

The present taxonomic position of these taxon/taxa:

Genus:	*Phi29-like viruses*	Fill in all that apply.
Subfamily:		
Family:	*Podoviridae*	
Order:	*Caudovirales*	

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:

See module 3

Part (b) re-assign to a higher taxon

Code	***2008.011gB.U***	(assigned by ICTV officers)

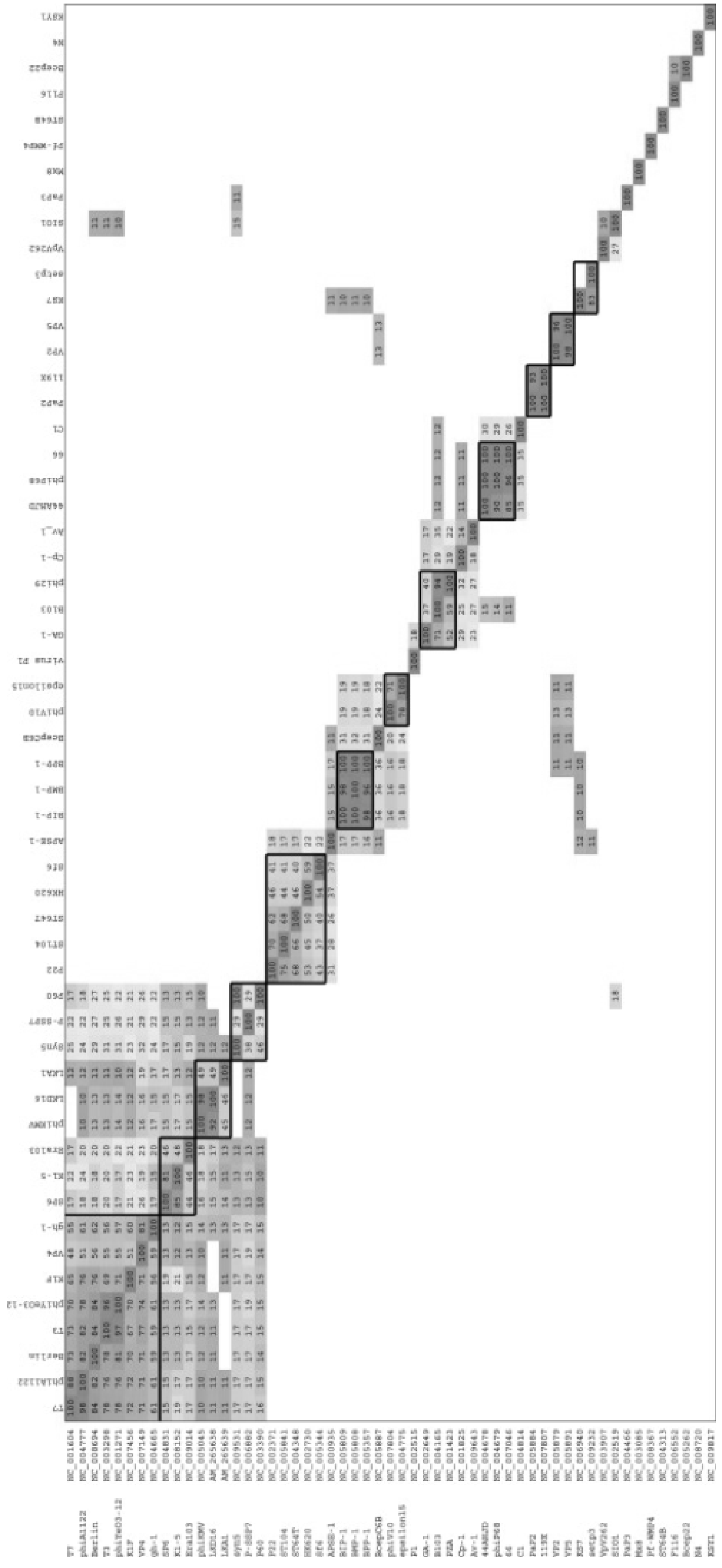
To re-assign the taxon (or taxa) listed in Part (a) as follows:

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

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 Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See module 3


T7
phiA1122
Berlin
T3
phiYeO3-12
K1F
VP4
gh-1
SP6
K1-5
Era103
phiKMV
LKD16
LKA1
syn5
P-SSP7
P60
P22
ST104
ST64T
HK620
Sf6
APSE-1
BIP-1
BMP-1
BPP-1
BcepC6B
phiV10
epsilon15
P1
GA-1
B103
PZA
Cp-1
AV-1
44AHJD
phiP68
66
C1
PaP2
119X
VP2
VP5
KS7
wetp3
VpV262
SIO1
PaP3
Mx8
PT-MNP4
ST64B
F116
Bcep22
N4
KSY1

B. PICOVIRINAE			
"phi29-like viruses"			
Bacillus phage φ29	NA	NA	NA
Bacillus phage PZA	NC_001423	100	100
Bacillus phage B103	NC_004165	94	63
Bacillus phage GA-1	NC_002649	40	56
The 44AHJD-like phages			
Staphylococcus phage 44AHJD	NC_004678	100	100
Staphylococcus phage P68	NC_004679	90	100
Staphylococcus phage 66	NC_007046	85	90
Staphylococcus phage SAP-2	NC_009875	ND	90
Streptococcus phage C1	NC_004814	35	38
Actinomyces phage Av-1	NC_009643	27	26
Streptococcus phage Cp-1	NC_001825	29	22

Fig. 1. A. Overview of the CoreExtractor comparison of the *Podoviridae*. Relative correlation scores (above 10%) are shown for the *Podoviridae* family and are based on the number homologous proteins between two phages. Color tags are added to visualize these correlations (from green to red for increasing correlation scores). B. Based on these values, a more precise comparison can be made for subsets of phages using CoreGenes (values in the right column)