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:	***2013.023a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *C5likevirus*, 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:

Evelien Adrieanssens Evelien.Adriaenssens@gmail.com
Andrew M. Kropinski kropinsk@queensu.ca
Rob Lavigne rob.lavigne@biw.kuleuven.be
John Nash, john.nash@phac-aspc.gc.ca

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):	July 2014

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	***2013.023aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***C5likevirus* (new)**
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:
Lactobacillus phage c5 *Lactobacillus phage LLKu*	EU340421 AY739900

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 five *Streptococcus* phages are related and distinct from any other phage. We have chosen 95% DNA sequence identity as the criterion for demarcation of species.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.023bB***	(assigned by ICTV officers)

To create a new genus within:

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.023cB***	(assigned by ICTV officers)

To name the new genus: *C5likevirus*

Assigning the type species and other species to a new genus

Code	***2013.023dB***	(assigned by ICTV officers)

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

Lactobacillus phage c5	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

The two phages belonging to this genus were previously described as grouping together [1]. Phages belonging to this genus have small, isometric heads, and long non-contractile tails. Furthermore, they share a comparable genome size and packaging mechanism (Table 1).

We propose 40% shared proteins with the type phage for new phages to be included in the new genus, as calculated with CoreGenes [2–4].

Origin of the new genus name:

Lactobacillus phage c5

Reasons to justify the choice of type species:

One of the first isolates of this group.

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. Both species differ more than 5% based on an EMBOSS stretcher alignment.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Riipinen K-A, Forsman P, Alatossava T (2011) The genomes and comparative genomics of Lactobacillus delbrueckii phages. Archives of virology 156: 1217–1233. doi:10.1007/s00705-011-0980-5.

2. Mahadevan P, King JF, Seto D (2009) CGUG: in silico proteome and genome parsing tool for the determination of “core” and unique genes in the analysis of genomes up to ca. 1.9 Mb. BMC research notes 2: 168. doi:10.1186/1756-0500-2-168.

3. Mahadevan P, King JF, Seto (2009) Data mining pathogen genomes using GeneOrder and CoreGenes and CGUG: gene order, synteny and in silico proteomes. International Journal of Computational Biology and Drug Design 2: 100–114.

4. Zafar N, Mazumder R, Seto D (2002) CoreGenes: A computational tool for identifying and cataloging “core” genes in a set of small genomes. BMC Bioinformatics 3: 12. doi:10.1186/1471-2105-3-12.

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)	Packaging – termini	% DNA sequence relatedness (a)	% Protein relatedness (b)
Lactobacillus phage C5	EU340421	31841	*cos* site	100	100
Lactobacillus phage LL-Ku	AY739900	31080	*cos* site	82.8	88.0

(a) EMBOSS Stretcher (relative to c5)
(b) CoreGenes 3.5 (relative to c5)

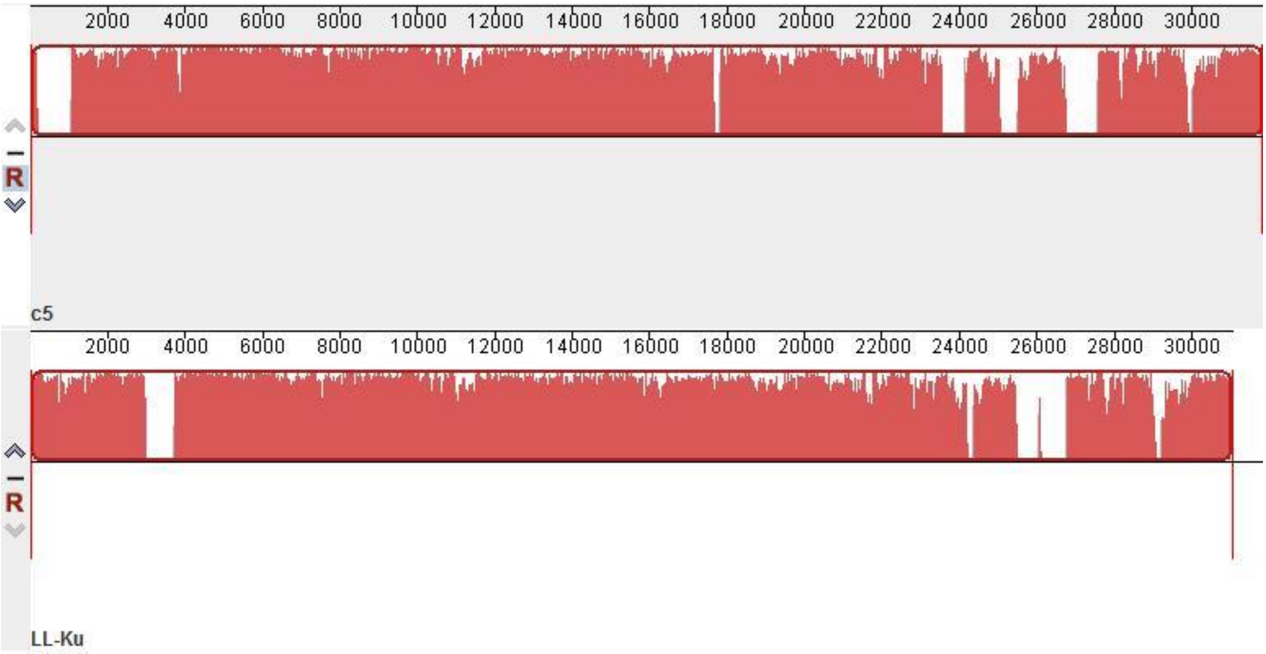

Figure 1. progressiveMauve alignment of the phage genomes belonging to the proposed genus (2). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

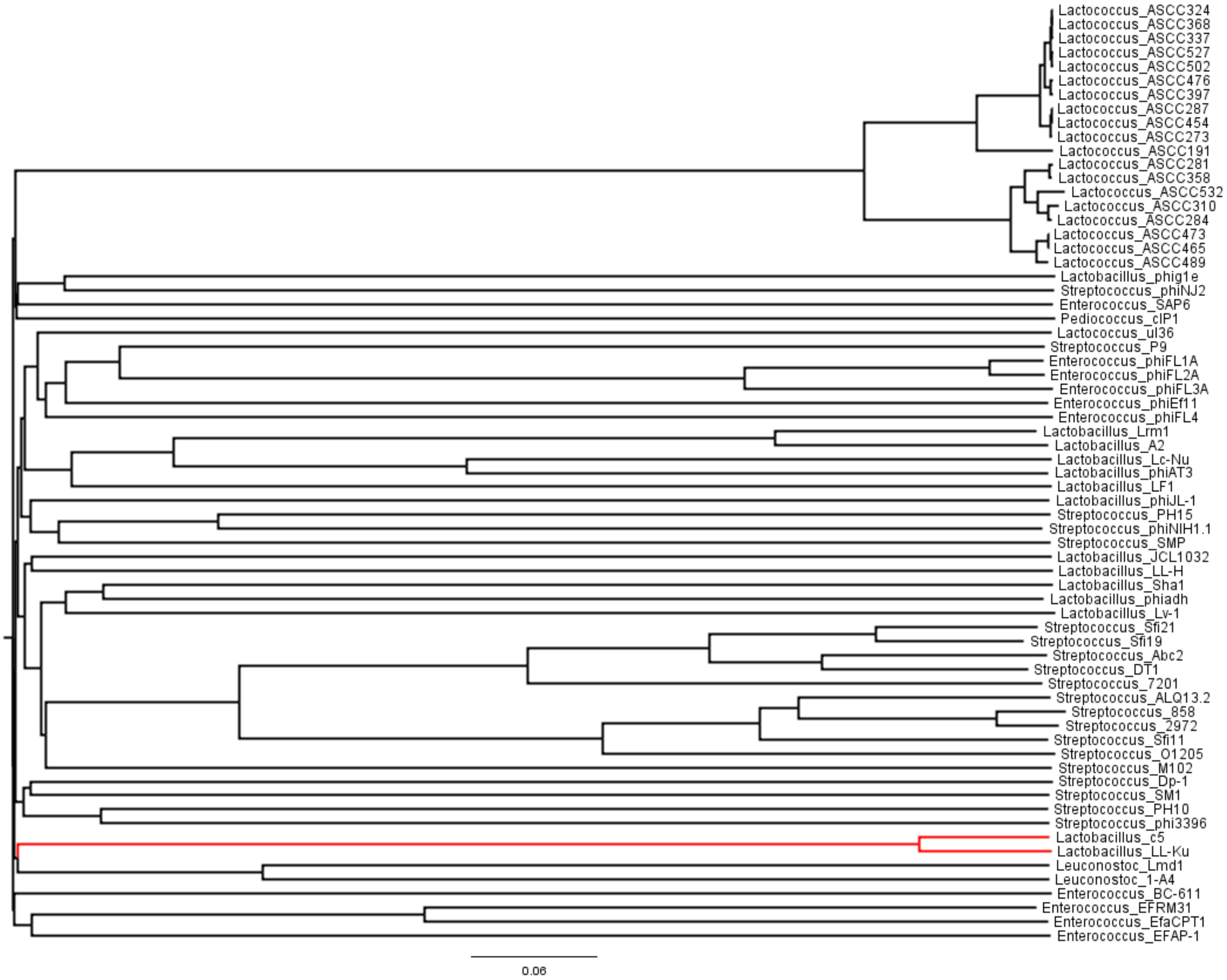

Figure 2: Whole genome phylogenetic tree of selected low GC content *Siphoviridae* phages in the NCBI database in November 2012. Genome sequences were aligned and the tree (NJ) was created with ClustalW 2.0 and visualized with FigTree. The newly proposed genus is colored in red.