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:	***2009.002a-gB***	(to be completed by ICTV officers)

Short title: Create new genus named *Bcep781likevirus* 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:

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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	***2009.002aB***	(assigned by ICTV officers)

To create 5 new species with the name(s):

Burkholderia phage Bcep781
Burkholderia phage Bcep43
Burkholderia phage Bcep1
Burkholderia phage BcepNY3
Xanthomonas phage OP2

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	***2009.002bB***	(assigned by ICTV officers)

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

Genus:	***Bcep781likevirus*** (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

"Bcep" stands for ***B**urkholderia* ***cep**acia*, and phages with this designation infect bacteria belonging to the *B. cepacia* genomic complex. The proposed genus ***Bcep781likevirus*** comprises a group of virulent myophages of which the genome sequence of five members, Bcep781 (NC_004333), Bcep1 (NC_009015), Bcep43 (NC_005342), BcepNY3 (NC_009604) and *Xanthomonas* phage OP2 (NC_007710), is known. The Bcep781 phages are small viruses with distinctly shorter tails than P2, Mu, and BcepMu.

The genomes of these phages range from 46 to 49 kb in size and encode 66 to 71 proteins. The four Bcep phages encode a single tRNA each. They form a homogeneous phage group not just in terms of sequence**,** but also by their distinctive genome organization compared to other groups (Figures 1).

The genomes of the Bcep781 phages are divided into four gene clusters encoded on alternate strands such that, using Bcep781 as the example, genes *1* through *19* and *29* through *51* are present on the bottom strand while genes *20* through *28* and *52* through *66* are present on the top strand (Figure 2). Head genes are located in the first cluster and tail genes are located in the third cluster. The virion major capsid and decoration proteins, Bcep781 gp*12* and gp*13*, were identified by protein sequencing and show some similarity to head proteins from the "PB1-like viruses". Several tail morphogenesis proteins, corresponding to Bcep781 gp*29* through gp*52*, can be linked to P2 tail genes by PSI-BLAST. In contrast to structural genes, genes for DNA replication and lysis are scattered throughout the genome. The lysis genes of these phages are not organized into a cassette but instead overlapping Rz and Rz1 genes are separated from the endolysin and holin genes. A distinctive feature of these phages is the presence of highly, maybe completely, circularly permuted genomes. The terminases of these phages are strongly related to other *pac*-type phages that also have highly permuted genomes.

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	***2009.002cB***	(assigned by ICTV officers)

To create a new genus to contain the species listed below

Code	***2009.002dB***	(assigned by ICTV officers)

To name the new genus: *Bcep781likevirus* (new)

assigning a new genus to higher taxa

Code	***2009.002eB***	(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	***2009.002fB***	(assigned by ICTV officers)

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

Burkholderia phage Bcep781

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

Code	***2009.002gB***	(assigned by ICTV officers)

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

Burkholderia phage Bcep781
Burkholderia phage Bcep43
Burkholderia phage Bcep1
Burkholderia phage BcepNY3
Xanthomonas phage OP2

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)

Origin of the new genus name:

Named after type species Bcep781

Reasons to justify the choice of type species:

Bcep781 was the first sequenced phage within this genus

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

See module 2

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Summer EJ, Gonzalez CF, Bomer M, Carlile T, Morrison W, Embry A et al.: Divergence and mosaicism among virulent soil phages of the Burkholderia cepacia complex. Journal of Bacteriology 2006, 188: 255-268.

Inoue Y, Matsuura T, Ohara T, Azegami K: Sequence analysis of the genome of OP2, a lytic bacteriophage of Xanthomonas oryzae pv. oryzae. Journal of General Plant Pathology 2006, 72: 104-110.

Summer EJ, Berry J, Tran TA, Niu L, Struck DK, Young R: Rz/Rz1 lysis gene equivalents in phages of Gram-negative hosts. Journal of Molecular Biology 2007, 373: 1098-1112.

Casjens SR, Gilcrease EB, Winn-Stapley DA, Schicklmaier P, Schmieger H, Pedulla ML et al.: The generalized transducing Salmonella bacteriophage ES18: complete genome sequence and DNA packaging strategy. Journal of Bacteriology 2005, 187: 1091-1104.

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.

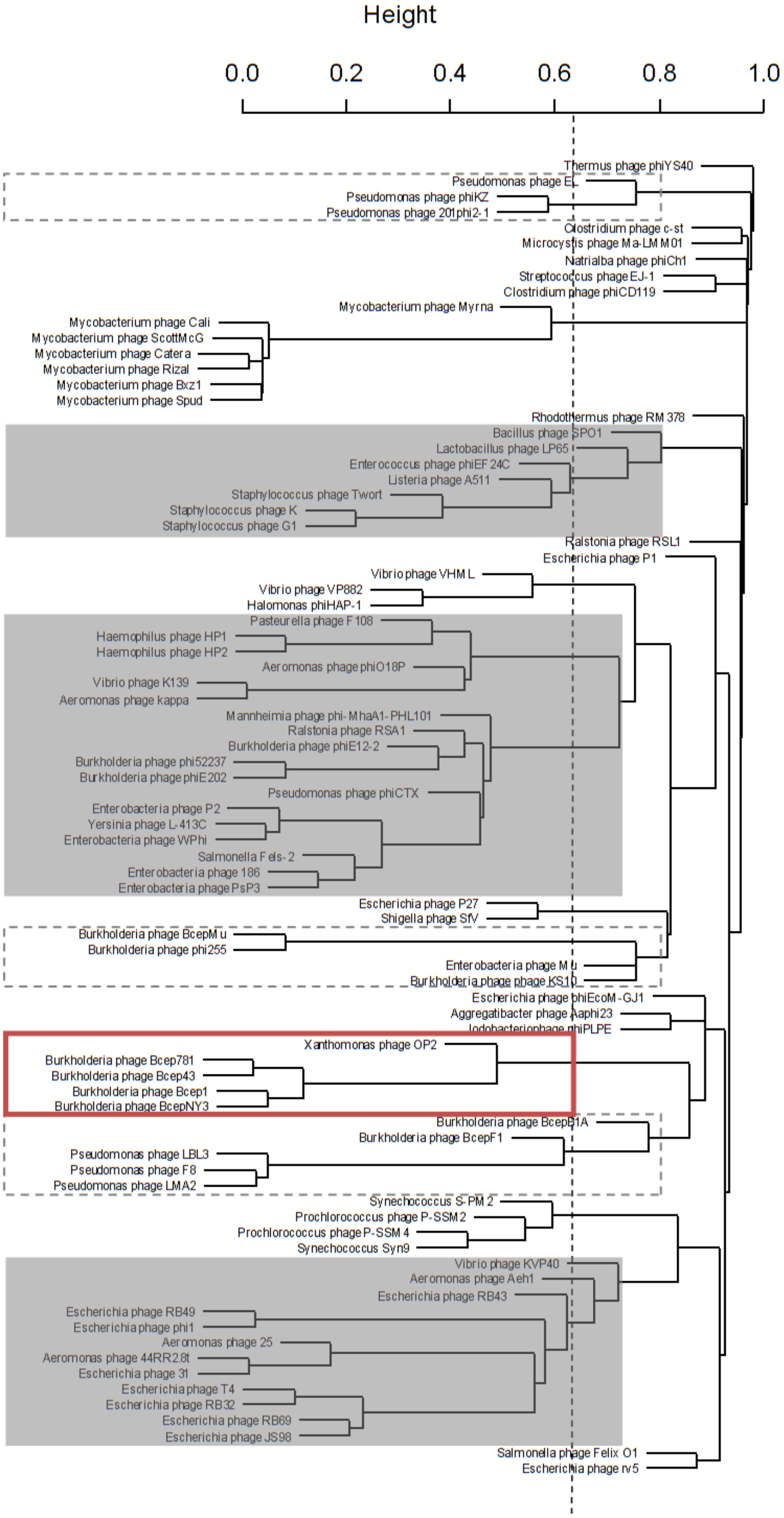

Figure 1: Hierarchical cluster dendrogram of the *Myoviridae*
The relative dissimilarity between the phage proteomes (between 0.0 and 1.0) forms the basis for the proposed groupings. The dotted lines reflects the cut-off value used for the establishement of genera, used consistently for all Myoviridae and the previously defined Podoviridae (Lavigne et al., 2008). Subfamily and tentative subfamily groupings are indicated in the grey and dotted boxes, respectively. The genus "Bcep781-like viruses" is highlighted in a red box

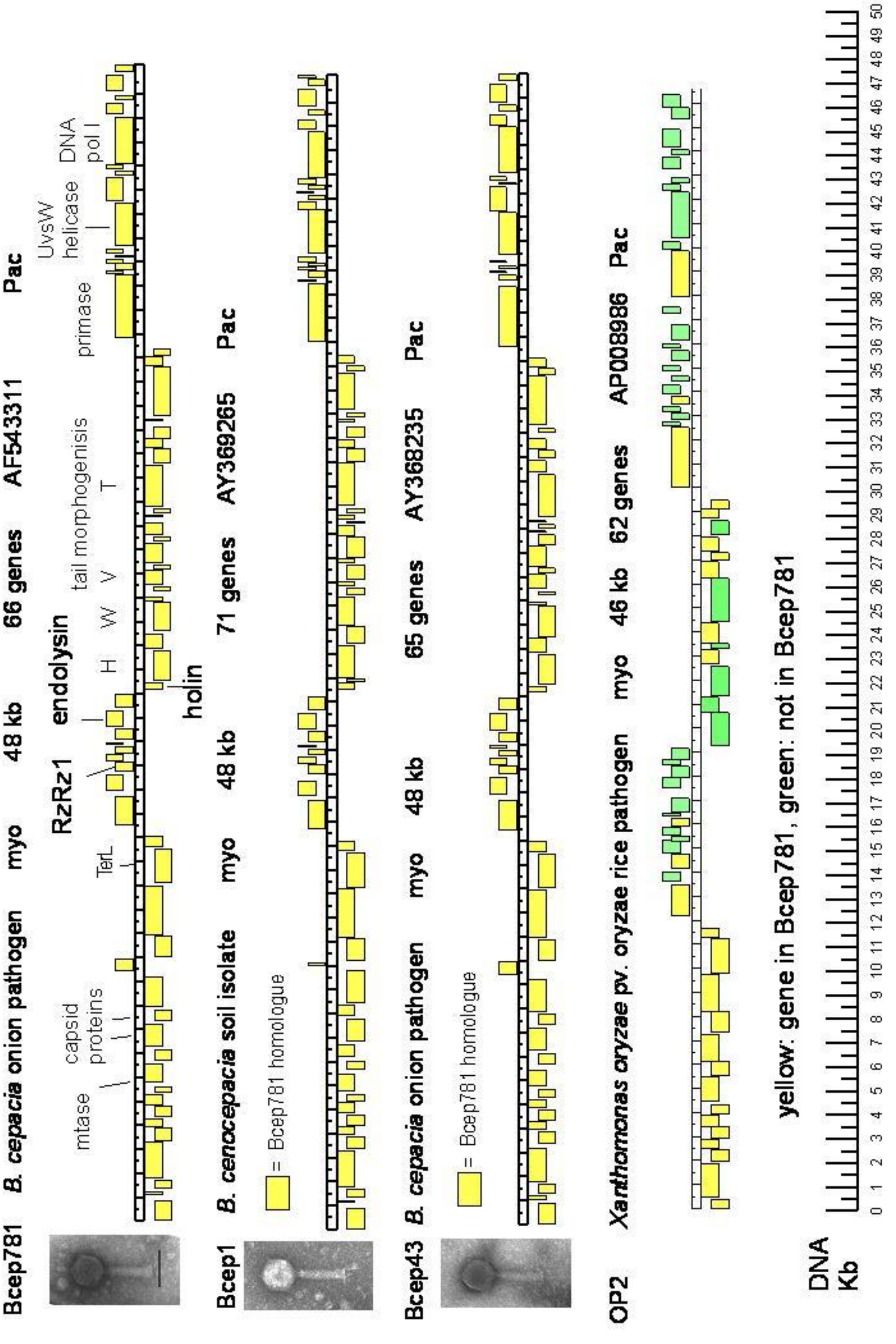

Figure 2: Genome organisation of the members of the “Bcep781-like viruses. Main predicted function are indicated and available EM micrographs have been added.