



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:	2016.005a-yB	(to be completed by ICTV officers)			
Short title: To create one (1) new subfamily, <i>Bclavirinae</i> , including four (4) new genera in the family <i>Siphoviridae</i> . (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/> 8 <input type="checkbox"/>	4 <input checked="" type="checkbox"/> 9 <input type="checkbox"/>	5 <input type="checkbox"/> 10 <input checked="" type="checkbox"/>

Author(s):

Andrew M. Kropinski—University of Guelph (Canada)
Jens H. Kuhn—NIH/NIAID/IRF-Frederick, Maryland (USA)
Evelien M. Adriaenssens—University of Pretoria (South Africa)

Corresponding author with e-mail address:

Andrew M. Kropinski Phage.Canada@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 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 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	2016.005aB	(assigned by ICTV officers)
To create 5 new species within:		
Genus:	<i>Pg1virus</i>	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.
Subfamily:	<i>Bclasvirinae (new)</i>	
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Mycobacterium virus Suffolk</i>	Mycobacterium phage Suffolk	KF713485.1
<i>Mycobacterium virus Manad</i>	Mycobacterium phage Manad	KJ595576.1
<i>Mycobacterium virus Soto</i>	Mycobacterium phage Soto	KJ174157.1
<i>Mycobacterium virus Apizium</i>	Mycobacterium phage Apizium	KR781349.1
<i>Mycobacterium virus Osmaximus</i>	Mycobacterium phage OSmaximus	JN006064.1

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. 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 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	2016.005bB	(assigned by ICTV officers)	
To create 1 new species within:			
Genus:		<i>Rosebushvirus</i> (new)	
Subfamily:		<i>Bclasvirinae</i> (new)	
Family:		<i>Siphoviridae</i>	
Order:		<i>Caudovirales</i>	
		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.	
Name of new species:		Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Mycobacterium virus Godines</i>		Mycobacterium phage Godines	KR997932

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. 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 3: **NEW GENUS**

creating a new genus

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

Code	2016.005cB	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	Bclavirinae (new)	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
Family:	Siphoviridae	
Order:	Caudovirales	

naming a new genus

Code	2016.005dB	(assigned by ICTV officers)
To name the new genus: <i>Rosebushvirus</i>		

Assigning the type species and other species to a new genus

Code	2016.005eB	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Mycobacterium virus Rosebush</i>		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:		
2		

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 viruses differ significantly from the type virus: Mycobacterium phage PG1 (see also Actinobacteriophage Database (<http://phagesdb.org/phages/PG1/>), where Mycobacterium phage Rosebush is listed as a Subcluster B2 phage). The (average) properties of the members of each subcluster are listed below:

Subgroup	Members	Avg Size (bp)	Avg GC%	Avg Genes	Avg tRNAs	Representative
B1	103	68,537	66.5	100.1	0	Mycobacterium phage PG1
B2	13	67,306	69.0	88.6	0	Mycobacterium phage Rosebush
B3	18	68,749	67.5	102.1	0	Mycobacterium phage Athena
B4	10	70,921	68.8	92.3	0.1	Mycobacterium phage Cooper
B5	5	70,038	68.0	96.0	0	Mycobacterium phage Acadian
B6	5	71,139	70.0	95.0	0	Not in GenBank

They all possess circularly permuted genomes (Fig. 1D). The next closest related phage to the members of the genus *Rosebushvirus* is Mycobacterium phage OrangeOswald, a member of the *Pipefishvirus* genus. Both phages share 30% overall sequence identity as shown using BLASTN analysis at NCBI.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this genus.

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 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	2016.005fB		(assigned by ICTV officers)
To create 2 new species within:			
Genus:	<i>Acadianvirus</i> (new)		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.
Subfamily:	<i>Bclasvirinae</i> (new)		
Family:	<i>Siphoviridae</i>		
Order:	<i>Caudovirales</i>		
Name of new species:		Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Mycobacterium virus Bae</i>		Mycobacterium phage Bae	KR080199.1
<i>Mycobacterium virus Reprobate</i>		Mycobacterium phage Reprobate	KF024727.1

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. 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 3: **NEW GENUS**

creating a new genus

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

Code	2016.005gB	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	<i>Bclavirinae</i>	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
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	

naming a new genus

Code	2016.005hB	(assigned by ICTV officers)
To name the new genus: <i>Acadianvirus</i> (new)		

Assigning the type species and other species to a new genus

Code	2016.005iB	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Mycobacterium virus Acadian</i>		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:		
3		

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 viruses differ significantly from the type virus: *Mycobacterium* phage PG1 (see also Actinobacteriophage Database (<http://phagesdb.org/phages/PG1/>) where phage Rosebush is listed as a Subcluster B2 phage). The (average) properties of the members of each subcluster are listed below:

Subgroup	Members	Avg Size (bp)	Avg GC%	Avg Genes	Avg tRNAs	Representative
B1	103	68,537	66.5	100.1	0	<i>Mycobacterium</i> phage PG1
B2	13	67,306	69.0	88.6	0	<i>Mycobacterium</i> phage Rosebush
B3	18	68,749	67.5	102.1	0	<i>Mycobacterium</i> phage Athena
B4	10	70,921	68.8	92.3	0.1	<i>Mycobacterium</i> phage Cooper
B5	5	70,038	68.0	96.0	0	<i>Mycobacterium</i> phage Acadian
B6	5	71,139	70.0	95.0	0	Not in GenBank

They all possess circularly permuted genomes (Fig. 1D). The next closest related phage to the members of the genus *Acadianvirus* is *Mycobacterium* phage Cooper, a member of the *Coopervirus* genus. They share 46% overall sequence identity as shown using BLASTN analysis at NCBI.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this genus.

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 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	2016.005jB	(assigned by ICTV officers)
To create 5 new species within:		
Genus:	<i>Coopervirus</i> (new)	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.
Subfamily:	<i>Bclasvirinae</i> (new)	
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Mycobacterium virus Adawi</i>	Mycobacterium phage Adawi	KF279411.1
<i>Mycobacterium virus JAMaL</i>	Mycobacterium phage JAMaL	KF493881.1
<i>Mycobacterium virus BrownCNA</i>	Mycobacterium phage BrownCNA	KT270441.1
<i>Mycobacterium virus Bane1</i>	Mycobacterium phage Bane1	KF279412.1
<i>Mycobacterium virus Vincenzo</i>	Mycobacterium phage Vincenzo	KR080194.1

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. 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 3: **NEW GENUS**

creating a new genus

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

Code	2016.005kB	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	Bclavirinae (new)	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
Family:	Siphoviridae	
Order:	Caudovirales	

naming a new genus

Code	2016.005lB	(assigned by ICTV officers)
To name the new genus: <i>Coopervirus</i> (new)		

Assigning the type species and other species to a new genus

Code	2016.005mB	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Mycobacterium virus Cooper</i>		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:		
10		

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 viruses differ significantly from the type virus: Mycobacterium phage PG1 (see also Actinobacteriophage Database (<http://phagesdb.org/phages/PG1/>) where phage PG1 is listed as a Subcluster B1 phage). The (average) properties of the members of each subcluster are listed below:

Subgroup	Members	Avg Size (bp)	Avg GC%	Avg Genes	Avg tRNAs	Representative
B1	103	68,537	66.5	100.1	0	Mycobacterium phage PG1
B2	13	67,306	69.0	88.6	0	Mycobacterium phage Rosebush
B3	18	68,749	67.5	102.1	0	Mycobacterium phage Athena
B4	10	70,921	68.8	92.3	0.1	Mycobacterium phage Cooper
B5	5	70,038	68.0	96.0	0	Mycobacterium phage Acadian
B6	5	71,139	70.0	95.0	0	Not in GenBank

They all possess circularly permuted genomes. The next closest related phage to members of the genus *Coopervirus* is Mycobacterium phage Reprobate, a member of the *Acadianvirus* genus. They share 48% overall sequence identity as shown using BLASTN analysis at NCBI.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this genus.

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 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	2016.005nB	(assigned by ICTV officers)	
To create 1 new species within:			
Genus: <i>Pipefishvirus</i> (new)		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.	
Subfamily: <i>Bclasvirinae</i> (new)			
Family: <i>Siphoviridae</i>			
Order: <i>Caudovirales</i>			
Name of new species:		Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Mycobacterium virus Bernardo</i>		Mycobacterium phage Bernardo	KF493879

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. 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 3: **NEW GENUS**

creating a new genus

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

Code	2016.005oB	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	Bclavirinae (new)	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
Family:	Siphoviridae	
Order:	Caudovirales	

naming a new genus

Code	2016.005pB	(assigned by ICTV officers)
To name the new genus: <i>Pipefishvirus</i> (new)		

Assigning the type species and other species to a new genus

Code	2016.005qB	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Mycobacterium virus Pipefish</i>		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

These viruses differ significantly from the type virus: *Mycobacterium* phage PG1 (see also Actinobacteriophage Database (<http://phagesdb.org/phages/PG1/>) where phage PG1 is listed as a Subcluster B1 phage). The (average) properties of the members of each subcluster are listed below:

Subgroup	Members	Avg Size (bp)	Avg GC%	Avg Genes	Avg tRNAs	Representative
B1	103	68,537	66.5	100.1	0	<i>Mycobacterium</i> phage PG1
B2	13	67,306	69.0	88.6	0	<i>Mycobacterium</i> phage Rosebush
B3	18	68,749	67.5	102.1	0	<i>Mycobacterium</i> phage Athena
B4	10	70,921	68.8	92.3	0.1	<i>Mycobacterium</i> phage Cooper
B5	5	70,038	68.0	96.0	0	<i>Mycobacterium</i> phage Acadian
B6	5	71,139	70.0	95.0	0	Not in GenBank

The genus *Pipefishvirus* represents subgroup B3 in this table. The closest relative of the type species *Mycobacterium virus Pipefish* is *Mycobacterium* phage Qyrzula, member of the genus *Rosebushvirus* and shares on average less than 60% sequence identity.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this genus.

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	2016.005rB	(assigned by ICTV officers)
To create a new subfamily within:		
Family:	<i>Siphoviridae</i>	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.
Order:	<i>Caudovirales</i>	

naming a new subfamily

Code	2016.005sB	(assigned by ICTV officers)
To name the new subfamily: <i>Bclasvirinae</i>		

genera and species assigned to the new subfamily

Code	2016.005tB	(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. <ul style="list-style-type: none"> • 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 		
<i>Pg1virus</i> <i>Rosebushvirus</i> (new) <i>Acadianvirus</i> (new) <i>Coopervirus</i> (new) <i>Pipefishvirus</i> (new)		
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		
<i>Recognized by the Actinobacteriophage Database (http://phagesdb.org/clusters/B/) and ourselves as being distinct, but related.</i>		
Origin of the new subfamily name:		
<i>Bclasvirinae</i> , includes the abbreviation “BCLAS” which indicates that the viruses are part of the B Cluster in the Actinobacteriophage Database of Siphoviruses.		

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	2016.005uB	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
<i>Mycobacterium virus Acadian</i> , <i>Mycobacterium virus Athena</i> , <i>Mycobacterium virus Chrisnmich</i> , <i>Mycobacterium virus Cooper</i> , <i>Mycobacterium virus Gadjet</i> , <i>Mycobacterium virus Nigel</i> , <i>Mycobacterium virus Pipefish</i> , <i>Mycobacterium virus Rosebush</i> , <i>Mycobacterium virus Stinger</i> , <i>Mycobacterium virus Zemanar</i>		
The present taxonomic position of these taxon/taxa:		
Genus:	<i>Pg1virus</i>	Fill in all that apply.
Subfamily:	<i>Bclavirinae</i> (new)	
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	
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

These viruses differ significantly from the type virus: *Mycobacterium* phage PG1 (see also Actinobacteriophage Database (<http://phagesdb.org/phages/PG1/>) where phage *Mycobacterium* phage PG1 is listed as a Subcluster B1 phage). The (average) properties of the members of each subcluster are listed below:

Subgroup	Members	Avg Size (bp)	Avg GC%	Avg Genes	Avg tRNAs	Representative
B1	103	68,537	66.5	100.1	0	<i>Mycobacterium</i> phage PG1
B2	13	67,306	69.0	88.6	0	<i>Mycobacterium</i> phage Rosebush
B3	18	68,749	67.5	102.1	0	<i>Mycobacterium</i> phage Athena
B4	10	70,921	68.8	92.3	0.1	<i>Mycobacterium</i> phage Cooper
B5	5	70,038	68.0	96.0	0	<i>Mycobacterium</i> phage Acadian
B6	5	71,139	70.0	95.0	0	Not in GenBank

Part (b) re-assign to a higher taxon

Code	2016.005vB	(assigned by ICTV officers)
To re-assign the following taxon (or taxa): <i>Mycobacterium virus Acadian</i>		
Genus:	<i>Acadianvirus</i> (new)	<p>Fill in all that apply.</p> <ul style="list-style-type: none">If the higher taxon has yet to be created write “(new)” after its proposed name and complete relevant module to create it. <p>If no genus is specified, enter “unassigned” in the genus box.</p>
Subfamily:	<i>Bclavirinae</i> (new)	
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	

Part (b) re-assign to a higher taxon

Code	2016.005wB	(assigned by ICTV officers)
To re-assign the following taxon (or taxa): <i>Mycobacterium virus Chrisnmich, Mycobacterium virus Cooper, Mycobacterium virus Nigel, Mycobacterium virus Stinger, Mycobacterium virus Zemanar</i>		
Genus:	<i>Coopervirus</i> (new)	<p>Fill in all that apply.</p> <ul style="list-style-type: none">If the higher taxon has yet to be created write “(new)” after its proposed name and complete relevant module to create it. <p>If no genus is specified, enter “unassigned” in the genus box.</p>
Subfamily:	<i>Bclavirinae</i> (new)	
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	

Part (b) re-assign to a higher taxon

Code	2016.005xB	(assigned by ICTV officers)
To re-assign the following taxon (or taxa): <i>Mycobacterium virus Athena, Mycobacterium virus Gadjet, Mycobacterium virus Pipefish</i>		
Genus:	<i>Pipefishvirus</i> (new)	<p>Fill in all that apply.</p> <ul style="list-style-type: none">If the higher taxon has yet to be created write “(new)” after its proposed name and complete relevant module to create it. <p>If no genus is specified, enter “unassigned” in the genus box.</p>
Subfamily:	<i>Bclavirinae</i> (new)	
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	

Part (b) re-assign to a higher taxon

Code	2016.005yB	(assigned by ICTV officers)
To re-assign the following taxon (or taxa): <i>Mycobacterium virus Rosebush</i>		
Genus:	<i>Rosebushvirus</i> (new)	<p>Fill in all that apply.</p> <ul style="list-style-type: none">If the higher taxon has yet to be created write “(new)” after its proposed name and complete relevant module to create it. <p>If no genus is specified, enter “unassigned” in the genus box.</p>
Subfamily:	<i>Bclavirinae</i> (new)	
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. 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.
2. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6):e39107.

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.

Fig. 1. Gegenees BLASTN [2] analysis of members of each genus plus one outsider. The genus *Pg1virus*, *sensu stricto*, includes 55 phages and is too large to show. The bordered data are assumed to be phages which are related at the strain level.

A. *Coopervirus*

PHAGE	ACCESSION NO.	DQ398044.1	KF279411.1	JN699011.1	UE770221.1	KF493881.1	JF704094.1	kt270441.1	JF704104.1	KF279413.1	KF279412.1	KR080194.1	KR080200.1	KF024727.1
Cooper	DQ398044.1	100.0	76.6	70.7	67.9	69.2	70.7	67.7	67.0	68.0	68.0	58.6	58.4	42.9
Adawi	KF279411.1	76.4	100.0	70.7	68.6	69.6	69.8	66.5	67.2	67.8	67.9	58.3	58.1	41.7
Stinger	JN699011.1	71.0	71.1	100.0	77.5	72.5	73.0	67.7	68.0	69.5	69.5	60.8	60.7	36.2
Nigel	UE770221.1	68.4	68.8	77.7	100.0	76.1	71.4	67.8	67.5	68.3	68.3	61.7	61.2	36.3
JAMaL	KF493881.1	69.5	69.3	72.3	76.8	100.0	81.4	80.2	78.6	80.6	80.6	60.0	59.6	37.9
ChrisnMich	JF704094.1	71.0	69.7	72.7	71.3	81.0	100.0	79.9	78.7	80.5	80.5	59.8	59.4	41.8
BrownCNA	kt270441.1	68.3	67.0	68.1	67.9	80.0	80.6	100.0	90.0	87.5	87.5	57.1	56.9	40.5
Zemanar	JF704104.1	67.8	67.1	67.9	67.8	78.5	79.0	89.6	100.0	88.3	88.2	58.5	58.4	42.8
Bane2	KF279413.1	68.4	68.1	68.9	67.8	80.6	80.9	87.6	88.9	100.0	99.9	58.1	57.7	41.7
Bane1	KF279412.1	68.4	68.2	68.9	67.9	80.6	80.9	87.6	88.8	99.9	100.0	57.9	57.5	41.7
Vincenzo	KR080194.1	58.1	57.7	61.0	62.0	59.2	59.2	56.9	58.1	57.8	57.7	100.0	99.6	34.2
AlanGrant	KR080200.1	57.2	57.0	60.3	60.9	59.4	58.5	56.6	58.2	57.6	57.4	99.5	100.0	33.4
Reprobate	KF024727.1	41.7	42.8	36.0	36.8	38.6	41.8	40.7	41.3	41.4	41.4	35.3	34.2	100.0

B. *Pipefishvirus*

PHAGE	ACCESSION NO.	DQ398048.1	DQ398049.1	KF493879.1	JN699006.1	KR080203.1	KR080205.1	KP027207.1	KJ194581.1	KJ194584.1	JF704095.1	JN699003.1	EU816589.1	JN699018.1	FJ641182.1	JN698992.1
Qyrzula	DQ398048.1	100.0	59.6	58.6	60.5	60.4	63.5	63.5	63.8	60.2	60.7	68.6	33.2	33.0	33.0	32.9
Pipefish	DQ398049.1	58.7	100.0	93.8	90.8	90.6	91.0	90.7	90.8	90.6	90.4	90.4	90.2	90.8	90.8	90.5
Bernardo	KF493879.1	59.4	93.5	100.0	92.9	92.0	92.5	91.5	92.5	92.5	91.6	91.6	91.2	92.4	92.5	92.6
Akoma	JN699006.1	59.9	91.0	93.6	100.0	97.6	96.8	96.1	95.5	96.4	94.9	94.6	94.9	95.2	96.1	94.2
OrangeOswald	KR080203.1	59.9	90.4	92.4	97.7	100.0	98.2	97.6	96.6	96.8	96.1	95.7	95.1	95.7	96.2	94.5
Corofin	KR080205.1	64.1	91.1	93.2	96.8	98.2	100.0	96.9	96.6	96.1	96.3	95.4	95.5	95.8	96.0	94.5
Chandler	KP027207.1	62.9	90.5	91.8	96.1	97.5	96.8	100.0	95.8	95.8	96.0	95.6	94.8	95.4	95.7	93.9
Audrey	KJ194581.1	63.6	90.8	93.0	95.5	96.6	96.6	95.9	100.0	96.4	95.7	95.9	94.7	95.2	94.9	94.2
Heathcliff	KJ194584.1	58.2	90.7	93.0	96.5	96.8	96.2	95.9	96.4	100.0	95.3	95.2	94.7	95.1	96.3	94.2
Daisy	JF704095.1	58.4	90.5	92.3	95.0	96.2	96.2	96.1	95.6	95.2	100.0	95.7	95.3	95.4	95.5	94.2
Athena	JN699003.1	68.5	90.6	92.0	94.5	95.5	95.4	95.6	95.7	95.1	95.7	100.0	95.0	96.0	95.1	94.0
Phaedrus	EU816589.1	38.1	90.2	91.9	95.2	95.4	95.6	95.1	94.9	94.8	95.5	95.2	100.0	96.4	95.5	93.9
Kamiyu	JN699018.1	33.7	90.8	92.9	95.3	95.7	95.9	95.6	95.2	95.1	95.6	96.1	96.2	100.0	95.7	94.0
Phyler	FJ641182.1	34.0	90.6	92.8	96.0	96.2	95.9	95.8	94.8	96.2	95.5	95.2	95.3	95.6	100.0	93.2
Gadget	JN698992.1	31.6	90.6	93.0	94.0	94.4	94.2	93.7	93.9	93.7	93.8	93.9	93.5	93.6	93.1	100.0

C. *Acadianvirus*

PHAGE	ACCESSION NO.	DQ398044	KR080199	JN699007	KF024727	KF416341
Cooper	DQ398044	100.0	32.2	40.3	42.9	42.7
Baee	KR080199	31.8	100.0	76.1	62.3	62.3
Acadian	JN699007	41.7	75.9	100.0	64.1	64.2
Reprobate	KF024727	41.7	62.0	64.3	100.0	99.3
Phelemich	KF416341	42.4	62.2	64.1	99.3	100.0

D. *Rosebushvirus*

PHAGE	ACCESSION NO.	AY129334.1	JN698991.1	KT365402.1	JN618996.1	KM101117.1	KF024722.1	JN699004.1	DQ398048.1	KR997932.1	EU816589.1
Rosebush	AY129334.1	100.0	99.0	97.9	97.4	96.7	95.8	97.8	96.8	94.3	37.4
Hedgerow	JN698991.1	99.0	100.0	98.0	97.2	96.5	95.7	98.0	96.6	94.4	37.6
Tres	KT365402.1	98.1	98.1	100.0	96.6	96.0	95.9	97.4	95.9	95.0	35.9
Arbiter	JN618996.1	97.5	97.3	96.6	100.0	96.8	95.6	97.1	97.2	94.1	33.2
LizLemon	KM101117.1	96.7	96.5	96.0	96.7	100.0	95.8	96.8	96.7	94.3	37.4
TA17A	KF024722.1	95.9	95.8	96.0	95.6	95.9	100.0	95.8	95.0	94.0	37.1
Arres	JN699004.1	97.8	98.0	97.3	97.1	96.8	95.8	100.0	96.9	94.6	37.9
Qyrzula	DQ398048.1	96.8	96.6	95.9	97.3	96.8	95.2	97.0	100.0	94.1	33.2
Godines	KR997932.1	94.4	94.6	95.0	94.4	94.4	94.0	94.7	94.2	100.0	35.7
Phaedrus	EU816589.1	39.7	39.6	37.9	37.9	39.8	39.5	39.8	38.1	38.0	100.0

Table 1. Details on the Cluster B phages (taken from: <http://phagesdb.org/clusters/B/>)

Subgroup	Members	Avg Size (bp)	Avg GC%	Avg Genes	Avg tRNAs	Representative
B1	103	68,537	66.5	100.1	0	Mycobacterium phage PG1
B2	13	67,306	69.0	88.6	0	Mycobacterium phage Rosebush
B3	18	68,749	67.5	102.1	0	Mycobacterium phage Athena
B4	10	70,921	68.8	92.3	0.1	Mycobacterium phage Cooper
B5	5	70,038	68.0	96.0	0	Mycobacterium phage Acadian
B6	5	71,139	70.0	95.0	0	Not in GenBank

Table 2. Phages belonging to a species within the genus *Pg1virus*.

Phage	Accession No
ThreeOh3D2	JN699009.1
Badfish	KJ194580.1
ABU	JF704091.1
Kikipoo	JN699017.1
IsaacEli	JN698990.1
Hertubise	JF937097.1
Oosterbaan	JF704109.1
Serendipity	JN006063.1
Serpentine	JX649096.1
Piglet	JX649097.1
Alex	JX649100.1
Chah	FJ174694.1
Orion	DQ398046.1
Scoot17C	GU247134.1
Sigman	KP027209.1
JacAttac	JN698989.1
ShiVal	KC576784.1
Thora	JF957056.1
Nacho	JX649098.1
Numberten	KJ194583.1
Colbert	GQ303259.1
EmpTee	KJ567044.1
Hetaeria	KT364588.1
Lasso	KM408320.1
Phamished	KR816508.1
Fang	GU247133.1
Yoshand	JF937109.1
Vista	JN699008.1
Swish	KJ194579.1
Phipps	JF704102.1
FluffyNinja	KP027197.1
KLucky39	JF704099.1
Newman	KC691258.1
Suffolk	KF713485.1
Eremos	KM236502.1
Pops	KR997967.1
Puhitonio	GQ303264.1
Murdoc	JN638752.1
Morgushi	JN638753.1
TallGRassMM	JN699010.1
UncleHowie	GQ303266.1
Pipsqueak	KP027208.1

Vortex	JF704103.1
Harvey	JF937095.1
Gyarad	JX649099.1
Manad	KJ595576.1
Soto	KJ174157.1
Apizium	KR781349.1
Vivaldi	KM347890.1
SDcharge11	KC661274.1
KingVeveve	KJ538723.1
Zonia	KM363597.1

Table 3. Phages belonging to a species within the genus *Coopervirus*.

Phage	Accession No.
Bane2	KF279413.1
AlanGrant	KR080200.1

Table 4. Phages belonging to a species within the genus *Acadianvirus*

Phage	Accession No.
Phelemich	KF416341

Table 5. Phages belonging to a species within the genus *Pipefishvirus*

Phage	Accession No.
Akoma	JN699006.1
OrangeOswald	KR080203.1
Corofin	KR080205.1
Chandler	KP027207.1
Audrey	KJ194581.1
Heathcliff	KJ194584.1
Daisy	JF704095.1
Phaedrus	EU816589.1
Kamiyu	JN699018.1
Phyler	FJ641182.1

Table 6. Phages belonging to a species within the genus *Rosebushvirus*.

Phage	Accession No.
Hedgerow	JN698991.1
Tres	KT365402.1
Arbiter	JN618996.1
LizLemon	KM101117.1
TA17A	KF024722.1

Arres	JN699004.1
Qyrzula	DQ398048.1

Fig. 3. Phylogenetic analysis of large subunit terminase proteins of PG1-like viruses with the TerL protein of Mycobacterium phage Dori (outlier; singleton) constructed using “one click” at phylogeny.fr [1]. "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 clusters are illustrated as follows: *Rosebushvirus* (**red**), *PgIvirus* (**blue**), *Acadianvirus* (**green**), *Coopervirus* (**black**), and *Pipefishvirus* (**orange**)

A. Summary figure

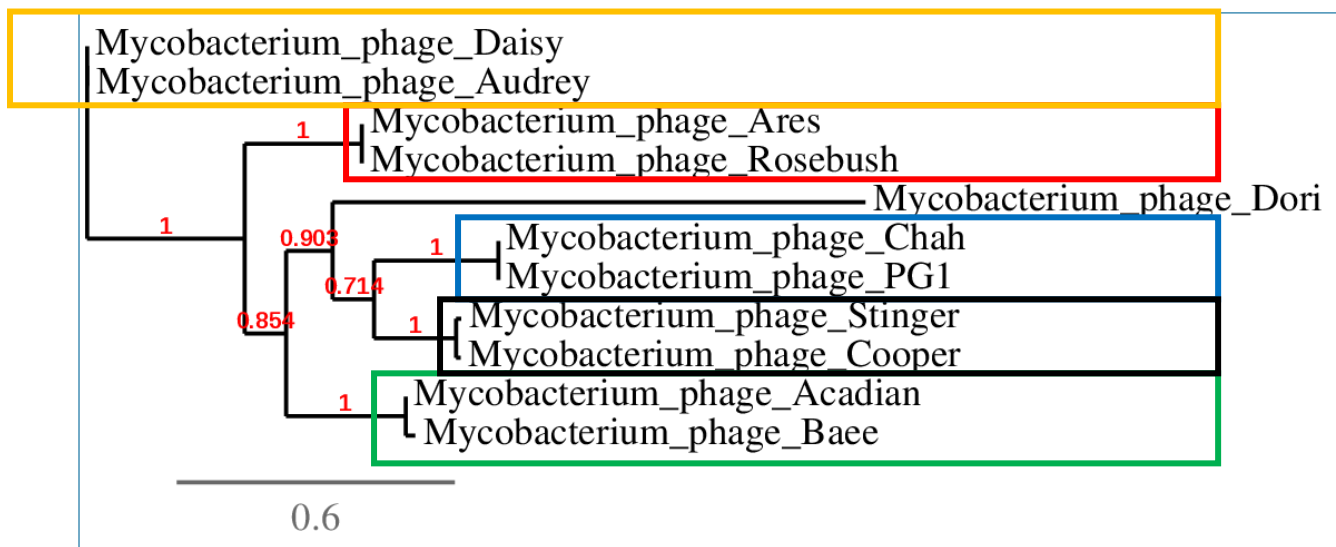
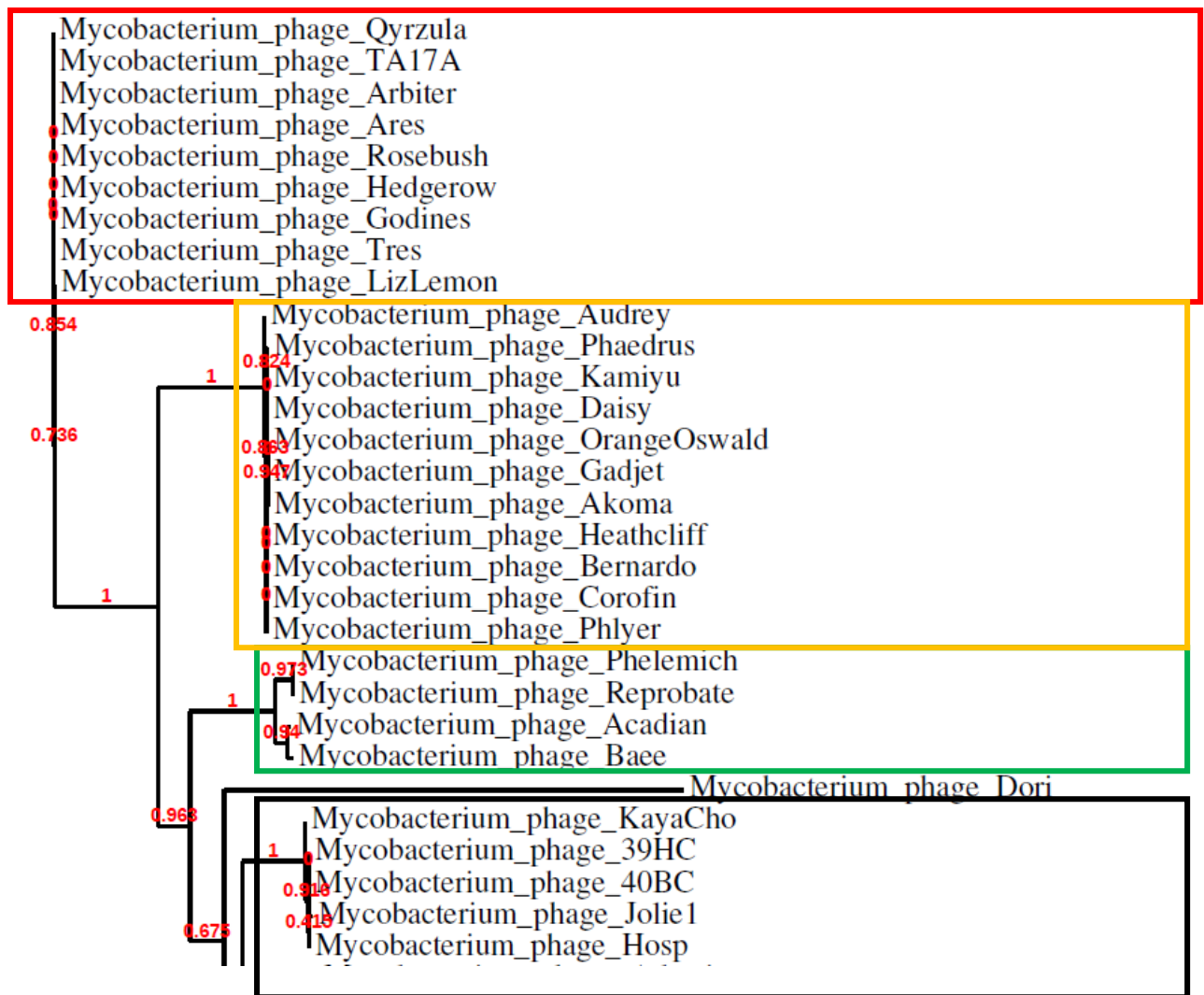
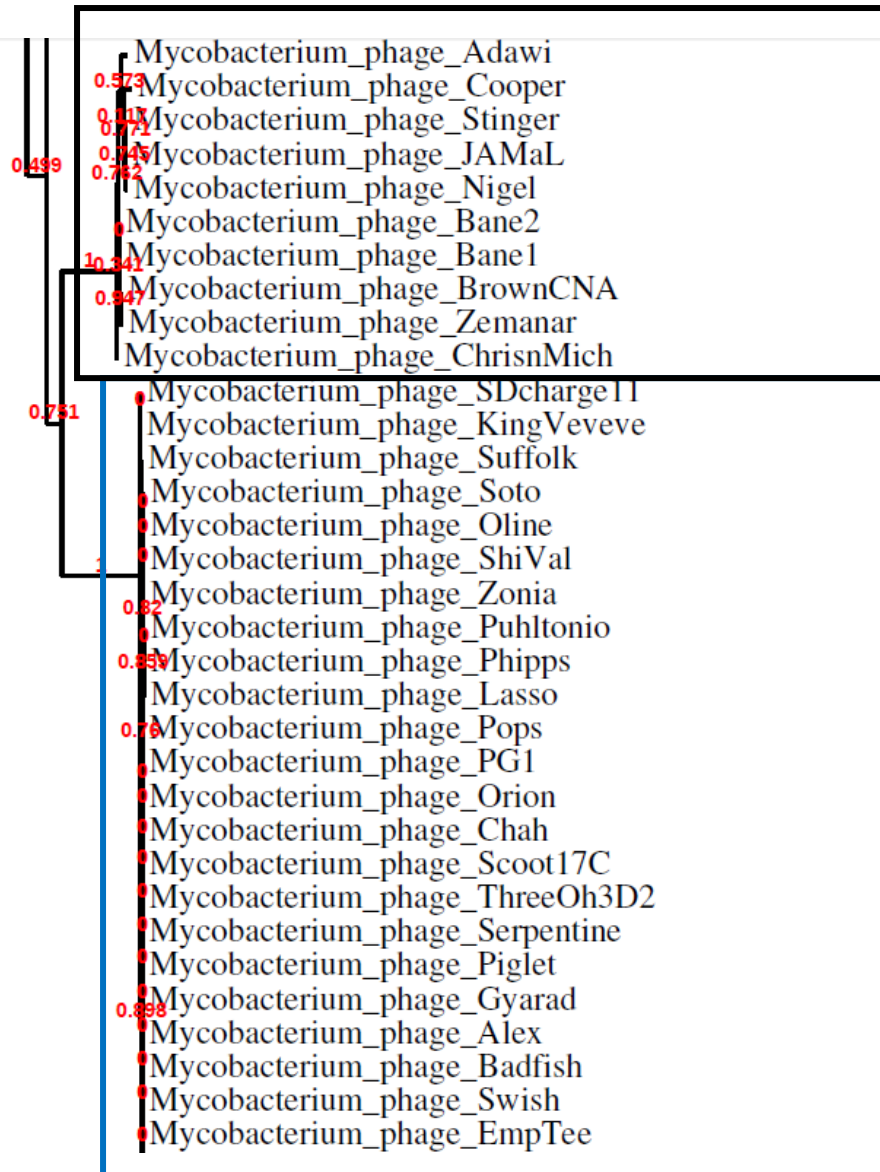


Figure 1: Phylogenetic tree (the branch length is proportional to the number of substitutions per site).

B. Detailed figure





Mycobacterium_phage_OSmaximus
Mycobacterium_phage_Murdoc
Mycobacterium_phage_Hetaeria
Mycobacterium_phage_Newman
Mycobacterium_phage_Vista
Mycobacterium_phage_JacAttac
Mycobacterium_phage_Manad
Mycobacterium_phage_UncleHowie
Mycobacterium_phage_Colbert
Mycobacterium_phage_Fang
Mycobacterium_phage_Thora
Mycobacterium_phage_Serendipity
Mycobacterium_phage_ABU
Mycobacterium_phage_KLucky39
Mycobacterium_phage_Vortex
Mycobacterium_phage_Oosterbaan
Mycobacterium_phage_Harvey
Mycobacterium_phage_Hertubise
Mycobacterium_phage_Yoshand
Mycobacterium_phage_Morgushi
Mycobacterium_phage_TallGRassMM
Mycobacterium_phage_Kikipoo
Mycobacterium_phage_Nacho
Mycobacterium_phage_Numberten
Mycobacterium_phage_Vivaldi
Mycobacterium_phage_FluffyNinja
Mycobacterium_phage_Sigman
Mycobacterium_phage_Pipsqueak
Mycobacterium_phage_Apizium
Mycobacterium_phage_Phamished