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:	***2012.005aB***	(to be completed by ICTV officers)

Short title: To create six new species in the genus, "T5-like viruses" (proposed name *T5likevirus*), 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:

Andrew M. Kropinski kropinsk@queensu.ca
Rob Lavigne rob.lavigne@biw.kuleuven.be

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:

note there are 7 species. Add core genes references and global comparisons; include species demarcation criteria.

Date first submitted to ICTV:
Date of this revision (if different to above):

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	***2012.005aB***	(assigned by ICTV officers)

To create six new species within:

Genus:	***T5likevirus****
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:	**GenBank sequence accession number(s) of reference isolate:**
Escherichia phage T5	AY543070
Escherichia phage Akfv33	HQ665011
Escherichia phage Eps7	CP000917
Salmonella phage Spc35	HQ406778
Escherichia phage Bf23	DQ097178
Escherichia phage H8	AC171169

***T5likevirus** is the new name for the genus "T5-like viruses" proposed in <2011.010aB.A.v1.Caudovirales_genus-ren>, an EC-approved proposal currently awaiting ratification by the ICTV membership

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

As shown by whole genome alignments (Figure 1) using progressiveMauve the genomes of these three phages are collinear and significantly related to coliphage T5. All authors have noted the relationship between these phages and T5 (References 1-3). The sequence of phage BF23 (Reference 4) is also compelling evidence that it is a member of the *T5likevirus* genus. In addition, phage BF23 has long been considered a T5 relative (Reference 5).

The species demarcation criteria include a difference in DNA similarity of more than 5% and differences in host range as described in the respective papers (References 1 – 7)

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Niu YD, Stanford K, Kropinski AM, Ackermann HW, Johnson RP, She YM, Ahmed R, Villegas A, McAllister TA. Genomic, proteomic and physiological characterization of a T5-like bacteriophage for control of Shiga toxin-producing *Escherichia coli* O157:H7. PLoS One. 2012; 7(4):e34585.

2. Hong J, Kim KP, Heu S, Lee SJ, Adhya S, Ryu S. Identification of host receptor and receptor-binding module of a newly sequenced T5-like phage EPS7. FEMS Microbiol Lett. 2008 Dec;289(2):202-9.

3. Kim M, Ryu S. Characterization of a T5-like coliphage, SPC35, and differential development of resistance to SPC35 in *Salmonella enterica* serovar typhimurium and *Escherichia coli*. Appl Environ Microbiol. 2011;77(6):2042-50.

4. Mondigler M, Ayoub AT, Heller KJ. The DNA region of phage BF23 encoding receptor binding protein and receptor blocking lipoprotein lacks homology to the corresponding region of closely related phage T5. J Basic Microbiol. 2006;46(2):116-25.

5. McCorquodale, D. J., and H. R. Warner. 1988. Bacteriophage T5 and related phages, p. 439-475. In R. Calender (ed.), The bacteriophages. Plenum Publishing Corp., New York.

6. Rabsch W, Ma L, Wiley G, Najar FZ, Kaserer W, Schuerch DW, Klebba JE, Roe BA, Laverde Gomez JA, Schallmey M, Newton SM, Klebba PE. FepA- and TonB-dependent bacteriophage H8: receptor binding and genomic sequence. J Bacteriol. 2007; 189(15):5658-74.

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.

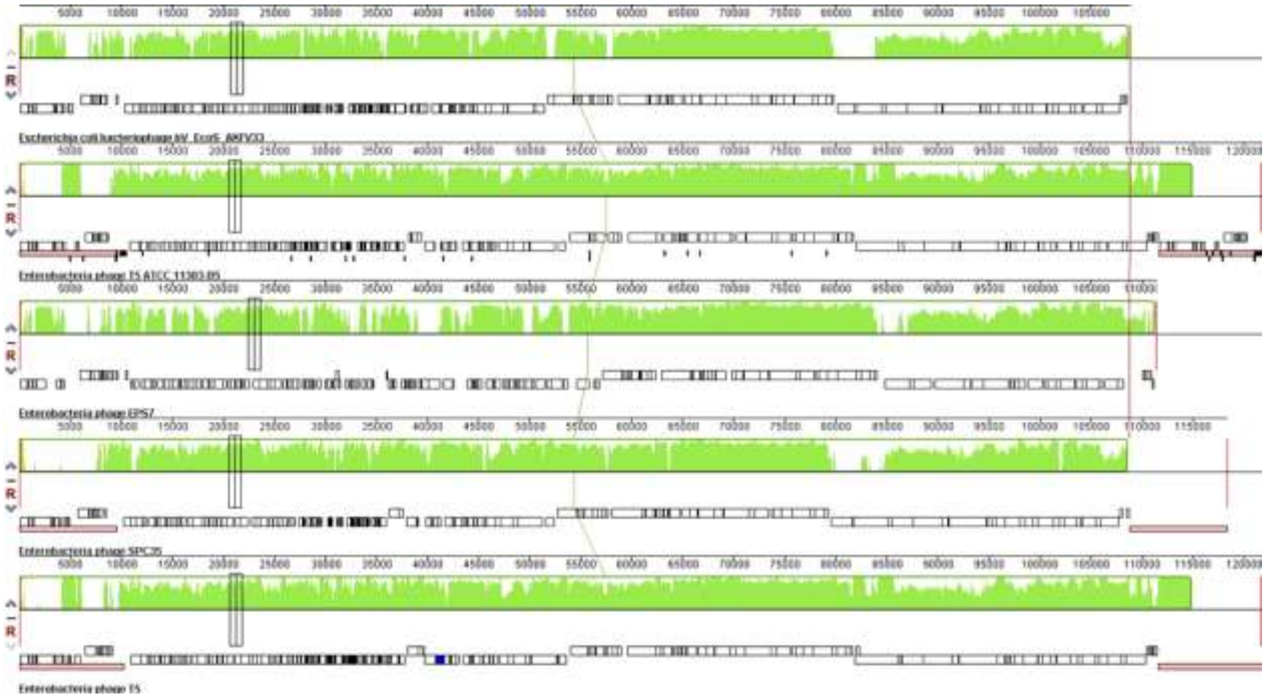

Figure 1. ProgessiveMauve alignment of the genomes of five T5-like phages