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:	***2015.044a-nB***	(to be completed by ICTV officers)

Short title: To add one (1) existing, and two (2) new genera to a new subfamily – *Guernseyvirina*e.
(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** ☒

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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 Study Group comments (if any) and response of the proposer:

Please note that the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

Date first submitted to ICTV: June 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	***2015.044aB***	(assigned by ICTV officers)

To create 6 new species within:

Genus:	***Jerseylikevirus*** **(**proposed name: ***Jerseyvirus*****)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Salmonella virus AG11	Salmonella phage vB_SenS_AG11	JX297445
Salmonella virus SETP7	Salmonella phage SETP7	KF562865
Salmonella virus SP101	Salmonella phage FSL SP-101	KC139511
Salmonella virus SETP13	Salmonella phage SETP13	KF562864
Salmonella phage LSPA1	Salmonella phage LSPA1	KM272358
Salmonella phage L13	Salmonella phage L13	KC832325

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

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

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 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	***2015.044bB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Sp31virus (new)***
Subfamily:	***Guernseyvirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Salmonella virus SP31	Salmonella phage FSL SP-031	KC139518

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

Please note that we have chosen to refer to this new genus as *Sp31virus* rather than *Sp3unalikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

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 3: **NEW GENUS**

creating a new genus

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

Code	***2015.044cB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Guernseyvirinae* (new)**
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	***2015.044dB***	(assigned by ICTV officers)

To name the new genus: *Sp31virus*

Assigning the type species and other species to a new genus

Code	***2015.044eB***	(assigned by ICTV officers)

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

Salmonella virus SP31

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:**

1

Reasons to justify the creation of a new genus:

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

On the basis of extensive morphological, and comparative genomic and proteomic analyses combined with whole genome and specific protein phylogenetic analyses Anany et al. (2) proposed the creation of a new subfamily, "Jerseyvirinae" to encompass these phages. In addition, they proposed the creation of three genera within this subfamily - "Jerseylikevirus", "K1glikevirus" and "Sp3unalikevirus." Jerseylikevirus (proposed to be renamed *Jerseyvirus*) has already been approved by ICTV. This proposal integrates the other two proposed genera. As addition information we have provided a whole genome tree based upon BLASTN analysis (Fig. 1).

Origin of the new genus name:

Derived from name of first isolate: *Salmonella* phage FSL SP-031

Reasons to justify the choice of type species:

First representative of this type of phage.

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 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	***2015.044fB***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***K1gvirus (new)***
Subfamily:	***Guernseyvirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus K1ind1	Escherichia phage K1ind1	GU196279
Escherichia virus K1G	Escherichia phage K1G	GU196277
Escherichia virus K1ind2	Escherichia phage K1ind2	GU196280
Escherichia virus K1H	Escherichia phage K1H	GU196278

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

Please note that we have chosen to refer to this new genus as *K1gvirus* rather than *K1glikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

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 3: **NEW GENUS**

creating a new genus

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

Code	***2015.044gB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Guernseyvirinae* (new)**
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	***2015.044hB***	(assigned by ICTV officers)

To name the new genus: *K1gvirus*

Assigning the type species and other species to a new genus

Code	***2015.044iB***	(assigned by ICTV officers)

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

Escherichia virus K1G

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:**

4

Reasons to justify the creation of a new genus:

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

On the basis of extensive morphological, and comparative genomic and proteomic analyses combined with whole genome and specific protein phylogenetic analyses Anany et al. (2) proposed the creation of a new subfamily, "Jerseyvirinae" to encompass these phages. In addition, they proposed the creation of three genera within this subfamily - "Jerseylikevirus", "K1glikevirus" and "Sp3unalikevirus." Jerseylikevirus (proposed to be renamed Jerseyvirus) has already been approved by ICTV. This proposal integrates the other two proposed genera. As addition information we have provided a whole genome tree based upon BLASTN analysis (Fig. 1).

Origin of the new genus name:

Derived from name of first isolate: *E.coli* phage K1G

Reasons to justify the choice of type species:

First representative of this type of phage.

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 4: **NEW SUBFAMILY**

creating a new subfamily

A subfamily can only be created within a family.

Code	***2015.044jB***	(assigned by ICTV officers)

To create a new subfamily within:

Family:	***Siphoviridae***
Order:	***Caudovirales***

If the family has yet to be created (in Module 5) please write "**(new)**" after the proposed name.

- If there is no Order, write "**unassigned**" here.

naming a new subfamily

Code	***2015.044kB***	(assigned by ICTV officers)

To name the new subfamily: *Guernseyvirinae*

genera and species assigned to the new subfamily

Code	***2015.044lB***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family

Jerseylikevirus – existing (proposed name: ***Jerseyvirus***)

Sp31virus – new

K1gvirus – new

The new subfamily 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 unassigned species that the subfamily will contain (those NOT within any of the genera listed above):**

0

Reasons to justify the creation of the new subfamily:

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

On the basis of extensive morphological, and comparative genomic and proteomic analyses combined with whole genome and specific protein phylogenetic analyses Anany et al. (2) proposed the creation of a new subfamily, "Jerseyvirinae" to encompass these phages. In addition, they proposed the creation of three genera within this subfamily - "Jerseylikevirus", "K1glikevirus" and "Sp3unalikevirus." Jerseylikevirus (proposed to be renamed *Jerseyvirus*) has already been approved by ICTV. This proposal integrates the other two proposed genera. As addition

information we have provided a whole genome tree based upon BLASTN analysis (Fig. 1).
Origin of the new subfamily name:
Derived from the name of the Channel Island closest to Jersey. It was considered inappropriate to name the subfamily Jerseyvirinae because of its similarity to *Jerseyvirus*.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2015.044mB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Jerseylikevirus (proposed name ***Jerseyvirus***)

The present taxonomic position of these taxon/taxa:

Genus:	-
Subfamily:	**unassigned**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

see 2015.019sB, above

Part (b) re-assign to a higher taxon

Code	***2015.044nB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	
Subfamily:	***Guernseyvirinae*** **(new)**
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

see 2015.019sB, above

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. 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.
2. Anany H, Switt AI, De Lappe N, Ackermann HW, Reynolds DM, Kropinski AM, Wiedmann M, Griffiths MW, Tremblay D, Moineau S, Nash JH, Turner D. A proposed new bacteriophage subfamily: "Jerseyvirinae". Arch Virol. 2015;160(4):1021-33.

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 type viruses for each of the three genera which belong to the *Guernseyvirina*e.

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**
Jersey	KF148055	43.45	50.0	69	100	100
K1G	GU196277	43.59	51.1	52	55	59.4
SP-031	KC139518	42.22	51.1	59	34	66.7

* Determined using BLASTN; ** Determined using CoreGenes (1);

Table 2. Phages which should be considered as strains within the subfamily *Guernseyvirina*e.

Phage	**GenBank Accession Number**
Salmonella phage vB_SenS-Ent2	HG934469
Salmonella phage vB_SenS-Ent3	HG934470
Escherichia phage K1ind3	GU196281

Fig. 1. Whole genome DNA tree – a BLASTN search was conducted at NCBI with the phage Jersey DNA sequence and the homologous sequences were selected for "Distance tree of results" analysis. The Neighbor Joining tree method was selected, and the results downloaded in "Newick Format." This file was edited with Notepad, and saved in dnd format. This was opened in FigTree (http://tree.bio.ed.ac.uk/software/figtree/) to produce the accompanying whole genome tree.