Taxonomic proposal to the ICTV Executive Committee

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:	***2008.015B***	(to be completed by ICTV officers)

Short title: Create species Pseudomonas phage 119X in the Podoviridae family
(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 5: **NEW SPECIES**

Code	***2008.015B***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	**unassigned**
Subfamily:	
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:

Pseudomonas phage 119X

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.

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).

The lytic Pseudomonas phage 119X (NC_007807; 43,365 nt) is part of the Colindale *Pseudomonas aeruginosa* typing set (Lindberg and Latta, 1974) is remarkably similar to later described *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.

References:

Vandenbergh,P.A., Wright,A.M. and Vidaver,A.K. Partial Purification and Characterization of a Polysaccharide Depolymerase Associated with Phage-Infected Erwinia amylovora. Appl. Environ. Microbiol. 49 (4), 994-996 (1985)

Annexes:

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