MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2015.047aB*	(to be completed by ICTV officers)

Short title: To add seven (7) new species to *Felixounalikevirus* (proposed name *Felixo1virus*)
(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:

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

Date first submitted to ICTV: June 2015
Date of this revision (if different to above):

ICTV-EC comments 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.

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	*2015.047aB*		(assigned by ICTV officers)

To create 7 new species within:

Genus:	*Felixounalikevirus* (proposed name *Felixo1virus*)	Fill in all that apply.
Subfamily:		• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Family:	*Myoviridae*	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Caudovirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Salmonella virus UAB87	Enterobacteriaphage UAB_Phi87	JN225449
Escherichia virus VpaE1	Escherichia phage vB_EcoM-VpaE1	KM657822
Salmonella virus Mushroom	Salmonella phage Mushroom	KP143762
Escherichia virus JH2	Escherichia phage JH2	KF055347
Escherichia virus AYO145A	Escherichia phage vB_EcoM_AYO145A	KR014248
Salmonella virus HB2014	Salmonella phage HB-2014	KP010413
Escherichia virus EC6	Escherichia phage EC6	JX560968

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

Several new FelixO1-like phage genomes have recently been deposited to GenBank, and in certain case a publication is also available (2-4). This proposal recognizes the fact that they are part of the *Felixo1virus* genus.

Please note that we have chosen to refer to this new genus as *Felixo1virus* rather than *Felixounalikevirus* 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. On average the genomes of this genus are 86.9 kb (38.9 mol% G+C), and encode 133 proteins and 21 tRNAs.

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.Tolen TN, Xie Y, Hernandez AC, Kuty Everett GF. Complete Genome Sequence of *Salmonella enterica* Serovar Typhimurium Myophage Mushroom. Genome Announc. 2015 Apr 9;3(2). pii: e00154-15.

3. Cowley LA, Beckett SJ, Chase-Topping M, Perry N, Dallman TJ, Gally DL, Jenkins C. Analysis of whole genome sequencing for the *Escherichia coli* O157:H7 typing phages. BMC Genomics. 2015 Apr 8;16(1):271. E.coli typing phages

4. Tiwari BR, Kim J. Complete Genome Sequence of Bacteriophage EC6, Capable of Lysing *Escherichia coli* O157:H7. Genome Announc. 2013 Jan;1(1). pii: e00085-12. doi: 10.1128/genomeA.00085-12.

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.

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Table 1. Properties of the seven new phages belonging to the *Felixo1likevirus* plus the type virus.

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
FelixO1	NC_005282	86.16	39.0	131	22	100	100
UAB_Phi87	JN225449	87.60	39.0	147	22	91	90.8
vB_EcoM-VpaE1	KM657822	84.40	38.9	132	22	91	90.1
Mushroom	KP143762	87.71	39.0	128	21	92	87.0
JH2	KF055347	87.71	38.8	131	20	88	87.0

vB_EcoM_AYO145A	KR014248	87.37	39.0	131	19	89	90.8
HB-2014	KP010413	87.51	38.8	126	21	88	83.2
EC6	JX560968	86.23	38.9	136	20	86	86.3

* Determined using BLASTN relative to T5; ** Determined using CoreGenes (1). The GenBank accession number for FelixO1 contains numerous annotation errors

Table 2. Phages which could be considered strains of FelixO1 or its relatives

Phage	GenBank accession No.
Escherichia coli O157 typing phage 12	KP869110
Escherichia coli O157 typing phage 11	KP869109
Escherichia coli O157 typing phage 8	KP869106
Escherichia coli O157 typing phage 15	KP869113
Salmonella phage FO1a	JF461087

Fig. 1. Whole genome DNA tree – a BLASTN search was conducted at NCBI, 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. The *Staphylococcus* phage is a chimera; and SPT_1 is a partial sequence.

Citrobacter_phage_Moogle

Escherichia_phage_EC6

Escherichia_coli_O157_typing_phage_15

Escherichia_coli_O157_typing_phage_1

Escherichia_coli_O157_typing_phage_12

Enterobacteria_phage_WV8

Escherichia_coli_O157_typing_phage_11

Escherichia_coli_O157_typing_phage_8

Staphylococcus_phage_SA1

Salmonella_phage_HB_2014

Escherichia_phage_JH2

Escherichia_phage_vB_EcoM_VpaE1

Escherichia_phage_vB_EcoM_AYO145A

Salmonella_phage_FO1a

Salmonella phage_Felix_01

Salmonella_phage_SPT_1

Salmonella_phage_Mushroom

Salmonella phage_UAB_Phi87

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