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:	***2013.022a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *Tm4likevirus*, 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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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	***2013.022aB***	(assigned by ICTV officers)

To create 9 new species within:

Genus:	***Tm4likevirus (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Mycobacterium phage TM4	AF068845
Mycobacterium phage angelica	HM152764
Mycobacterium phage jaws	JN185608
Mycobacterium phage crimd	HM152767
Mycobacterium phage anaya	JF704106
Mycobacterium phage pixie	JF937104
Mycobacterium phage macncheese	JX042579
Mycobacterium phage larva	JN243855
Mycobacterium phage fionn	JN831653

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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the EMBOSS Stretcher algorithm.

MODULE 3: NEW GENUS

creating a new genus

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

Code	***2013.022bB***	(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	***2013.022cB***	(assigned by ICTV officers)

To name the new genus: *Tm4likevirus*

Assigning the type species and other species to a new genus

Code	***2013.022dB***	(assigned by ICTV officers)

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

Mycobacterium phage TM4

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:**

9

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 Mycobacteriophage group (www.phagesdb.org) as belonging to cluster K. Phages belonging to this genus share a comparable genome size (52 – 62 kb), a comparable GC content (65 – 68 %), and a genome with defined physical end and a comparable 3' overhang. Members of this genus also have a comparable morphology, with an isometric head and a long, non-contractile tail (Figure 1).
A ClustalW analysis of the complete genomes of this genus with all other *Mycobacterium* phages belonging to the *Siphoviridae* reveals that this genus is a clearly separate group (Figures 2 and 3). We propose a shared protein content of at least 40% with the type phage, *Mycobacterium phage TM4*. We performed a CoreGenes 3.5 analysis [1–3] with the four phages of this genus (Table 1). The CoreGenes analysis was also performed against the type species of other proposed genera of siphoviruses infecting *Mycobacterium* and the shared protein content was consistently below 40% (data not shown).

Origin of the new genus name:

Mycobacterium phage TM4

Reasons to justify the choice of type species:

The genus *Tm4likevirus* is named after the first isolated and sequenced phage of this group, *Mycobacterium* phage Tm4 [4].

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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the EMBOSS Stretcher algorithm. The isolates BarrelRoll and Adephagia share 95.8% and 95.3% DNA identity with *Mycobacterium phage Jaws*, respectively, and thus belong to the same species.

MODULE 9: APPENDIX: supporting material

additional material in support of this proposal

References:

1. Mahadevan P, King JF, Seto (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: 100–114.

2. Mahadevan P, King JF, Seto D (2009) CGUG: in silico proteome and genome parsing tool for the determination of "core" and unique genes in the analysis of genomes up to ca. 1.9 Mb. BMC Res Notes 2: 168. doi:10.1186/1756-0500-2-168.

3. Zafar N, Mazumder R, Seto D (2002) CoreGenes: A computational tool for identifying and cataloging "core" genes in a set of small genomes. BMC Bioinformatics 3: 12. doi:10.1186/1471-2105-3-12.

4. Ford ME, Stenstrom C, Hendrix RW, Hatfull GF (1998) Mycobacteriophage TM4: genome structure and gene expression. Tuber lung Dis 79: 63–73. doi:10.1054/tuld.1998.0007.

5. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147. doi:10.1371/journal.pone.0011147.

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.

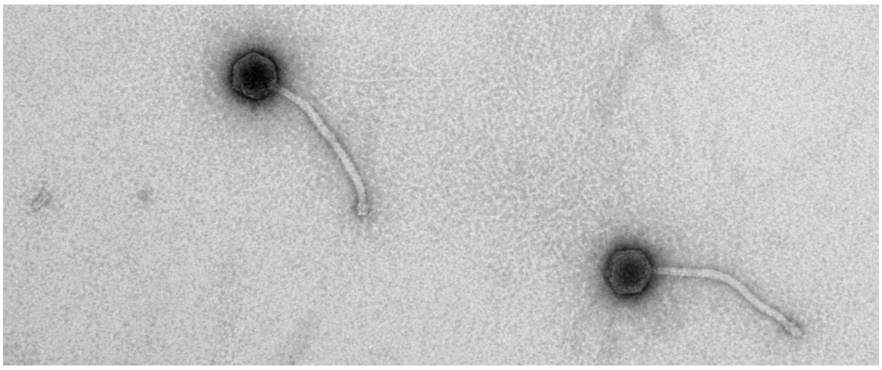

Figure 1: EM picture of isolates of phage Tm4, the type species of the genus *Tm4likevirus* (http://phagesdb.org/media/emPics/Tm4.tif).

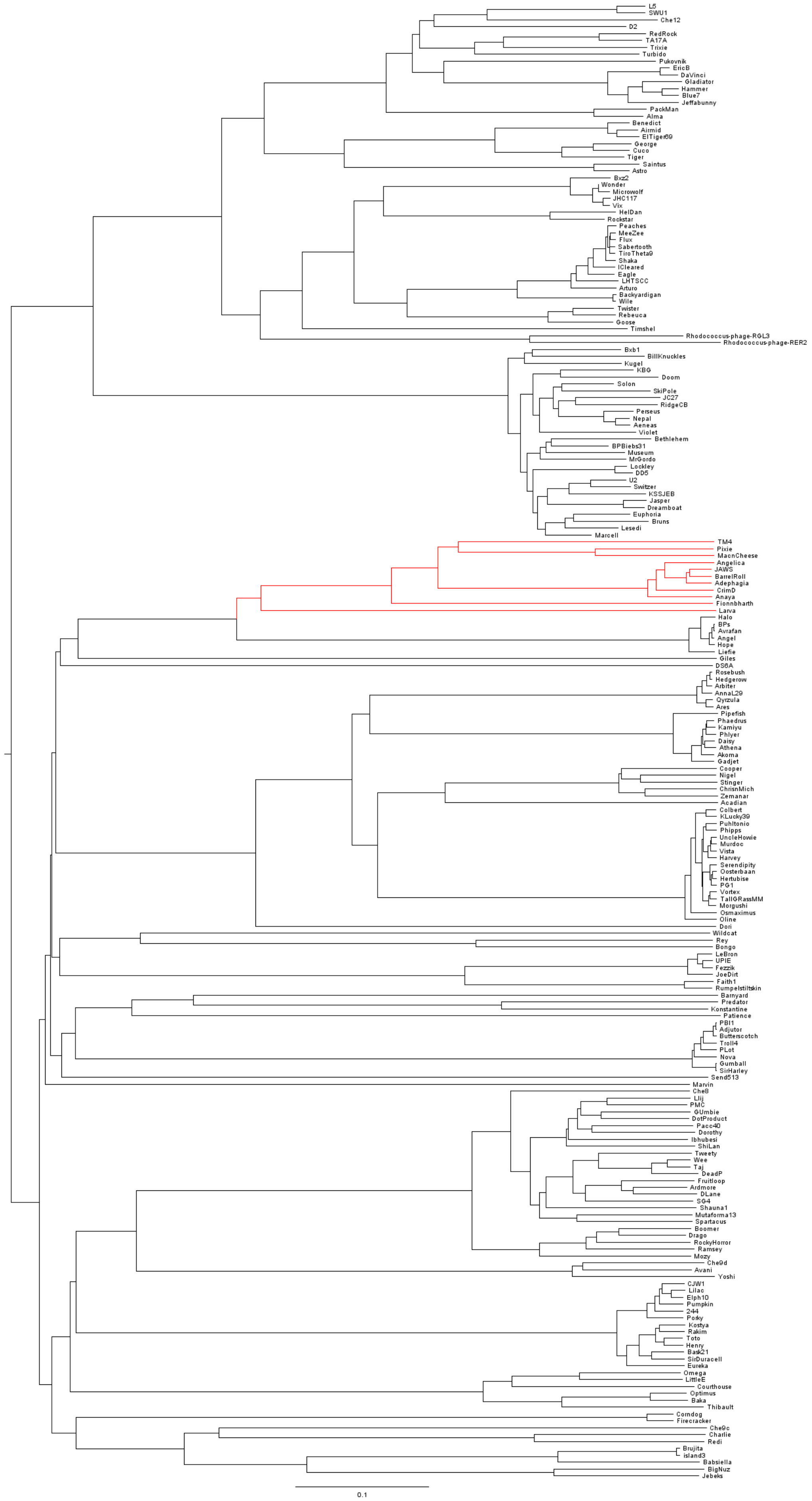
L5
SWU1
Che12
D2
RedRock
TA17A
Trixie
Turbido
Pukovnik
EricB
DaVinci
Gladiator
Hammer
Blue7
Jeffabunny
PackMan
Alma
Benedict
Airmid
ElTiger69
George
Cuco
Tiger
Saintus
Astro
Bxz2
Wonder
Microwolf
JHC117
Vix
HelDan
Rockstar
Peaches
MeeZee
Flux
Sabertooth
TiroTheta9
Shaka
ICleared
Eagle
LHTSCC
Arturo
Backyardigan
Wile
Twister
Rebeuca
Goose
Timshel
Rhodococcus-phage-RGL3
Rhodococcus-phage-RER2
Bxb1
BillKnuckles
Kugel
KBG
Doom
Solon
SkiPole
JC27
RidgeCB
Perseus
Nepal
Aeneas
Violet
Bethlehem
BPBiebs31
Museum
MrGordo
Lockley
DD5
U2
Switzer
KSSJEB
Jasper
Dreamboat
Euphoria
Bruns
Lesedi
Marcell
TM4
Pixie
MacnCheese
Angelica
JAWS
BarrelRoll
Adephagia
CrimD
Anaya
Fionnbharth
Larva
Halo
BPs
Avrafan
Angel
Hope
Liefie
Giles
DS6A
Rosebush
Hedgerow
Arbiter
AnnaL29
Qyrzula
Ares
Pipefish
Phaedrus
Kamiyu
Phlyer
Daisy
Athena
Akoma
Gadjet
Cooper
Nigel
Stinger
ChrisnMich
Zemanar
Acadian
Colbert
KLucky39
Puhltonio
Phipps
UncleHowie
Murdoc
Vista
Harvey
Serendipity
Oosterbaan
Hertubise
PG1
Vortex
TallGRassMM
Morgushi
Osmaximus
Oline
Dori
Wildcat
Rey
Bongo
LeBron
UPIE
Fezzik
JoeDirt
Faith1
Rumpelstiltskin
Barnyard
Predator
Konstantine
Patience
PBI1
Adjutor
Butterscotch
Troll4
PLot
Nova
Gumball
SirHarley
Send513
Marvin
Che8
Llij
PMC
GUmbie
DotProduct
Pacc40
Dorothy
Ibhubesi
ShiLan
Tweety
Wee
Taj
DeadP
Fruitloop
Ardmore
DLane
SG4
Shauna1
Mutaforma13
Spartacus
Boomer
Drago
RockyHorror
Ramsey
Mozy
Che9d
Avani
Yoshi
CJW1
Lilac
Elph10
Pumpkin
244
Porky
Kostya
Rakim
Toto
Henry
Bask21
SirDuracell
Eureka
Omega
LittleE
Courthouse
Optimus
Baka
Thibault
Corndog
Firecracker
Che9c
Charlie
Redi
Brujita
island3
Babsiella
BigNuz
Jebeks
0.1

Figure 2: ClustalW phylogenetic tree (NJ) of complete genomes of all *Mycobacterium* siphoviruses in the NCBI database in November 2012. The proposed genus is colored in red. The scale bar represents 0.1 substitutions per site.

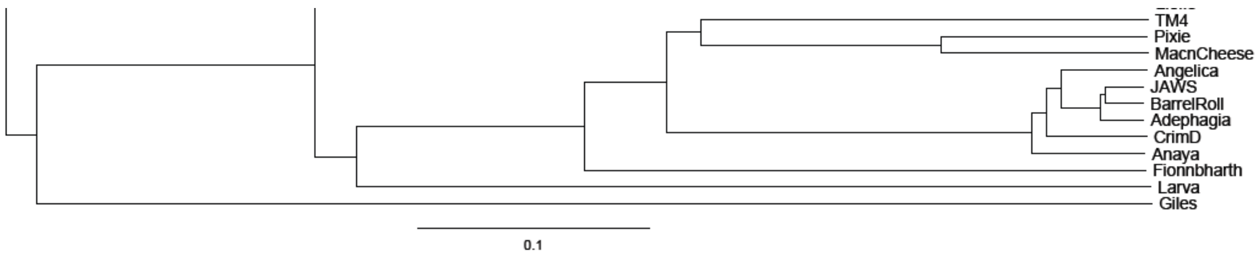

Figure 3: ClustalW phylogenetic tree of complete genomes of the isolates belonging to the genus *Tm4likevirus*, excerpt of Figure 2.

Figure 4: progressiveMauve alignment of the phage genomes belonging to the proposed genus [5]**. 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.**

Table 1: CoreGenes 3.5 (protein) and EMBOSS Stretcher (DNA) analysis of selected phages with the type phage of the genus, *Mycobacterium phage tm4*.

Phage Name	**% proteins in common with TM4**	**% DNA similarity with TM4**
Mycobacterium phage angelica	60.9	55.6

Mycobacterium phage jaws	64.1	56.1
Mycobacterium phage crimd	63.0	56.7
Mycobacterium phage anaya	62.0	55.9
Mycobacterium phage pixie	64.1	55.8
Mycobacterium phage macncheese	66.3	55.4
Mycobacterium phage larva	56.5	53.4
Mycobacterium phage fionn	46.7	55.7