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:	***2015.052aB***	(to be completed by ICTV officers)

Short title: To amend the description of the *Schizot4likevirus*; and, add one (1) new species
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s):

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 Study Group comments (if any) and response of the proposer:

Please note that the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

Date first submitted to ICTV: June 2015
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	***2015.052aB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Schizot4likevirus*** (proposed renaming to ***Schizot4virus***)
Subfamily:	***Tevenvirinae***
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Vibrio virus ValKK3	Vibrio phage ValKK3	KP671755

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

Several new Schizo T4-like phage genomes have recently been deposited to GenBank. This proposal recognizes the fact that they are part of the *Schizot4virus* genus.

Please note that we have chosen to refer to this new genus as *Schizot4virus* rather than *Schizot4virus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

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 BLASTN algorithm.

BLASTN, CoreGenes (1) (Table 1), and progressiveMauve alignment (2) (Fig. 1), and phylogenetic analyses (Fig 2ABC) all indicate that the proposed species is part of the *Schizot4virus*.

MODULE 10: **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.
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.

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 *Vibrio* phage ValKK3 which belongs to the *Schizot4virus* along with the type virus (KVP40).

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
Vibrio phage ValKK3	KP671755	246.09	41.23	390	29 ***	71	88.7
Vibrio phage KVP40	AY283928.2	244.83	42.6	381	29	100	100

* Determined using BLASTN relative to KVP40; ** Determined using CoreGenes (2) relative to KVP40;*** None indicated in GenBank file

Table 2. Phages which are closely related to KVP40 or ValKK3, and should be considered strains

Phage	GenBank accession No.
Vibrio phage VH7D	KC131129♥
Vibrio phage phi-pp2	JN849462

♥N.B. Normally this strain would have been chosen as the species because it has been accorded RefSeq status but it is severely underannotated.

Fig. 1. progressiveMauve alignment (1) of the annotated genomes of , from top to bottom: KVP40, ValKK3 and nt-1. 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).

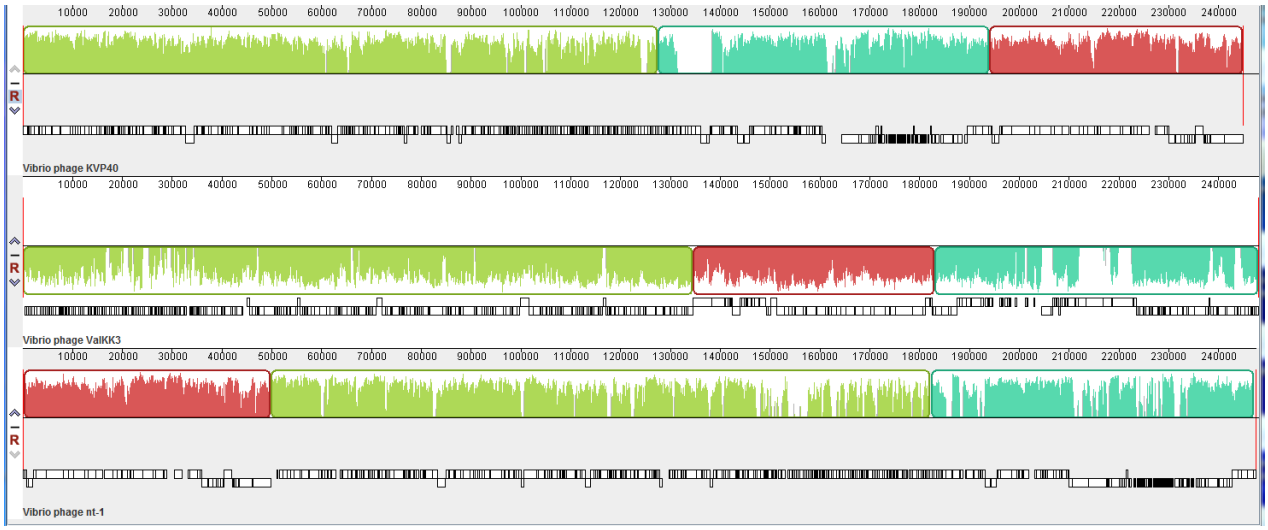

Fig. 2. Phylogenetic analysis of (A) the terminase, large subunit proteins, (B) DNA polymerase and (C) the major capsid protein of *Schizot4virus* and variety of other phages constructed using "one click" at phylogeny.fr (3). "The "One Click mode" targets users that do not wish to deal with program and 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."

A. Terminase, large subunit

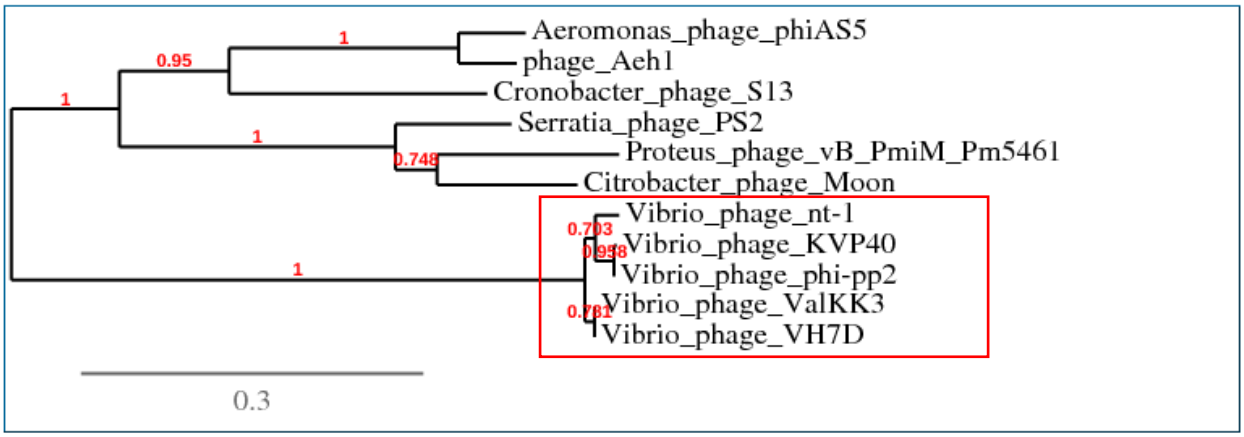

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

B. DNA polymerase

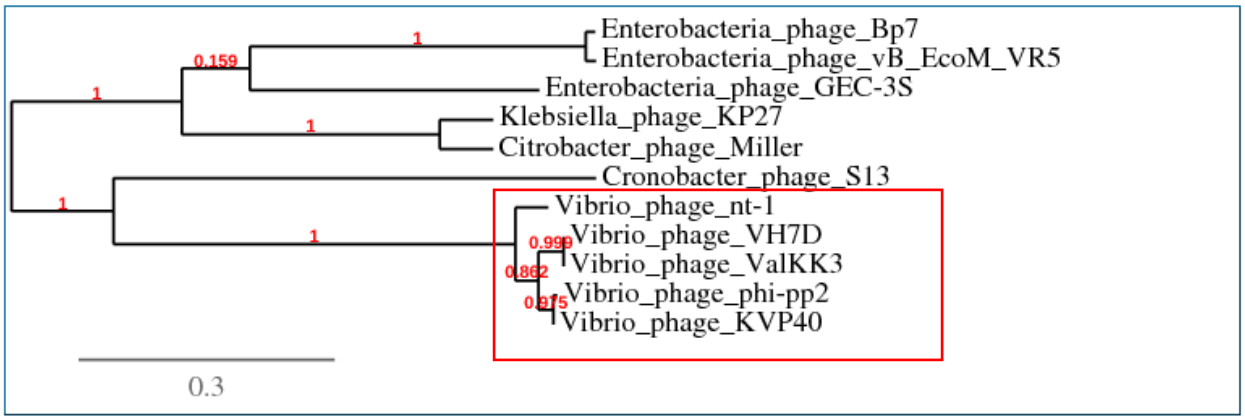

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

C. Major capsid protein

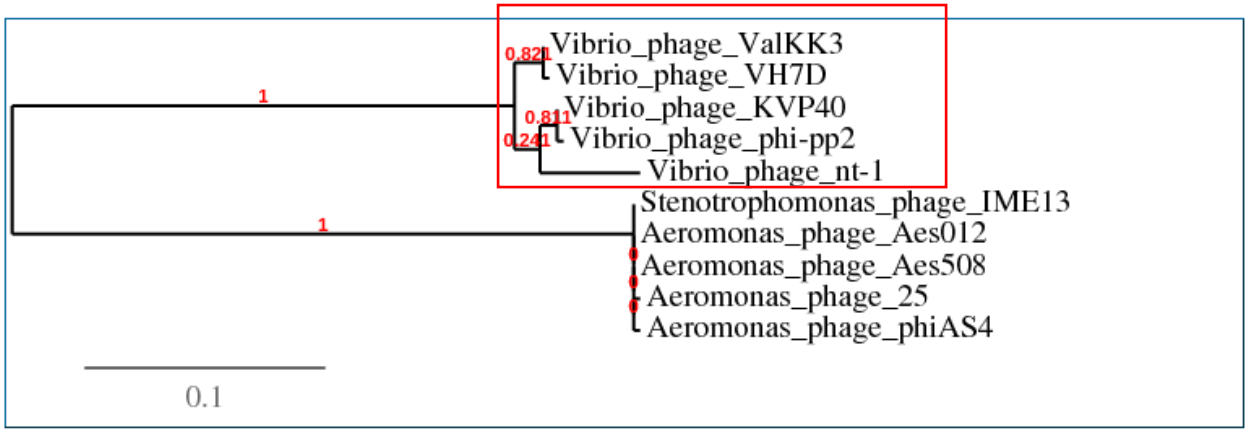

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*