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:	***2015.022a-dB***	(to be completed by ICTV officers)

Short title: To create one (1) new genus, *Tg1virus*, including two (2) new species within the family *Myoviridae*.
(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):

Carlos G. Leon-Velarde – University of Guelph (Canada)
Andrew M. Kropinski – University of Guelph (Canada)
Evelien M. Adriaenssens – University of Pretoria (South Africa)

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)	Bacterial & 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 *Tg1virus* rather than *Tg1likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" from phage genus names. Since the committee is currently studying how to define, at a molecular level, subfamilies, families and orders it does not make sense further classify these T4-like phages.

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	***2015.022aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Tg1virus (new)***
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 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)**
Yersinia virus TG1	Yersinia phage vB_YenM_TG1	KP202158
Yersinia virus R1RT	Yersinia phage phiR1-RT	HE956709

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

Yersinia phages vB_YenM_TG1 and phiR1-RT were isolated in Guelph (Canada) in 2014, and Helsinki (Finland) in 2012, respectively. These communities are approximately 6,644 kilometres apart, yet the two viruses show a 98% identity with query coverage of 93% at the DNA level, for an overall DNA sequence identity of 91%.

Yersinia phage phiR1-RT was isolated from raw sewage (Mikail Skurnik, personal communication) while vB_YenM_TG1 phage was isolated from pig manure. The isolation host for vB_YenM_TG1 was *Yersinia enterocolitica* of serotype O:9, yet its host range also includes strains of serotypes O:3, O:5, and O5,27. *Yersinia* phage phiR1-RT also displays a similar host range (Mikail Skurnik, personal communication). Electron micrographs of vB_YenM_TG1 (Fig. 1) show that the phage exhibits an elongated head measuring 115 nm in length and 91 nm in diameter. The extended tail shows transverse striations and has a length and width of 129 nm and 23 nm, respectively. A clearly defined neck, collar, baseplate, and associated fibrous structures (neck fibers and long tail fibers) were present. Phages with contracted tails measuring 50 nm in length were also observed. Collectively, these morphological features indicate that this virus belongs to the *Myoviridae* family.

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.

The relatedness of these two phages was confirmed using CoreGenes (2) which the Bacterial and Archaeal Virus Subcommittee of ICTV has extensively used to compare the total proteomes (Table 1) of two viruses; progressiveMauve (Fig. 2; 1); and, by phylogenetic analysis (3) of their large subunit terminase proteins (Fig.3) and whole genome sequences (Fig.4.)

Please note that we have chosen to refer to this new genus as *Tg1virus* rather than *Tg1likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" from phage genus names.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.022bB***	(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	***2015.022cB***	(assigned by ICTV officers)

To name the new genus: *Tg1virus*

Assigning the type species and other species to a new genus

Code	***2015.022dB***	(assigned by ICTV officers)

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

Yersinia virus TG1

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:**

2

Reasons to justify the creation of a new genus:

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

Both vB_YenM_TG1 and phiR1-RT display a low GC% content genome, containing only 4 tRNA genes, exhibit similar morphology, and gene arrangement. Phylogenetic analysis of large subunit terminase proteins and whole genome sequences show that vB_YenM_TG1 and its closest relative phiR1-RT form a distinct clade. Additionally less than 34% overall DNA similarity exists with the closest neighbors within the *Myoviridae*.

Origin of the new genus name:

Named after *Yersinia enterocolitica* phage vB_YenM_TG1

Reasons to justify the choice of type species:

Of the two bacteriophages, phage vB_YenM_TG1 is the most recently isolated, has the most complete characterization regarding morphology and host range available. Plus the name phiR1-RT does not lend itself to easy ease of naming 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.
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. Saitou N, Nei M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Bio. Evol. 1987; 4(4):406-25.

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 two phages belonging to the *Tg1virus*

Phage	Genome length (bp)	Genome (mol%G+C)	No. CDSs	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
vB_YenM_TG1	162,101	34.6	262	4	100	100
phiR1-RT	168,809	34.5	262	4	91	89.7

* Determined using BLASTN; ** Determined using CoreGenes (4)

Fig. 1. Electron micrograph of *Yersinia* phage vB_YenM_TG1 negatively stained with uranyl acetate.

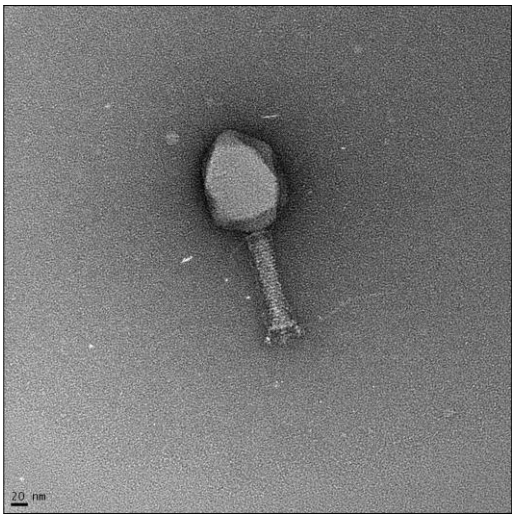

Fig. 2. progressiveMauve alignment of the annotated genomes of phiR1-RT (top) and vB_YenM_TG1 (bottom) (1). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication).

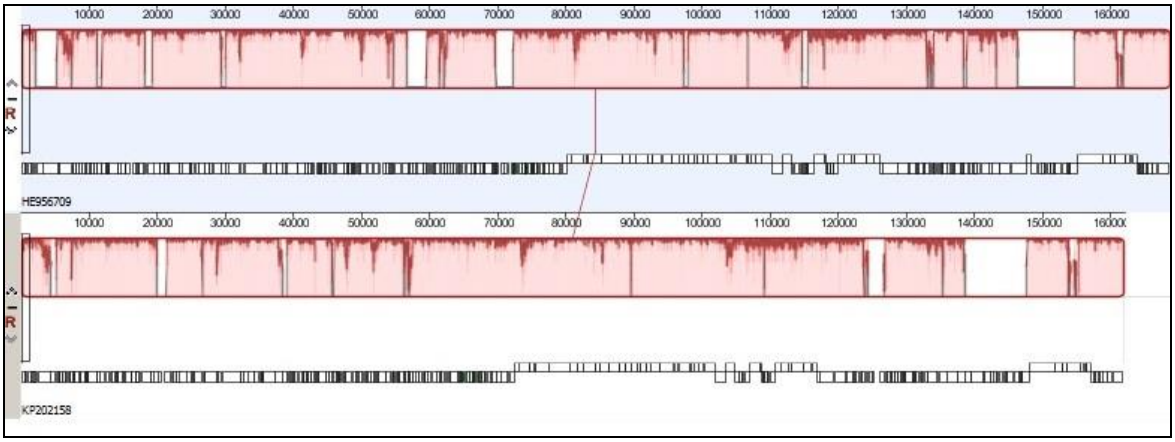

Fig. 3. Phylogenetic analysis of large subunit terminase proteins of tg1viruses and other related bacteriophage proteins constructed using “one click” at phylogeny.fr (3). "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already 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."

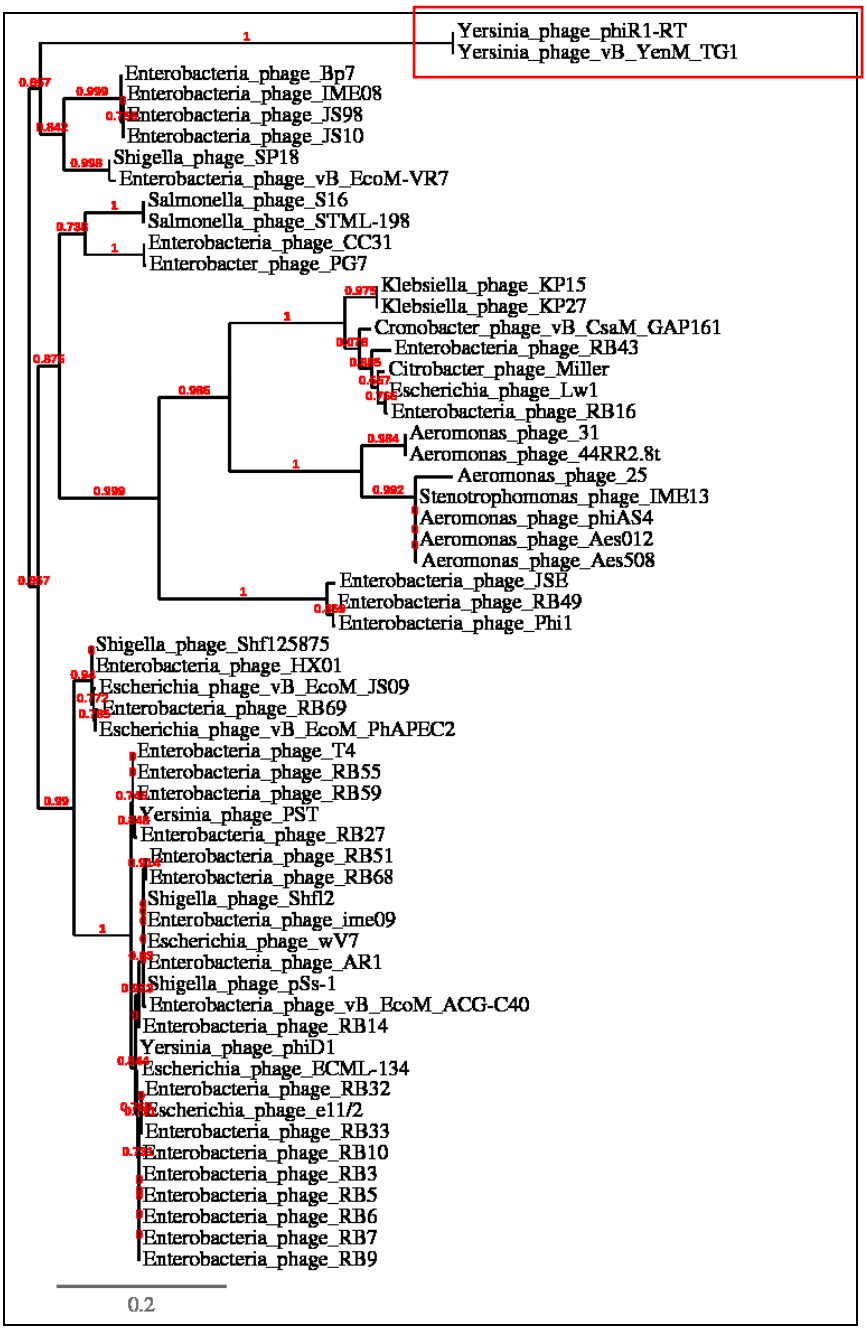

Fig. 4. Whole genome phylogeny. Based on joining neighbor analysis (4). The vB_YenM_TG1 genome sequence was first submitted to BLASTN analysis with query results selected for the nearest 20 complete genomes. Genomes that were > 0.75 similar were included in the analysis.