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:	***2012.002a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *Corndoglikevirus*, comprising two new species, 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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Rob Lavigne rob.lavigne@biw.kuleuven.be
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John Nash, john.nash@phac-aspc.gc.ca

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:	2012
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	***2012.002aB***	(assigned by ICTV officers)

To create two new species within:

Genus:	***Corndoglikevirus* (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 corndog	AY129335
Mycobacterium phage firecracker	JN698993

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

BLASTN analysis revealed that these phages are related and distinct from any other phages. We have chosen 95% DNA identity as species demarcation criterion.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2012.002bB***	(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	***2012.002cB***	(assigned by ICTV officers)

To name the new genus: *Corndoglikevirus*

Assigning the type species and other species to a new genus

Code	***2012.002dB***	(assigned by ICTV officers)

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

Mycobacterium phage corndog

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

Mycobacterium smegmatis phages Corndog and Firecracker possess elongated heads (average dimensions: 173 x 43nm) with a noncontractile tail 258nm in length (Figure 1). The average genome size for these viruses is 71.0 kb with 4bp 3’extensions. These phages show similar properties (Table 1) and genome homology (Figure 2)

Other *Mycobacterium* phages exist which possesses elongated heads, namely Babsiella, Brujita and island3 (Figures 3 and 4). The latter phages possess small genomes (47.1 – 48.4 kb), a higher mol%G+C content (66.8-67.1) and 11bp 3’extended termini.

Origin of the new genus name:

Named after the well characterized *Mycobacterium* phage Corndog

Reasons to justify the choice of type species:

First member of this proposed genus to be full 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.

BLASTN analysis revealed that these phages are related and distinct from any other phages. We have chosen 95% DNA identity as species demarcation criterion.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Pedulla ML, Ford ME, Houtz JM, Karthikeyan T, Wadsworth C, Lewis JA, Jacobs-Sera D, Falbo J, Gross J, Pannunzio NR, Brucker W, Kumar V, Kandasamy J, Keenan L, Bardarov S, Kriakov J, Lawrence JG, Jacobs WR Jr, Hendrix RW, Hatfull GF. Origins of highly mosaic mycobacteriophage genomes. Cell. 2003; 113(2):171-82.

2. De Los Santos, C., Homan, D., Morales, J., Shepard, E., Hwang, Y-C., Ilagan, J., Donohue, J-P., Chan, P., Lowe, T., and Hartzog, G. 2011. BMEThesis. Annotation and analysis of newly discovered mycobacteriophage genomes. University of California Santa Cruz.

3. 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.

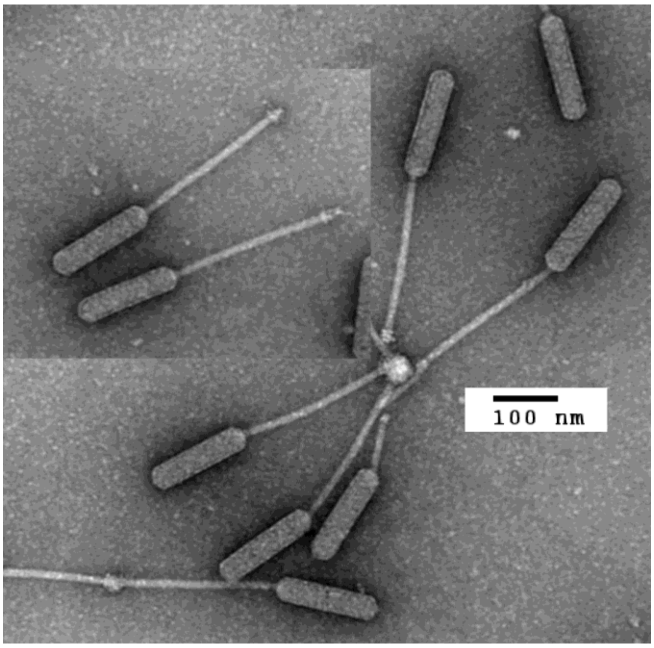

Figure 1. Electron micrograph of phage Corndog (modified from http://phagesdb.org/phages/Corndog/)

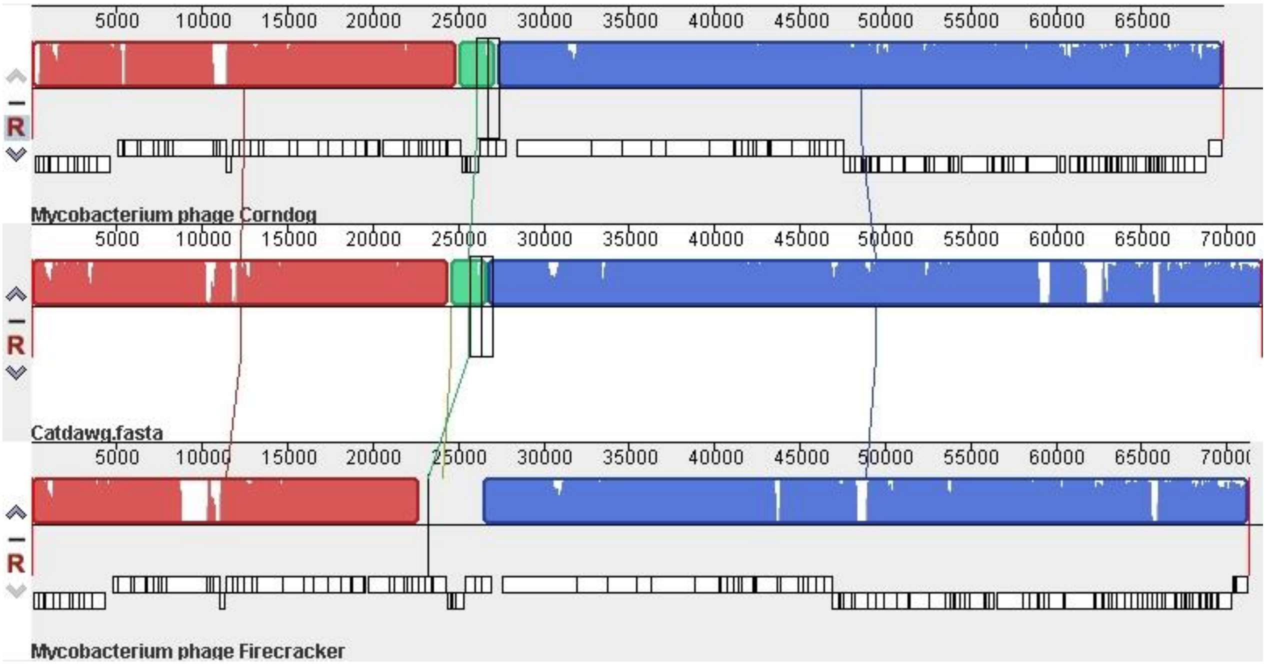

Figure 2. progressiveMauve (3) alignment of the phage genomes belonging to the proposed genus (full genome represented by its annotated ORFs in white blocks) (Darling et al, 2010). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. 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. Phage Catdawg has not been deposited in the NCBI database, and is therefore not an official member of this genus.

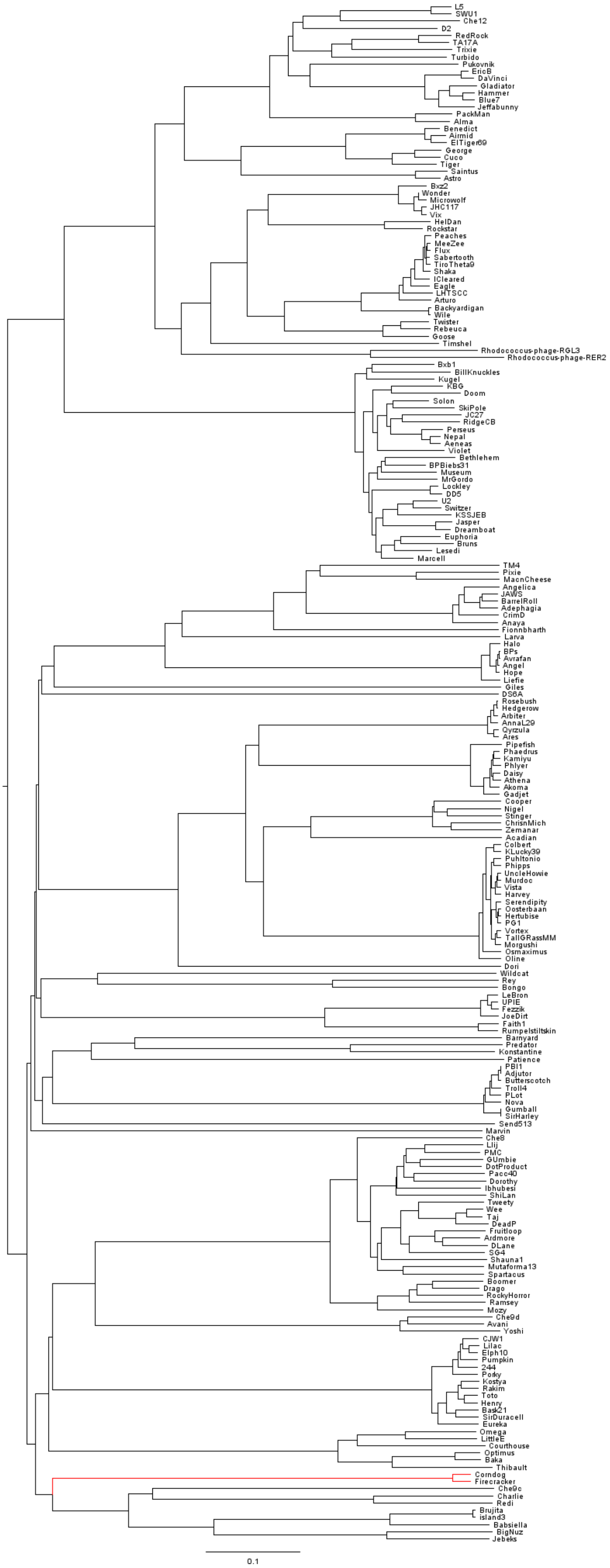
L5
SWU1
Che12
D2
RedRock
TA17A
Trixie
Turbido
Pukovnik
EricB
DaVinci
Gladiator
Hammer
Blue7
Jeffabunny
PackMan
Alma
Benedict
Airmid
ElTiger69
George
Cuco
Tiger
Saintus
Astro
Bxz2
Wonder
Microwolf
JHC117
Vix
HelDan
Rockstar
Peaches
MeeZee
Flux
Sabertooth
TiroTheta9
Shaka
ICleared
Eagle
LHTSCC
Arturo
Backyardigan
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 3. 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.

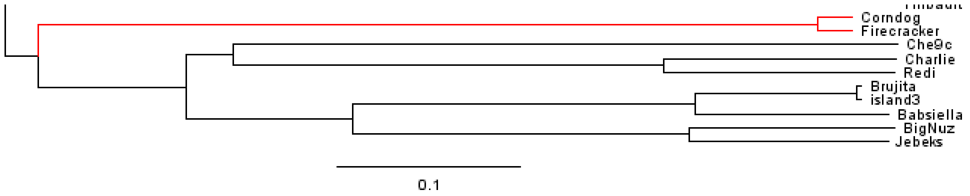

Figure 4. ClustalW phylogenetic tree of complete genomes of the isolates belonging to the genus *Corndoglikevirus*, excerpt of Figure 3.

Table 1. Properties of members of this new genus group determined using CoreGenes 3.0

Phage		**Corndog**	**Firecracker**
Isolated by		W. Brucker	J. Morales & D. Homan
Isolation source		Pittsburgh, PA USA	Santa Cruz, CA USA
Isolation year		2001	2009
Dimensions(*)			
	Head (LxW)	167 x 42 nm	178 x 44 nm
	Tail (L)	263 nm	253 nm
Genome length (bp)		69777	71341
GC content		65.4%	65.5
Genome ends	Extension	3’	3’
	Sequence	GTCT	GTGT
No. proteins		122	126
No. tRNAs		0	0
No. proteins shared with type species (&%)			118 (96.7%)
GenBank accession No.		AY129335	JN698993
Mycobacterio-phage database cluster		O	O
Source of data:		http://phagesdb.org /phages/Corndog/	http://phagesdb.org/ phages/Firecracker/

* = calculated from electron micrographs on Mycobacteriophage Database site.