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:	***2009.006a-gB***	(to be completed by ICTV officers)

Short title: Create new genus named *Felixo1likevirus* in the family *Myoviridae*
(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:

Rob Lavigne rob.lavigne@biw.kuleuven.be
Andrew Kropinski kropinsk@queensu.ca
Hans-Wolfgang Ackermann ackermann4@gmail.com

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

ICTV-EC or Study Group comments and response of the proposer:

[previous (EC41) decision: inconsistent with naming rules.]

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

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	**2009.006aB**	(assigned by ICTV officers)

To create 3 new species with the name(s):

Salmonella phage FelixO1
Erwinia phage phiEa21-4
Escherichia phage wV8

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	**2009.006bB**	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***Felixo1likevirus*** (new)
Subfamily:	
Family:	***Myoviridae***
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.

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.
- Provide GenBank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

BLASTX analysis of the genome of *Salmonella* phage FelixO1 (AF320576) reveals little homology between its proteins and those of other bacteriophages, with the notable exceptions of the recently characterized *Erwinia* phage phiEa21-4 (EU710883) and coliphage wV8 (EU877232). All the authors of manuscripts on these three phages noted their similarity.

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	**2009.006cB**	(assigned by ICTV officers)

To create a new genus to contain the species listed below

Code	**2009.006dB**	(assigned by ICTV officers)

To name the new genus: *Felixo1likevirus*

assigning a new genus to higher taxa

Code	**2009.006eB**	(assigned by ICTV officers)

To assign the new genus as follows: Ideally, a genus should be placed within a higher taxon, but if not, write "**unassigned**" in the box below.

Subfamily:	
Family:	***Myoviridae***
Order:	***Caudovirales***

If any of these taxa has yet to be created (in module 4, 5 or 6) please write "**(new)**" after its proposed name.

assigning type species and other species to a new genus

Code	**2009.006fB**	(assigned by ICTV officers)

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

Salmonella phage FelixO1

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

Bacteriophage O1 (also called phage Felix O1, 01 or 0-1) is a member of the A1 group of the *Myoviridae* with an icosahedral head approximately 70 nm in diameter and a contractile tail (18 x 138 nm) characterized by subunits overlapping each other like roof tiles and showing a criss-cross terminating in six straight tail fibres (Ackermann 2007). It was first used by Felix and Callow in the original scheme for the identification and typing of *Salmonella enterica* subsp. *enterica* serovar Typhi (Felix and Callow 1943). Phage O1 is fairly unique among *Salmonella* bacteriophages because of its broad host range within this genus and its specificity for the genus (Kallings and Lindberg 1967; Kallings 1967).

Code	**2009.006gB**	(assigned by ICTV officers)

To assign the following as additional species of the new genus:

Erwinia phage *phiEa21-4*
Escherichia phage wV8

Reasons to justify the creation of a new genus:
Additional material in support of this proposal may be presented in the Appendix, Module 9

All members described encapsulate linear, non-permuted genomes of 84-88 kb within an isometric capsid (diameter: ca. 73 nm) and carry non-flexible, contractile tails of approximately 140 nm.

Based on these observations, these phages can be classified into the A1 morphological group of the *Myoviridae* (Table 1; Figure 1).

Whole genome comparisons were made at the protein level using CoreGenes (Zafar et al. 2002) revealed that FelixO1 and wV8 share 92% of their proteins in common. The authors (Villegas et al. 2009) of the paper on wV8 remarked that "This level of similarity indicates that wV8 should be classified into the newly proposed genus, "FelixO1-like viruses" (the proposed name of the genus has since been changed to *Felixo1likevirus*), along with *Erwinia amylovora* phage phiEa21-4." Similarly the authors of the paper on the *Erwinia* phage (Lehman et al. 2009) state "The only phage genome to which φEa21-4 is substantially similar is that of the *Salmonella* typing phage FelixO1. In fact, phiEa21-4 has the first reported FelixO1-like genome. The similarity between these two genomes extends beyond the fact that both are members of the *Myoviridae* family. Proteomic work did confirm the existence of shared structural genes, but these two phages also share a total of 32 genes that are not shared with other *Myoviridae* and that may be unique to the Felix O1-like genus." The level of DNA relatedness is relatively low (Fig 2).

Origin of the new genus name:

Named after type species FelixO1

Reasons to justify the choice of type species:

The strictly virulent and historically important *Salmonella* phage FelixO1 was first described almost 70 years ago and has been used extensively as a typing phage for this bacterial genus.

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.
- Provide GenBank accession numbers (not RefSeq accessions) for genomic sequences of new species

Phage	Host genus	Genome size (%GC)	ORFs	tRNAs	% Proteins related to FelixO1(*)	Accession No.
FelixO1	*Salmonella*	86,155 (39.0)	131	22		AF320576
φEa21-4	*Erwinia*	84,576 (43.8)	117	26	53	EU710883
wV8	*Escherichia*	88,487 (38.9)	138	23	92	EU877232

*Relatedness determined using CoreGenes.

Clearly the *Erwinia* phage shows differences in genome size, mol%GC; possesses a unique set of consensus rho-independent terminators; and, many of its proteins are significantly different from those of Felix O1.

Phage wV8 does not infect *Salmonella*; it appears to recognize both OMP and LPS receptors in *Escherichia coli* O157:H7. Contains a gene (No. 95), the protein of which shows sequence similarity to proteins from florescent pseudomonads (*P. aeruginosa* hypothetical protein PLES_07941, & *P. putida* hypothetical protein PputGB1_3399).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Ackermann,H.-W. 2007. Salmonella phages examined in the electron microscope. Methods Mol. Biol. 394:213-34.: 213-234.

Darling,A.C., Mau,B., Blattner,F.R., and Perna,N.T. 2004. Mauve: multiple alignment of conserved genomic sequence with rearrangements. Genome Research 14: 1394-1403.

Felix,A. and Callow,B.R. 1943. Typing of paratyphoid B bacilli by means of Vi bacteriophage. British Medical Journal ii: 127-130.

Kallings,L.O. 1967. Sensitivity of various salmonella strains to felix 0-1 phage. Acta Pathologica et Microbiologica Scandinavica 70: 446-454.

Kallings,L.O. and Lindberg,A.A. 1967. Resistance to Felix 0-1 phage in salmonella bacteria. Acta Pathologica et Microbiologica Scandinavica 70: 455-460.

Lehman,S.M., Kropinski,A.M., Castle,A.J., and Svircev,A.M. 2009. Complete genome of the broad-host-range Erwinia amylovora phage Ea21-4 and its relationship to Salmonella phage felix O1. Applied & Environmental Microbiology 75: 2139-2147.

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.

Table 1:

Phage	Isolation details Source, Location & Year		Genome size (%GC)	ORFs	tRNAs	% Proteins related to FelixO1(*)	Accession No.
FelixO1	Germany	1940s	86,155 (39.0)	131	22		AF320576
φEa21-4	Sewage, St. Catharines, ON, Canada	2000	84,576 (43.8)	117	26	53	EU710883
wV8	Sewage, Winnipeg, MB, Canada	1987	88,487 (38.9)	138	23	92	EU877232

(*) shown using CoreGenes

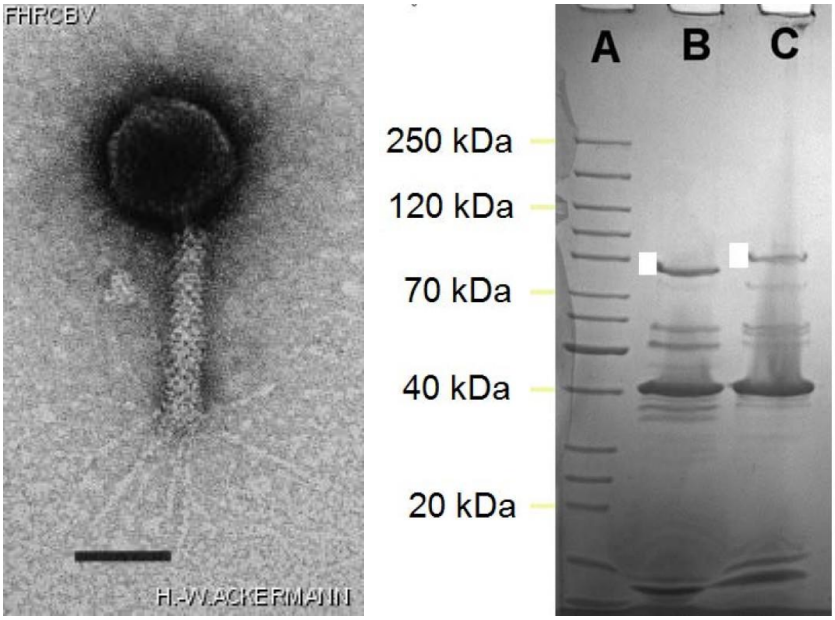

Figure 1:
Left: Electron microscopic images of negatively stained FelixO1 particles. Scale bar represents 100 nm
Right: A. Structural proteins of phages Felix O1 (lane B) and wV8 (lane C) revealed by SDS-PAGE. Clear boxes are to the left side of the phage tail fibre protein bands (taken from: http://www.virologyj.com/content/6/1/41).

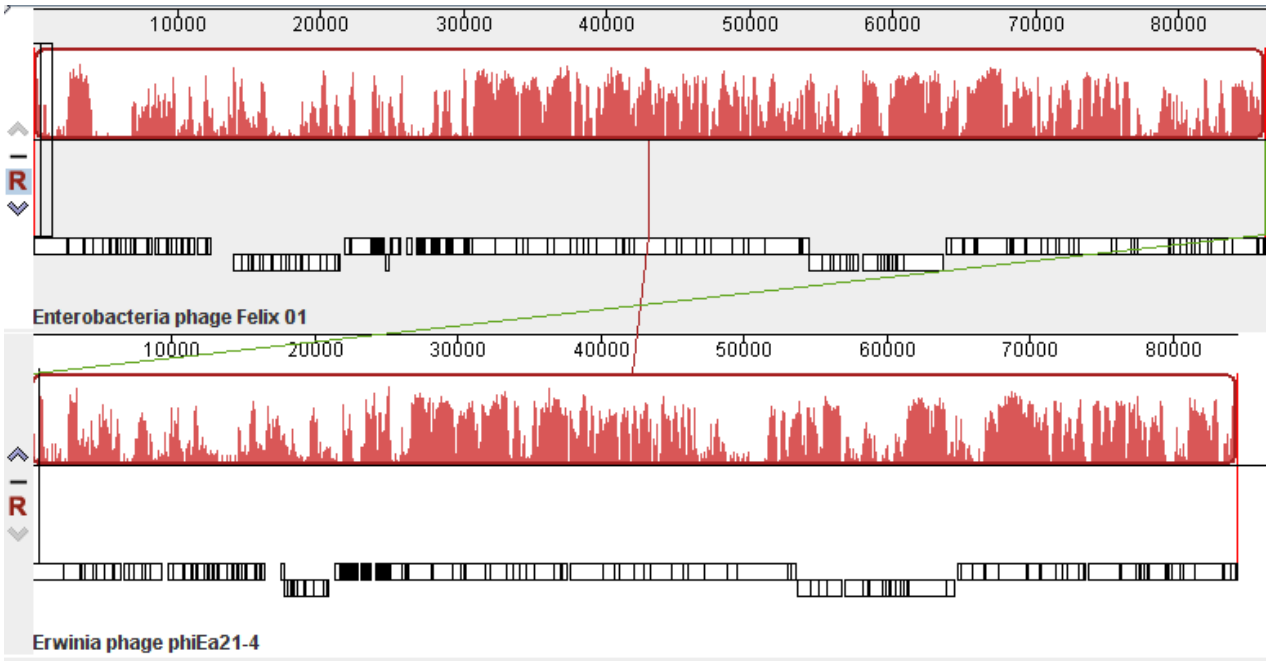

Figure 2. Comparison, at the DNA sequence level using Mauve (Darling et al. 2004), of FelixO1 (Top) to φEa21-4 (Bottom). Both show five transcriptional blocks and 50% of the proteins are related but little overall DNA sequence identity.