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:	***2012.004aB***	(to be completed by ICTV officers)

Short title: To create eight new species in the genus "T1-like viruses" (proposed name *Tunalikevirus*) in the family *Siphoviridae*, order *Caudovirales*
(e.g. 6 new species in the genus *Zetavirus*)

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

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:

Improve species name, add CEV2 Genbank accession, supply species demarcation criteria and change 'homology' to 'similarity'.

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	***2012.004aB***

(assigned by ICTV officers)

To create eight new species within:

Genus:	**“T1-like viruses”** (to be renamed *Tunalikevirus**)
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.

	GenBank sequence accession number(s) of reference isolate:
Escherichia phage Rogue1	JQ182736
Escherichia phage Jk06	DQ121662
Escherichia phage Eb49	JF770475
Escherichia phage Rtp	AM156909
Escherichia phage Tls	AY308796
Cronobacter phage Esp2949-1	JF912400
Enterobacter phage F20	JN672684
Shigella phage Shfl1	HM035024

*genus to be renamed *Tunalikevirus*, see proposal <2011.010aB.A.v2.Caudovirales_genus-ren>

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 CoreGenes analysis (http://binf.gmu.edu:8080/CoreGenes2.0/) of the proteomes the genomes of these three phages are collinear and significantly related (>47% homologous proteins) to coliphage T1. Battaglioli et al. and Wietzorrek et al. both noted the relationship between these phages and T1 (References 1-2). The interpretation of their electron micrographs by Lee et al. (Reference 3) was incorrect. Two of the interesting properties of these phages is that the small early region genes tend not to be conserved; and, these phages possess homologs to coliphage lambda gpH, gpL, gpI, gpFII, gpU, and gpV indicating a phylogenetic relationship between the tail modules of the T1 and lambdoid phages.

Species demarcation criteria: For the phages to belong to different species, we propose a difference in DNA identity of more than 5% in combination with differences in host range.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Battaglioli EJ, Baisa GA, Weeks AE, Schroll RA, Hryckowian AJ, Welch RA. Isolation of generalized transducing bacteriophages for uropathogenic strains of *Escherichia coli.* Appl Environ Microbiol. 2011 Sep;77(18):6630-5.

2. Wietzorrek A, Schwarz H, Herrmann C, Braun V. The genome of the novel phage Rtp, with a rosette-like tail tip, is homologous to the genome of phage T1. J Bacteriol. 2006 Feb;188(4):1419-36.

3. Lee YD, Kim JY, Park JH, Chang H. Genomic analysis of bacteriophage ESP2949-1, which is virulent for *Cronobacter sakazakii*. Arch Virol. 2012 Jan;157(1):199-202.

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.

Phage	**Number of homologous proteins to T1**	**% similarity**
Escherichia phage Rogue1	42	53.8
Escherichia phage Jk06	37	47.4
Escherichia phage Eb49	42	53.8
Escherichia phage Rtp	44	56.4
Escherichia phage Tls	51	65.4
Cronobacter phage Esp2949-1	37	47.4
Enterobacter phage F20	45	57.7
Shigella phage Shfl1	66	84.6

Table 1. CoreGene Analysis of the proteome of the proposed genera in comparison to that of coliphage T1.

Based upon our proposal that phages which share 40% of their proteins in common belong to the same genus, all of these viruses should be confirmed as members of the *Tunalikevirus* genus.