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:	***2013.037a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *Andromedalikevirus*, within the family *Siphoviridae*, containing 8 new species
(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	***2013.037aB***	(assigned by ICTV officers)

To create 8 new species within:

Genus:	***Andromedalikevirus* (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 andromeda	KC330684
Bacillus phage eoghan	KC330680
Bacillus phage taylor	KC330682
Bacillus phage curly	KC330679
Bacillus phage finn	KC330683
Bacillus phage glittering	KF669651
Bacillus phage blastoid	KF669648
Bacillus phage riggi	KF669659

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.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.037bB***	(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	***2013.037cB***	(assigned by ICTV officers)

To name the new genus: *Andromedalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.037dB***	(assigned by ICTV officers)

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

Bacillus phage andromeda

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:**

8

Reasons to justify the creation of a new genus:

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

These are *Bacillus* siphoviruses with genomes of ~49,500bp, and a G+C content of approximately 42%. The heads measure ~48 to 57 nm in diameter and the flexible tails varying in length from 11 to 149 nm (Figure 1). All have ~800bp terminal repeats, similar gene content, and host range. BLASTN and BLASTX analyses against NCBI's Viruses (taxid:10239) database demonstrates no homologs. They share a high degree of DNA identity and shared protein content (Table 1).

Origin of the new genus name:

Bacillus phage Andromeda

Reasons to justify the choice of type species:

The isolate chosen by the isolators as the type species

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. Therefore, *Bacillus* phage Gemini, which shares 99.8% sequence similarity with *Bacillus* phage Andromeda is considered a strain.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1: Laura Lorenz; Bridget Lins, Jonathan Barrett, Andrew Montgomery; Stephanie Trapani, Anne Schindler; Steven G Cresawn, Gail Christie, Louise Temple. Genomic characterization of six novel *Bacillus pumilus* bacteriophages. Virology, 444(1-2):374-83, 2013

2: Matthew,S.P., Decker,S.L., Chamakura,K.R. and Kuty Everett,G.F. Complete Genome of *Bacillus pumilus* Siphophage Glittering. Genome Announc 1 (6), e00856-13 (2013)

3: Still,E.L., Riggi,C.F., Chamakura,K.R. and Kuty Everett,G.F. Complete Genome of *Bacillus pumilus* Siphophage Riggi. Genome Announc 1 (6), e00861-13 (2013)

4: Mash,S.J., Minahan,N.T., Chamakura,K.R. and Kuty Everett,G.F. Complete Genome of *Bacillus pumilus* Siphophage Blastoid. Genome Announc 1 (6), e00854-13 (2013)

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

Table 1. Phage genomes

Phage	GenBank Accession No.	Genome size (bp)	Mol%G+C	Termini	% DNA sequence identity (a)	% Shared proteins (b)
Bacillus phage Andromeda	KC330684	49,259	41.91	~800bp terminal repeats; defined ends	100%(c)	100%
Bacillus phage Eoghan	KC330680	49,458	42.21	~800bp terminal repeats; defined ends	75.4	86.1
Bacillus phage Taylor	KC330682	49,492	42.29	~800bp terminal repeats; defined ends	75.7	86.1

Bacillus phage Gemini	KC330681	49,362	41.90	~800bp terminal repeats; defined ends	99.8**(c)**	98.7
Bacillus phage Curly	KC330679	49,425	41.82	~800bp terminal repeats; defined ends	91.1	92.4
Bacillus phage Finn	KC330683	50,161	41.69	~800bp terminal repeats; defined ends	73.3	88.6
Bacillus phage Glittering	KF669651	49,246	42.05	unknown	94.5	92.4
Bacillus phage Blastoid	KF669648	50,354	42.23	unknown	71.2	86.1
Bacillus phage Riggi	KF669659	49,836	41.46	unknown	71.9	89.9

(a) EMBOSS Stretcher (relative to Andromeda)
(b) CoreGenes 2.0
(c) Strain of same species

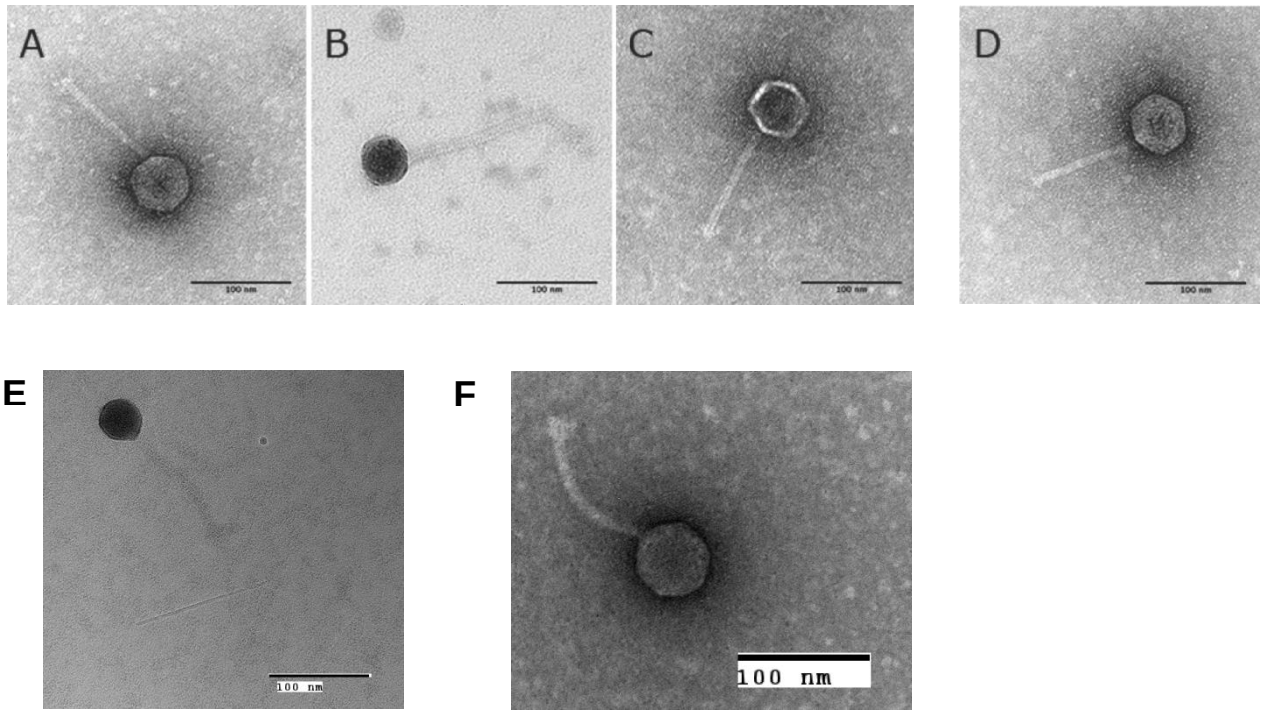

Figure 1. Electron micrographs of negatively stained *Bacillus pumilus* phages Curly, A; Gemin,i B; Eoghan, C; Taylor, D; Finn, E; and Andromeda, F.

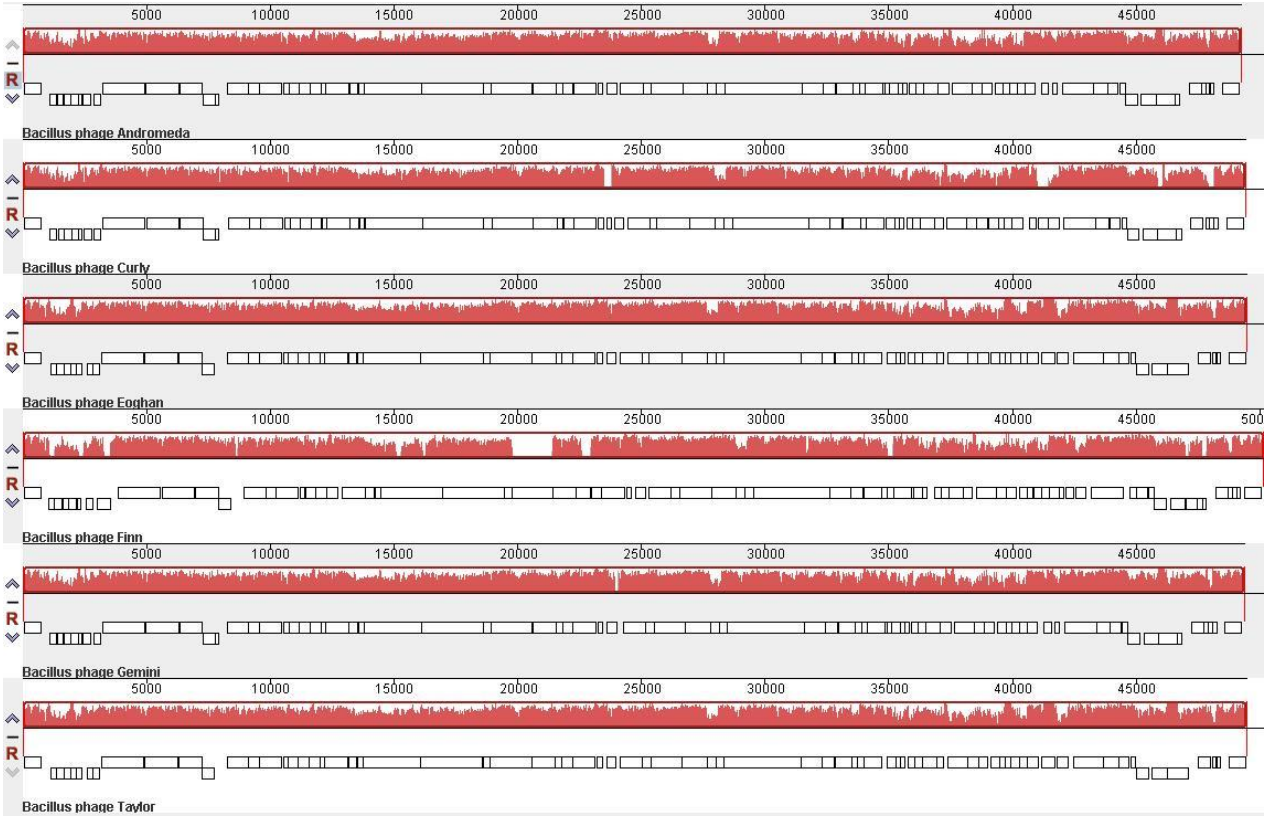

Figure 2. progressiveMauve alignment of the phage genomes belonging to the proposed genus (full genome represented by its annotated ORFs in white blocks) (2). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence 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.

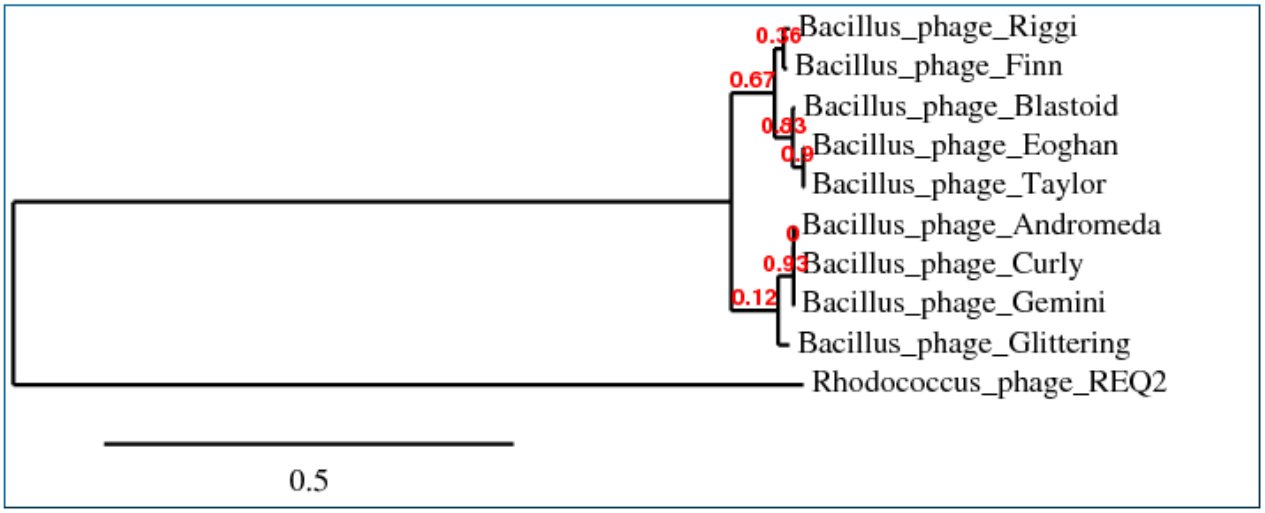

Fig.3. Phylogenetic analysis of the major capsid protein from this group of phages (One Click phylogeny.fr).