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:	***2013.030a-dB***	(to be completed by ICTV officers)

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

Hans-Wolfgang Ackermann ackermann4@gmail.com
Evelien Adriaenssens Evelien.Adriaenssens@gmail.com
Sylvain Moineau Sylvain.Moineau@bcm.ulaval.ca
Andrew M. Kropinski akropins@uoguelph.ca
Rob Lavigne rob.lavigne@biw.kuleuven.be
Niall De Lappe niall.delappe@hse.ie
Hany Anany hanany@uoguelph.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	***2013.030aB***	(assigned by ICTV officers)

To create 6 new species within:

Genus:	***Jerseylikevirus* (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:
Salmonella phage jersey	KF148055
Salmonella phage SETP3	EF177456
Salmonella phage Ent1	HE775250
Salmonella phage SE2	JQ007353
Salmonella phage wksl3	JX202565
Salmonella phage SS3e	AY730274

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 *Salmonella* 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	***2013.030bB***	(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	***2013.030cB***	(assigned by ICTV officers)

To name the new genus: *Jerseylikevirus*

Assigning the type species and other species to a new genus

Code	***2013.030dB***	(assigned by ICTV officers)

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

Salmonella phage jersey

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:**

6

Reasons to justify the creation of a new genus:

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

BLASTN analyses reveal that these six *Salmonella* phages are related and distinct from any other phage. vB_SenS-Ent1 possesses "an icosahedral head 64 nm in diameter and a flexible, non-contractile tail of 116 × 8.5 nm possessing terminal fibres." (1). Lyses *S*. Enteritidis, *S.* Typhimurium, *S*.Heidelberg, and several other *S*. enterica serovars. "Phage SE2 could lyse planktonic and biofilm cells of S. enterica serovar Enteritidis PT-4." (2). Phage "SS3e, is able to lyse not only various *Salmonella* serovars but also *Escherichia coli*, *Shigella sonnei*, *Enterobacter cloacae*, and *Serratia marcescens*" (3). SETP3 heads "measured 62.5 nm and were icosahedral. Tails were rigid, non-contractile, measured 120 x 7 nm, had striations with a periodicity of 4 nm, and carried a 20 nm wide baseplate with spikes." SETP3 was adsorbed by group B (O4,12) and D1 (O 9,12) *Salmonella* and not by group D3 (O 9,46) *Salmonella*. SETP3 was adsorbed by lipopolysaccharide purified from *S*. Enteritidis (O 9,12) but not with lipopolysaccharide purified from *S.* Minnesota (O 21). The results were consistent with adsorption to the O 12 antigen.
General characteristics of these phages are listed in Table 1.

Origin of the new genus name:

Salmonella phage Jersey

Reasons to justify the choice of type species:

The original historical isolate 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.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1: Turner D, Hezwani M, Nelson S, Salisbury V, Reynolds D. Characterization of the *Salmonella* bacteriophage vB_SenS-Ent1. J Gen Virol. 2012; 93(Pt 9):2046-56.

2: Tiwari BR, Kim S, Kim J. Complete genomic sequence of *Salmonella enterica* serovar Enteritidis phage SE2. J Virol. 2012; 86(14):7712.

3: Kim SH, Park JH, Lee BK, Kwon HJ, Shin JH, Kim J, Kim S. Complete genome sequence of *Salmonella* bacteriophage SS3e. J Virol. 2012; 86(18):10253-4.

4. Kang,H.W., Kim,J.W., Jung,T.S. and Woo,G.J. 2013. wksl3, a New Biocontrol Agent for *Salmonella enterica* Serovars Enteritidis and Typhimurium in Foods: Characterization, Application, Sequence Analysis, and Oral Acute Toxicity Study. Appl. Environ. Microbiol. 79 (6), 1956-1968

5. Ackermann HW, Gershman M. Morphology of phages of a general *Salmonella* typing set. Res Virol. 1992; 143(5):303-10. (Jersey phage reference)

6. Darling AE, Mau B, Perna NT (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5: e11147

N.B. 02.066.0.00.045. Enterobacteria phage Jersey (Jersey)

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	GenBank Accession No.	Genome size (bp)	Mol%G+C	% DNA sequence identity (a)	% Shared proteins (b)
Salmonella phage Jersey	KF148055	43,447	49.97	ND[(c)]	ND[(c)]

Salmonella phage SETP3	EF177456.1	42,572	49.85	100%	100%
Salmonella phage vB_SenS-Ent1	HE775250.1	42,391	49.79	85.7%	92.5
Salmonella phage SE2	JQ007353.1	43,221	49.64	79.5%	86.8
Salmonella phage wksl3	JX202565.1	42,633	49.80	79.2%	94.3
Salmonella phage SS3e	AY730274.2	40,793	50.08	75.8%	83.0

(a) EMBOSS Stretcher (relative to SETP3; genome reoriented for comparison)
(b) CoreGenes 2.0
(c) Not determined since sequence has not been released by GenBank

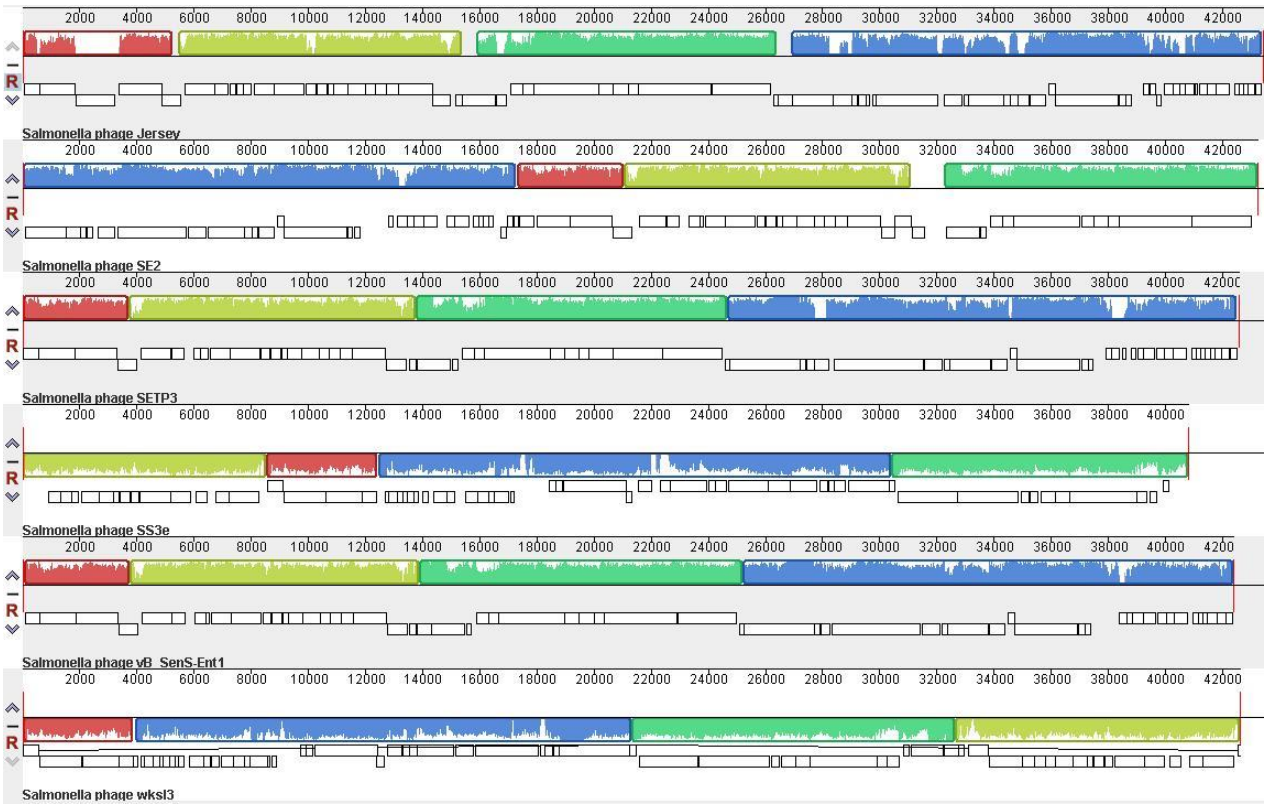

Figure 1. progressiveMauve alignment of the phage genomes belonging to the proposed genus (full genome represented by its annotated ORFs in white blocks) (6). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence 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. The alignment indicates that the phages are very similar, but not collinearly organized.

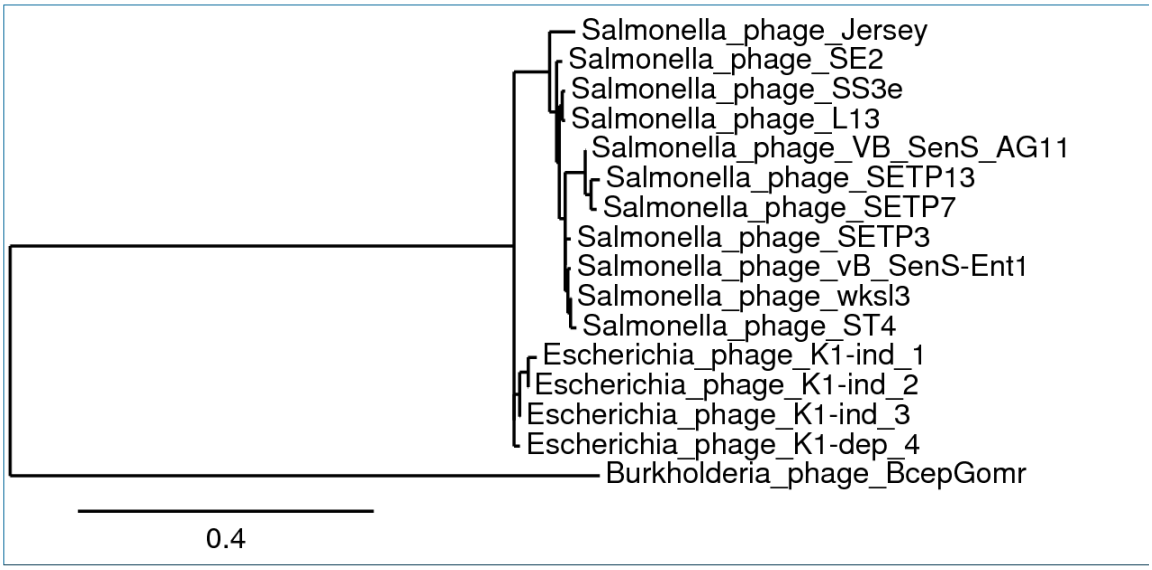

Figure 2: Phylogenetic tree of the major capsid proteins of phages belonging to the proposed genus *Jerseylikevirus*.

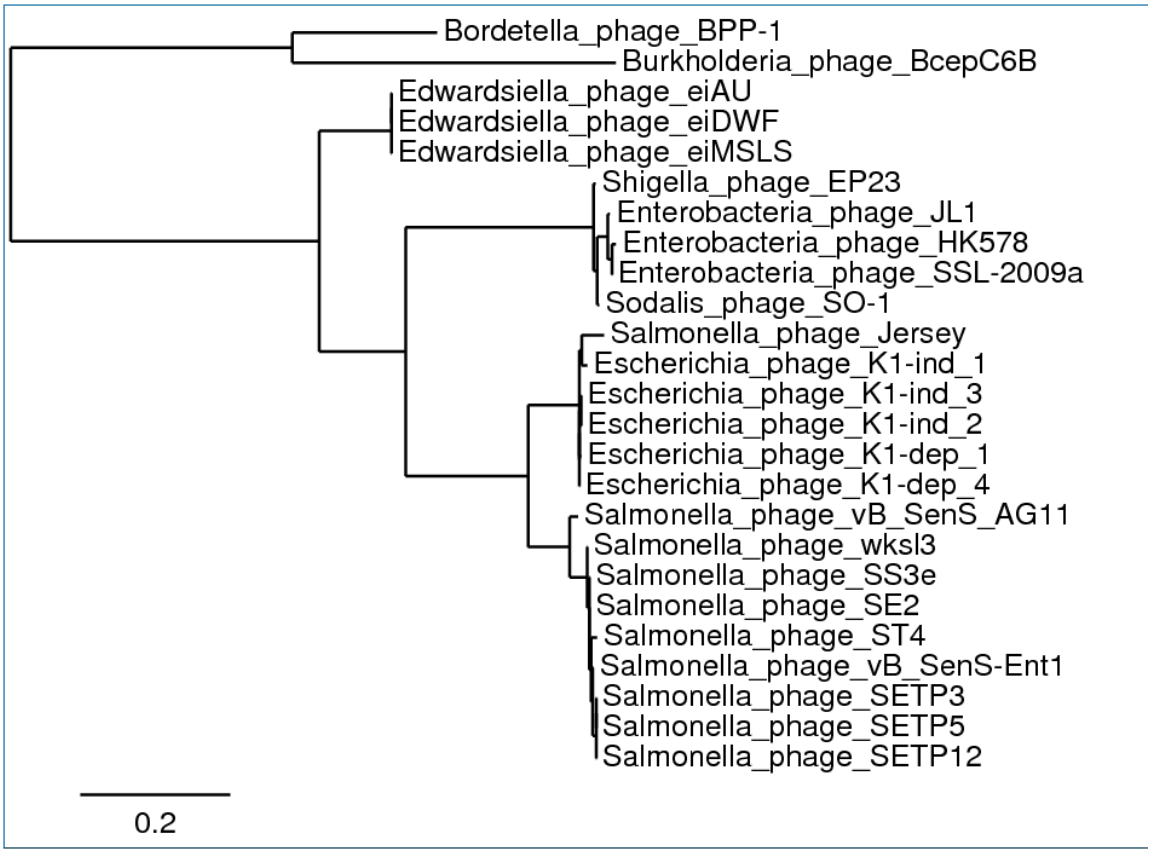

Figure 2: Phylogenetic tree of the DNA polymerase of phages belonging to the proposed genus *Jerseylikevirus*.