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:	***2016.071a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, *Jd18virus*, including two (2) new species, in the subfamily *Tevenvirinae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

Author(s):

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Andrew M. Kropinski—University of Guelph, Canada

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: July 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	***2016.071aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Jd18virus* (new)**
Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Klebsiella virus JD18 *Klebsiella virus PKO111*	Klebsiella phage JD18 Klebsiella phage PKO111	KT239446 KR269720

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 11

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	***2016.071bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Tevenvirinae***
Family:	***Myoviridae***
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	***2016.071cB***	(assigned by ICTV officers)

To name the new genus: *Jd18virus*

Assigning the type species and other species to a new genus

Code	***2016.071dB***	(assigned by ICTV officers)

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

Klebsiella virus JD18

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 11

The phages belonging to this genus, Klebsiella phages JD18 and PKO11, possess genomes of ca. 167.5kb (39.5 mol%G+C) and encode 240 proteins and 16 tRNAs on average. Neither has been described in the scientific literature, but JD18 was isolated in Shanghai (China) and PKO111 is from Yongin, Gyeonggi-do, South Korea.
BLASTN analyses (Table 1), coupled with progressiveMauve (Fig. 1), proteomic analyses using CoreGenes (Table 1); and, phylogenetic analysis (Fig. 2) all indicate that this is a cohesive group of viruses.

Origin of the new genus name:

Named after Klebsiella phage JD18

Reasons to justify the choice of type species:

This was 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 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.

2. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013; 6:140. doi: 10.1186/1756-0500-6-140.

3. 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.

4. 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.

Table 1. Properties of the two phages belonging to the genus *Jd18virus*.

Klebsiella phage	GenBank Accession No.	RefSeq No.	Genome size (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	% Homologous proteins **
JD18	KT239446	NC_028686	166.31	39.6	278	16#	100	100
PKO111	KR269720	-	168.76	39.4	203	16#	91	70.1***

* Determined using BLASTN; ** Determined using CoreGenes [2]; # none indicated in GenBank file; *** the reciprocal CoreGenes analysis reveals 96.1% identity suggesting that the annotation of these phages are not equivalent.

Fig. 1. progressiveMauve alignment [1] of the annotated genomes of members of the *Jd18virus* genus – from top to bottom: JD18 and PKO111. 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 (Aaron Darling, personal communication). N.B. the genomes of some of these phages are not collinear with that of Klebsiella phage JD18.

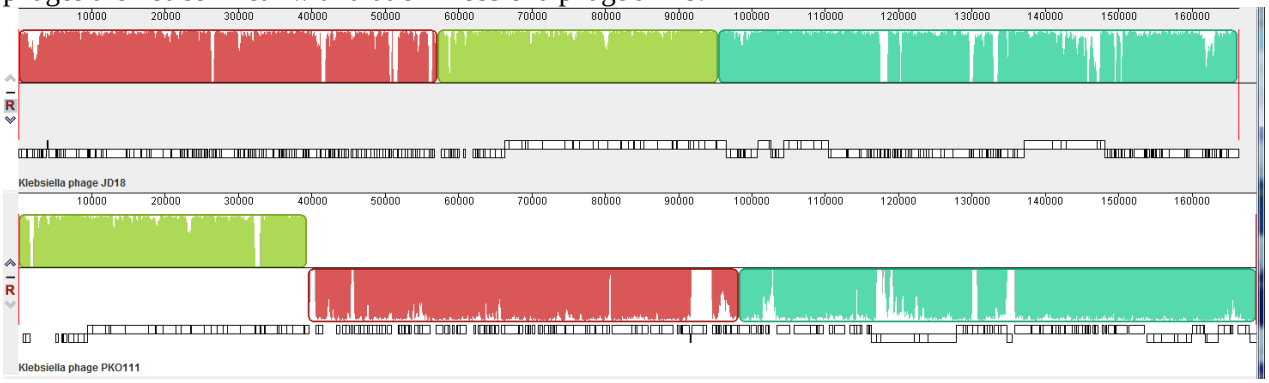
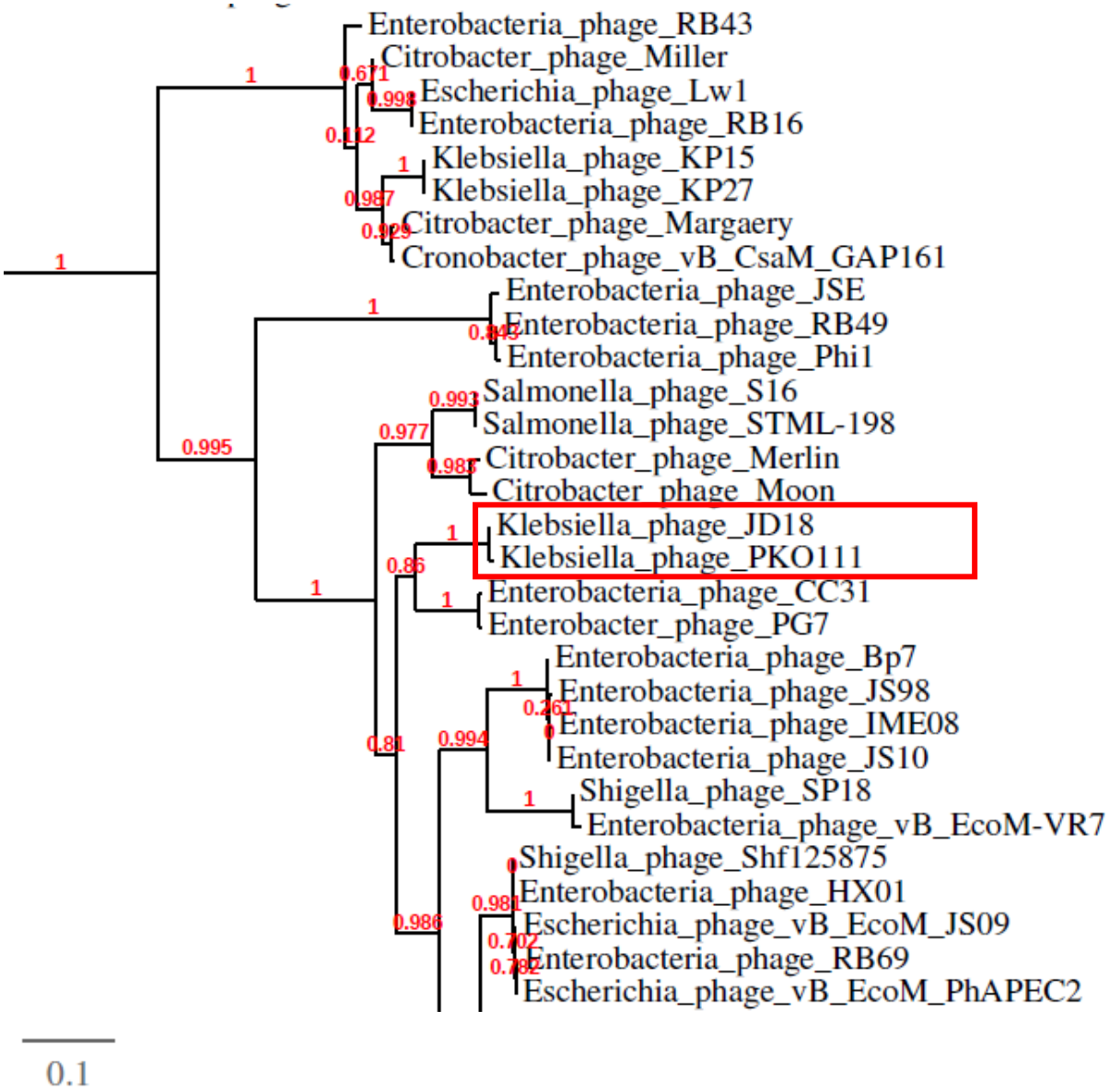


Fig. 2. Phylogenetic analysis of the large subunit terminase proteins the *Klebsiella* JD18/PKO111 phages and homologous proteins from a variety of other phages constructed using "one click" at phylogeny.fr [3]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. 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. **Red box** = *Jd18virus*


Enterobacteria_phage_RB43
Citrobacter_phage_Miller
Escherichia_phage_Lw1
Enterobacteria_phage_RB16
Klebsiella_phage_KP15
Klebsiella_phage_KP27
Citrobacter_phage_Margaery
Cronobacter_phage_vB_CsaM_GAP161
Enterobacteria_phage_JSE
Enterobacteria_phage_RB49
Enterobacteria_phage_Phi1
Salmonella_phage_S16
Salmonella_phage_STML-198
Citrobacter_phage_Merlin
Citrobacter_phage_Moon
Klebsiella_phage_JD18
Klebsiella_phage_PKO111
Enterobacteria_phage_CC31
Enterobacter_phage_PG7
Enterobacteria_phage_Bp7
Enterobacteria_phage_JS98
Enterobacteria_phage_IME08
Enterobacteria_phage_JS10
Shigella_phage_SP18
Enterobacteria_phage_vB_EcoM-VR7
Shigella_phage_Shf125875
Enterobacteria_phage_HX01
Escherichia_phage_vB_EcoM_JS09
Enterobacteria_phage_RB69
Escherichia_phage_vB_EcoM_PhAPEC2
0.1