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:	***2013.032a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *Wbetalikevirus*, within the family *Siphoviridae*
(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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Rob Edwards raedwards@gmail.com

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	***2013.032aB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Wbetalikevirus* (new)**
Subfamily:	
Family:	***Siphoviridae***
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.

	GenBank sequence accession number(s) of reference isolate:
Bacillus phage Wbeta	DQ289555

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

Bacillus phage Wβ (WBeta) is a temperate member of *Siphoviridae*, which gave rise to a number of lytic derivatives important in the typing of *Bacillus anthracis* (Table 1). Since these phages all appear to have derived from *Bacillus* phage Wbeta through a variety of mutations they should all be classified into a single species.

MODULE 3: NEW GENUS

creating a new genus

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

Code	***2013.032bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Siphoviridae***
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	***2013.032cB***	(assigned by ICTV officers)

To name the new genus: *Wbetalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.032dB***	(assigned by ICTV officers)

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

Bacillus phage Wbeta

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:**

1

Reasons to justify the creation of a new genus:

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

Bacillus phage WBeta is a temperate member of *Siphoviridae*, which gave rise to a number of lytic derivatives important in the typing of *Bacillus anthracis* (Table 1). Since these phages all appear to have derived from *Bacillus* phage Wbeta through a variety of mutations they should all be classified into a single species. The lytic derivatives Fah, Cherry and γ (Gamma) have been reported previously to be in essence the same phage containing variations at three places in the genome (1, 2, 3). Table 1 lists the general characteristics of these phages.

We propose 40% shared proteins with the type phage for new phages to belong to this genus.

Origin of the new genus name:

Bacillus phage Wbeta

Reasons to justify the choice of type species:

The original isolate of this group.

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.

Since these phages all appear to have derived from *Bacillus* phage Wbeta through a variety of mutations they should all be classified into a single species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Fouts DE, Rasko DA, Cer RZ, Jiang L, Fedorova NB, Shvartsbeyn A, Vamathevan JJ, Tallon L, Althoff R, Arbogast TS, Fadrosh DW, Read TD, Gill SR. Sequencing *Bacillus anthracis* typing phages gamma and cherry reveals a common ancestry. J Bacteriol. 2006; 188(9):3402-8.

2. Schuch R, Fischetti VA. Detailed genomic analysis of the Wbeta and gamma phages infecting *Bacillus anthracis*: implications for evolution of environmental fitness and antibiotic resistance. J Bacteriol. 2006; 188(8):3037-51.

3. Minakhin L, Semenova E, Liu J, Vasilov A, Severinova E, Gabisonia T, Inman R, Mushegian A, Severinov K. Genome sequence and gene expression of *Bacillus anthracis* bacteriophage Fah. J Mol Biol. 2005 Nov 18;354(1):1-15.

4. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147

5. Rohwer F, Edwards RE (2002) The Phage Proteomic Tree: a genome-based taxonomy for phage. Journal of Bacteriology 184: 4529-4535

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.

Table 1. Phage genomes belonging to the proposed genus

Phage	GenBank Accession No.	Genome size (bp)
Gamma-LSU (Wγ^L)	DQ222855	38,067
Gamma-USAMRIID (Wγ^U)	DQ222853	37,253
Cherry (Wγ^C)	DQ222851	36,615
Gamma-d'Herelle (Wγ^d)	DQ289556	37,373
Wbeta (Wβ)	DQ289555	40,864
Gamma-	DQ221100	36,083

Porton (Wγ^P)		
Fah	DQ150593	37,974

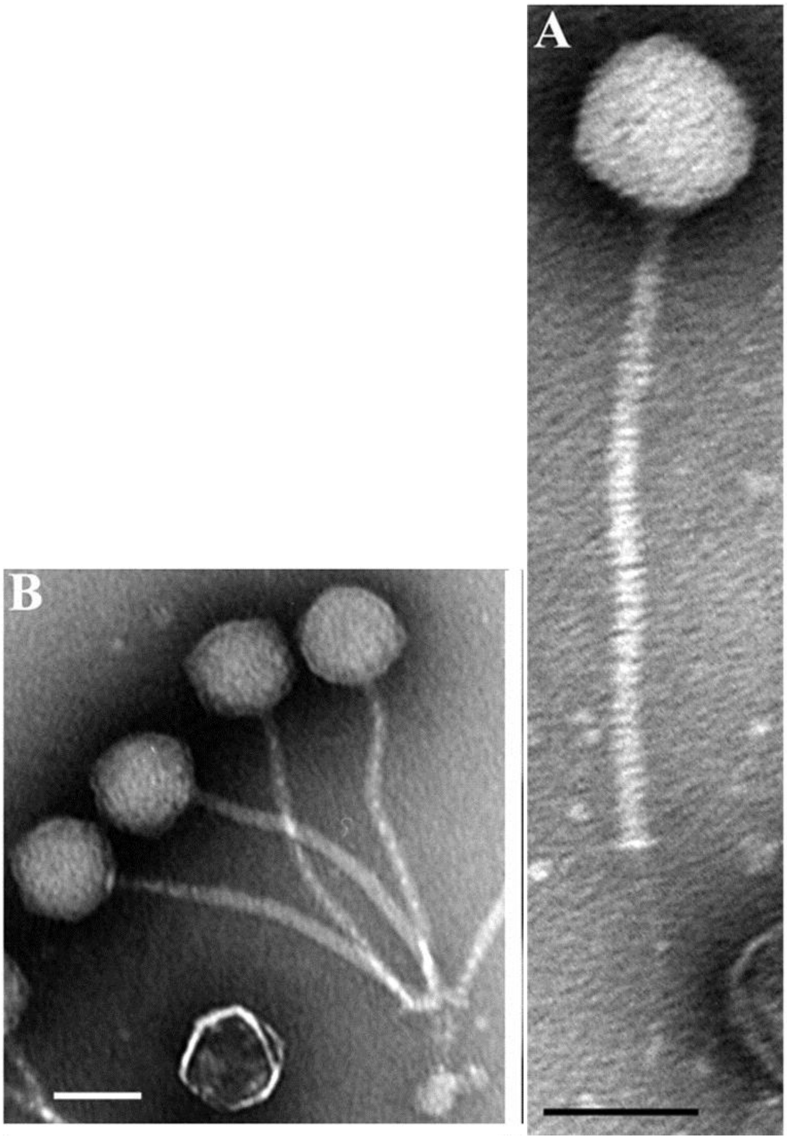

Figure 1. Electron micrograph of *Bacillus* phage Gamma (http://jb.asm.org/content/188/8/3037/F1.expansion.html)

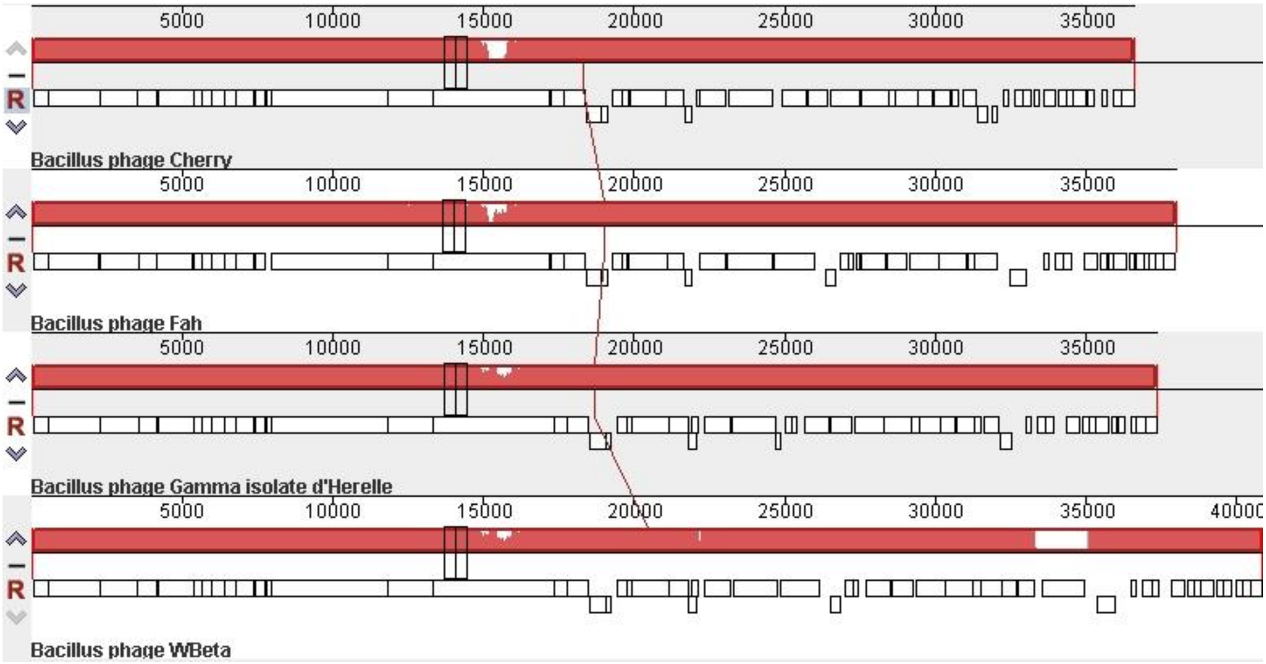

Figure 2. progressiveMauve alignment of the genomes of *Bacillus* phages Wβ, Cherry, Gamma d'Herelle and Fah indicates that they are very similar. Alignment of the phage genomes belonging to the proposed genus (full genome represented by its annotated ORFs in white blocks) (4). Colored blocks indicate 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.

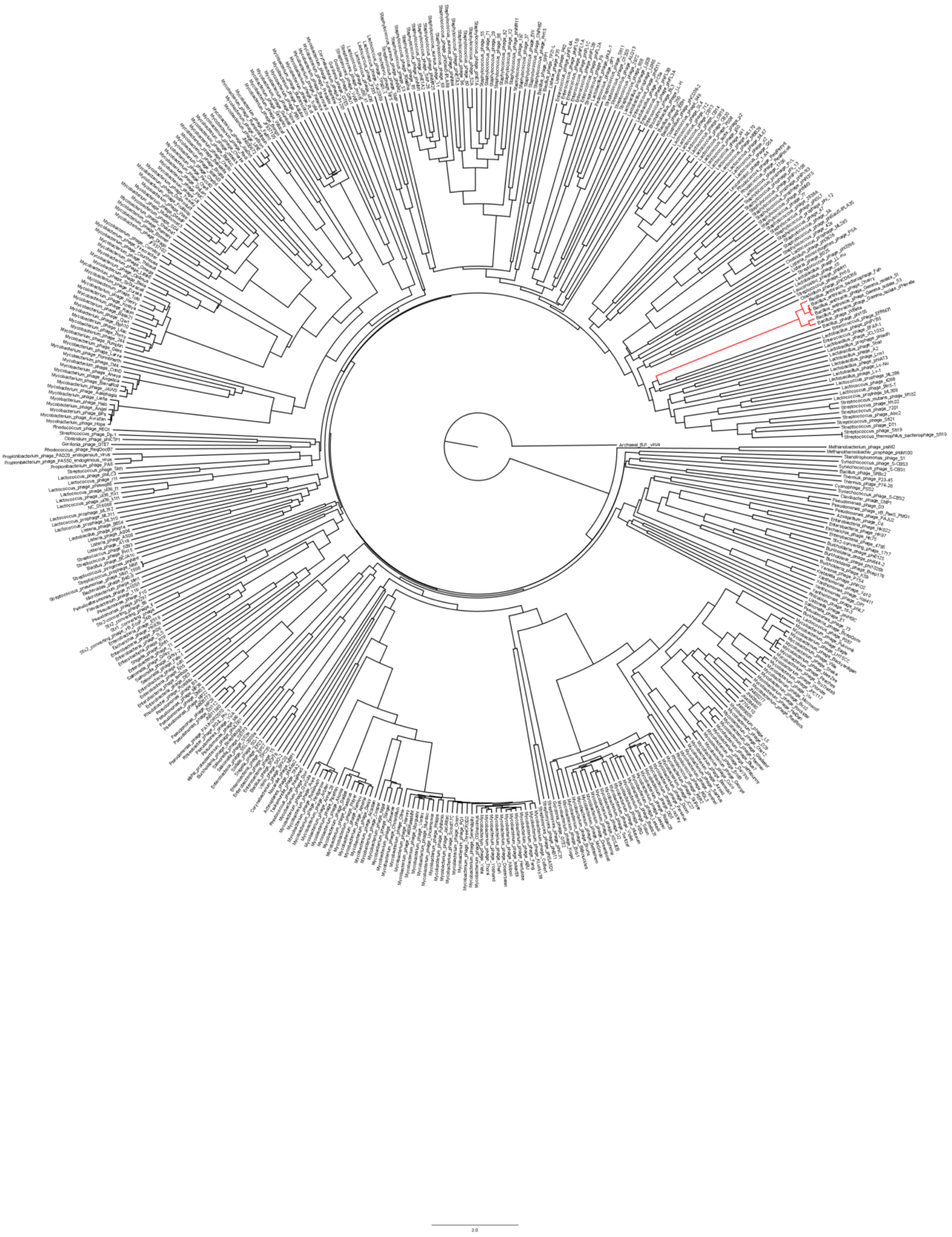

Figure 3: Phage Proteomic Tree (Rohwer & Edwards, 2002) of all the *Siphoviridae* phages in the NCBI database November 2012. Briefly, all predicted proteins sequences are compared with all others and a length-corrected protein distance matrix was calculated based on CLUSTALW alignment of sequences with a BLASTP e value < 0.001, with missing protein penalties of 10 and gap extension penalties of 0.20 (5). The tree was generated using FITCH. The proposed genus is in red. The scale bar represents protein distances of 2.0..

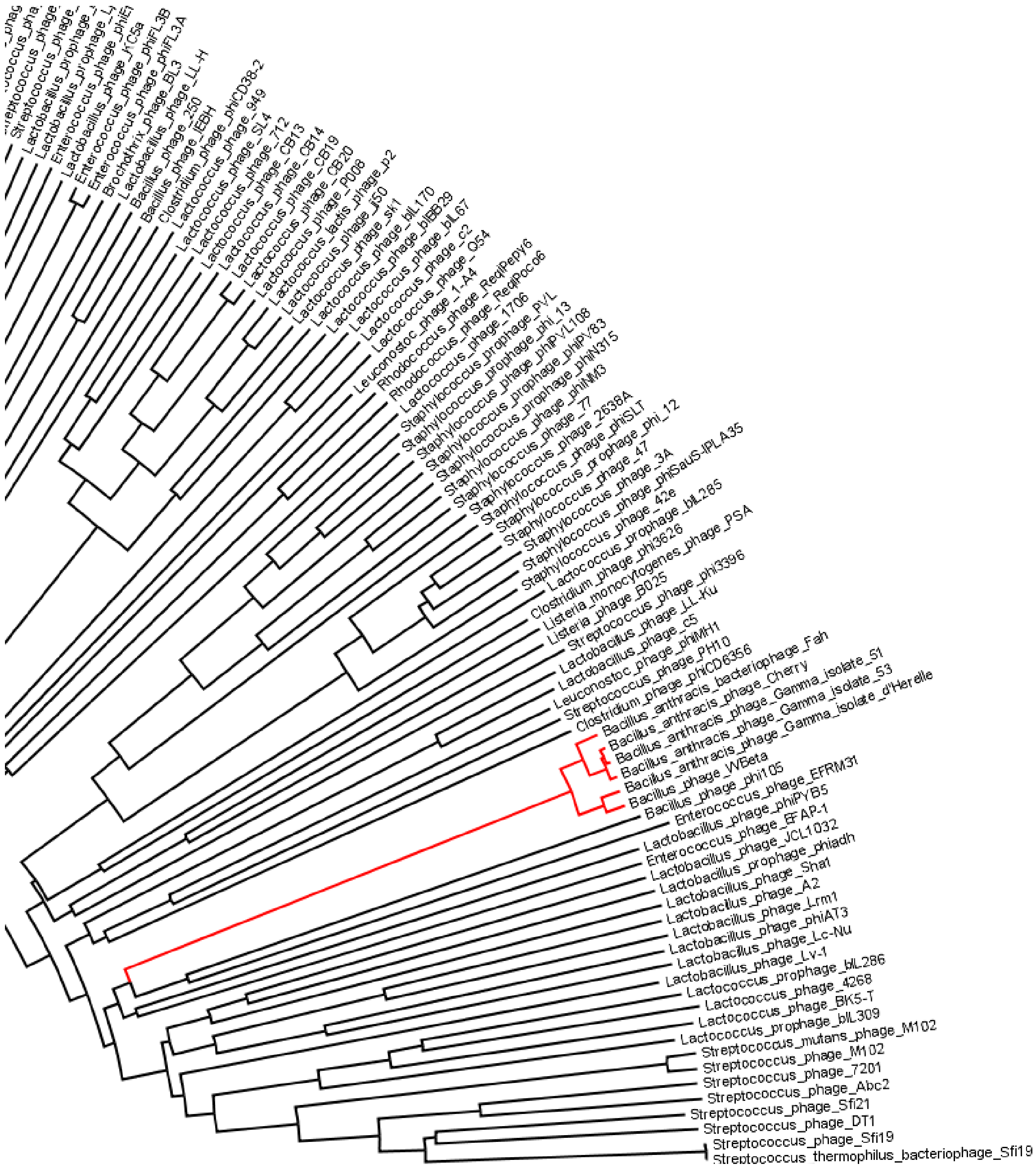

Figure 4: Fragment of the phylogenetic tree of Figure 3, zoomed in on the proposed genus.