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.

MODULE1: **TITLE, AUTHORS, etc**

Code assigned:	***2016.080a-abB***	(to be completed by ICTV officers)

Short title: A complete reanalysis of the family *Inoviridae* rearranging two (2) existing genera; creating five (5) new genera and seventeen (17) new species; reassigning twelve (12) previously approved species, and removing twenty nine (29) species.

(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** ☒	

Author(s):

Petar Knezevic— University of Novi Sad (Serbia)
Andrew M. Kropinski—University of Guelph (Canada)
Evelien M. Adriaenssens—University of Pretoria (South Africa)
Rob Lavigne—KU Leuven (Belgium)

Corresponding author with e-mail address:

Petar Knezevic (Chair, Inoviridae Study Group)
petar.knezevic@dbe.uns.ac.rs

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 Bacterial and Archaeal Virus Subcommittee

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

Date first submitted to ICTV: July 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

Decision taken at EC48: "Uc. Remove Fig 2".

In reply, Petar Knezevic writes: The taxonomy of *Inoviridae* is based on coatB protein sequence, so I consider this phylogenetic tree crucial."

Proposal Secretary's action: Advance proposal to U for further consideration by the EC.

MODULE2: **NEW SPECIES**

creatingand 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	***2016.080aB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Fibrovirus* (new)**
Subfamily:	
Family:	***Inoviridae***
Order:	

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)**
Vibrio virus VGJ	Vibrio phage VGJ	AY242528

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

Please note that the species belongs to the new genus *Fibrovirus*, along with previously approved species of *Vibrio virus fs1***.**

MODULE3: **NEW GENUS**

creating a new genus

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

Code	***2016.080bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Inoviridae***
Order:	

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	***2016.080cB***	(assigned by ICTV officers)

To name the new genus: *Fibrovirus*

Assigning the type species and other species to a new genus

Code	***2016.080dB***	(assigned by ICTV officers)

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

Vibrio virus fs1	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 analyses performed using Gegenees BLASTN and TBLASTX (Table 1 and 2), and "One click" phylogeny.fr of the Zot, CoatB and Coat A proteins indicate significant relatedness between Vibrio phages fs1 and VGJ (Figure 1, 2 and 3, respectively). According to BLASTN, CoreGenes and BLASTP of key genes (Table 3), the phages are similar at both DNA level 88% and protein level 53%. The phages of this genus possess a genome of approx. 6.3-7.5 kb (43 mol% G+C) which encodes 11-15 proteins. The phylogenetic analyses of the Zot and CoatB proteins confirmed that the proposed genus is cohesive and distinct from the other genera in the family, and analysis of the CoatA protein confirmed the differences among species.

The next closest inovirus, Vibrio phage KSF1 shares only 27% of DNA and 20% of proteome similarity with the type species of the genus *Fibrovirus*, *Vibrio virus fs1*. Figure 4 derived from progressiveMauve (Darling et al, 2004) analysis reveals the overall sequence similarity between the members of this genus.

There are several phages, i.e. Vibrio phage ND1fs1, VSK, VSKK and VEJ, considered as variants of *Vibrio virus fs1,* according to DNA similarity higher than 95% (the proteome is not considered according to probable annotation issues). Although ND1fs1 connects all the phages, fs1 was selected as a type strain (the reason is indicated below).

Virions of fs1 and VGJ are filamentous, approximately 7 nm wide and 1000-1200 nm long. The

phages were isolated from *Vibrio cholera* O139 strains and for phage VGJ and VEJ it was confirmed that the mannose-sensitive hemagglutinin (MSHA) is a receptor (type IV pilus). The phages are able to integrate genome into host DNA (Kar et al, 1996; Honma et al., 1997; Ehara et al., 1997; Campos et al, 2003; Campos et al., 2010; Nguyen et al., 2012).

Origin of the new genus name:

Fibra (latin) = "fiber"

Reasons to justify the choice of type species:

The first member of this genus to be described fully.

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. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

MODULE2: **NEW SPECIES**

creatingand 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	***2016.080eB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Saetivirus* (new)**
Subfamily:	
Family:	***Inoviridae***
Order:	

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)**
Vibrio virus VFJ	Vibrio phage VFJ	KC357596

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

Please note that the species belongs to a new genus *Saetivirus*, along with the previously approved species of *Vibrio virus fs2***.**

MODULE3: **NEW GENUS**

creating a new genus

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

Code	***2016.080fB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Inoviridae***
Order:	

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	***2016.080gB***	(assigned by ICTV officers)

To name the new genus: *Saetivirus*

Assigning thetype species and other species to a new genus

Code	***2016.080hB***	(assigned by ICTV officers)

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

Vibrio virus fs2	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 analyses based on Gegenees, CoreGenes and "One click" phylogeny.fr for relevant genes clearly indicate that the two species, *Vibrio virus fs2* and *Vibrio virus VFJ* are related and distinct from other members of the family *Inoviridae* (Table 1 and 2; Fig. 1, 2 and 3). The phages of this genus possess genomes of approx. 8.5 kb (44 mol% G+C). The phages share 80% DNA sequence identity and 100% homologous proteins and the genome of phage VFJ encodes three additional proteins (Table 4). They show some similarity to Vibrio phage VEJ (genus *Fibrovirus*) at protein level (53% with type strain), but there is no obvious DNA sequence similarity. Figure 5 derived from progressiveMauve analysis reveals the overall sequence similarity between the two members of genus *Saetivirus*.

The Vibrio phages fs2 and VFJ are morphologically similar: 7 nm in width and 1200 (fs2)-1400 (VFJ) nm in length. They not integrate into bacterial DNA and rather persist as a plasmid. The classical O1 type *V. cholerae* shows high level of resistance to these phages (Ikema and Honma, 1998; Wang et al. 2013).

Origin of the new genus name:

Saeta (latin) = "horse hair"

Reasons to justify the choice of type species:

The first member of this genus to be described fully.

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. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

MODULE2: **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	***2016.080iB***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Habenivirus* (new)**
Subfamily:	
Family:	***Inoviridae***
Order:	

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)**
Ralstonia virus RSM1	Ralstonia phage RSM1	AB259123.2
Ralstonia virus RSM3	Ralstonia phage RSM3	AB434711
Ralstonia virus RS603	Ralstonia phage RS603	AB937974

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

Please note that the species are assigned to a new genus *Habenivirus*.

MODULE3: **NEW GENUS**

creating a new genus

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

Code	***2016.080jB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Inoviridae***
Order:	

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	***2016.080kB***	(assigned by ICTV officers)

To name the new genus: *Habenivirus*

Assigning thetype species and other species to a new genus

Code	***2016.080lB***	(assigned by ICTV officers)

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

Ralstonia virus RSM1	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:**

3

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 Gegenees, CoreGenes and "One click" phylogeny.fr analyses showed a close relationship between the Ralstonia phages RSM1, RSM3 and RS603 and indicated that the proposed genus is cohesive and distinct from the other genera in the family (Table 1 and 2; Fig. 1, 2 and 3). The phages of this genus possess genomes of approx. 7.6-9.0 kb (59-60 mol% G+C), and encode 13-15 proteins. They share 56-91% DNA sequence identity and 60-80% homologous proteins (Table 5). Figure 6 derived from progressiveMauve analysis reveals the overall sequence similarity between the members of this genus.
The phage RSMSuper, which is similar to RSM3 at the DNA sequence and proteome level 99% and 100%, respectively, should be considered a strain of Ralstonia phage RSM3 within this genus.
RSM1 is a filamentous virus approx. 1400 nm in length and 10 nm in width (Yamada, 2013). Ralstonia phage RSM3 decreases *R. solanacearum* growth rate, twitching motility, movement in tomato plant stems, extracellular polysaccharide (EPS) production, and *phcA* expression, resulting in loss of virulence (Addy et al, 2012).

Origin of the new genus name:

Habena (Latin) = "strap, bridle, reins, whip"

Reasons to justify the choice of type species:

The first member of this genus to be described fully.

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. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

MODULE2: **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	***2016.080mB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Vespertiliovirus* (new)**
Subfamily:	
Family:	***Inoviridae***
Order:	

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)**
Spiroplasma virus SkV1CR23x	Spiroplasma phage SkV1CR23x	EF506570

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

Please note that the species belongs to a new genus *Vespertiliovirus*, along with previously determined species *Spiroplasma virus R8A2B* and *C74*.

MODULE3: **NEW GENUS**

creating a new genus

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

Code	***2016.080nB***	(assigned by ICTV officers)

Tocreate a new genus within:

Subfamily:	
Family:	***Inoviridae***
Order:	

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	***2016.080oB***	(assigned by ICTV officers)

Toname the new genus: *Vespertiliovirus*

Assigning thetype species and other species to a new genus

Code	***2016.080pB***	(assigned by ICTV officers)

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

Spiroplasma virus R8A2B

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:**

3

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 hosts of the phages are members of the genus *Spiroplasma*: *S. citri* for phages R8A2B and C74 (sometimes denoted as SpV1), and *S. kunkelii* for phage SkV1CR23x. The phages of the genus are rod-shaped viruses with a genome of approx. 8000 nucleotides (GC% = 22-23) encoding 11-12 ORFs. The phylogenetic analyses performed by Gegenees and "One click" phylogeny.fr clearly showed that the phages belonging to this genus (Spiroplasma phages SkV1CR23x, C74 and R8A2B) are related (Tables 1, 2; Figures 1, 2, 3). They share 67-70% DNA sequence identity and 75-83% homologous proteins (Table 6). In this case, UGA is not a stop codon, but as in the host bacterium encodes tryptophan (Renaudin et al., 1990). Spiroplasma phages are 230–280 nm long and 10–15 nm in diameter (Day, 2012). The phages can enter the lysogenic cycle (Renaudin et al, 1990; Bebear et al, 1996). The next closest phage that infects *Spiroplasma melliferum* (Spiroplasma phage SVTS2) shows no DNA similarity to any member of this genus and only 33% of protein homology. Figure 7 derived from progressiveMauve analysis reveals the overall sequence similarity between the members of this genus.

Origin of the new genus name:

Vespertilio (latin) = "bat"

Reasons to justify the choice of type species:

The first member of this genus to be described fully.

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. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

MODULE2: **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	***2016.080qB***	(assigned by ICTV officers)

To create 11 new species within:

Genus:	**unassigned**
Subfamily:	
Family:	***Inoviridae***
Order:	

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)**
Propionibacterium virus B5	Propionibacterium phage B5	AF428260
Stenotrophomonas virus SMA6	Stenotrophomonas phage SMA6	HG315669
Stenotrophomonas virus SMA7	Stenotrophomonas phage SMA7	HG007973
Stenotrophomonas virus SMA9	Stenotrophomonas phage SMA9	AM040673
Stenotrophomonas virus PSH1	Stenotrophomonas phage PSH1	EF489910
Ralstonia virus PE226	Ralstonia phage PE226	HM064452
Vibrio virus VCY	Vibrio phage VCY	JN848801
Spiroplasma virus SVTS2	Spiroplasma phage SVTS2	AF133242.2
Ralstonia virus RSS1	Ralstonia phage RSS1	AB259124
Vibrio virus VfO3K6	Vibrio phage VfO3K6	AB043678
Vibrio virus KSF1	Vibrio phage KSF1	AY714348

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

Propionibacterium phage B5 is the only member of the family that infect the Gram-positive bacterium (*Propionibacterium freudenreichii*). Its genome contains 5806 bases (GC%: 64.3), encoding 10 proteins. The virions are 620 nm long and 12 nm wide (Chopin et al, 2002).
Stenotrophomonas phage SMA6 and SMA7 are isolated from a *Stenotrophomonas maltophilia* strain Khak84, and has a genome of 7648 and 7069 bases, respectively. Each phage possesses 11 potential open reading frames and is able to integrate into host genome (Petrova et al., 2014).
Stenotrophomonas phage SMA9 is isolated from a strain c5 and it genome consists of 6907 bases and 7 ORFs (Hagemann et al, 2006).
Stenotrophomonas phage PSH1 is isolated from a *Stenotrophomonas maltophilia* strain P2 and the virions are 2100 nm long. The genome consists of 6867 bases with 10 ORFs (Liu et al, 2012). The phage genome is deposited in the GenBank as a plasmid sequence, although it is indicated in the reference that it is a replicative form of the phage and the phage is described in details.
Ralstonia phage PE226 was isolated from plant rhizosphere using *Ralstonia solanacearum* as a host. It has a genome of 5475 bases (GC%: 61.7) that encodes 9 proteins. The phage is able to form clear plaques, and virion average size range of the phages was 1050 ± 200 nm in length and 6–9 nm in width (Murugaiyan et al, 2011).
Vibrio phage VCY is a phage of *Vibrio cholerae*, 1600 nm long and 7 nm wide with the overall genome size of 7103 kb and 11 putative ORFs. The phage is able to integrate into host DNA (Xue et al, 2011).
Spiroplasma phage SVTS2 infects *Spiroplasma melliferum*. The genome is 6825 bases (GC%: 22.7) encodes 13 proteins (Sha et al, 2000).
Ralstonia phage RSS1 contains genome of 6633 bp and 11 ORFs. The phage infect *Ralstonia solanacearum* and able to integrate in bacterial genome (Kawasaki et al, 2007). The filaments are approx. 1100 nm in length and 10 nm in width (Yamada, 2013).
The species of phage *Vibrio virus VfO3K6* comprises 2 strains, VfO3K6 (sometimes designated as f237) and VfO4K8, isolated from pandemic strains of *Vibrio parahaemolyticus*. The size of their genomes is in a range 6.9-8.8 kb (approx. 45% GC), and the difference is a result of a deletion present in the strain VfO4K6. The DNA similarity is 99%, while proteome contains 8-10 proteins, and amino acid sequences of core genes of the two strains are identical (Table 12). The bacteriophage VfO3K6 has dimensions 2500 x 8 nm, while *VfO4K68* has 1300 x 6 nm (Nasu et al, 2000; Chan et al, 2002); this morphological difference have to be further confirmed. It is reported that VfO4K68 is able to infect O3:K6 strain (Chan et al, 2002). The phage show similarity to Vf33 phages of *V. parahaemolyticus*, but only 21% at DNA and 30% at proteome level, with very low similarity of core genes.
Vibrio phage KSF1 is a virus of *Vibrio cholera* that use MSHA type pili IV as receptors. Its genome contains 7107 nucleotides, with 14 ORFs. Its virions are 1200 nm in length and 7 nm in width (Faraque et al, 2005).
All these phages do not meet criteria to be assigned to any genus of family *Inoviridae*.

The sequences of uncultured phages obtained from environmental samples were not considered: Uncultured phage WW-nAnB (Access. No. JN402401), Uncultured phage WW-nAnB strain 2 (Access. No. KJ003981), Uncultured phage WW-nAnB strain 3 (Access. No. KJ003982) and *Ralstonia* phage 1 NP-2014 (Access. No. KF887906). Similarly, the existing sequences for which it is not clear whether they are phage or prophage sequences, i.e. Ralstonia phage p12J (Access. No. AY374414.2), Stenotrophomonas phage SHP2 (Acces. No. HM150760) and Spiroplasma phage SVGII3 (Access. No. AJ969242) were not considered. The genome of Ralstonia phage RSS20 (Access. No. AB830321) was not analyzed as it is incomplete (more than 2/3 of the genome is not determined), while RSS30 (Access. No. AB828698) is excluded since it has to be re-annotated because of lack of core genes - only 3

genes are annotated, but according to Glimmer (Delcher et al, 1999) there are 17 putative ORFs and according to GeneMarkS (Besemer et al, 2001) 19 ORFs. The partial sequences of phages were not included in the analysis (e.g. Bacteriophage ZJ2, Xanthomonas phage Cf, Cf16, Cf1t, Lf, Xf, phiLF, phiXo and phiXv; Inovirus C2, Shigella phage SfX and Thermus phage PH75).

MODULE3: **NEW GENUS**

creating a new genus

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

Code	***2016.080rB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Inoviridae***
Order:	

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	***2016.080sB***	(assigned by ICTV officers)

To name the new genus: *Lineavirus*

Assigning thetype species and other species to a new genus

Code	***2016.080tB***	(assigned by ICTV officers)

To designate the following as the type species of thenew genus

Salmonella virus IKe

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 phages of this genus, *Salmonella virus IKe* and *Escherichia virus I22* cluster together when analysis is carried out using the Gegenees and "One click" phylogeny.fr for Zot, Coat B and Coat A proteins (Table 1 and 2; Fig. 1, 2 and 3). They possess genomes of approx. 6.8 kb (41-43 mol%G+C) and encode 9-10 proteins. They share 42% DNA sequence identity when examined by BLASTN and 80% homologous proteins when examined by CoreGenes (Table 8). The next closest member is Enterobacteria phage M13 which shares only 1% DNA sequence identity, but 70% of proteome homolog is detected. The two species, IKe and I22 show similarity to other enterobacterial phages, but they are mutually more closely related, based on amino-acid sequences of Zot and Coat B proteins (Fig. 2 and 3; Table 7). While they share high level of protein homology with M13 and If1 (80 ad 50%, respectively), as well as amino-acid sequence of Zot

protein (50-55%), there is no similarity of Coat B protein and DNA sequences. Figure 8 derived from progressiveMauve analysis reveals the similarity of the genus member with other viruses of enterobacteria and overall sequence similarity between the two members of the genus *Lineavirus* (Fig. 8 A and B).
The phages are able to infect enterobacteria with Inc2-type plasmid (both IKe and I22), but also IncN and IncP-1 (only IKe) (Peeters et al, 1985; Stassen et al, 1992).

Origin of the new genus name:

Linea (latin) = "line"

Reasons to justify the choice of type species:

The first member of this genus to be described fully.

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. For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTN, phage should have significant similarity of both Zot and Coat B proteins. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Each of the proposed genus comprise phages with similar DNA sequences; the phages differ from the others with more than 50% at the amino-acid level for CoatB and Zot proteins, as confirmed with the BLASTP algorithm.

MODULE7: **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	***2016.080uB***	(assigned by ICTV officers)

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

Escherichia virus AE2; Salmonella virus C2; Escherichia virus DeltaA; Escherichia virus Ec9; Escherichia virus f1; Escherichia virus fd; Escherichia virus HR; Escherichia virus PR64FS; Escherichia virus SF; Escherichia virus tf1; Escherichia virus X; Escherichia virus X2; Escherichia virus ZJ2; Pseudomonas virus Pf2; Vibrio virus 493; Vibrio virus v6; Vibrio virus Vf12; Vibrio virus VSK; Xanthomonas virus Cf16; Xanthomonas virus Cf1t; Xanthomonas virus Cf1tv; Xanthomonas virus Lf; Xanthomonas virus Xf; Xanthomonas virus Xfo; Xanthomonas virus Xfv

The present taxonomic position of these taxon/taxa:

Genus:	***Inovirus***
Subfamily:	
Family:	***Inoviridae***
Order:	

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	**YES**

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

The previously approved species should be removed because their genome sequences are absent, incomplete (less than 2/3 of genome is sequenced), only sequences of prophages exist or other crucial data are missing. The exceptions are Vibrio phage Vf12, that should be removed as it is the same species as *Vibrio virus Vf33,* Vibrio phage VSK which is a strain of species *Vibrio virus fs1*, as well as Escherichia phage fd and Escherichia phage f1, as they are the strains of the species *Escherichia virus M13*.

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

Code	***2016.080vB***	(assigned by ICTV officers)

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

Escherichia virus I22; Salmonella virus IKe; Pseudomonas virus Pf1;Pseudomonas virus Pf3; Escherichia virus If1;Vibrio virus CTXphi; Vibrio virus fs1; Vibrio virus fs2; Vibrio virus Vf33; Xanthomonas virus Cf1c

The present taxonomic position of these taxon/taxa:

Genus:	***Inovirus***
Subfamily:	

Fill in all that apply.

Family:	***Inoviridae***
Order:	

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

The species should be excluded from genus *Inovirus* and left as unassigned members of family *Inoviridae* or re-assign to new genera (please see part b).

Part (b)re-assign to a higher taxon

Code	***2016.080wB***	(assigned by ICTV officers)

To re-assign the following taxa as follows:
Escherichia virus If1, Vibrio virus CTXphi, Pseudomonas virus Pf1, Pseudomonas virus Pf3, Vibrio virus Vf33 and *Xanthomonas virus Cf1c*

Genus:	***unassigned***
Subfamily:	
Family:	***Inoviridae***
Order:	

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

The viral species *Escherichia virus If1, Vibrio virus CTXphi, Pseudomonas virus Pf1, Pseudomonas virus Pf3, Vibrio virus Vf33* and *Xanthomonas virus Cf1c* should be excluded from the genus *Inovirus*, but maintained in the family *Inoviridae* as unassigned species. Although phage If1 shows considerable protein homology with Enterobacteria phage M13 (60%) and amino-acid sequence similarity with this phage for Zot (64%) and Coat B protein (57%) there is no DNA homology between them (Table 1, 2 and 8; Fig. 1, 2, 3 and 8A). In addition, it was proven that If1 uses different mechanism to infect the host in comparison to fd phage, a strain of species *Enterobacteria virus M13* (Lorenz et al, 2011).
Vibrio phage CTXphi is previously approved as a species according to a prophage sequence and all other existing sequences of CTXphi and preCTXphi seems to be prophage sequences. It is the reason why they were not considered here.
Pseudomonas phage Pf1 shows many specificities and it is not phylogenetically related to Pseudomonas phage Pf3, particularly when Zot and Coat B proteins are considered.
Xanthomonas virus Cf1c is represented with two strains Cf1c and XacF1. The both strains are classified in the GenBank as "*Caudovirales*; *Podoviridae*; *Autographivirinae*; *T7likevirus*; unclassified T7-like viruses" but they belong to family *Inoviridae*.

Part (b) re-assign to a higher taxon

Code	***2016.080xB***	(assigned by ICTV officers)

To re-assign the following taxon as follows:

Vibrio virus fs1

Genus:	***Fibrovirus (new)***
Subfamily:	
Family:	***Inoviridae***
Order:	

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

The species *Vibrio virus fs1* should be included in a new genus *Fibrovirus*, along with the new species *Vibrio virus VGJ*.

Part (b) re-assign to a higher taxon

Code	***2016.080yB***	(assigned by ICTV officers)

To re-assign the following taxon as follows:

Vibrio virus fs2

Genus:	***Saetivirus (new)***
Subfamily:	
Family:	***Inoviridae***
Order:	

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

The species *Vibrio virus fs2* should be included in a new genus *Saetivirus*, along with the new species *Vibrio virus VFJ*.

Part (b) re-assign to a higher taxon

Code	***2016.080zB***	(assigned by ICTV officers)

To re-assign the following taxa as follows:

Salmonella virus IKe and *Escherichia virus I22*

Genus:	***Lineavirus (new)***
Subfamily:	
Family:	***Inoviridae***
Order:	

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

Salmonella virus IKe and *Escherichia virus I22* should be included in a new genus *Lineavirus*.

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

Code	***2016.080aaB***	(assigned by ICTV officers)

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

Spiroplasma virus 1aa; Spiroplasma virus KC3; Spiroplasma virus S102; Spiroplasma virus T78; Spiroplasma virus R8A2B and *Spiroplasma virus C74*

The present taxonomic position of these taxon/taxa:

Genus:	***Plectrovirus***
Subfamily:	
Family:	***Inoviridae***
Order:	

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	**YES: 4 of these 6 species to be abolished**

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

The sequences of the previously approved species *Spiroplasma virus 1aa; Spiroplasma virus KC3; Spiroplasma virus S102* and *Spiroplasma virus T78* are absent and the species should be removed. The only member of the genus is *Acholeplasma virus MVL51 (renamed MV-L51)*. The phages *Spiroplasma virus R8A2B* and *Spiroplasma virus C74* should be re-assigned (please see part b).

Part (b) re-assign to a higher taxon

Code	***2016.080abB***	(assigned by ICTV officers)

To re-assign the following taxa as follows:

	Spiroplasma virus R8A2B and *Spiroplasma virus C74*
Genus:	***Vespertiliovirus (new)***
Subfamily:	
Family:	***Inoviridae***
Order:	

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

The species *Spiroplasma virus R8A2B* and *Spiroplasma virus C74* are re-assign to new genus *Vespertiliovirus* along with a new species *Spiroplasma virus SkV1CR23x*.

MODULE9: **NON-STANDARD**
Template for any proposal not covered by modules 2-8.

non-standard proposal

Code		(assigned by ICTV officers)

Title of proposal: ***Etymology of family name***

Text of proposal:

In the 9th edition of Virus Taxonomy (Day, 2012), the etymology of the family name is described as:
Ino: from Greek *nos*, "muscle filament".
It should be changed as follows:
Ino: from Greek *is, inos* (ἴς**,** gen. ἰνός), "fiber, fibrous" (muscle fiber, sinew, tendon, fibrin, plant rib, plant fiber)

Henry George Liddell; Robert Scott [1940], A Greek-English Lexicon; Machine readable text (Trustees of Tufts University, Oxford) [word count] [greatscott36].
Wilhelm Pape: Handwörterbuch der griechischen Sprache. Braunschweig 31914, Band 1, S. 1262.
http://www.zeno.org/nid/20008450226
http://medical-dictionary.thefreedictionary.com/ino-
Thanks to Prof. Dr. Milena Jovanovic, University of Belgrade, Sebia

MODULE10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Addy H. S., Askora A., Kawasaki T., Fujie M., Yamada T. 2012. Loss of Virulence of the phytopathogen *Ralstonia solanacearum* through infection by ϕRSM filamentous Phages. Phytopathology 102, 469–477.

Addy, H.S., Askora, A., Kawasaki, T., Fujie, M., Yamada, T. 2012. Utilization of Filamentous Phage RSM3 to Control Bacterial Wilt Caused by *Ralstonia solanacearum*. Plant Disease, 96(8):1204-1209.

Addy,H.S., Askora,A., Kawasaki,T., Fujie,M. and Yamada,T. 2012. The Filamentous Phage varphiRSS1 Enhances Virulence of Phytopathogenic *Ralstonia solanacearum* on Tomato. Phytopathology 102 (3), 244-251

Agren, J., Sundstrom, A., Hafstrom, T., Segerman, B. 2012. Gegenees: Fragmented Alignment of Multiple Genomes for Determining Phylogenomic Distances and Genetic Signatures Unique for Specified Target Groups. PLoS ONE 7(6): e39107.

Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative (Syst Biol. 2006;55(4):539-52.

Bebear,C.M., Aullo,P., Bove,J., Renaudin,J. 1996. *Spiroplasma citri* virus SpV1. Characterization of viral sequences present in the spiroplasma host chromosome. Curr. Microbiol. 32, 134-140.

Besemer, J., Lomsadze, A., Borodovsky, M. 2001. GeneMarkS: a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions. Nucleic Acids Research, 29: 2607-2618.

Campos, J., Martínez, E., Suzarte, E., Rodríguez, B.L., Marrero, K., Silva, Y., Ledón, T., del Sol, R., Fando, R. 2003. VGJφ, a Novel Filamentous Phage of *Vibrio cholerae*, Integrates into the Same Chromosomal Site as CTXφ. J Bacteriol., 185(19): 5685–5696.

Campos,J., Martinez,E., Izquierdo,Y. and Fando,R. 2010. VEJ{phi}, a novel filamentous phage of *Vibrio cholerae* able to transduce the cholera toxin genes. Microbiology, 156 (PT 1), 108-115.

Chan,B., Miyamoto,H., Taniguchi,H., Yoshida,S. 2002. Isolation and genetic characterization of a novel filamentous bacteriophage, a deleted form of phage f237, from a pandemic *Vibrio parahaemolyticus* O4:K68 strain. Microbiol. Immunol. 46 (8), 565-569.

Chang, B., Taniguchi, H., Miyamoto, H., Yoshida,S. 1998. Filamentous bacteriophages of *Vibrio parahaemolyticus* as a possible clue to genetic transmission. J. Bacteriol. 180 (19), 5094-5101.

Chopin,M.C., Rouault,A., Ehrlich,S.D., Gautier,M. 2002. Filamentous phage active on the gram-positive bacterium

References:

Propionibacterium freudenreichii. J. Bacteriol. 184 (7), 2030-2033.

Darling, A.C.E., Mau, B., Blattner, F.R., Perna, N.T. 2004. Mauve: multiple alignment of conserved genomic sequence with rearrangements. Genome Res14 (7), 1394-1403.

Day, L.A. 2012. Inoviridae. Ninth Report of the International Committee on Taxonomy of Viruses. (2012) Ed: King, A.M.Q., Adams, M.J., Carstens, E.B. and Lefkowitz, E.J. San Diego: Elsevier Academic Press.

Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. Improved microbial gene identification with GLIMMER, Nucl Acids Res. 27:23 (1999), 4636-4641.

Ehara,M., Shimodori,S., Kojima,F., Ichinose,Y., Hirayama,T., Albert,M.J., Supawat,K., Honma,Y., Iwanaga,M. and Amako,K. 1997. Characterization of filamentous phages of *Vibrio cholerae* O139 and O1. FEMS Microbiol. Lett. 154 (2), 293-301.

Faruque,S.M., Bin Naser,I., Fujihara,K., Diraphat,P., Chowdhury,N., Kamruzzaman,M., Qadri,F., Yamasaki,S., Ghosh,A.N., Mekalanos,J.J. 2005. Genomic sequence and receptor for the Vibrio cholerae phage KSF-1phi: evolutionary divergence among filamentous vibriophages mediating lateral gene transfer. J. Bacteriol. 187 (12), 4095-4103.

Hagemann, M., Hasse, D., Berg, G. 2006. Detection of a phage genome carrying a zonula occludens like toxin gene (zot) in clinical isolates of *Stenotrophomonas maltophilia*.Arch Microbiol, 185 (6): 449-458.

Hagemann, M., Hasse,D. and Berg,G. 2006. Detection of a Phage Genome Carrying a Zonula Occludens like Toxin Gene (zot) in clinical isolates of *Stenotrophomonas maltophilia.* Arch. Microbiol. 185 (6), 449-458.

Honma,Y., Ikema,M., Toma,C., Ehara,M. and Iwanaga,M. 1997. Molecular analysis of a filamentous phage (fsl) of *Vibrio cholerae* O139. Biochim. Biophys. Acta 1362 (2-3), 109-115.

Ikema,M. and Honma,Y. 1998. A novel filamentous phage, fs-2, of *Vibrio cholerae* O139. Microbiology 144 (Pt 7), 1901-1906.

Kar, S., Ghosh, R.K., Ghosh, A.N., Ghosh, A. 1996. Integration of the DNA of a novel filamentous bacteriophage VSK from *Vibrio cholerae* 0139 into the host chromosomal DNA. FEMS Microbiology Letters, 145(1): 17–22.

Kawasaki,T., Nagata,S., Fujiwara,A., Satsuma,H., Fujie,M., Usami,S. and Yamada,T. 2007. Genomic characterization of the filamentous integrative bacteriophages {phi}RSS1 and {phi}RSM1, which infect *Ralstonia solanacearum*. J. Bacteriol. 189 (16), 5792-5802.

Kawasaki,T., Nagata,S., Fujiwara,A., Satsuma,H., Fujie,M., Usami,S., Yamada,T. 2007. Genomic characterization of the filamentous integrative bacteriophages {phi}RSS1 and {phi}RSM1, which infect *Ralstonia solanacearum*. J. Bacteriol. 189 (16), 5792-5802.

Liu, J., Liu, Q., Shen, P., Huang, Y.P. 2012. Isolation and characterization of a novel filamentous phage from *Stenotrophomonas maltophilia*. , Arch Virol. 157(9):1643-50.

Lorenz, S.H., Jakob, R.P., Weininger, U., Balbach, J., Dobbek, H., Schmid, F.X. 2011. The filamentous phages fd and IF1 use different mechanisms to infect *Escherichia coli*. J Mol Biol., 405(4):989-1003.

Luiten, R. G. M., Putterman, D. G., Schoenmakers, J. G. G., Konings, R. N. H., Day, L. A. 1985. Nucleotide Sequence of the Genome of Pf3, an IncP-1 Plasmid-Specific Filamentous Bacteriophage of *Pseudomonas aeruginosa*. J. Virol., 268-276.

Murugaiyan, S., Bae, J.Y., Wu, J., Lee, S.D., Um, H.Y., Choi, H.K., Chung, E., Lee, J.H. Lee, S.W. 2011. Characterization of filamentous bacteriophage PE226 infecting *Ralstonia solanacearum* strains. J. Appl. Microbiol., 110(1): 296-303.

Nasu, H., Iida, T., Sugahara, T., Yamaichi, Y., Park, K., Yokoyama, K., Makino, K., Shinagawa, H., Honda, T. A Filamentous Phage Associated with Recent Pandemic *Vibrio parahaemolyticus* O3:K6 Strains. J Clin Microbiol. 38(6): 2156–2161.

Newman, J., L. A. Day, G. W. Dalack, D. Eden. 1982. Hydrodynamic determination of molecular weight, dimensions, and structural parameters of Pf3 virus. Biochemistry, 21:3352-3358.

Nguyen, D.T., Ngo, T.C., Tran, H.H., Le, T.H., Nguyen, H.T., Nguyen, B.M., Tran, N.D., Yamashiro, T., Ehara, M. 2012. Characterization of *Vibrio cholerae* O139 of an Aquatic Isolate in Northern Vietnam. Open Microbiol J., 6: 14–21.

Peeters,B.P., Peters,R.M., Schoenmakers,J.G. and Konings,R.N. 1985. Nucleotide sequence and genetic organization of the genome of the N-specific filamentous bacteriophage IKe. Comparison with the genome of the F-specific filamentous phages M13, fd and f1. J. Mol. Biol. 181 (1), 27-39.

Peeters,B.P., Peters,R.M., Schoenmakers,J.G., Konings,R.N. 1985. Nucleotide sequence and genetic organization of the genome of the N-specific filamentous bacteriophage IKe. Comparison with the genome of the F-specific filamentous phages M13, fd and f1. J. Mol. Biol. 181 (1), 27-39.

Peterson, C., G. W. Dalack, L. A. Day, W. T. Winter. 1982. Structure of the filamentous bacteriophage, Pf3, by X-ray fiber diffraction. J. Mol. Biol. 162:877-881.

References:

Petrova, M., Shcherbatova, N., Kurakov, A., Mindlin, S. 2014. Genomic characterization and integrative properties of phiSMA6 and phiSMA7, two novel filamentous bacteriophages of *Stenotrophomonas maltophilia*. Arch. Virol. 159 (6), 1293-1303.

Petrova,M., Shcherbatova,N., Kurakov,A. and Mindlin,S. 2014. Genomic characterization and integrative properties of phiSMA6 and phiSMA7, two novel filamentous bacteriophages of *Stenotrophomonas maltophilia*. Arch. Virol. 159 (6), 1293-1303.

Renaudin,J., Aullo,P., Vignault,J.C.,Bove,J.M. 1990. Complete nucleotide sequence of the genome of *Spiroplasma citri* virus SpV1-R8A2 B Nucl Acids Res. 18 (5), 1293.

Sha,Y., Melcher,U., Davis,R.E. and Fletcher,J. 2000. Common elements of spiroplasma plectroviruses revealed by nucleotide sequence of SVTS2. Virus Genes 20 (1), 47-56.

Stassen,A.P., Schoenmakers,E.F., Yu,M., Schoenmakers,J.G. Konings,R.N.1992. Nucleotide sequence of the genome of the filamentous bacteriophage I2-2: module evolution of the filamentous phage genome. J. Mol. Evol. 34 (2): 141-152.

Stassen,A.P., Schoenmakers,E.F., Yu,M., Schoenmakers,J.G., Konings,R.N. 1992. Nucleotide sequence of the genome of the filamentous bacteriophage I2-2: module evolution of the filamentous phage genome. J. Mol. Evol. 34 (2), 141-152.

Taniguchi, H, Sato, K, Ogawa, M, Udou, T, Mizuguchi, Y. 1984. Isolation and characterization of a filamentous phage, Vf33, specific for *Vibrio parahaemolyticus*. Microbiol Immunol. 28(3):327-37.

Van, T.T., Yoshida, S., Miki, K., Kondo, A., Kamei, K. 2014. Genomic characterization of ϕRS603, a filamentous bacteriophage that is infectious to the phytopathogen *Ralstonia solanacearum*.Microbiol. Immunol, 58(12):697-700.

Van, T.T.B., Yoshida, S., Miki, K., Kondo, A., Kamei, K. 2015. Complete genome sequence of a filamentous bacteriophage, RS611, that infects the phytopathogen *Ralstonia solanacearum*. Arch Virol, 160(3): 865-867.

Wang,Q., Kan,B. and Wang,R. 2013. Isolation and Characterization of the New Mosaic Filamentous Phage VFJ Phi of *Vibrio cholera*. PLoS ONE 8 (8), E70934.

Wang,Q., Kan,B., Wang,R. 2013. Isolation and Characterization of the New Mosaic Filamentous Phage VFJ Phi of *Vibrio cholera*. PLoS ONE 8 (8), E70934.

Xue,H., Xu,Y., Boucher,Y., Polz,M.F. 2011. High Frequency of a Novel Filamentous Phage, VCY{Phi}, within an Environmental *Vibrio cholerae* Population. Appl. Environ. Microbiol. 78(1):28-33.

Yamada, T. 2013. Filamentous phages of Ralstonia solanacearum: double-edged swords for pathogenic bacteria. Front Microbiol. 4: 325.

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.BLASTN of the *Inoviridae* constructed using Gegenees (Agren et al, 2012) with fragment size= 100 bases; and, step size = 50 bases.

Bacteriophage	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
1: Acholeplasma virus MVL1 X58839	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2: Xanthomonas phage Cf1c M57538.1	0	100	99	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3: Xanthomonas phage XacF1 AB910602.1	0	98	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4: Enterobacteria phage If1 U02303.1	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5: Propionibacterium phage B5 AF428260.1	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6: Pseudomonas phage Pf1 X52107.1	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7: Spiroplasma phage SVTS2 AF133242.2	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8: Ralstonia phage PE226 HM064452.1	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0
9: Stenotrophomonas phage SMA6 HG315669	0	0	0	0	0	0	0	0	100	2	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10: Stenotrophomonas phage PSH1 EF489910.	0	0	0	0	0	0	0	0	3	100	6	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11: Stenotrophomonas phage SMA7 HG00797	0	0	0	0	0	0	0	0	1	7	100	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12: Stenotrophomonas phage SHP2 HM150760	0	0	0	0	0	0	0	0	3	6	15	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13: Vibrio phage CTX KJ619459.1	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14: Vibrio phage VCY JN848801.1	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	1	0	0	0	0	0	0	0	0	0	3	2	1	0	2	2	1	0	0	0	0	0	0	0	0	0	0	0
15: Enterobacteria phage I22 X14336.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16: Enterobacteria phage Ike X02139.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
17: Vibrio phage fs2 AB002632.1	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	100	84	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18: Vibrio phage VFJ KC357596.1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	85	100	0	0	0	0	0	0	0	0	0	0	2	1	0	2	2	2	0	0	0	0	0	0	0	0	0	0	0
19: Spiroplasma phage 1R8A2B X51344.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	52	41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20: Spiroplasma phage 1C74 U28974.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54	100	59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21: Spiroplasma phage SkV1_CR23x EF506570.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	45	59	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22: Pseudomonas phage Pf3 M11912.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23: Pseudomonas phage Pf3 NY M19377.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24: Vibrio phage VfO3K6 AB043678.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	78	17	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25: Vibrio phage VfO4K68 AB043679.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	20	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26: Vibrio phage Vf12 AB012574.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	18	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27: Vibrio phage Vf33 AB012573.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	18	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28: Vibrio phage KSF1 AY714348.1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	100	21	19	18	19	18	18	0	0	0	0	0	0	0	0	0	0	0
29: Vibrio phage VGJ AY242528.1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	19	100	63	60	68	60	59	0	0	0	0	0	0	0	0	0	0	0
30: Vibrio phage VEJ FJ904927.1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	20	70	100	81	82	72	71	0	0	0	0	0	0	0	0	0	0	0
31: Vibrio phage fs1 D89074.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	22	71	87	100	85	77	75	0	0	0	0	0	0	0	0	0	0	0
32: Vibrio phage ND1fs1 AB572858.1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	20	77	81	78	100	93	91	0	0	0	0	0	0	0	0	0	0	0
33: Vibrio phage VSKK AF452449.2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	19	70	73	70	92	100	82	0	0	0	0	0	0	0	0	0	0	0
34: Vibrio phage VSK AF453500.3	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	18	68	71	71	90	82	100	0	0	0	0	0	0	0	0	0	0	0
35: Ralstonia phage RS603 AB937974.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	51	52	51	0	0	0	3	3	5	5
36: Ralstonia phage RSM1 AB259123.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	44	100	78	78	0	0	0	0	0	0	0
37: Ralstonia phage RSMSuper AB981170.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	44	79	100	99	0	0	0	0	0	0	0
38: Ralstonia phage RSM3 AB434711.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	44	78	99	100	0	0	0	0	0	0	0
39: Enterobacteria phage fd J02451.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	86	84	0	0	0	0
40: Enterobacteria phage f1 J02448.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86	100	97	0	0	0	0
41: Enterobacteria phage M13 V00604.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84	97	100	0	0	0	0
42: Ralstonia phage RSSTH1 LC066596.1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	100	80	85	80
43: Ralstonia phage RS611 AB931172.1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	91	100	90	81
44: Ralstonia phage RSS0 JQ408219.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	85	79	100	91
45: Ralstonia phage RSS1 AB259124.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	88	77	100	100

Table 2.TBLASTX of the *Inoviridae* constructed using Gegenees (Agren et al, 2012) with fragment size= 100 bases; and, step size = 50 bases. Bacteriophages of *Spiroplasma* and *Acholeplasma* were not included in the analysis, because of different genetic code (translation table 4 instead of 11).

Bacteriophage	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
1: Enterobacteria phage If1 U02303.1	100	28	27	20	20	19	20	19	18	18	20	19	20	20	20	20	21	20	24	24	20	20	19	20	20	20	20	20	20	19	19	32	33	33	20	20	20	20	20	20
2: Enterobacteria phage I22 X14336.1	32	100	56	20	20	19	19	19	19	19	20	20	20	20	21	20	21	21	26	26	21	21	20	20	20	20	20	21	21	21	21	31	31	32	20	20	20	20	20	20
3: Enterobacteria phage Ike X02139.1	30	53	100	19	19	19	18	16	15	16	17	20	20	20	21	21	20	20	25	25	20	20	19	19	19	18	19	19	19	18	18	33	34	34	20	20	20	20	20	20
4: Xanthomonas phage Cf1c M57538.1	21	20	20	100	92	27	24	21	23	21	23	20	20	21	21	21	21	20	21	21	21	21	22	23	22	23	23	22	23	23	23	20	19	19	21	21	21	21	21	20
5: Xanthomonas phage XacF1 AB910602.1	20	20	20	90	100	28	24	22	23	21	23	20	20	21	21	21	21	21	20	21	21	21	22	23	22	22	22	22	23	23	23	19	19	19	20	21	21	20	21	20
6: Stenotrophomonas phage SMA6 HG315	20	19	19	27	28	100	36	27	28	23	23	21	20	20	21	21	21	21	20	20	21	20	24	24	24	24	24	23	24	24	24	20	20	20	20	20	20	20	20	20
7: Stenotrophomonas phage PSH1 EF4899	21	20	20	24	24	37	100	39	37	22	23	21	21	20	21	21	21	21	20	20	21	20	25	24	23	24	23	22	23	23	22	20	19	19	21	21	21	21	21	20
8: Stenotrophomonas phage SMA7 HG007	19	18	17	23	23	28	37	100	34	14	13	21	20	20	21	21	20	20	20	21	20	20	21	20	21	21	21	22	21	22	22	12	12	12	21	21	21	20	20	20
9: Stenotrophomonas phage SHP2 HM150	20	16	13	24	24	29	38	36	100	14	11	20	18	20	21	21	20	20	21	21	21	21	23	21	22	22	22	21	22	22	22	10	8	9	19	20	20	20	20	20
10: Propionibacterium phage B5 AF42826(	21	18	20	23	23	24	22	17	18	100	22	20	20	20	21	21	21	20	21	20	20	20	23	22	22	23	22	23	23	23	23	17	16	16	20	20	20	19	20	19
11: Pseudomonas phage Pf1 X52107.1	20	19	19	21	21	22	22	14	15	20	100	22	20	20	21	21	22	21	21	21	20	20	21	21	22	21	21	22	21	21	21	18	17	17	20	20	19	21	19	20
12: Vibrio phage CTX KJ619459.1	21	20	20	20	20	20	19	18	19	17	21	100	21	23	22	22	23	23	24	20	20	20	19	19	19	19	18	21	21	20	20	20	19	20	22	22	22	22	22	23
13: Vibrio phage VCY JN848801.1	21	20	20	20	20	19	20	19	17	17	20	20	100	41	23	23	27	24	24	28	20	20	20	21	20	20	20	20	20	20	20	20	20	19	25	24	27	27	27	23
14: Vibrio phage KSF1 AY714348.1	20	20	20	20	20	20	21	19	20	19	21	23	41	100	24	24	27	26	20	20	19	19	20	20	20	20	19	20	20	20	20	20	20	20	34	36	36	35	37	36
15: Vibrio phage Vf12 AB012574.1	20	20	20	20	19	20	19	20	20	18	20	22	22	23	100	99	43	39	22	24	20	20	20	20	20	20	20	21	20	21	21	19	19	19	32	33	34	35	35	32
16: Vibrio phage Vf33 AB012573.1	20	20	20	20	19	20	19	20	20	18	20	22	22	23	99	100	43	39	22	24	20	20	20	20	20	20	20	21	20	21	21	19	19	19	32	33	34	35	35	32
17: Vibrio phage VfO3K6 AB043678.1	20	20	20	20	20	20	19	19	19	19	21	22	25	25	41	41	100	82	22	22	20	20	19	20	20	20	20	20	21	21	20	20	19	19	23	24	25	25	25	24
18: Vibrio phage VfO4K68 AB043679.1	20	20	19	21	21	21	20	21	20	20	21	23	24	26	42	42	100	100	21	20	20	20	19	21	20	21	21	20	21	21	21	20	19	19	22	23	24	23	23	24
19: Vibrio phage fs2 AB002632.1	24	24	24	21	21	20	20	20	19	20	19	22	23	20	22	22	22	20	100	80	20	20	20	19	19	19	19	21	21	20	20	23	23	23	22	22	24	24	24	23
20: Vibrio phage VFJ KC357596.1	24	24	24	21	21	20	19	20	18	19	20	20	26	20	24	24	23	20	82	100	21	21	20	20	19	19	19	20	20	20	20	23	23	23	24	24	27	26	26	23
21: Pseudomonas phage Pf3 NY M19377.1	21	21	21	22	21	19	19	19	21	19	20	19	21	20	21	21	20	20	21	20	100	100	20	20	20	20	20	21	21	21	21	20	20	20	20	20	21	20	20	20
22: Pseudomonas phage Pf3 M11912.1	20	21	20	21	21	19	19	19	21	19	20	19	20	19	21	21	21	20	21	20	100	100	20	21	20	20	20	21	21	20	20	20	20	20	20	20	20	20	20	20
23: Ralstonia phage PE226 HM064452.1	20	20	20	23	23	25	25	23	24	23	23	20	20	20	21	21	21	21	20	20	21	21	100	36	35	36	36	24	24	23	24	20	19	19	21	20	20	20	21	21
24: Ralstonia phage RSSTH1 LC066596.1	21	20	20	23	23	23	23	22	23	23	23	21	20	20	21	21	21	21	21	20	21	21	32	100	85	90	85	28	23	25	25	18	18	18	21	20	21	21	20	20
25: Ralstonia phage RS611 AB931172.1	21	20	20	23	23	23	23	22	23	23	24	21	20	20	21	21	21	21	21	21	21	21	34	94	100	93	86	29	23	25	25	18	18	18	21	20	21	21	20	20
26: Ralstonia phage RSS0 JQ408219.1	21	20	20	23	23	24	24	22	23	22	23	21	20	20	21	21	21	21	21	20	21	21	33	90	84	100	93	29	24	25	25	19	19	19	21	21	21	21	21	20
27: Ralstonia phage RSS1 AB259124.1	21	19	20	23	23	24	23	23	23	23	23	21	20	20	21	21	21	21	21	20	21	21	34	91	84	99	100	30	24	25	25	18	18	18	21	21	21	21	20	20
28: Ralstonia phage RS603 AB937974.1	20	20	20	22	22	23	22	21	21	22	23	21	20	20	21	21	21	21	21	21	21	21	23	28	27	30	30	100	65	67	68	19	19	19	20	20	20	20	20	20
29: Ralstonia phage RSM1 AB259123.1	21	21	19	22	23	23	23	22	21	22	23	21	20	20	21	21	21	21	21	21	20	20	24	24	23	23	23	59	100	81	82	20	20	20	21	21	21	20	21	20
30: Ralstonia phage RSM3 AB434711.1	20	20	19	23	22	23	22	22	21	22	22	20	20	20	21	21	21	21	21	21	20	21	23	25	24	25	25	59	83	100	96	20	20	19	21	21	20	21	21	21
31: Ralstonia phage RSMSuper AB981170.1	20	20	19	22	22	23	22	22	21	22	22	20	20	20	21	21	21	21	21	21	21	21	23	25	24	25	25	61	83	97	100	20	20	20	21	21	20	20	21	21
32: Enterobacteria phage fd J02451.1	37	28	37	19	19	18	18	10	9	11	14	21	20	19	20	20	20	19	26	26	20	20	17	15	17	16	16	18	19	18	18	100	94	95	20	20	20	21	20	19
33: Enterobacteria phage M13 V00604.2	36	28	37	19	19	18	18	10	9	11	15	20	20	20	20	20	20	19	26	26	20	20	16	16	17	16	16	18	18	17	17	94	100	98	19	20	20	20	20	20
34: Enterobacteria phage f1 J02448.1	37	28	37	19	19	19	18	10	9	10	14	20	20	19	20	20	20	19	26	26	20	20	16	16	16	16	16	17	18	17	18	95	98	100	19	20	20	20	20	20
35: Vibrio phage VSK AF453500.3	20	20	20	20	20	20	19	20	18	18	19	21	25	34	34	34	25	23	24	26	20	20	19	20	19	20	20	20	20	20	20	19	19	20	100	68	66	68	73	67
36: Vibrio phage VSKK AF452449.2	21	20	20	20	21	20	19	20	19	18	19	23	25	35	35	35	25	23	23	26	19	19	19	19	19	19	19	20	20	20	20	20	20	20	67	100	71	73	74	72
37: Vibrio phage VGJ AY242528.1	20	20	20	20	20	20	19	20	19	18	19	22	27	35	36	36	26	23	24	28	20	20	19	19	19	20	19	19	21	21	21	19	19	19	64	67	100	77	76	71
38: Vibrio phage VEJ FJ904927.1	21	20	19	19	19	19	19	19	18	18	19	22	27	36	38	38	26	23	25	28	20	20	18	20	19	20	20	20	21	20	20	18	18	18	67	71	82	100	84	80
39: Vibrio phage ND1fs1 AB572858.1	21	20	19	20	20	20	19	19	19	18	19	22	27	38	38	38	27	24	25	29	20	20	19	19	19	19	19	19	20	21	20	19	19	19	74	76	80	83	100	78
40: Vibrio phage fs1 D89074.1	21	20	19	20	20	19	20	19	18	17	19	22	23	38	36	36	25	23	25	24	20	20	19	19	19	19	19	19	20	20	20	19	19	19	70	72	80	83	84	100

Fig. 1. Phylogenetic analysis of the Zot protein (morphogenesis protein) of phages from family *Inoviridae* constructed using "one click" at phylogeny.fr (13). The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences (Anisimova and Gascuel, 2006). The phages of the same genera are outlined by the same color: Orange- *Habenivirus*; Green-*Fibrovirus*; Blue- *Saetivirus*; Red- *Lineavirus*; Violet- *Inovirus*; Brown-*Vespertiliovirus*.

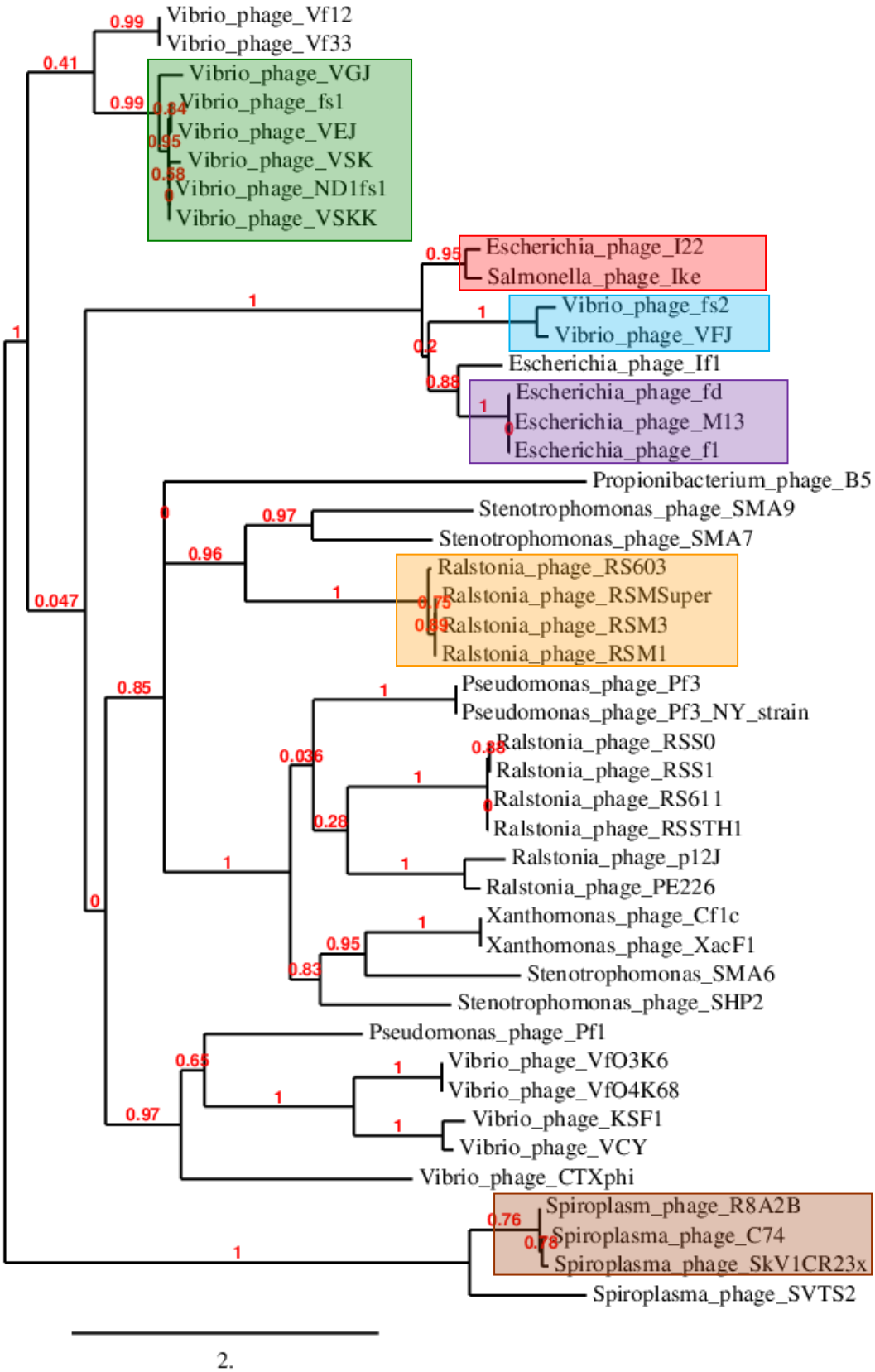


Fig.2 . Phylogenetic analysis of the major coat protein (Coat B) of phages from family *Inoviridae* constructed using "one click" at phylogeny.fr (13). The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences (Anisimova and Gascuel, 2006). The phages of the same genera are outlined by the same color: Orange- *Habenivirus*; Green-*Fibrovirus*; Blue- *Saetivirus*; Red- *Lineavirus*; Violet- *Inovirus*; Brown-*Vespertiliovirus*.

.

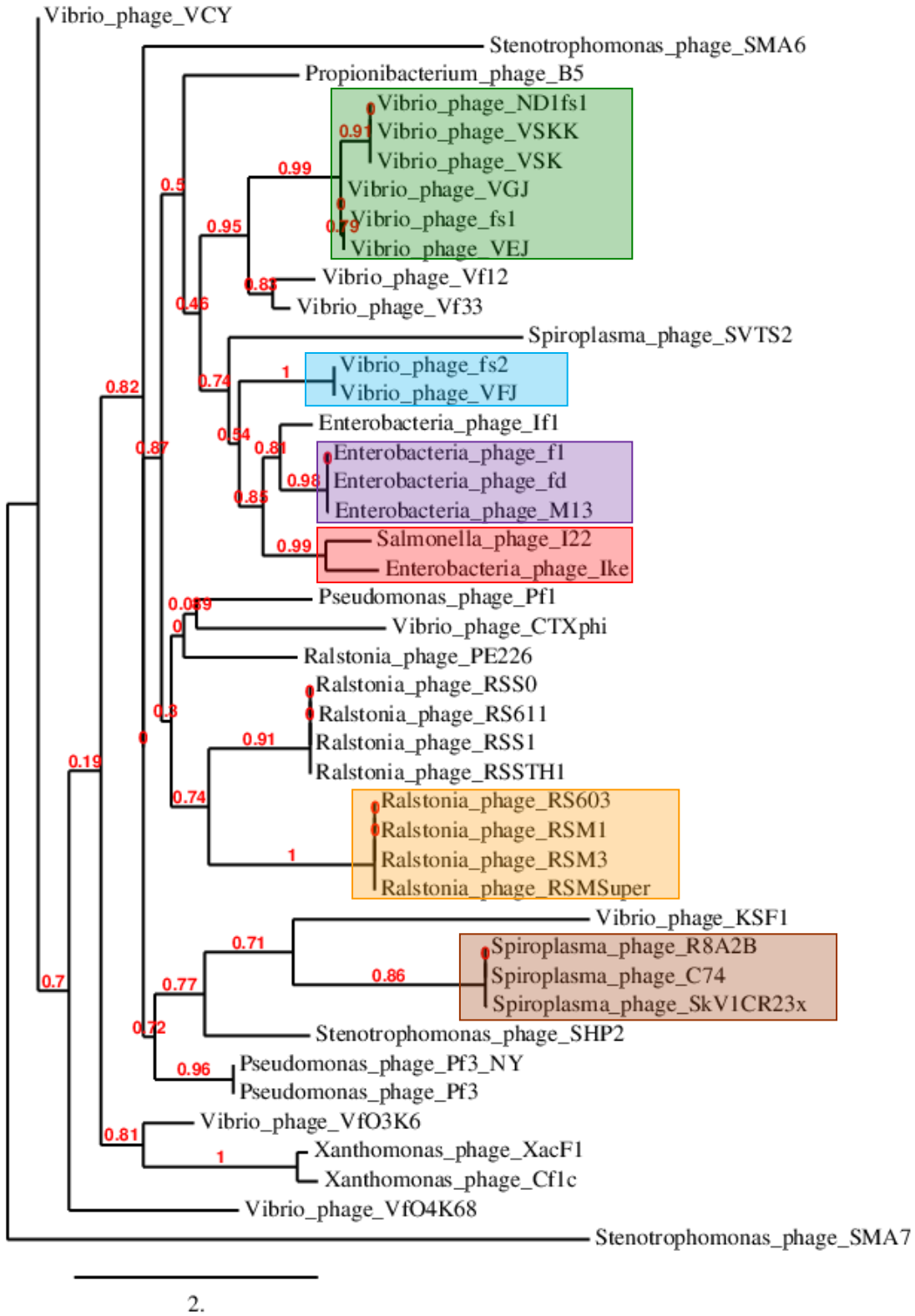


Fig. 3. Phylogenetic analysis of the minor coat protein (adhesion host specific protein) of phages from the family *Inoviridae* constructed using "one click" at phylogeny.fr (13). The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences (Anisimova and Gascuel, 2006). The phages of the same genera are outlined by the same color: Orange- *Habenivirus*; Green-*Fibrovirus*; Blue- *Saetivirus*; Red- *Lineavirus*; Violet- *Inovirus*; Brown- *Vespertiliovirus*.

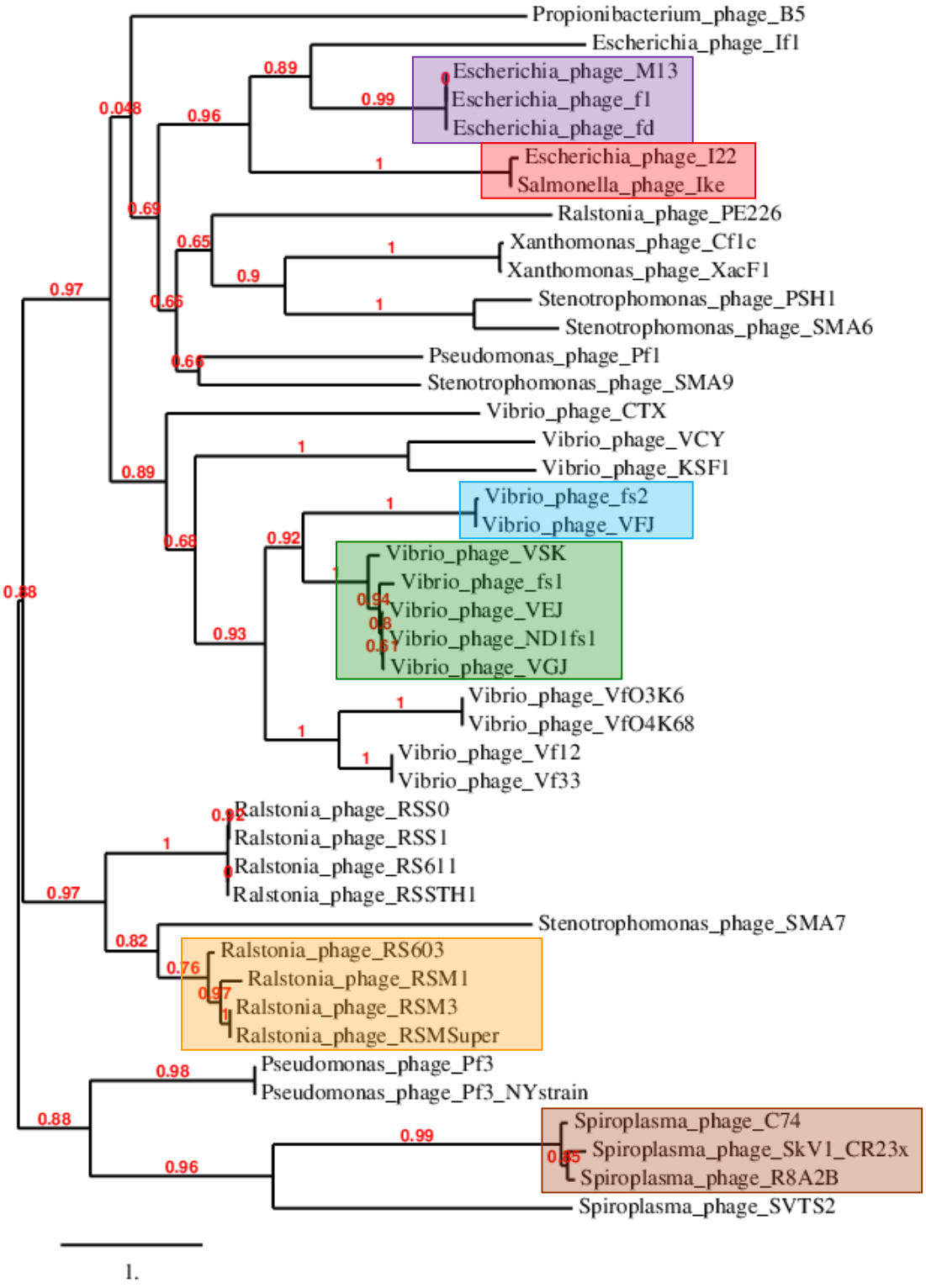


Table 3. Properties of two phages belonging to the genus *Fibrovirus* and the peripherally related viruses (Vibrio phage Vf33, FSK1 and VCY)

Vibrio phage	GenBank accession No.	Genome length (bp)	Genome (mol% G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**	Zot***	CoatB	CoatA
fs1*****	D89074.1	6340	43.4	15	100	100	100	100	100
VGJ	AY242528.1	7542	43.4	13	88	53	82	97	86
Vf33	AB012574.1	7965	45.7	7	0	47	47	63	0
KSF1	AY714348.1	7107	44.4	12	30	20	0	0	0
VCY	JN848801.1	7103	41.4	11	0	0	0	0	0

* Determined using BLASTN; ** Determined using CoreGenes ***Determined using BLASTP; **** Re-annotated protein; ***** Vibrio phages VEJ, ND1fs1, VSK and VSKK should be considered strains of Vibrio phage fs1 within this genus.

Fig. 4. ProgressiveMauve alignment (Darling et al, 2004) of the genomes of phages from genus *Fibrovirus (Vibrio virus fs1* and *Vibrio virus VGJ)*.

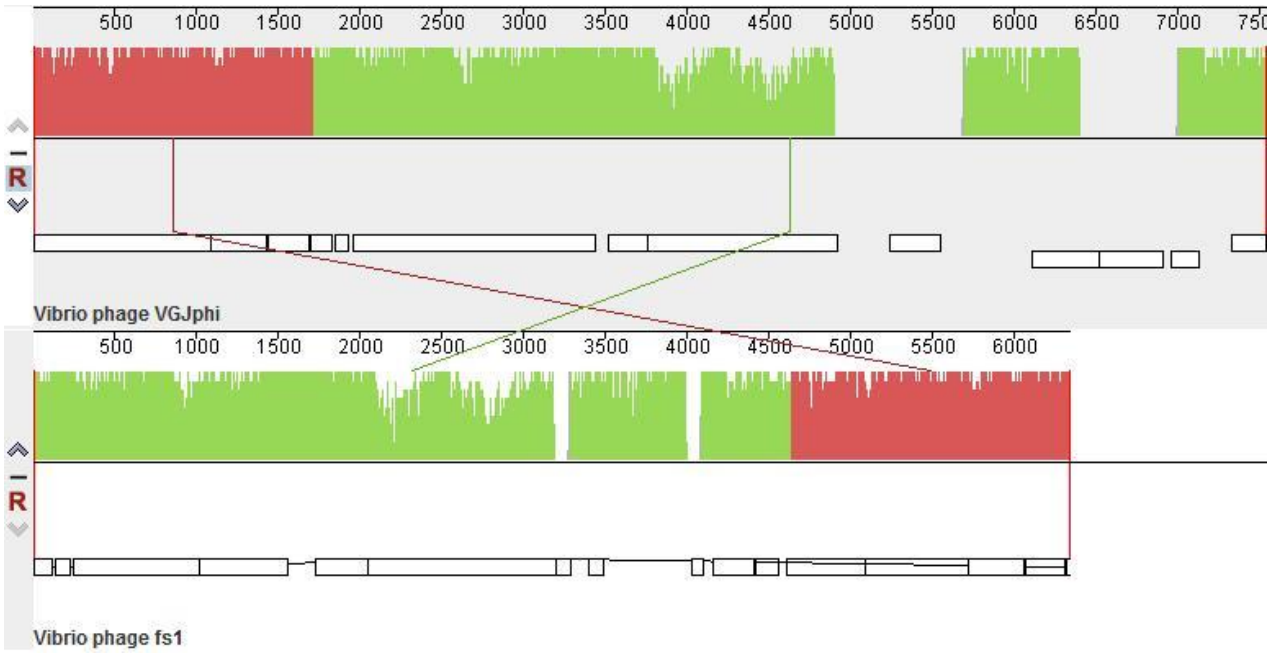


Table 4. Properties of the phages belonging to the genus *Saetivirus*, Vibrio phage fs2 and Vibrio phage VFJ, and related phages.

Vibrio phage	GenBank accession No.	Genome length (bp)	Genome (mol% G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**	Zot***	Coat B	Coat A
fs2	**AB002632.1**	**8651**	**44.5**	**9**	**100**	**100**	**100**	**100**	**100**
VFJ	**KC357596.1**	**8555**	**44.3**	**12**	**88**	**100**	**89**	**100**	**98**
M13	V00604.2	6407	40.7	10	0	44	44	29	7
IKe	X02139.1	6883	40.5	10	0	22	46	15	10
fs1	D89074.1	6340	43.4	15	1	11	16	0	8

* Determined using BLASTN; ** Determined using CoreGenes ***Determined using BLASTP

Fig. 5. ProgressiveMauve alignment (Darling et al, 2004) of the two species of the genus *Saetivirus*.

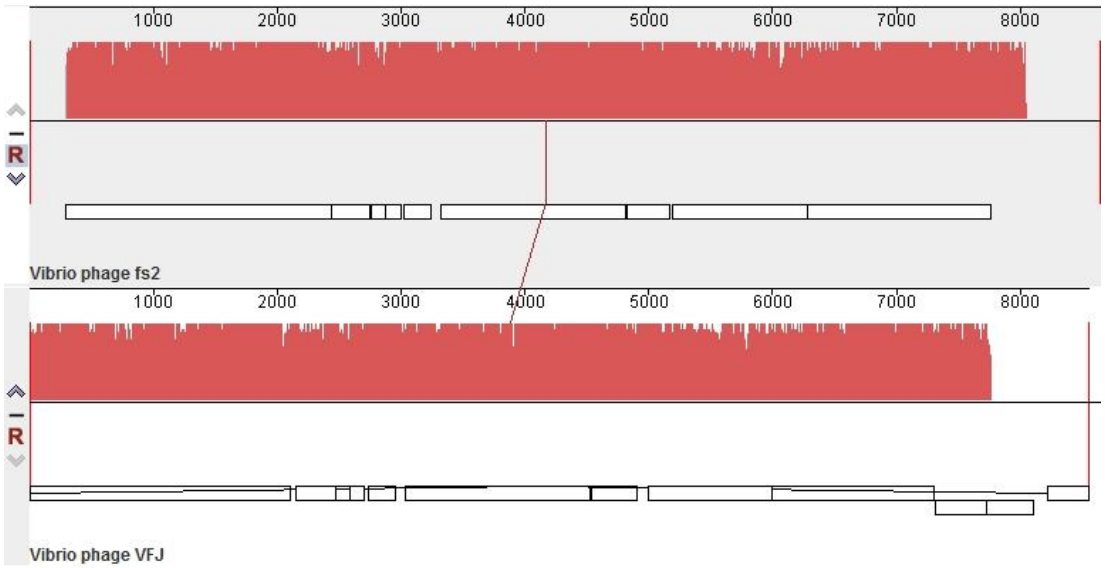


Table 5. Properties of the three phages belonging to the genus *Habenivirus* and a peripherally related Ralstonia phage RSS1

Ralstonia phage	GenBank accession No.	Genome length (bp)	Genome (mol%G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**	Zot***	CoatB	CoatA
RSM1	**AB259123.2**	**9004**	**60.0**	**15**	**100**	**100**	**100**	**100**	**100**
RSM3	**AB434711.1**	**8929**	**59.6**	**14**	**91**	**80**	**99**	**95**	**81**
RS603	**AB937974.1**	**7679**	**59.4**	**13**	**56**	**60**	**93**	**100**	**75**
RSS1	AB259124.1	6662	62.6	12	0	20	10	0	10

* Determined using BLASTN; ** Determined using CoreGenes ***Determined using BLASTP

Fig. 6. ProgressiveMauve alignment (Darling et al, 2004) of the three species of the genus *Habenivirus*.

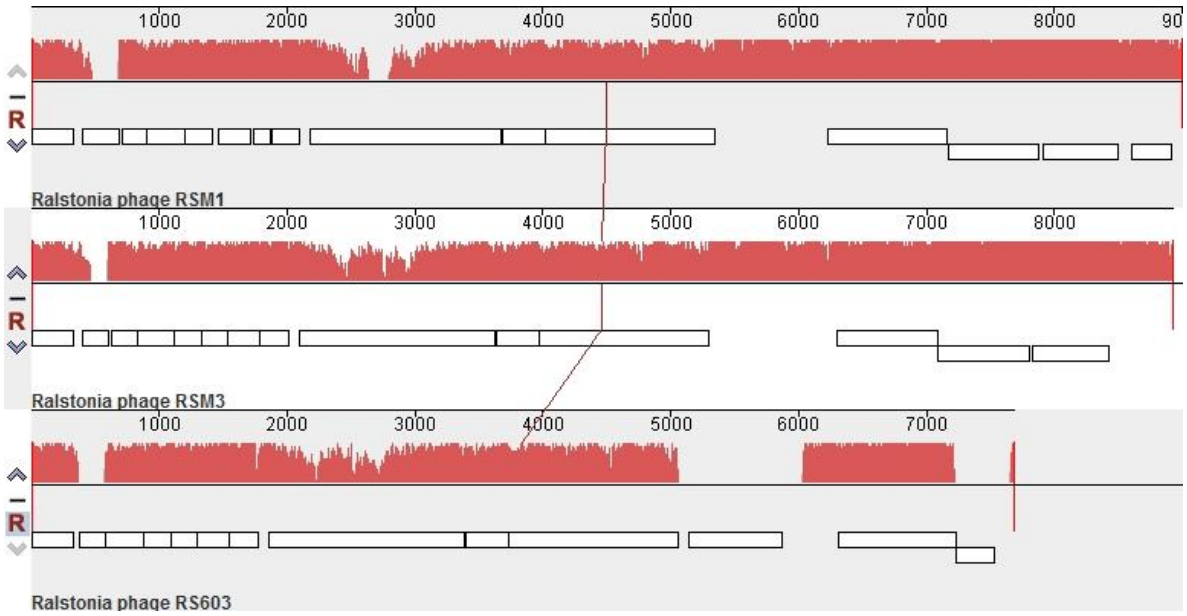


Table 6. Properties of the phages belonging to the genus *Vespertiliovirus* and an outlier (Spiroplasma phage SVST2).

Spiroplasma phage	GenBank accession No.	Genome length (bp)	Genome (mol%G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**	Zot***	CoatB****	CoatA*****
R8A2B	**X51344.1**	**8273**	**22.9**	**12**	**100**	**100**	**100**	**100**	**100**
SkV1CR23x	**EF506570.1**	**7870**	**22.2**	**13**	**70**	**83**	**94**	**99**	**86**
C74	**U28974.1**	**7768**	**23.2**	**13**	**67**	**75**	**96**	**100**	**91**
SVST2	AF133242.2	6825	22.7	13	0	33	37	0	3.2

* Determined using BLASTN; ** Determined using CoreGenes ***Determined using BLASTP: Zot homologs to NP_040337.2 of reference strain; **** Coat B homologs to NP_040339.1 of reference strain; *****Coat A homologs to NP_040340.1 of reference strain

Fig. 7. ProgressiveMauve alignment (Darling et al, 2004) of the species of the genus *Vespertiliovirus*.

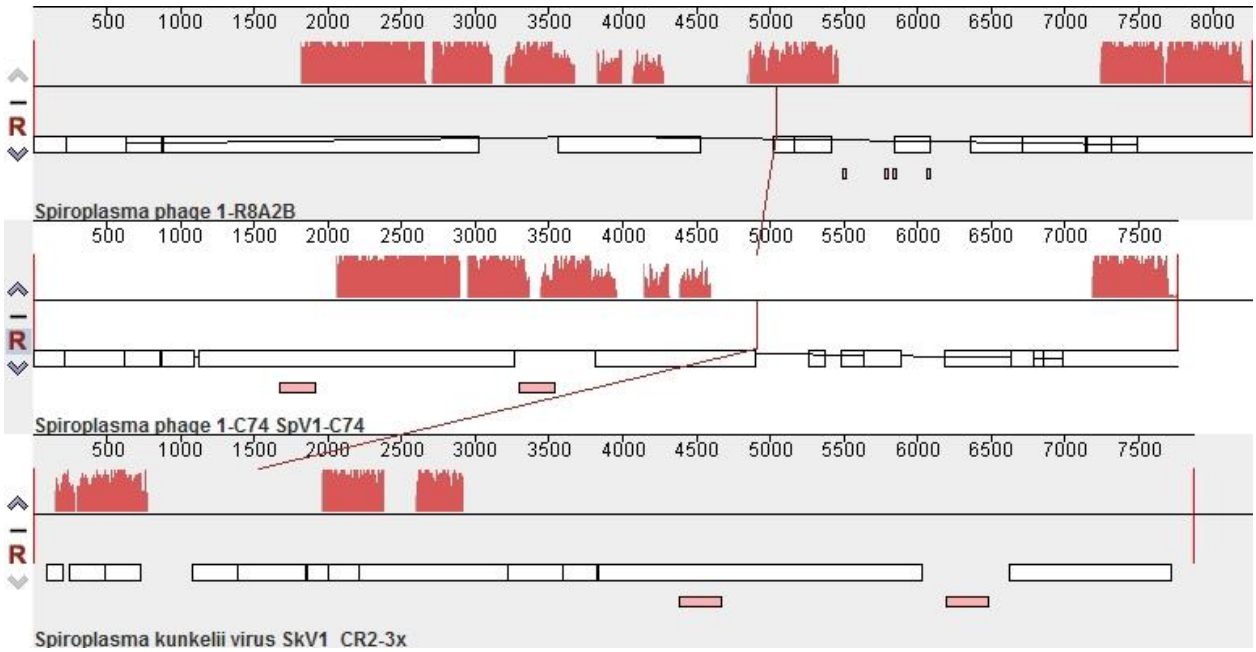


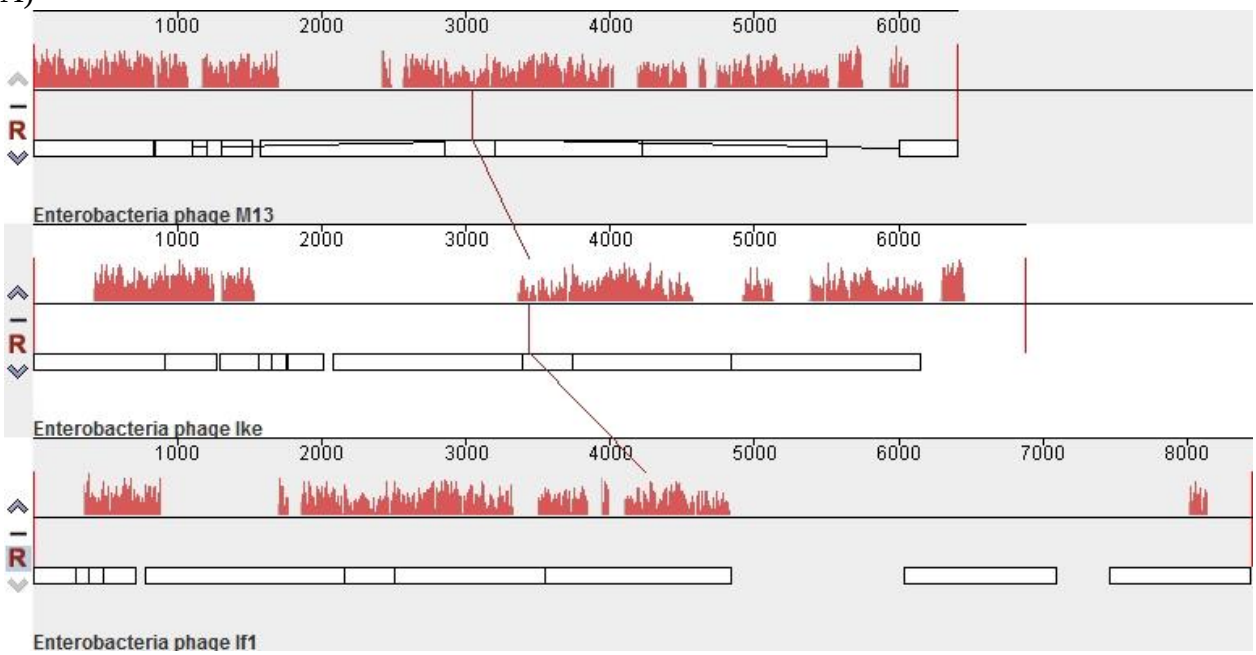
Table 7. Properties of the phages belonging to the genus *Lineavirus* and two outliers (Enterobacteria phages M13 and If1).

Phage	GenBank accession No.	Genome length (bp)	Genome (mol%G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**	Zot***	CoatB	Coat A
IKe	**X02139.1**	**6883**	**40.5**	**10**	**100**	**100**	**100**	**100**	**100**
I22	**X14336.1**	**6744**	**42.7**	**9**	**42**	**70**	**85**	**69**	**93**
M13	V00604.2	6407	40.7	10	1	80	50	0	15
If1	U02303	8454	43.7	10	0	50	55	0	11

* Determined using BLASTN; ** Determined using CoreGenes ***Determined using BLASTP

Fig. 8. ProgressiveMauve alignment (Darling et al, 2004) of A) the representatives of enterobacteria phages: Escherichia phage M13 (genus *Inovirus*), *Salmonella* phage IKe (genus *Lineavirus*) and *Escherichia* phage If1 (unassigned) and B) the species of genus *Lineavirus*

A)



B)

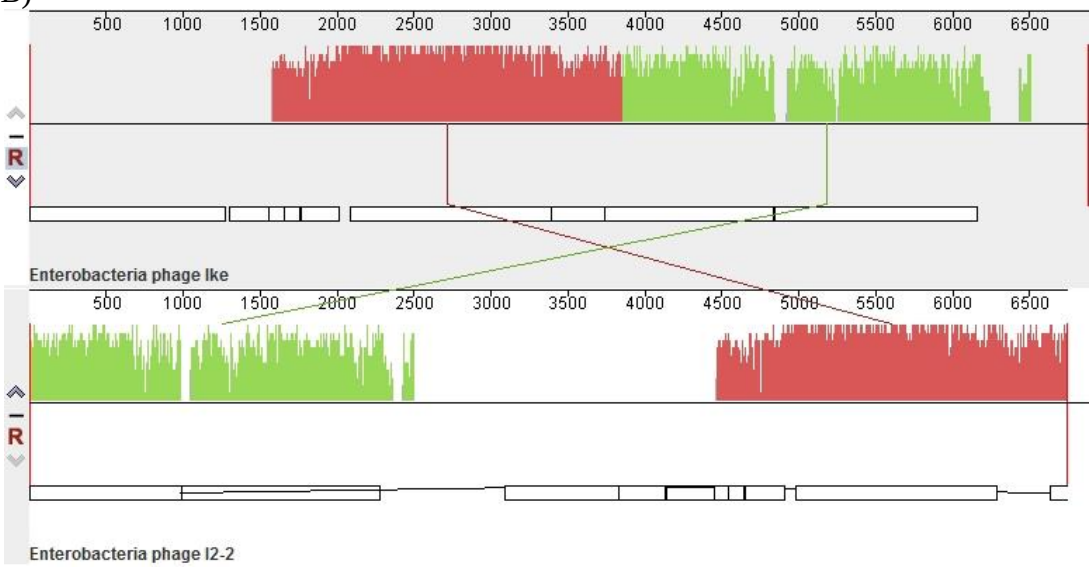


Table 8. Properties of the phages belonging to the genus *Inovirus* and the peripherally related viruses (*Salmonella* phage IKe and *Escherichia* phage If1)

Phage	GenBank accession No.	Genome length (bp)	Genome (mol%G+C)	No. CDS	DNA (% sequence identity)*	Proteome (% homologous proteins)**	Zot***	CoatB	CoatA
M13	V00604.2	6407	40.7	10	100	100	100	100	100
f1	J02448.1	6407	40.9	10	99	100	100	97	99
fd	J02451.1	6408	40.9	10	97	100	99	99	99
IKe	X02139.1	6883	40.5	10	1	80	51	27	13
If1	U02303	8454	43.7	10	0	60	64	57	24

* Determined using BLASTN; ** Determined using CoreGenes ***Determined using BLASTP