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: ***2008.059B*** (to be completed by ICTV officers)

Short title: create species named Phormidium phage Pf-WMP3 to be unassigned within 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	***2008.059B***	(assigned by ICTV officers)

To create 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:

Phormidium phage Pf-WMP3

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 Pf-WMP3 genome contains 43,249 bp with 234 bp direct terminal repeats (NC_009551). The overall genome organization and core genes of this phage are distantly related to the *Autographivirinae*.

The GC content of Pf-WMP3 genome is 46.49%. Based on the results of BLAST searches and modified by visual inspection, 41 potential ORFs were identified on the Pf-WMP3 genome, occupying 89.2% of the Pf-WMP3 genome. Considering putative gene functions and transcription direction, two functional genomic regions can be delineated. The left arm is transcribed rightward and comprises genes coding for DNA replication; the right arm is transcribed leftward and codes for structural proteins. This separates Pf-WMP3 from the Autographivirinae, but more importantly, this phage has no RNA polymerase gene.

Compared with Pf-WMP4, cyanophage Pf-WMP3 has diverged extensively at the DNA level; however, they are closely related at the protein level and genome architecture. The left arm genes for the two phages, which mainly encode the DNA replication machinery, are not conserved in the gene order. Whereas the right arm genes of the two phages coding for structural proteins show high similarity in amino acid sequences and modular architecture, indicating that they have retained similar development strategies. The differences in similarity levels between the left and right arm genes suggest that the structural genes are the most conserved elements for a phage.

References:

** Xinyao Liu , Shuanglei Kong , Miao Shi , Liwen Fu , Yin Gao and Chengcai An (2008) Genomic Analysis of Freshwater Cyanophage Pf-WMP3 Infecting Cyanobacterium Phormidium foveolarum: The Conserved Elements for a Phage. 10.1007/s00248-008-9386-7

Annexes:

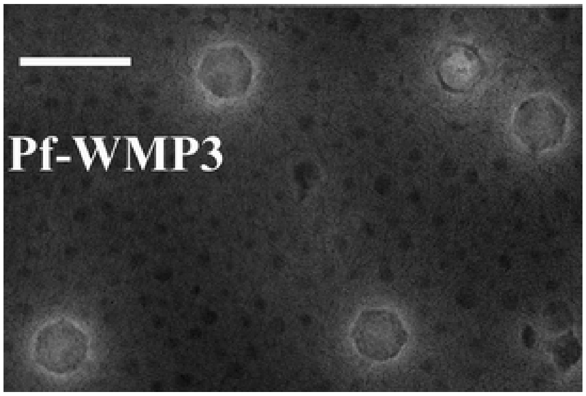

Figure 1 Electron micrograph of cyanophage Pf-WMP3 (Bar = 100 nm)