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:	***2016.028a-jB***	(to be completed by ICTV officers)

Short title: To amend the description of the genus *Reyvirus*, creating one (1) new subfamily *Mclasvirinae* within the *Siphoviridae*.
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☐	**3** ☒	**4** ☒	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☐	**10** ☒

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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 Bacterial and Archaeal Viruses Subcommittee

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.028aB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Mclasvirinae* (new)**
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	***2016.028bB***	(assigned by ICTV officers)

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

Assigning the type species and other species to a new genus

Code	***2016.028cB***	(assigned by ICTV officers)

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

Mycobacterium virus Bongo

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

The Actinobacteriophage Database (http://phagesdb.org/clusters/M/) recognizes that the Cluster M Mycobacterium phages fall into two groups: M1, represented by Mycobacterium phage Bongo and M2, represented by Mycobacterium phage Rey. These clusters are based upon overall DNA sequence relatedness. Phage Rey has an 83.7 kb genome (60.9 mol% G+C) and encodes 153 CDS and 21 tRNAs. The averages for the M1 phages are: 80.8 kb genome length, 61.6 mol% G+C, 135.5 CDS, and 17.5 tRNAs. The data in 2013.021a-dB revealed distant DNA relatedness and phylogenetic distance. Mycobacterium phage Bongo only shares 49% overall DNA sequence identity with Mycobacterium phage Rey. They are also phylogenetically distinct (Fig. 1).

Origin of the new genus name:

Mycobacterium phage Bongo.

Reasons to justify the choice of type species:

The first of its type to be sequenced.

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. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 4: **NEW SUBFAMILY**

creating a new subfamily

A subfamily can only be created within a family.

Code	***2016.028dB***	(assigned by ICTV officers)

To create a new subfamily within:

Family:	***Siphoviridae***
Order:	***Caudovirales***

If the family has yet to be created (in Module 5) please write "**(new)**" after the proposed name.

- If there is no Order, write "**unassigned**" here.

naming a new subfamily

Code	***2016.028eB***	(assigned by ICTV officers)

To name the new subfamily: *Mclasvirinae* (new)

genera and species assigned to the new subfamily

Code	***2016.028fB***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family

Reyvirus (existing genus currently unassigned in the family *Siphoviridae*)

Bongovirus (new genus)

The new subfamily 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 unassigned species that the subfamily will contain (those NOT within any of the genera listed above):**

0

Reasons to justify the creation of the new subfamily:

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

The Actinobacteriophage Database (http://phagesdb.org/clusters/M/) recognizes that the Cluster M Mycobacterium phages fall into two groups: M1, represented by Mycobacterium phage Bongo and M2, represented by Mycobacterium phage Rey. These clusters are based upon overall DNA sequence relatedness. Phage Rey has an 83.7 kb genome (60.9 mol% G+C) and encodes 153 CDS and 21 tRNAs. The averages for the M1 phages are: 80.8 kb genome length, 61.6 mol% G+C, 135.5 CDS, and 17.5 tRNAs. The data in 2013.021a-dB revealed distant DNA relatedness and phylogenetic distance. Mycobacterium phage Bongo only shares 49% overall DNA sequence identity with Mycobacterium phage Rey. They are also phylogenetically distinct (Fig. 1)

Origin of the new subfamily name:

Sigil for **Cl**uster **M** **A**cinobacteriophage database **s**iphovirus.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2016.028gB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Mycobacterium virus Bongo

The present taxonomic position of these taxon/taxa:

Genus:	***Reyvirus***
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Member significantly different from Mycobacterium phage Rey.
We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

Part (b) re-assign to a higher taxon

Code	***2016.028hB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Bongovirus*** **(new)**
Subfamily:	***Mclasvirinae*** **(new)**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Part (c) taxon/taxa to be removed or moved

Code	***2016.028iB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Genus ***Reyvirus***

The present taxonomic position of these taxon/taxa:

Genus:	
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

See below

Part (d) re-assign to a higher taxon

Code	***2016.028jB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (c) as follows:

Genus:	
Subfamily:	***Mclasvirinae*** **(new)**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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 accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See section 2016.028fB

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008; 36(Web Server issue):W465-9.

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. Characteristics of Mycobacterium phages Bongo and Rey. These two viruses share ca. 50% sequence identity, which we consider too low to be considered members of the same genus.

Mycobacterium phage	**Actinobacter-iophage database cluster**	**GenBank Accession No.**	**Genome length (bp)**	**Mol% G+C**	**CDS**	**tRNA**	**Termini**
Bongo	M1	JN699628	80228	61.6	132	19	11-bp 3'-cohesive terminus (ACCTCCTGCAA)
Rey	M2	JF937105	83724	60.9	153	21	11-bp 3'-cohesive terminus (ACCCCATGCAA)

Table 2. Phages which are strains of the virus Mycobacterium phage Bongo.

Phage	**Accession No.**
Mycobacterium phage Bricole	KT591491.1
Mycobacterium phage PegLeg	KC900379.1

Fig. 1. Phylogenetic analysis of (A) large subunit terminase proteins, (B) major capsid proteins, and (C) major tail proteins of Mycobacterium phage Rey-related viruses and variety of other phage proteins constructed using "one click" at phylogeny.fr [3]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative (Syst Biol. 2006;55(4):539-52.) for details". The *Reyvirus, Bongovirus* cluster (*Mclasvirinae*) is indicated in red.

A. TerL protein

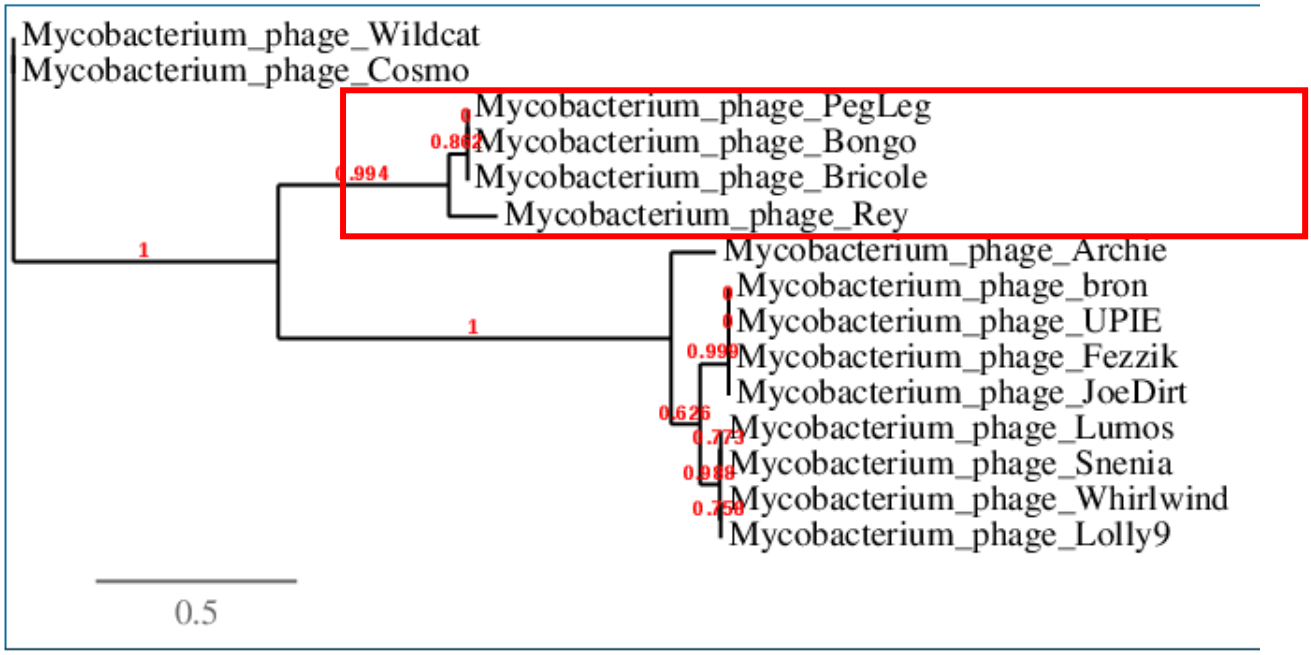

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

B. Major capsid proteins

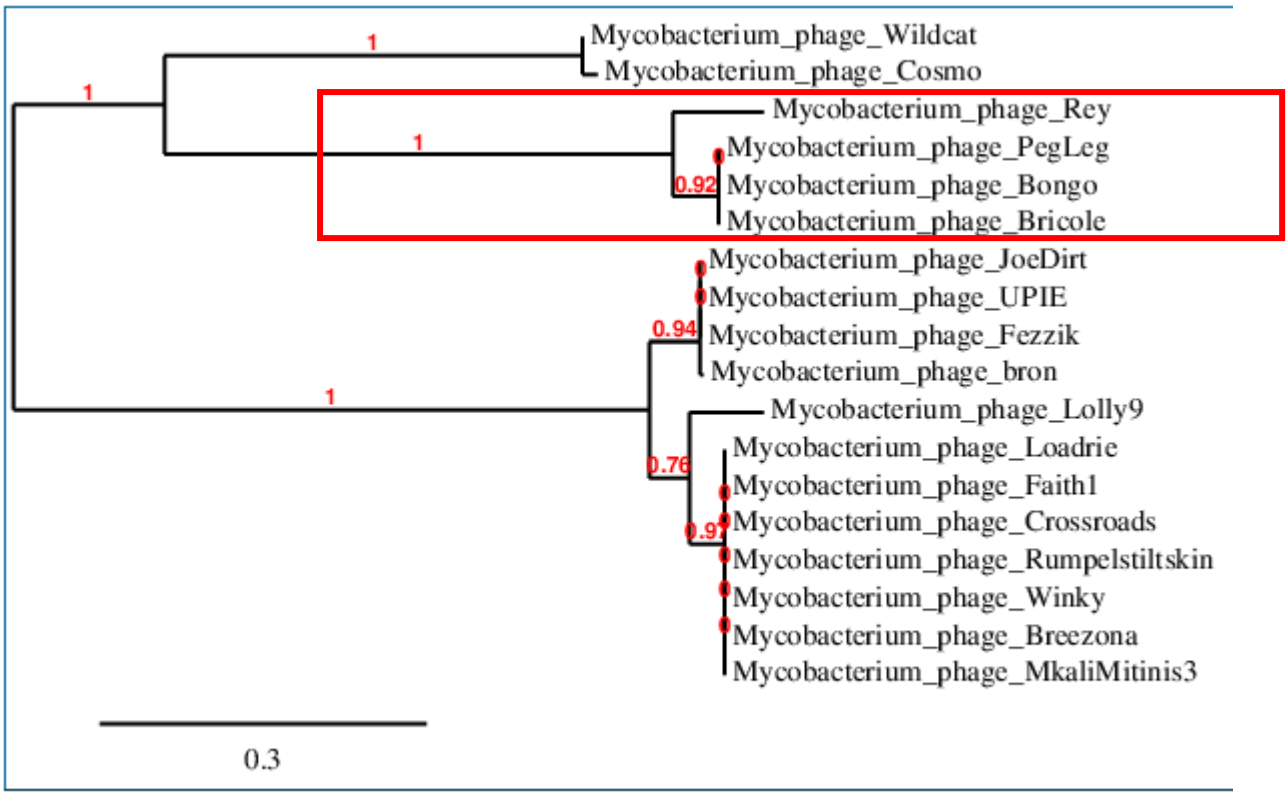

Figure 1: *Phylogenetic tree.*

C. Major tail proteins

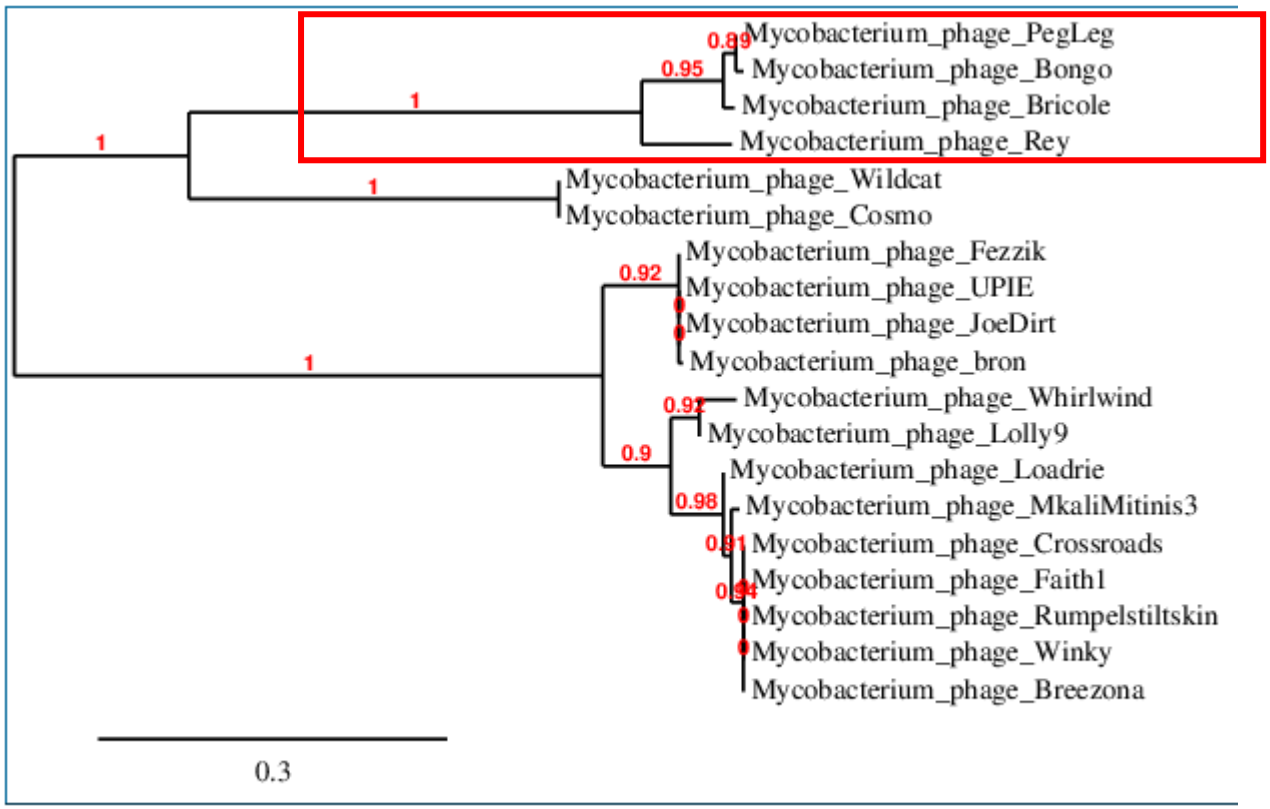

Figure 1: *Phylogenetic tree.*