This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2009.005a-gB***	(to be completed by ICTV officers)

Short title: Create new genus named *Phicd119likevirus* in the family *Myoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

Rob Lavigne rob.lavigne@biw.kuleuven.be
Andrew Kropinski kropinsk@queensu.ca
Pieter-Jan Ceyssens pieterjan.ceyssens@biw.kuleuven.be

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

ICTV-EC or Study Group comments and response of the proposer:

[previous (EC41) decision: inconsistent with naming rules.]

Date first submitted to ICTV:
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.005aB***	(assigned by ICTV officers)

To create 3 new species with the name(s):

Clostridium phage phiCD119
Clostridium phage phiC2
Clostridium phage phiCD27

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.005bB***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***Phicd119likevirus*** (new)
Subfamily:	
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

These are all integrative temperate phages of *Clostridium difficile* with genomes ranging from 51-60 kb in size and a mol%G+C of 28.7-29.4 (NC_007917; NC_009231; NC_011398). In each case, the electron micrographs are preliminary due to variable measurements. Virus head diameters are given as 50-65 nm and tail lengths are said to range from 110 to 210 nm (Figure 1).

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	***2009.005cB***	(assigned by ICTV officers)

To create a new genus to contain the species listed below

Code	***2009.005dB***	(assigned by ICTV officers)

To name the new genus: *Phicd119likevirus*

assigning a new genus to higher taxa

Code	***2009.005eB***	(assigned by ICTV officers)

To assign the new genus as follows: Ideally, a genus should be placed within a higher taxon, but if not, write "**unassigned**" in the box below.

Subfamily:	
Family:	***Myoviridae***
Order:	***Caudovirales***

If any of these taxa has yet to be created (in module 4, 5 or 6) please write "**(new)**" after its proposed name.

assigning type species and other species to a new genus

Code	***2009.005fB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Clostridium phage phiCD119

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

Code	***2009.005gB***	(assigned by ICTV officers)

To assign the following as additional species of the new genus:

Clostridium phage phiC2
Clostridium phage phiCD27

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Based on proteomic comparison (Figure 1)

What unites these viruses, in addition to similar proteomes, is the presence in each of a cytosine-C5 specific DNA methylase (pfam00145, DNA_methylase, C-5 cytosine-specific DNA methylase; phiCD119 protein YP_529611.1) and a DNA replication cassette composed of three proteins: a DnaD (primosome recruiting protein, presumably analogous to lambda gp*O* and P22 gp*18*;

phiCD119 protein YP_529603.1), a hypothetical protein (misidentified in phiCD27 as a putative resolvase/integrase and missed entirely in the annotation of phiCD119) and a single-stranded DNA binding protein.

Origin of the new genus name:

The genus is named after its first fully sequenced member

Reasons to justify the choice of type species:

first fully sequenced member

Species demarcation criteria in the new 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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

Absence of genome-wide DNA homology and proteomic variation; differences in host range.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Mayer MJ, Narbad A, Gasson MJ: Molecular characterization of a Clostridium difficile bacteriophage and its cloned biologically active endolysin. Journal of Bacteriology 2008, 190: 6734-6740.

Goh S, Ong PF, Song KP, Riley TV, Chang BJ: The complete genome sequence of Clostridium difficile phage phiC2 and comparisons to fCD119 and inducible prophages of CD630. Microbiology 2007, 153: 676-685.

Govind R, Fralick JA, Rolfe RD: Genomic organization and molecular characterization of Clostridium difficile bacteriophage FCD119. Journal of Bacteriology 2006, 188: 2568-2577.

Goh S, Riley TV, Chang BJ: Isolation and characterization of temperate bacteriophages of Clostridium difficile. Appl Environ Microbiol 2005, 71: 1079-1083.

Narasimhan G, Bu C, Gao Y, Wang X, Xu N, Mathee K: Mining protein sequences for motifs. Journal of Computational Biology 2002, 9: 707-720.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.
The use of Figures and Tables is strongly recommended.

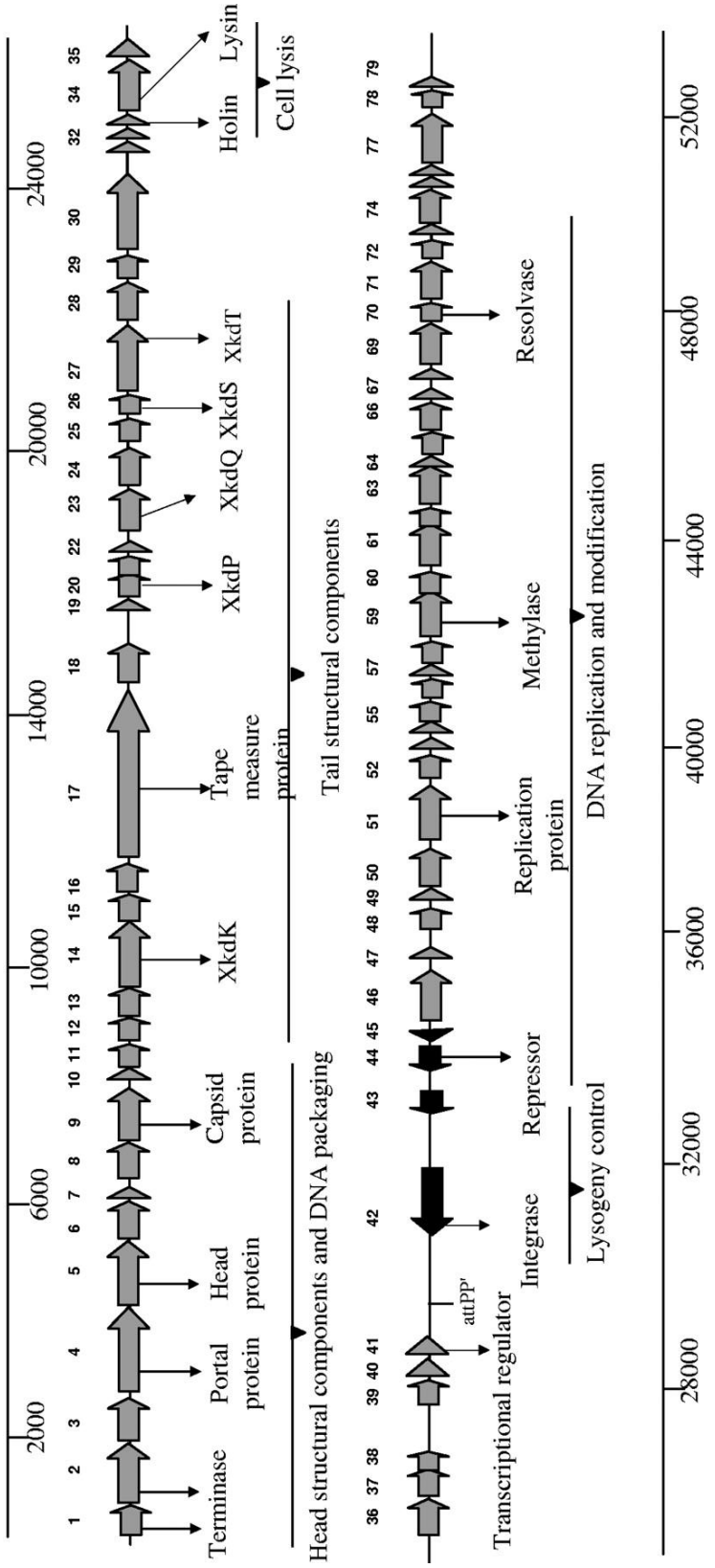

Figure 1: Genetic and physical organization of ΦCD119 genome with predicted ORFs and some functional assignments. The ORFs (1 to 79) are indicated by arrows or arrowheads pointing in the direction of transcription. The relative positions of the ORFs and the *attPP'* site in the genome are marked.

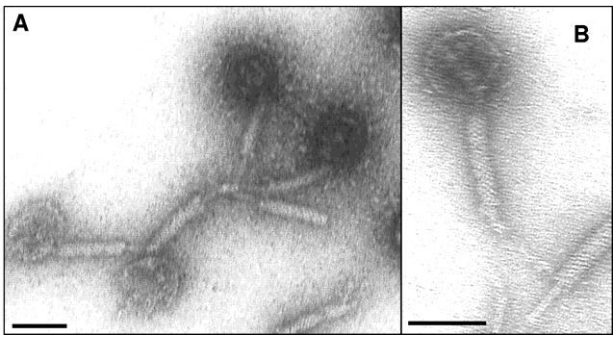

Figure 2. Electron microscopy of phage ΦCD119 showing its icosahedral capsid and a flexible tail. Bar, 50 nm.