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:	***2013.014a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *Cjwunalikevirus*, 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	***2013.014aB***	(assigned by ICTV officers)

To create 9 new species within:

Genus:	***Cjwunalikevirus (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 CJW1	AY129331
Mycobacterium phage pumpkin	GQ303265
Mycobacterium phage 244	DQ398041
Mycobacterium phage porky	EU816588
Mycobacterium phage Bask21	JF937091
Mycobacterium phage sirduracell	JF937106
Mycobacterium phage eureka	JN412590
Mycobacterium phage kostya	EU816591
Mycobacterium phage toto	JN006061

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 (Table 1).

MODULE 3: NEW GENUS

creating a new genus

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

Code	***2013.014bB***	(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	***2013.014cB***	(assigned by ICTV officers)

To name the new genus: *Cjwunalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.014dB***	(assigned by ICTV officers)

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

Mycobacterium phage CJW1	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 E. Phages belonging to this genus share a comparable genome size (74 - 76 kb), a comparable GC content (~63.1%), the presence of about 2 tRNAs and a genome with defined physical end with a comparable 9 bp 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 CJW1*. We performed a CoreGenes 3.5 analysis [1–3] with selected phages based on the results of the ClustalW analysis (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 CJW1

Reasons to justify the choice of type species:

The genus *Cjwunalikevirus* is named after the first isolated and sequenced phage of this group, *Mycobacterium* phage Cjw1 [4]. The number '1' is replaced with the word 'una' to avoid confusion with the adjacent letter 'l' in the genus name.

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.

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. Pedulla ML, Ford ME, Houtz JM, Karthikeyan T, Wadsworth C, et al. (2003) Origins of highly mosaic mycobacteriophage genomes. Cell 113: 171–182.

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.

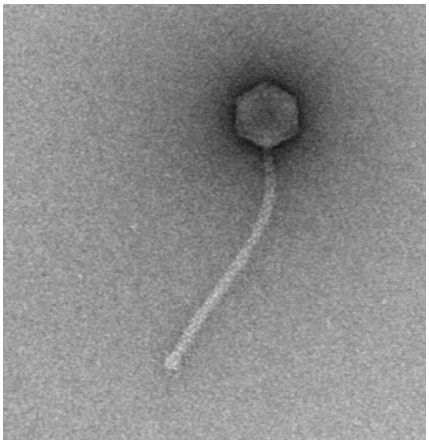

Figure 1: EM picture of phage Cjw1, a member of the genus *Cjwunalikevirus* (http://phagesdb.org/media/emPics/Cjw1.tif).

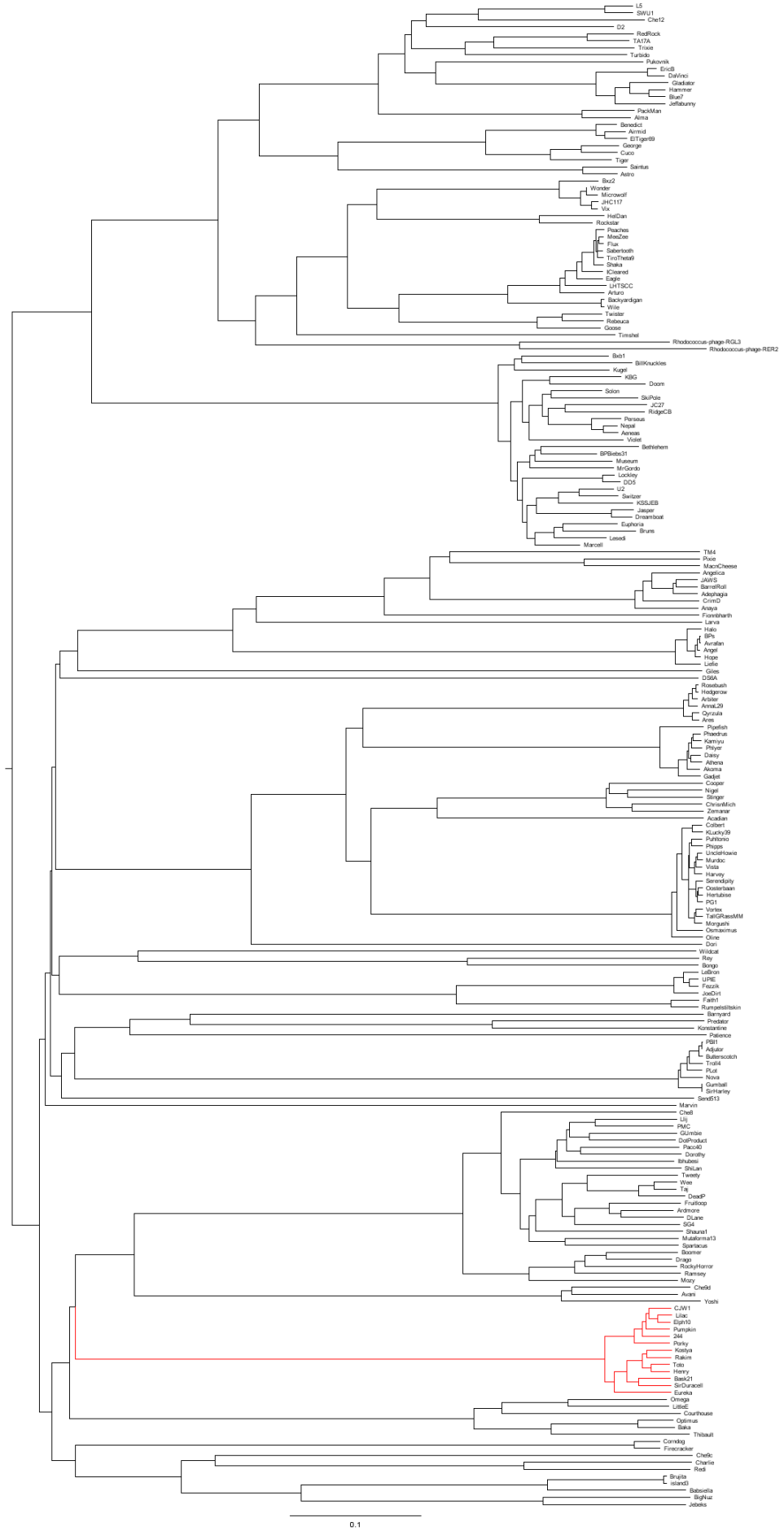
L5
SWU1
Che12
D2
RedRock
TA17A
Trixie
Turbido
Pukovnik
EricB
DaVinci
Gladiator
Hammer
Blue7
Jeffabunny
PackMan
Alma
Benedict
Airmid
ETiger89
George
Cuco
Tiger
Saintus
Astro
Bxz2
Wonder
Microwolf
JHC117
Vix
HelDan
Rockstar
Psaches
MeeZee
Flux
Saberlooth
TiroTheta9
Shaka
ICleared
Eagle
LHTSCC
Arturo
Backyardigan
Wille
Twister
Rebecca
Goose
Timshel
Rhodococcus-phage-RGL3
Rhodococcus-phage-RER2
Bxb1
BillKnuckles
Kugel
KBG
Doom
Solon
SkiPole
JC27
RidgeCB
Perseus
Nispit
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
Lollie
Giles
D29A
Rosebush
Hedgerow
Arbiter
AnnaL29
Qyrzula
Ares
Pipefish
Phaedrus
Kamiyu
Phlyer
Daisy
Athena
Akoma
Gadjet
Cooper
Nigel
Stinger
ChrisnMich
Zemanar
Acadian
Colbert
KLucky39
Puhitonio
Phipps
UncleHowie
Murdoc
Viola
Harvey
Serendipity
Oosterbaan
Hertubise
PG1
Vortex
TellGRaesMM
Morgushi
Osmaximus
Oline
Dori
Wildcat
Rey
Bongo
LeBron
UPIE
Feuzik
JoeDirt
Faith1
Rumpelstiltskin
Barnyard
Predator
Konstantine
Patience
PBI1
Adjutor
Butterscotch
Trish1
PLot
Nova
Gumball
SirHarley
Swed513
Marvin
Che8
Lili
PMC
GUmbie
DotProduct
Paco40
Dorothy
Ibhubesi
ShiLan
Tweety
Wee
Titi
DeadP
Fruitloop
Ardmore
DLane
SS4
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
BigHuz
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.

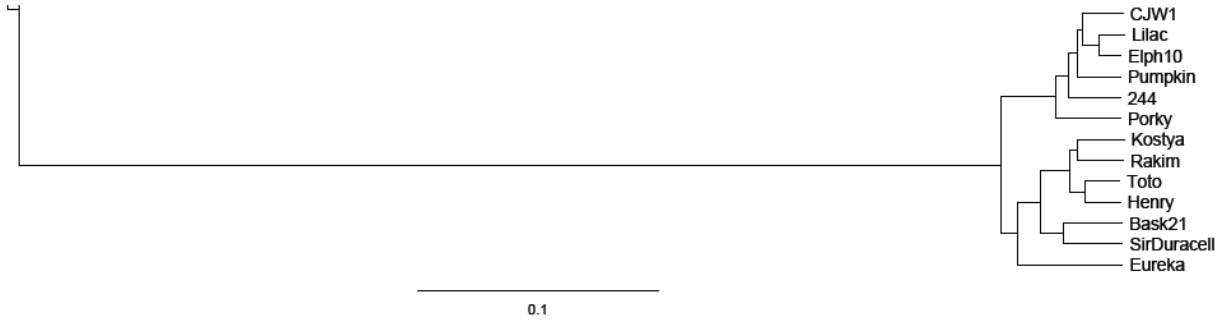

Figure 3: ClustalW phylogenetic tree of complete genomes of the isolates belonging to the genus *Cjwunalikevirus*, excerpt of Figure 2.

Figure 4: progressiveMauve alignment of the phage genomes belonging to the proposed [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: Selected EMBOSS Stretcher results in the genus *Cjwunalikevirus*.

Isolate Name	Isolate name	% DNA identity	Species
CJW1	Elph10	95.1	*Mycobacterium phage Cjw1*
Lilac	Elph10	95.8	*Mycobacterium phage Cjw1*

Kostya	Rakim	94.9	*Mycobacterium phage Kostya*
Toto	Henri	95.6	*Mycobacterium phage Toto*
CJW1	Pumpkin	93.1	Different species

Table 2: CoreGenes 3.5 and EMBOSS Stretcher analysis, showing the shared protein content and DNA similarity of selected phages of the genus *Cjwunalikevirus* with the type species of this genus.

Phage name	**% proteins shared with Cjw1**	**% DNA similarity with Cjw1**
Mycobacterium phage pumpkin	95.7	93.1
Mycobacterium phage 244	93.6	92.3
Mycobacterium phage porky	89.4	89.0
Mycobacterium phage Bask21	90.1	85.3
Mycobacterium phage sirduracell	87.9	84.2
Mycobacterium phage eureka	89.4	88.6
Mycobacterium phage kostya	87.9	87.8
Mycobacterium phage toto	90.1	90.0