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:	***2009.003a-gB***	(to be completed by ICTV officers)

Short title: Create new genus named *Bcepmulikevirus* 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	***2009.003aB***	(assigned by ICTV officers)

To create 2 new species with the name(s):

Burkholderia phage BcepMu
Burkholderia phage phiE255

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	***2009.003bB***	(assigned by ICTV officers)

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

Genus:	***Bcepmulikevirus*** (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

BcepMu was first identified as a functional virion that forms plaques on Burkholderia cenocepacia K56-2. BcepMu is present as a lysogen in many B.
cenocepacia strains of the human pathogenic ET2 lineage, including the sequenced strain J2315. However, like most Burkholderia strains, B.
cenocepacia J2315 is polylysogenic and also harbors another morphologically identical prophage element KS10. Phage phiE255 is a closely related phage of the soil saprophyte *B. thailandensis* [NC_009237].

BcepMu related prophage elements that have not been shown to produce functional virions are present in several other non-Burkholderia hosts including Salmonella typhi Ty2 [NC_004631], *Salmonella typhi* CT18 [NC_003198], *Photorhabdus luminescens* TT01 [NC_005126], and *Chromobacterium violaceum* [NP_901809].

This new genus was named *Bcepmulikevirus* because, like Mu and unlike most other phages, its members utilize transposition for replication. The distinctive genomic feature implicating the use of replicative transposition is the presence of random host DNA sequences at either end of the packaged virion DNA. These host sequences are derived from excision of prophage DNA from random sites scattered over the host genome. This requires fundamental differences in terminase function as compared to more typical terminases that utilize concatemers of phage genomic DNA as a substrate. This is reflected by the homology between BcepMu TerL and Mu TerL. Another genome feature shared by BcepMu and Mu is the presence of genomic terminal CA dinucleotide repeats, a feature common in many transposons. Furthermore, BcepMu and Mu seem to be morphologically identical.

Despite these similarities, BcepMu and its close relative phiE255 have marked differences in genome organization and minimal overall protein sequence similarity to Mu, explaining why they have not been grouped together.

-The putative BcepMu transposase is not related to the Mu transposase, TnpA, but instead is a distant member of the Tn552-IS1604 transposase family.
-The BcepMu genome is organized into two clusters, with genes 1 through 13 encoded on the bottom strand and genes 17 through 52 on the top strand.
-The cluster of bottom strand genes includes transcription regulators, the transposase, and a number of small genes of unknown function.
-The lysogeny control region is likely to include genes 16 and 17, located at the interface of the bottom strand/top strand gene clusters. This is followed by a lysis cassette consisting genes encoding a holin, endolysin, Rz and Rz1.
-Proteins 27 through 51 encompass the head and tail morphogenesis cassette.
The BcepMu tail biosynthetic cassette proteins are recognizably related both in sequence and in gene order to those of coliphage P2.

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	***2009.003cB***	(assigned by ICTV officers)

To create a new genus to contain the species listed below

Code	***2009.003dB***	(assigned by ICTV officers)

To name the new genus: *Bcepmulikevirus*

assigning a new genus to higher taxa

Code	***2009.003eB***	(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	***2009.003fB***	(assigned by ICTV officers)

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

Burkholderia phage BcepMu

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

Code	***2009.003gB***	(assigned by ICTV officers)

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

Burkholderia phage BcepMu
Burkholderia phiE255

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 BcepMu

Reasons to justify the choice of type species:

BcepMu was the first sequenced phage within this genus. EM images are appended (Figure 2)

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:

Langley R, Kenna DT, Vandamme P, Ure R, Govan JR: Lysogeny and bacteriophage host range within the Burkholderia cepacia complex. Journal of Medical Microbiology 2003, 52: 483-490.

Lavigne R, Seto D, Mahadevan P, Ackermann H-W, Kropinski AM: Unifying classical and molecular taxonomic classification: analysis of the Podoviridae using BLASTP-based tools. Research in Microbiology 2008, 159: 406-414.

Summer EJ, Gonzalez CF, Carlisle T, Mebane LM, Cass AM, Savva CG et al.: Burkholderia cenocepacia phage BcepMu and a family of Mu-like phages encoding potential pathogenesis factors. Journal of Molecular Biology 2004, 340: 49-65.

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.

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.

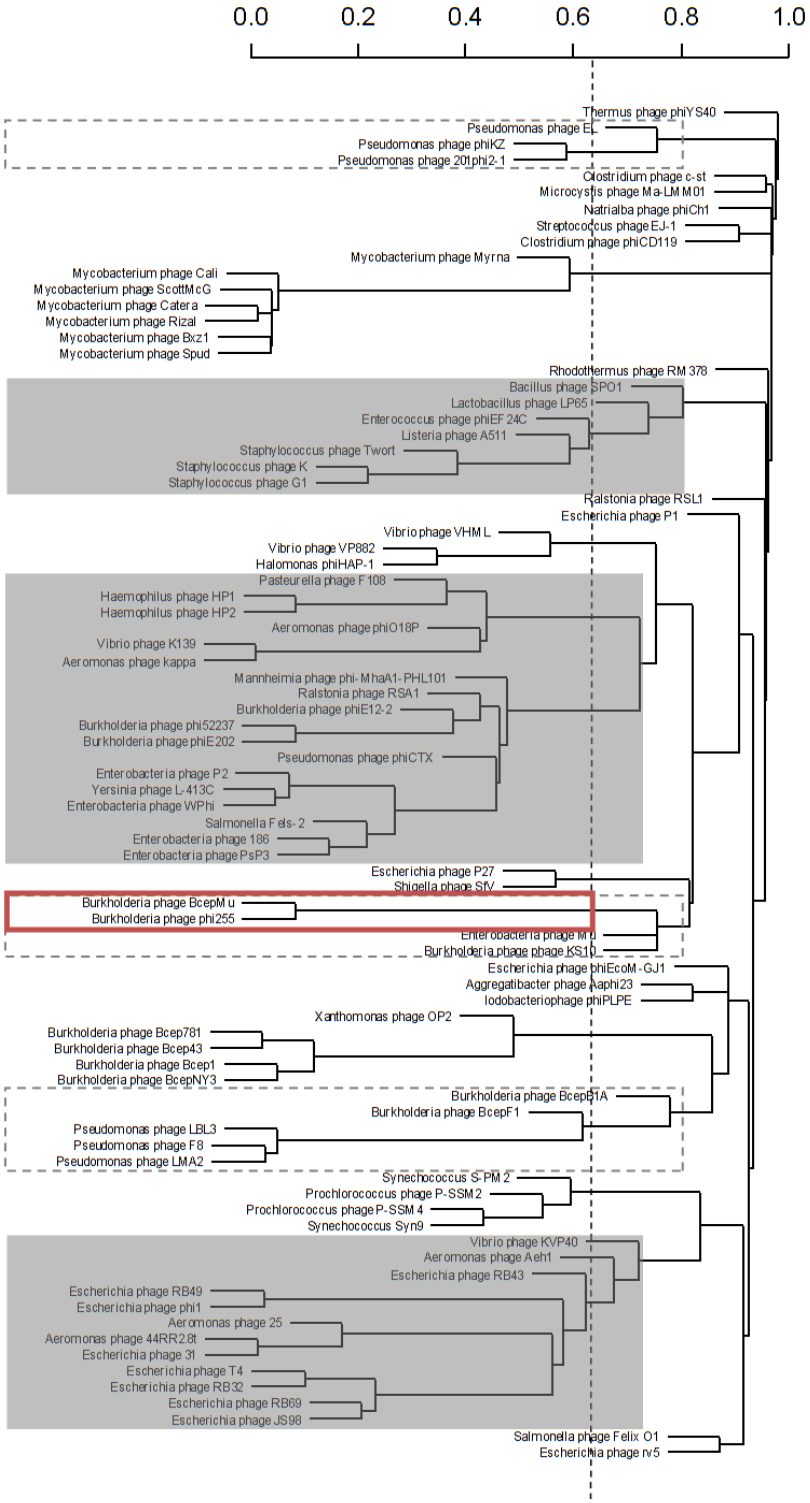

Figure 1: Hierarchical cluster dendrogram of the *Myoviridae*
The relative dissimilarity between the phage proteomes (between 0.0 and 1.0) forms the basis for the proposed groupings. The dotted lines reflects the cut-off value used for the establishement of genera, used consistently for all *Myoviridae* and the previously defined *Podoviridae* (Lavigne et al., 2008). Subfamily and tentative subfamily groupings are indicated in the grey and dotted boxes, respectively. The members of the genus *Bcepmulikevirus* are highlighted in the red box. Note the relationship with phage Mu, which is clearly present, but falls outside the correlation parameter for inclusion within the same genus.

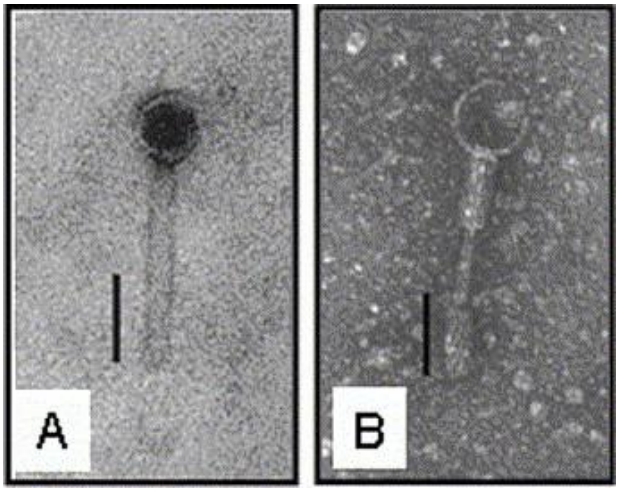

Figure 2. Morphology of intact (A) and inactivated (B) particles of BcepMu. The bar represents 100 nm. Phage lysates were prepared and either imaged immediately (A) or stored for one week at 4 °C prior to imaging (B). Image B shows a typical disintegrating particle with a broken head and partially exposed tail core.

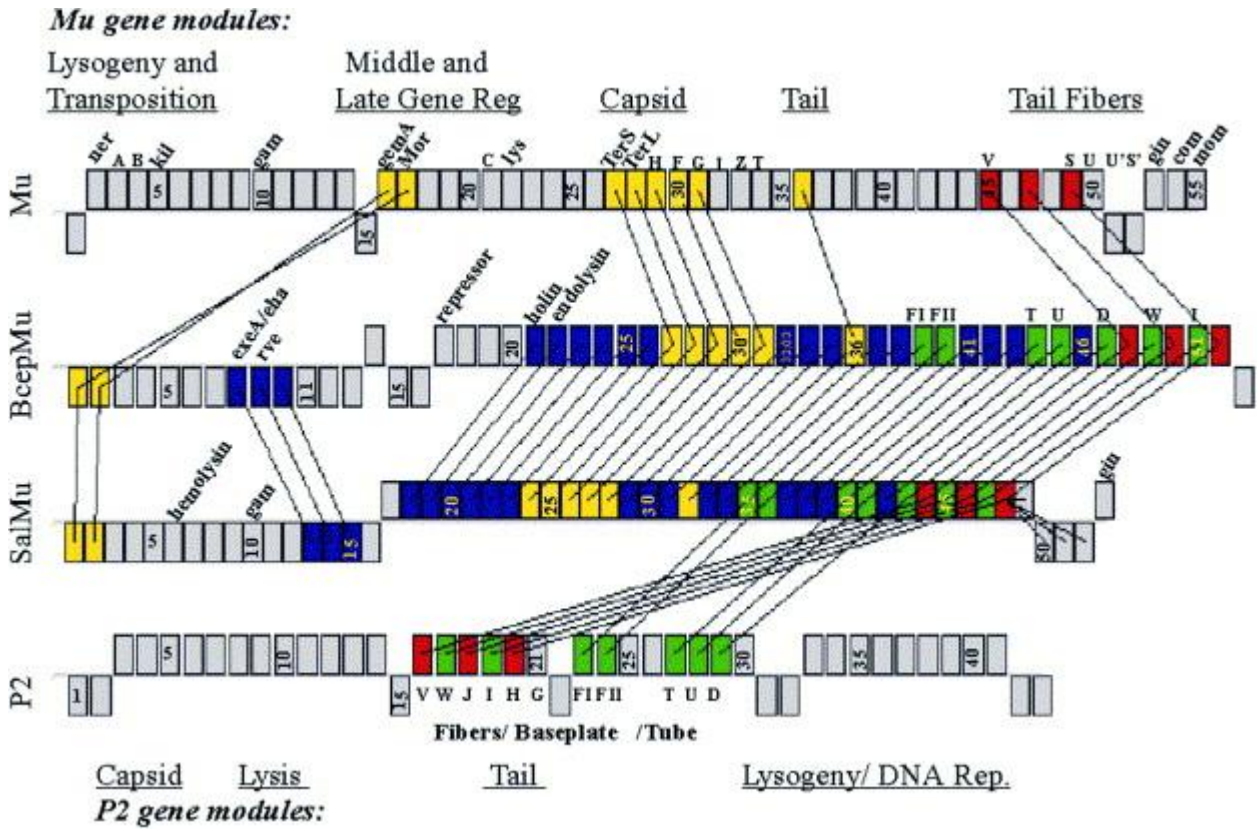

Figure 3. BcepMu shows modular homology with phages Mu and P2. GenomePixelizer (Allometra) representations of the Mu, BcepMu, (prophage SalMu) and P2 coding regions are shown, with lines connecting homologs. The Mu map was derived from NC_000929 and the P2 map was derived from entry NC_001895. Color coding: yellow, genes conserved between Mu, BcepMu and prophage SalMu; blue, genes conserved between BcepMu and prophage SalMu only; green, genes conserved between P2, BcepMu and prophage SalMu; red, genes homologous in all four phages; gray, genes not shared between any of these phages. Functional gene modules are labeled for Mu and P2. Relevant genes are annotated from the Mu and P2 maps.