



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:	2008.015- 018B.01	(to be completed by ICTV officers)
Short title: new genus the 119X-like viruses (e.g. 6 new species in the genus <i>Zetavirus</i> ; re-classification of the family <i>Zetaviridae</i> etc.)		
Modules attached (please check all that apply):	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input checked="" type="checkbox"/>
	5 <input type="checkbox"/>	6 <input type="checkbox"/>
	7 <input type="checkbox"/>	

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:

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MODULE 4: **NEW GENUS**

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

Code	2008.015B.01	(assigned by ICTV officers)
To create a new genus assigned as follows:		
Subfamily:		Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.
Family:	<i>Podoviridae</i>	
Order:	<i>Caudovirales</i>	

Code	2008.016B.01	(assigned by ICTV officers)
To name the new genus: <i>The 119X-like viruses</i>		

Code	2008.017B.01	(assigned by ICTV officers)
To assign the following as species in the new genus:		
<ul style="list-style-type: none">• <i>Pseudomonas</i> phage 119X (new)		

Code	2008.018B.01	(assigned by ICTV officers)
To designate the following as the type species in the new genus:		
<i>Pseudomonas</i> phage 119X		

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.

The lytic 119X-like phage group comprise phages 119X and PaP2. The former is part of the Colindale *Pseudomonas aeruginosa* typing set (Lindberg and Latta, 1974) and is remarkably similar to *P. aeruginosa* phage PaP2 (NC_005884). Dotplot alignments of the two genomes reveal that the differences between the two chromosomes can be largely accounted for by a small deletion and a small duplication in the sequence of PaP2, suggesting PaP2 can be considered as belonging to the 119X species.

Origin of the new genus name:

Named after the type species *Pseudomonas* phage 119X

Argument to justify the choice of type species:

Pseudomonas phage 119X 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.

Presence of genome-wide DNA homology; proteomic correlation

References:

Lindberg, R.B. and Latta, R.L. (1974) Phage typing of *Pseudomonas aeruginosa*: clinical and epidemiological considerations. *Journal of Infectious Diseases* 130, S33-S43.

Annexes:
