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:	***2008.033-036B***	(to be completed by ICTV officers)

Short title: Create new genus named "Epsilon15-like viruses" 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** ☐			

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

MODULE 4: **NEW GENUS**

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

Code	***2008.033B***	(assigned by ICTV officers)

To create a new genus assigned as follows:

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

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.

Code	***2008.034B***	(assigned by ICTV officers)

To name the new genus: "Epsilon15-like viruses"

Code	***2008.035B***	(assigned by ICTV officers)

To assign the following as species in the new genus:

- *Salmonella phage epsilon15* (proposed in 2008.037B)
- *Escherichia phage phiV10* (new)

Code	***2008.036B***	(assigned by ICTV officers)

To designate the following as the type species in the new genus:
Salmonella phage epsilon15

Argument to justify the creation of a new genus:

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. Hence, using this parameter, new genera may be defined. In figure 1 (appended), a cluster dendrogram of the *Podoviridae* family shows the demarcation criteria for subfamilies and genera. This dendrogram shows a correlation of the "epsilon15-like viruses" to BPP-1, BIP-1, BMP-1 and BcepC6B at the proteome level, but insufficient to include them within the same genus.

The temperate "epsilon15-like viruses" infect *Salmonella* (ε15) and *E.coli* (φV10),

Argument to justify the creation of a new genus:

respectively, and have unique serotype conversion modules (Kropinski et al., 2007). Their adenine methylases share homology only with Stx2-converting phage 86 (YP_794086.1), and containing a pfam05063 MT-A70 motif which is associated with the S-adenosylmethionine-binding subunit of human m6A methyltransferase.

Origin of the new genus name:

Named after the type species *Salmonella* phage ε15

Argument to justify the choice of type species:

Salmonella phage epsilon15 is the first sequenced member of this genus.

Species demarcation criteria in the genus:

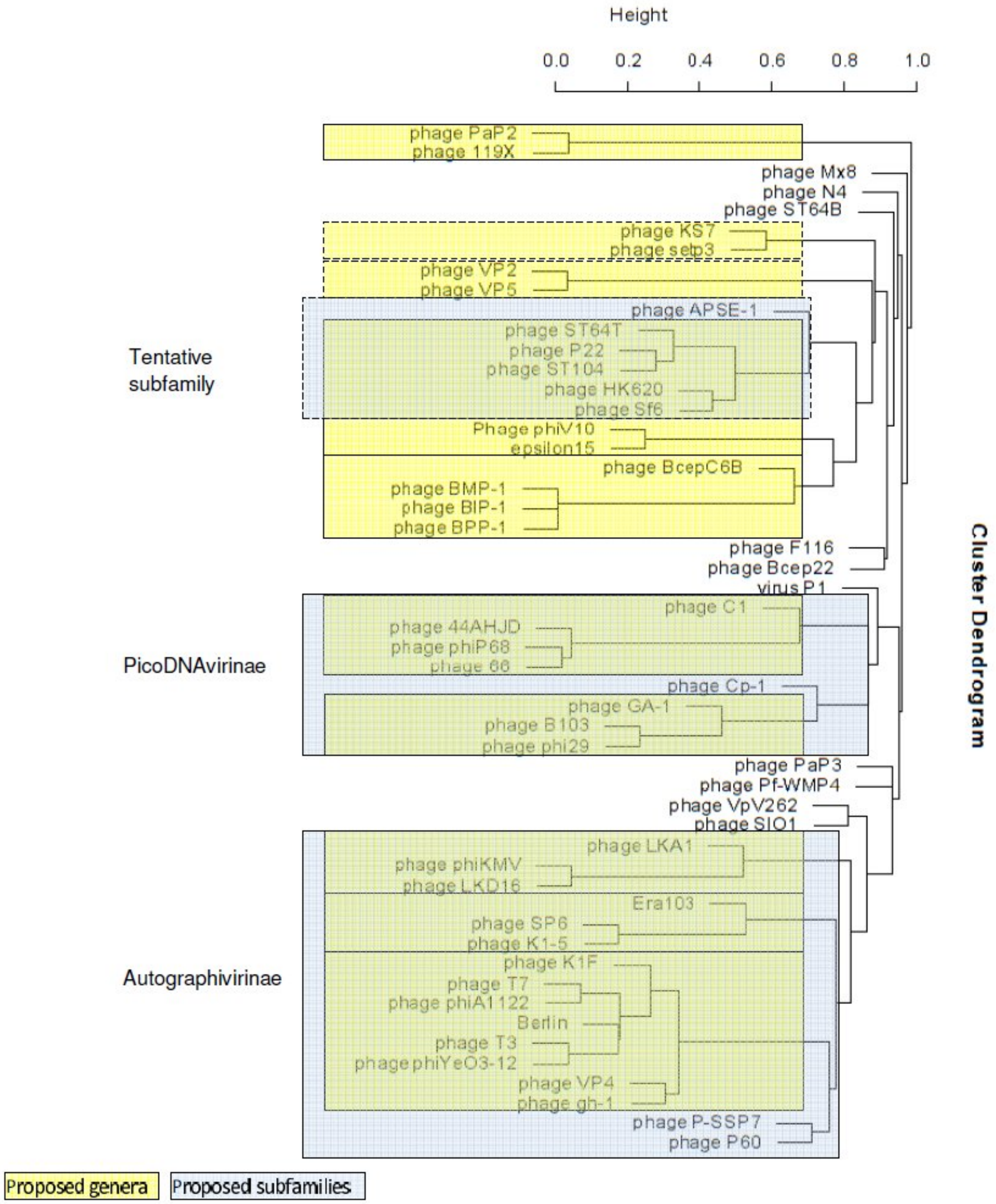
If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Absence of genome-wide DNA homology between ε15 and φV10; proteomic correlation

References:

Kropinski, A.M., Kovalyova, I.V., Billington, S.J., Butts, B.D., Patrick, A.N., Guichard, J.A., Hutson, S.M., Sydlaske, A.D., Day, K.R., Falk, D.R. and McConnell, M.R. (2007) The genome of e15, a serotype-converting, Group E1 *Salmonella* enterica-specific bacteriophage. Virology 369(2):234-44.

Annexes:



Cluster dendrogram of the Podoviridae family. This dendrogram shows the relative level of dissimilarity (Height: 0.0 = identical; 1.0 = dissimilar) between phage proteomes. Based on these correlations, groupings were made and evaluated based on biologically available data. From this, genera and proposed subfamily divisions were defined