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:	***2015.021a,bB***	(to be completed by ICTV officers)

Short title: To amend the description of the *T5likevirus*; and, add four (4) 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** ☒

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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 & Archaeal Virus Subcommittee

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: May 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	***2015.021aB***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***T5likevirus*** (proposed name, ***T5virus***)
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus FFH1	Escherichia phage vB_EcoS_FFH_1	KJ190157
Salmonella virus Shivani	Salmonella phage Shivani	KP143763
Salmonella virus Stitch	Salmonella phage Stitch	KM236244
Escherichia virus DT57C	Escherichia phage DT57C	KM979354

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 T5-like phage genomes have recently been deposited to GenBank. This proposal recognizes the fact that they are part of the *T5virus* genus.

Please note that we have chosen to refer to this new genus as *T5virus* rather than T5likevirus 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. *Escherichia* phage DT571/2 (KM979355) is a strain of DT57C. It shares 96% identity with DT57C.

BLASTN, CoreGenes (1) (Table 1), and progressiveMauve alignment (2) (Fig. 1) all indicate that the proposed these species are part of the *T5virus*.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2015.021bB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Vibrio phage 149 (type IV) from the *T5likevirus* genus

The present taxonomic position of these taxon/taxa:

Genus:	***T5virus***
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	YES

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

There are no sequence data to justify the presence of this virus in the genus *T5virus*.

Part (b) re-assign to a higher taxon

Code		(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	
Subfamily:	
Family:	
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

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.
4. Hong Y, Pan Y, Harman NJ, Ebner PD. Complete Genome Sequences of Two *Escherichia coli* O157:H7 Phages Effective in Limiting Contamination of Food Products. Genome Announc. 2014;2(5). pii: e00519-14. [vB_EcoS_FFH_1]
5. Grover JM, Luna AJ, Wood TL, Chamakura KR, Kuty Everett GF. Complete Genome of *Salmonella enterica* Serovar Typhimurium T5-Like Siphophage Stitch. Genome Announc. 2015;3(1). pii: e01435-14.

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 1A. Properties of the four phages belonging to the genus *T5virus* plus the type virus.

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
vB_EcoS_FFH_1	KJ190157.1	108.48	39.2	156	23	82	84.6
Shivani	KP143763	120.10	38.8	171	9	71	81.5
Stitch	KM236244	123.48	40.3	179	25	69	77.8
DT57C	KM979354	108.07	39.7	133	15	71	75.3
T5	AY543070.1	121.75	39.3	162	25	100	100

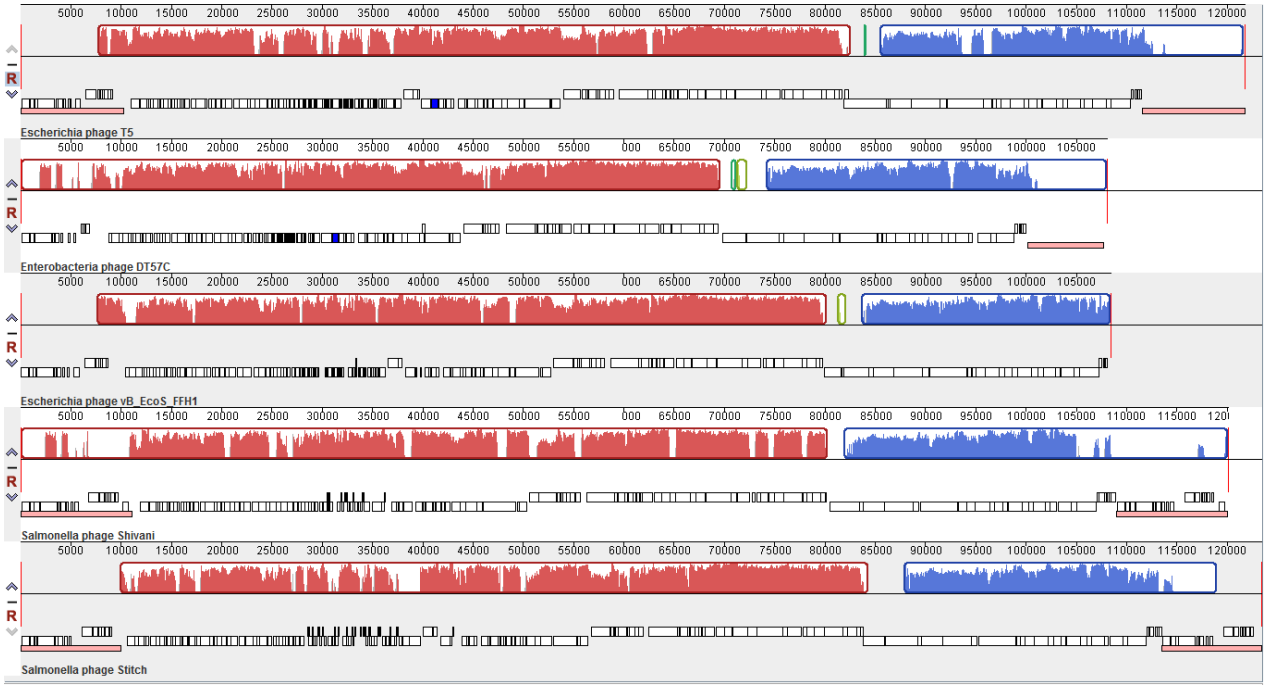
* Determined using BLASTN relative to T5; ** Determined using CoreGenes (2) relative to T5. N.B. *Escherichia* phage DT571/2 (KM979355) is a strain of DT57C.

Table 1B. Length of terminal direct repeats.

Phage	GenBank accession No.	Direct terminal repeat length (bp)
vB_EcoS_FFH_1	KJ190157	ND
Shivani	KP143763	11123
Stitch	KM236244	9982
DT57C	KM979354	7595
T5	AY543070	10219

ND = not determined

Fig. 1. progressiveMauve alignment (1) of the annotated genomes of , from top to bottom: T5, DT57C, FFH1, Shivani and Stich. 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).


Escherichia phage T5
Enterobacteria phage DT57C
Escherichia phage vB_EcoS_FFH1
Salmonella phage Shivani
Salmonella phage Stitch