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:	***2013.038a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *Bcep22likevirus* within the family *Podoviridae*
(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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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	

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

Date first submitted to ICTV: June 2013
Date of this revision (if different to above): July 2014

MODULE 2: NEW SPECIES

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.038aB***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Bcep22likevirus* (new)**
Subfamily:	
Family:	***Podoviridae***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Burkholderia phage Bcep22	AY349011.3
Burkholderia phage Bcepil02	FJ937737.2
Burkholderia phage Dc1	JN662425.1
Burkholderia phage Bcepmigl	JX104231.1

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus.

MODULE 3: NEW GENUS

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.038bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Podoviridae***
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.038cB***	(assigned by ICTV officers)

To name the new genus: *Bcep22likevirus*

Assigning the type species and other species to a new genus

Code	***2013.038dB***	(assigned by ICTV officers)

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

Burkholderia phage Bcep22

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

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

4

Reasons to justify the creation of a new genus:

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

This genus was originally recognized by the Gill et al. (1). These four phages infected *Burkholderia cenocepacia* strain (Phage DC1 (2) has a broader host range which includes *B. cepacia* and *B. stabilis*). They possess genomes ranging from 61.8 - 63.8 kb, with G+C contents of 65.3 - 66.2. In spite of producing clear plaques they possess repressor-type and recombinase proteins but do not appear to form lysogens (1). Bcep22 has a capsid diameter of 71 nm and a short, noncontractile tail measuring 15 nm in length by 14 nm in width. Unique characteristics of these phages include: (a) the physical separation of the genes for the small and large subunits of terminase; (b) the presence of a CsrA (carbon storage regulator) only previously found in *Pseudomonas* phage F116 and *Erwinia* phage PEp14; (c) an extremely large (4602-4667 amino acid residue), virion-associated, multidomain protein; (d) a RimL (COG1670, Acetyltransferases) only previously found in *Sinorhizobium* phage PBC5 and *Myxococcus* phage Mx8; and, (e) multiple putative tail fiber protein orthologs. They all possess a single tRNA. EMBOSS Stretcher analysis shows that these phages share 71-76% DNA sequence identity; while CoreGenes 2.0 (3,4) reveals that they share 68-79% homologous proteins.

Origin of the new genus name:

Burkholderia phage Bcep22

Reasons to justify the choice of type species:

The genus *Bcep22likevirus* is named after the first isolated and sequenced phage of this group, *Burkholderia cepacia* phage Bcep22.

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.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus.

MODULE 9: APPENDIX: supporting material

additional material in support of this proposal

References:

1. Gill JJ, Summer EJ, Russell WK, Cologna SM, Carlile TM, Fuller AC, Kitsopoulos K, Mebane LM, Parkinson BN, Sullivan D, Carmody LA, Gonzalez CF, LiPuma JJ, Young R. 2011. Genomes and characterization of phages Bcep22 and BcepIL02, founders of a novel phage type in *Burkholderia cenocepacia*. J Bacteriol. 193(19):5300-13
2. Lynch KH, Stothard P, Dennis JJ. 2012. Characterization of DC1, a broad-host-range Bcep22-like podovirus. Appl Environ Microbiol. 2012 78(3):889-91.
3. Mahadevan P, King JF, Seto D. 2009. Data mining pathogen genomes using GeneOrder and CoreGenes and CGUG: gene order, synteny and *in silico* proteomes. Int J Comput Biol Drug Des. 2(1):100-14.
4. Kropinski AM, Borodovsky M, Carver TJ, Cerdeño-Tárraga AM, Darling A, Lomsadze A, Mahadevan P, Stothard P, Seto D, Van Domselaar G, Wishart DS. 2009. *In silico* identification of genes in bacteriophage DNA. Methods Mol Biol. 502:57-89.
5. Darling AE, Mau B, Perna NT. 2010. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 5(6):e11147.

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 but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

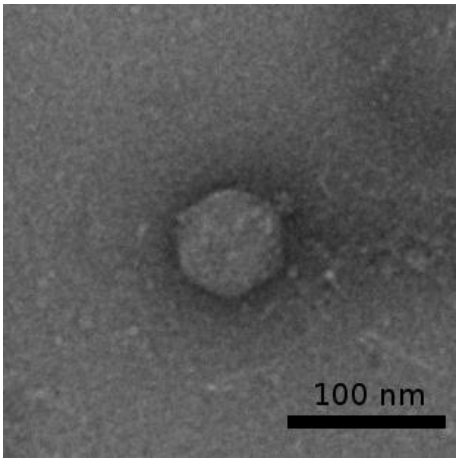

Figure 1. Electron micrograph of 2% (wt/vol) uranyl acetate-stained preparation of phage Bcep22 (kindly provided by J.J. Gill and R. Young) clearly showing that it is a member of the *Podoviridae*. Bar, 100 nm.

Table 1. Phage genomes

Phage	GenBank Accession No.	Genome size (bp)	Mol%G+C tRNA	Termini	% DNA sequence identity (a)	% Shared proteins (b)
Burkholderia phage Bcep22	AY349011.3	63,882	65.31	Circularly permuted	100%	100%
Burkholderia phage Bcepil02	FJ937737.2	62,715	66.20	Circularly permuted	71.2	70.1
Burkholderia phage Dc1	JN662425.1	61,847	66.21		71.2	67.5
Burkholderia phage Bcepmigl	JX104231.1	62,952	65.51		75.8	79.2

(a) EMBOSS Stretcher (relative to Bcep22)
(b) CoreGenes 2.0

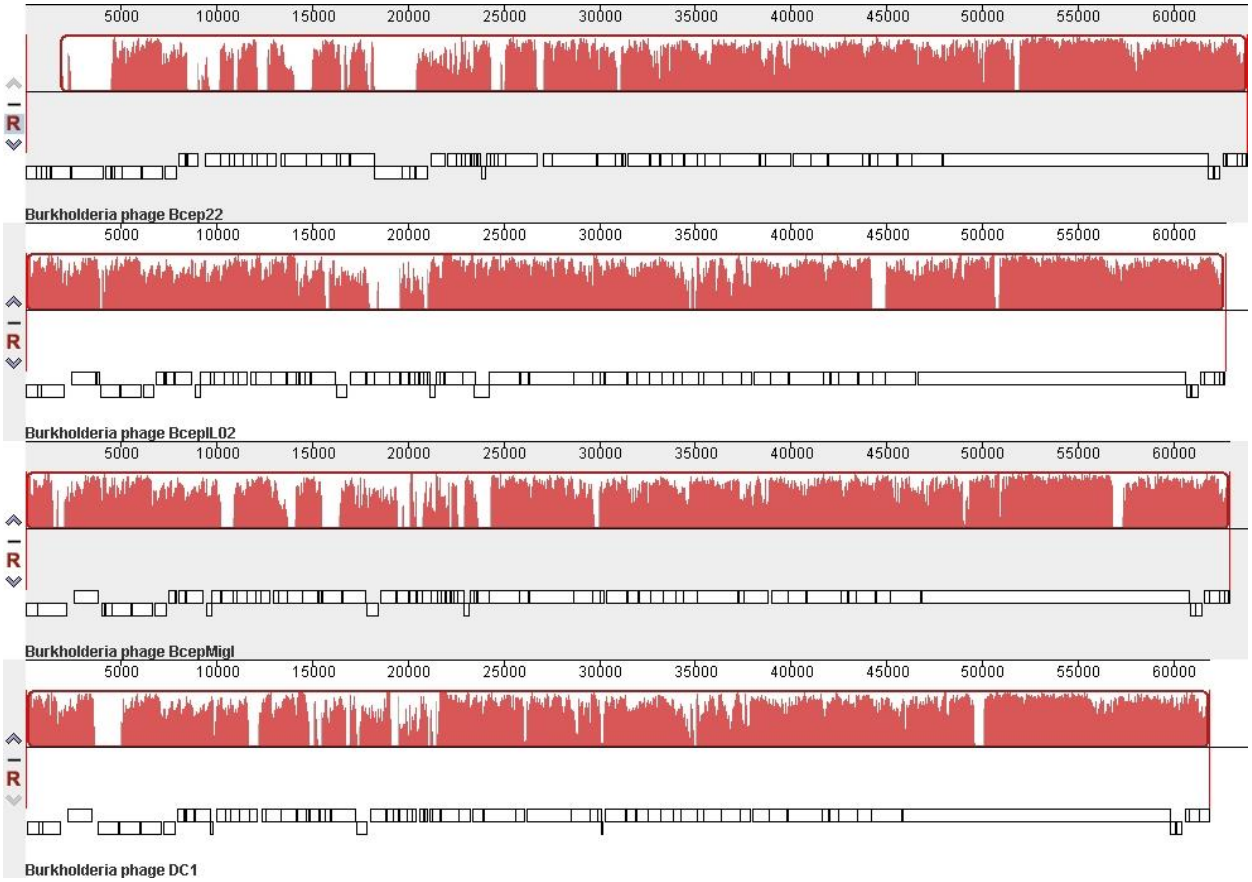

Figure 1. progressiveMauve alignment (Darling et al. 2010) of the genomes of the proposed genus *Bcep22likevirus* (full genome represented by its annotated ORFs in white blocks. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

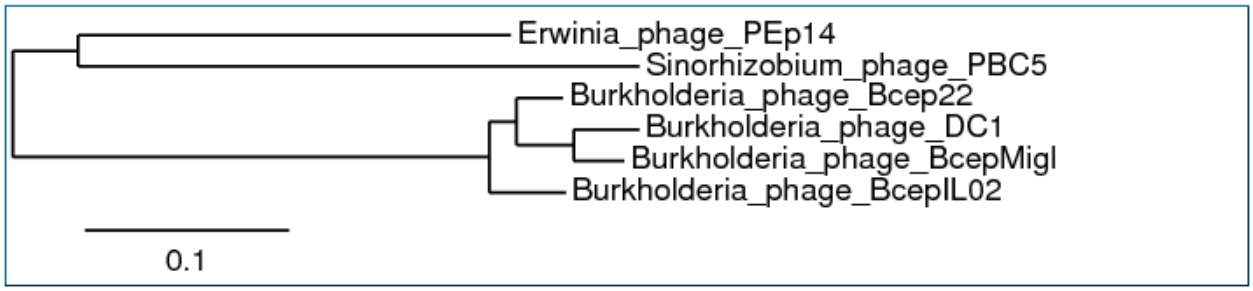

Figure 2. Phylogeny of capsid proteins from members of the *Bcep22likevirus* and relatives constructed using “one click” at phylogeny.fr. *Erwinia* phage PEp14 is also a member of the Podoviridae.