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:	***2008.011-014B.01***	(to be completed by ICTV officers)

Short title: introduction of the Picovirinae subfamily
(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:

Rob Lavigne (rob.lavigne@biw.kuleuven.be)
Hans-W. Ackermann (Ackermann@mcb.ulaval.ca)
Andrew M. Kropinski (Andrew_Kropinski@phac-aspc.gc.ca)

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	***2008.011B.01***	(assigned by ICTV officers)

To create a new Subfamily assigned as follows:

Family:	***Podoviridae***
Order:	***Caudovirales***

If there is no Order, put "unassigned" here.

Code	***2008.012B.01***	(assigned by ICTV officers)

To name the new Subfamily: *Picovirinae*

Code	***2008.013B.01***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:

- ***The ϕ29-like viruses (modified)***
- ***The 44AHJD-like viruses (new)***

Code	***2008.014B.01***	(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
Streptococcus phage Cp-1

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

Argument to justify the creation of a new Subfamily:

introduction of subfamilies. Subfamilies emphasize commonalities between related genera, prevent excessive subdivision during classification and solve classification difficulties with cross-family correlations.

The *Picovirinae*

The virus group is considered by the ICTV to include *Bacillu*s 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 "φ29-like phages" and the "44AHJD-like phages".

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.

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.

Annexes:

References:

See appended manuscript