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: ***2008.026B*** (to be completed by ICTV officers)

Short title: create species named Bordetella phage BPP-1 within the genus "Bpp1-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 5: **NEW SPECIES**

Code	***2008.026B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	**"Bpp1-like viruses"**
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:

Bordetella phage BPP-1

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.

Other members of this species include

Bordetella phage BMP-1	NC_005808
Bordetella phage BIP-1	NC_005809

BPP-1 is a temperate bacteriophage (Figure 1) initially found in a clinical isolate of *B. bronchiseptica* that displays a marked tropism for Bvg$^+$ phase *B. pertussis*, *B. parapertussis*, and *B. bronchiseptica*.(Liu et al., 2002)

BPP-1, BIP-1, and BMP-1 were independently determined to be 42,493 bp, 42,638 bp, and 42,663 bp, respectively (NC_005357; NC_005809; NC_005808). The length differences were due to a variable number of tandem repeats within the VR2 region of *bbp36*, and the three phage sequences are identical except for changes at variable regions 1 (134 bp) and 2 (consists of a series of identical 19-bp repeats separated by one of three 5-bp spacers), two single nucleotide polymorphisms within *mtd*, and single nucleotide insertions and deletions within a homopolymer tract "G-string" located within *bpm* (Liu et al., 2002)

References:

** Liu, M., R. Deora, S. R. Doulatov, M. Gingery, F. A. Eiserling, A. Preston, J. Duncan, R. W. Simons, P. A. Cotter, J. Parkhill, and J. F. Miller. 2002. Reverse transcriptase-mediated tropism switching in Bordetella bacteriophage. Science 295:2091-2094.

Annexes:

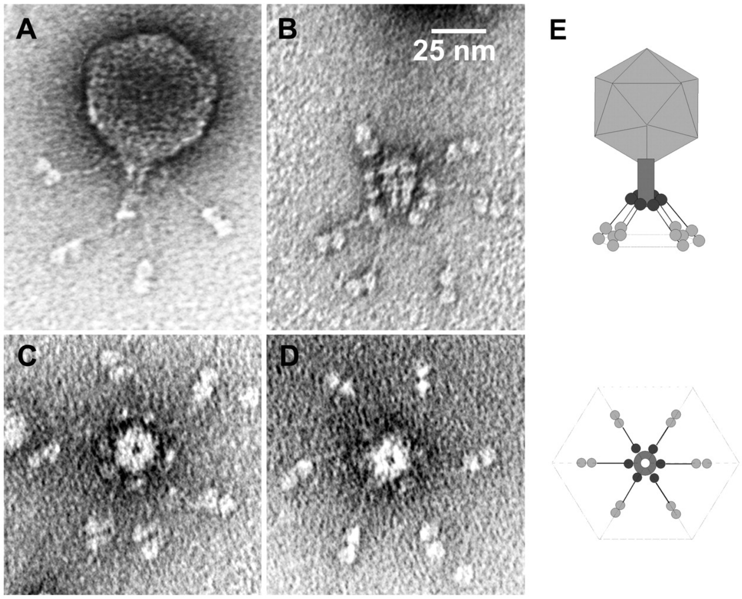

Figure 1: BPP-1 virion morphology. Negative-stain transmission electron micrographs of (A) an intact phage particle, (B) an isolated tail (side view), with partially dissociated tail fibers, and (C, D) isolated tails with tail fibers (top view). (E) Schematic diagram (not to scale) showing general particle morphology and hexagonal symmetry.