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:	***2015.031a-dB***	(to be completed by ICTV officers)

Short title: Create one (1) new genus, *Vp5virus*, including three (3) new species within the family *Podoviridae*
(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** ☒

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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)	Bacterial and Archaeal Virus Subcommittee

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

Please note that we have chosen to refer to this new genus as *B4virus* rather than *B4likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "like" 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	***2015.031aB***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Vp5virus* (new)**
Subfamily:	
Family:	***Podoviridae***
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 VP5	Vibriophage VP5	AY510084
Vibrio virus VC8	Vibrio phage phiVC8	JF712866
Vibrio virus VP2	Vibriophage VP2	AY505112

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 BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.031bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
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	***2015.031cB***	(assigned by ICTV officers)

To name the new genus: *Vp5virus*

Assigning the type species and other species to a new genus

Code	***2015.031dB***	(assigned by ICTV officers)

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

Vibrio virus VP5

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:**

3

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

These three phages are a phylogenetically unique group of *Vibrio cholerae*-specific viruses. Since descriptions of only one of these phages has been published (3), the following analysis is derived from the sequences in GenBank. While the presence of an integrase might lead one to suspect that these phages are temperate, a new analysis of these proteins reveals that they contain primase-polymerase domains (Prim_Pol, cd04859; Prim-Pol, pfam09250; PriCT_2, pfam08707; Prim-Pol, smart00943). These phages also contain an "adenylosuccinate synthetase" which is supported by motif anaylysis (Adenylsucc_synt, smart00788; PRK04293; PurA, COG0104; purA, TIGR00184; Adenylsucc_synt, pfam00709; AdSS, cd03108; and PLN02513, LN02513). Its closest homologs are to similarly named proteins from *Pithovirus sibericum* (YP_009000992) and *Megavirus courdo7* (AEX62163).

"Adenylosuccinate synthetase (AdSS) catalyzes the first step in the de novo biosynthesis of AMP. IMP and L-aspartate are conjugated in a two-step reaction accompanied by the hydrolysis of GTP to GDP in the presence of Mg2+" (NCBI).

It also encodes a DNA polymerase I homolog with 3'-5' exonuclease and polymerase domains whose primary homologs are to marine virioplankton proteins.

It would appear that these phages have global distribution having been isolated in China and Mexico.

A phylogenetic analysis is not called for since most of the proteins are poorly related to any other phage protein.

Origin of the new genus name:

Vibrio phage VP5

Reasons to justify the choice of type species:

The first fully 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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

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. doi: 10.1186/1756-0500-6-140.

3. Wang, D.; Wang, M.; Li, Y.; Dong, H.; Liu, Z.; Liu, Y.; Qi, G.; Gao, S.; Jin, W.; Kan, B. Complete genome sequence and analysis of *Vibrio cholerae* phage VP2. Bing Du Xue Bao. 2005, 21, 60-64.

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.

Fig. 1 Electron micrograph of uranyl acetate negatively stained phage phiVC8 (provided by Dr. Eslava Campos)

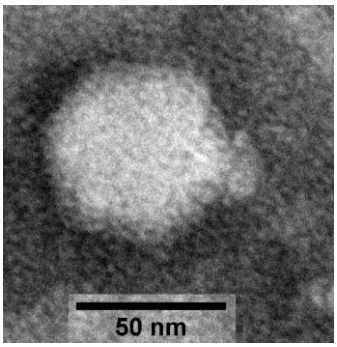

Table 1. Properties of the three phages belonging to the genus *Vp5virus*

Phage	GenBank Accession No.	Genome size (bp)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	% Homologous proteins **
VP5	AY510084	39,786	50.5	48	0	100	100
phiVC8	JF712866	39,422	50.8	48	0	82	100
VP2	AY505112	39,853	50.6	47	0	92	91.7

* Determined using BLASTN; ** Determined using CoreGenes

Table 2. Phages closely related to VP2

Vibrio phage QH	KM612259
Vibrio phage J2	KM612264
Vibrio phage J3	KM612265
Vibrio phage H3	KM612263
Vibrio phage H2	KM612262
Vibrio phage H1	KM612261
Vibrio phage CJY	KM612260

Fig. 2. progressiveMauve alignment (1) of the annotated genomes of members of the *Vp5virus* genus (from top to bottom: VP5, VP2, and phiVC8). 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).