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:	***2013.033aB***	(to be completed by ICTV officers)

Short title: To create 2 new species in the genus *Phic3unalikevirus*, 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:

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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:

Date first submitted to ICTV: June 2013
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	***2013.033aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Phic3unalikevirus***
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:
Streptomyces phage phibt1 *Streptomyces phage TG1*	AJ550940 JX182372

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

BLASTN analyses reveal that these two *Streptomyces* phages, phiBT1 [1] and TG1 (unpublished) are related to the type phage of this genus, *Streptomyces phage phiC31*. DNA (Table 1, Figure 1) and protein comparisons (Table 1) support the addition of these phages to the genus.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Gregory MA, Till R, Smith MCM (2003) Integration site for Streptomyces phage phiBT1 and development of site-specific integrating vectors. Journal of bacteriology 185: 5320–5323.

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. Phage genomes

Phage	**Accession No.**	**Size (bp)**	**% DNA sequence relatedness (a)**	**% Protein relatedness (b)**
Streptomyces phage phibt1	AJ550940	41831	69.4	84.9
Streptomyces phage TG1	JX182372	40474	65.5	86.8

(a) EMBOSS Stretcher (relative to phiC31)
(b) CoreGenes 3.5 (relative to phiC31)

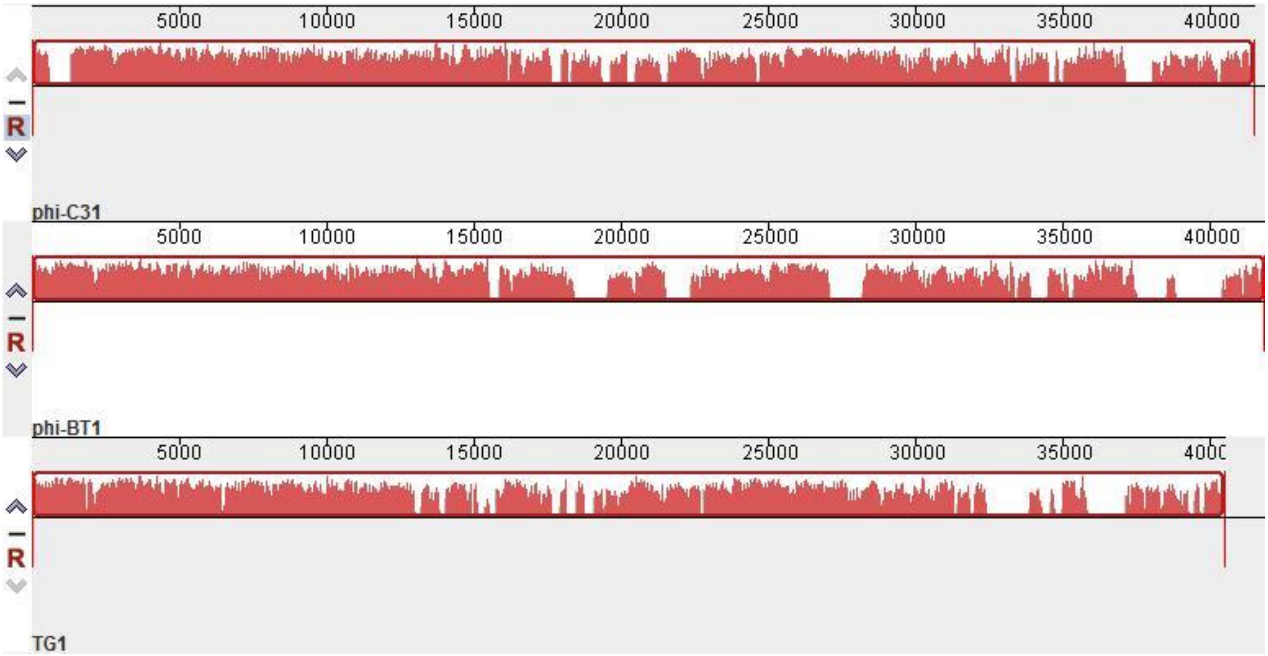

Figure 1. progressiveMauve alignment of the genomes of the newly proposed members of the genus *Phic3unalikevirus*.