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:	***2008.027-031B***	(to be completed by ICTV officers)

Short title: create genus "Bbp1-like viruses" within 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 4: **NEW GENUS**

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

Code	***2008.027B***	(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	***2008.028B***	(assigned by ICTV officers)

To name the new genus: "Bpp1-like viruses"

Code	***2008.029B***	(assigned by ICTV officers)

To assign the following as species in the new genus:

- *Bordetella* phage BPP-1 (new)
- *Burhkolderia* phage BcepC6B (new)

Code	***2008.030B***	(assigned by ICTV officers)

To designate the following as the type species in the new genus:
Salmonella phage BPP-1

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 (Figure 1).

The "Bpp1-like viruses" include temperate viruses (infecting members of the β-proteobacteria *Bordetella* (BPP-1, BMP-1 and BIP-1)(Liu et al., 2004) and *Burkholderia* (BcepC6B) (Summer et al., 2006). They share the presence of genes specifying DNA polymerase I, a helicase, and repressors.

Argument to justify the creation of a new genus:

BPP-1-like phages share some common gene products with the temperate VP2-like and ε15-like phages (Figure 1). However, this homology is largely restricted to the proteins involved in morphogenesis. This has led us to reject, at present, any consideration of subfamily status for these phages.

Origin of the new genus name:

Named after the type species *Bordetella* phage BPP-1

Argument to justify the choice of type species:

Bordetella phage BPP-1 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:

Liu, M., Gingery, M., Doulatov, S.R., Liu, Y., Hodes, A., Baker, S., Davis, P., Simmonds, M., Churcher, C., Mungall, K., Quail, M.A., Preston, A., Harvill, E.T., Maskell, D.J., Eiserling, F.A., Parkhill, J. and Miller, J.F. (2004) Genomic and genetic analysis of *Bordetella* bacteriophages encoding reverse transcriptase-mediated tropism-switching cassettes. Journal of Bacteriology 186, 1503-1517.

Summer, E.J., Gonzalez, C.F., Bomer, M., Carlile, T., Morrison, W., Embry, A., Kucherka, A.M., Lee, J., Mebane, L., Morrison, W.C., Mark, L., King, M.D., LiPuma, M.J., Vidaver, A.K. and Young, R. (2006) Divergence and mosaicism among virulent soil phages of the *Burkholderia cepacia* complex. Journal of Bacteriology 188, 255-268.

Annexes:

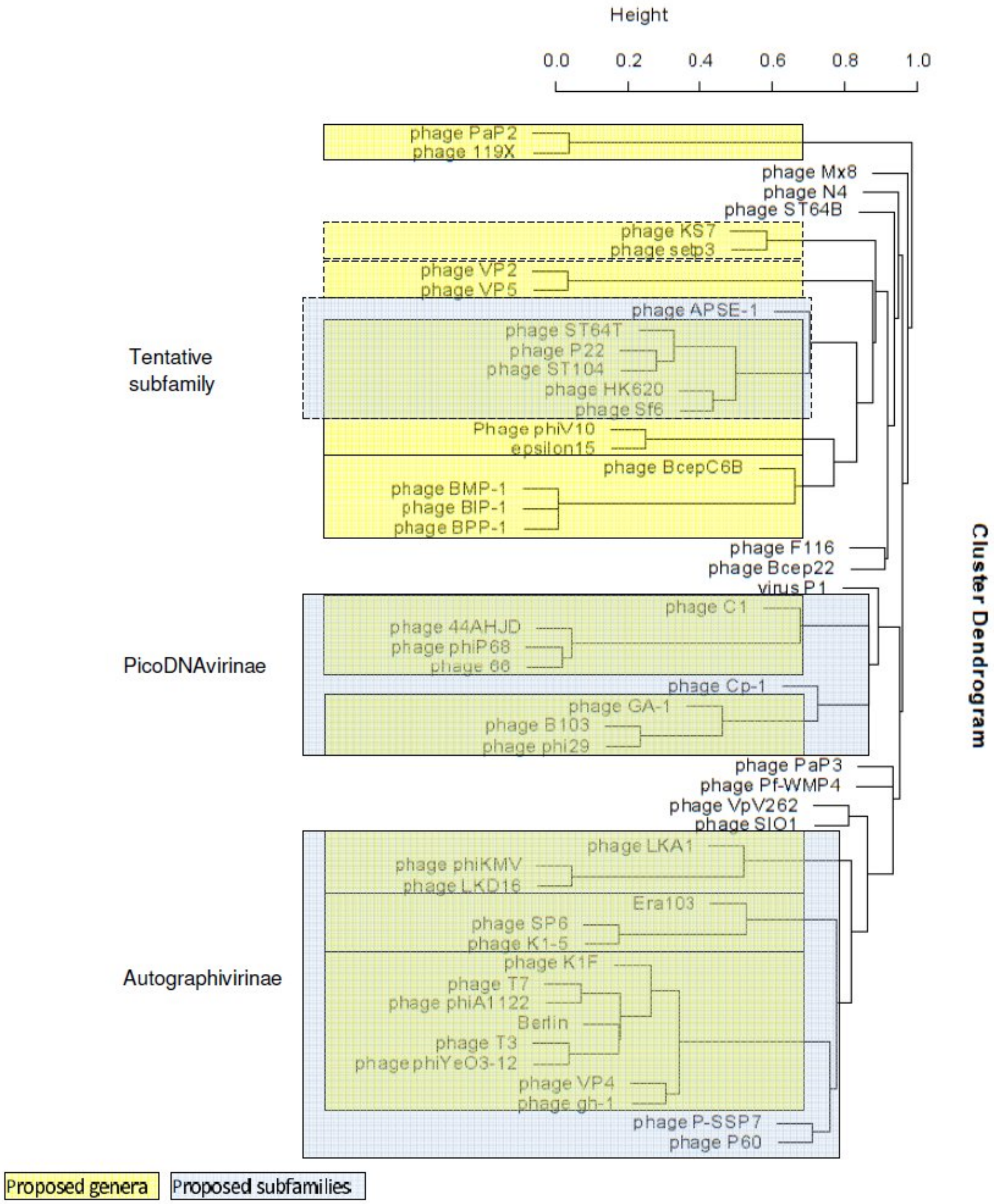

Figure 1: Cluster dendrogram based on the proteomic correlation scores among sequenced Podoviridae members

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. As observed, the proposed “BPP1-like viruses”consists of two species *Bordetella* phage BPP-1 (with highly similar phages BIP-1 and BMP-1) and *Burkholderia* phage BcepC6B