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:	***2016.031a-rB***	(to be completed by ICTV officers)

Short title: To amend the description of the *Felixo1virus* genus; and to create three (3) new genera within a new subfamily in the family *Myoviridae*.
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☒	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☐	**10** ☒

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	ICTV Bacterial and Archaeal Viruses Subcommittee

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

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

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2016.031aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Felixo1virus***
Subfamily:	***Ounavirinae*** **(new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus HY02 *Escherichia virus TP1*	Escherichia phage HY02 Escherichia typing phage 1	KM092515.1 KP869100.1

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

As defined by the Master Species List (2015), the *Felixo1virus* genus included 10 species: *Escherichia virus AYO145A, Escherichia virus EC6, Escherichia virus JH2, Escherichia virus VpaE1, Escherichia virus wV8, Salmonella virus FelixO1, Salmonella virus HB2014, Salmonella virus Mushroom, Salmonella virus UAB87,* and *Erwinia virus Ea214.* based on similar morphology, genome organization, and at least 53% conserved proteins of their members. We have subsequently realized that taxonomy based upon conservation of overall proteomes results in "lumping," and that Erwinia phage Ea21-4 is significantly different to deserve classification in a separate genus. Therefore, in this Taxonomic Proposal, we have reexamined all FelixO1-like phages using DNA and protein homology plus phylogenetic analysis to propose three new genera within a new subfamily.

The characteristics of members of the new species of the existing genus *Felixo1virus* are listed in Table 1.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2016.031bB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Suspvirus* (new)**
Subfamily:	***Ounavirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus SUSP1	Escherichia phage phiSUSP1	KT454805.1
Escherichia virus SUSP2	Escherichia phage phiSUSP2	KT454806.1

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 in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.031cB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Ounavirinae* (new)**
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2016.031dB***	(assigned by ICTV officers)

To name the new genus: *Suspvirus* (new)

Assigning the type species and other species to a new genus

Code	***2016.031eB***	(assigned by ICTV officers)

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

Escherichia virus SUSP1

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

BLASTN, CoreGenes (Table 2) [2], Gegenees BLAST and TBLASTX (Fig. 2) [4], progressiveMauve alignment (Fig. 5) [1], and phylogenetic analyses (Fig. 7) [3] all indicate that the proposed genus, *Suspvirus*, is cohesive and distinct from other genera. On average, the genomes of this genus are 89.7 kb (40.0 mol% G+C), and encode 135 proteins and 19 tRNAs. The host bacterium is *Escherichia coli*. By comparison, the phages of the *Felix01virus* genus have the following properties: genome length - 87.5 kb, mol% G+C - 38.9, proteins - 133, and tRNAs – 22.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this 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.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by

more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2016.031fB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Mooglevirus* (new)**
Subfamily:	***Ounavirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Citrobacter virus Moogle *Citrobacter virus Mordin*	Citrobacter phage Moogle Citrobacter phage Mordin	KM236239.1 KT363872.2

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 in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.031gB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Ounavirinae* (new)**
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2016.031hB***	(assigned by ICTV officers)

To name the new genus: *Mooglevirus* (new)

Assigning the type species and other species to a new genus

Code	***2016.031iB***	(assigned by ICTV officers)

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

Citrobacter virus Moogle

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

BLASTN, CoreGenes (Table 3) [2], Gegenees BLAST and TBLASTX (Fig. 2) [4], progressiveMauve alignment (Fig. 4) [1], and phylogenetic analyses (Fig. 7) [3] all indicate that the proposed genus, *Mooglevirus*, is cohesive and distinct from other genera. On average, the genomes of this genus are 88.8 kb in length (38.9 mol% G+C), and encode 132 proteins and 23 tRNAs. The host bacterium is *Citrobacter freundii.* By comparison, the phages of the *Felix01virus* genus have the following properties: genome length - 87.5 kb, mol% G+C - 38.9, proteins - 133, and tRNAs - 22.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this 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.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this

new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2016.031jB***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Ea214virus* (new)**
Subfamily:	***Ounavirinae* (new)**
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Erwinia virus M7	Erwinia phage vB_EamM-M7	HQ728263.1

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 in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.031kB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Ounavirinae* (new)**
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2016.031lB***	(assigned by ICTV officers)

To name the new genus: *Ea214virus* (new)

Assigning the type species and other species to a new genus

Code	***2016.031mB***	(assigned by ICTV officers)

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

Erwinia virus Ea214	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

BLASTN, CoreGenes (Table 4) [2], Gegenees BLAST and TBLASTX (Fig. 2) [4], progressiveMauve alignment (Fig. 6) [1], and phylogenetic analyses (Fig. 7) [3] all indicate that the proposed genus, *Ea214virus*, is cohesive and distinct from other genera. On average, the genomes of this genus are 85.1 kb in length (43.6 mol% G+C), and encode 117 proteins and 26 tRNAs. The host is *Erwinia amylovora*. By comparison, the phages of the *Felix01virus* genus have the following properties: genome length - 87.5 kb, mol%G+C - 38.9, proteins - 133, and tRNAs - 22.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this genus. The species was originally called *Erwinia phage phiEa21-4* but following the Subcommittee vote on the use of "phi" and hyphens in taxon names is renamed *Erwinia virus Ea214*.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 4: **NEW SUBFAMILY**

creating a new subfamily

A subfamily can only be created within a family.

Code	***2016.031nB***	(assigned by ICTV officers)

To create a new subfamily within:

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

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

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

naming a new subfamily

Code	***2016.031oB***	(assigned by ICTV officers)

To name the new subfamily: *Ounavirinae* (new)

genera and species assigned to the new subfamily

Code	***2016.031pB***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:

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

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

Felixo1virus

***Suspvirus* (new)**

***Mooglevirus* (new)**

***Ea214virus* (new)**

The new subfamily will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of unassigned species that the subfamily will contain (those NOT within any of the genera listed above):**

0

Reasons to justify the creation of the new subfamily:

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

As defined by the Master Species List (2015), the *Felixo1virus* genus included 10 species: *Escherichia virus AYO145A, Escherichia virus EC6, Escherichia virus JH2, Escherichia virus VpaE1, Escherichia virus wV8, Salmonella virus FelixO1, Salmonella virus HB2014, Salmonella virus Mushroom, Salmonella virus UAB87,* and *Erwinia virus Ea214.* based on similar morphology, genome organization, and at least 53% conserved proteins of their members. We have

subsequently realized that taxonomy based upon conservation of overall proteomes results in "lumping," and that Erwinia phage Ea21-4 is significantly different to deserve classification in a separate genus. Therefore, in this Taxonomic Proposal, we have reexamined all FelixO1-like phages using DNA and protein homology plus phylogenetic analysis to propose three new genera within a new subfamily.
Origin of the new subfamily name:
Salmonella phage Felix O1 was originally called phage O1.

MODULE 7: **REMOVE and MOVE**

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

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

Code	***2016.031qB***	(assigned by ICTV officers)

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

Erwinia virus Ea214

The present taxonomic position of these taxon/taxa:

Genus:	***Felixo1virus***
Subfamily:	
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

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

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

This TaxoProp reveals that this phage is significantly different from Salmonella phage Felix O1.

Part (b) re-assign to a higher taxon

Code	***2016.031rB***	(assigned by ICTV officers)

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

Genus:	***Ea214virus* (new)**
Subfamily:	***Ounavirinae* (new)**
Family:	***Myoviridae***
Order:	***Caudovirales***

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

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

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See above.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

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

2. 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. doi: 10.1186/1756-0500-6-140.

3. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008; 36(Web Server issue):W465-9.

4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6):e39107.

Felix O1-like phages:

5. 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;16:271. [*Escherichia coli* O157 typing phage 1]

6. Tiwari BR, Kim J. Complete Genome Sequence of Bacteriophage EC6, Capable of Lysing *Escherichia coli* O157:H7. Genome Announc. 2013;1(1). pii: e00085-12. [EC6]

7. Wang J, Niu YD, Chen J, McAllister TA, Stanford K. Complete Genome Sequence of *Escherichia coli* O145:NM Bacteriophage vB_EcoM_AYO145A, a New Member of O1-Like Phages. Genome Announc. 2015;3(3). pii: e00539-15. [vB_EcoM_AYO145A]

References:

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

Moogle-like viruses

9. Bernal CL, Berkowitz VE, Cahill JL, Rasche ES, Kuty Everett GF. Complete Genome Sequence of *Citrobacter freundii* Myophage Michonne. Genome Announc. 2015;3(5). pii: e01134-15. [Michonne]

10. Guan J, Snowden JD, Cahill JL, Rasche ES, Kuty Everett GF. Complete Genome Sequence of *Citrobacter freundii* Myophage Mordin. Genome Announc. 2015;3(5). pii: e01203-15. [Mordin]

11. Nguyen QT, Luna AJ, Hernandez AC, Kuty Everett GF. Complete Genome Sequence of *Citrobacter freundii* Myophage Moogle. Genome Announc. 2015;3(1). pii: e01426-14. [Moogle]

Erwinia phages

12. Born Y, Fieseler L, Marazzi J, Lurz R, Duffy B, Loessner MJ. Novel virulent and broad-host-range *Erwinia amylovora* bacteriophages reveal a high degree of mosaicism and a relationship to Enterobacteriaceae phages. Appl Environ Microbiol. 2011;77(17):5945-54. [vB_EamM-M7]

13. Lehman SM, Kropinski AM, Castle AJ, Svircev AM. Complete genome of the broad-host-range *Erwinia amylovora* phage phiEa21-4 and its relationship to Salmonella phage felix O1. Appl Environ Microbiol. 2009;75(7):2139-47. [phiEa21-4]

14. Müller I, Kube M, Reinhardt R, Jelkmann W, Geider K. Complete genome sequences of three *Erwinia amylovora* phages isolated in north america and a bacteriophage induced from an Erwinia tasmaniensis strain. J Bacteriol. 2011;193(3):795-6. [phiEa104]

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.

Fig. 1. Electron micrograph of **Left** negatively stained Erwinia phage phi21-4 (provided by Antonet Svircev, Agricullture and AgriFood Canada, 4902 Victoria Avenue North, Vineland, Ontario L0R 2E0, Canada) and **Right** Citrobacter phage Moogle (provided by Gabby Everett).

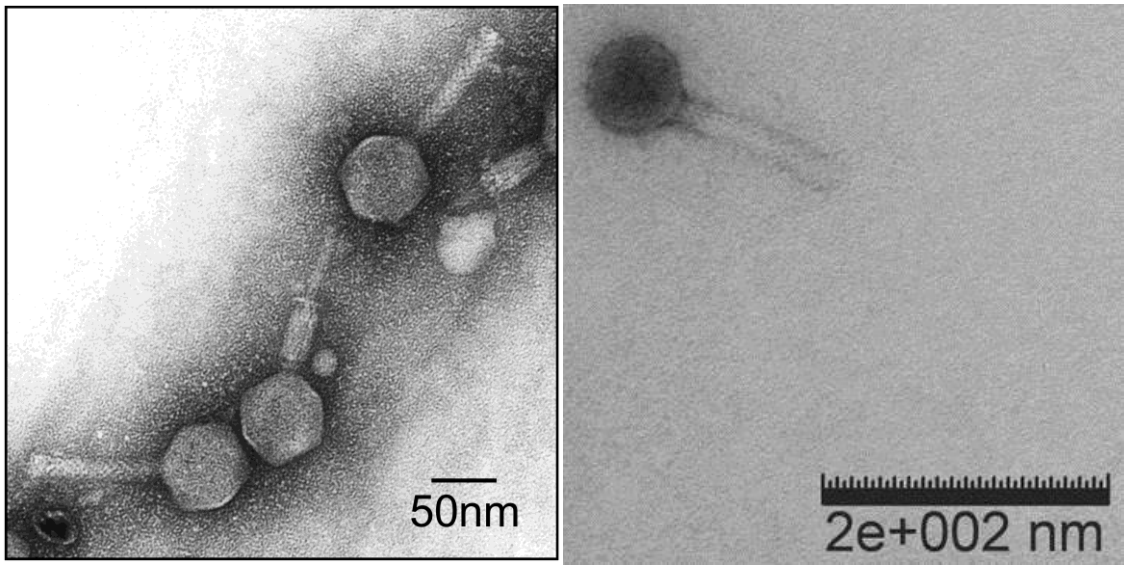


Fig. 2. Gegenees BLASTN (A) and TBLASTX (B) analysis in accurate mode (fragment size: 200 bp; step size: 100 bp) of Salmonella phage FelixO1-like viruses. "Phage SA1" (GU169904.1) is an artifact in GenBank and indicated in red. The phages boxed in black on the left diagram should be considered as strains of the phages described below.

PHAGE NAME	ACCESSION	AF320576.1	JF461087.1	KP143762.1	KM657822.1	KR014248.1	JN225449.1	KF055347.1	KP010413.1	JX560968.1	KM092515.1	KP869100.1	EU877232.1	KP869110.1	KP869109.1	KP869106.1	GU169904.1	KT454806.1	KT454805.1	KM236239.1	KT001916.1	KT363872.2	KT934943.1	JN641803.1	KF550303.1	JN882284.1	GU070616.1	JX181824.1	HQ728263.1	FQ482083.1	EU710883.1
Salmonella phage FelixO1	AF320576.1	100.0	96.3	83.1	74.3	72.7	75.1	69.6	67.4	66.8	69.8	70.6	70.0	70.1	70.1	70.0	76.2	20.8	19.5	15.6	14.3	13.9	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.2	0.2
Salmonella phage FO1a	JF461087.1	99.6	100.0	83.5	74.7	73.1	75.7	69.9	68.0	66.8	70.5	71.1	70.2	70.2	70.2	70.2	76.4	21.2	20.2	15.6	14.7	14.3	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2
Salmonella phage Mushroom	KP143762.1	81.2	79.0	100.0	76.1	74.2	75.2	71.4	68.7	67.1	69.4	70.5	70.4	70.5	70.5	70.4	73.9	22.6	21.5	16.8	14.7	14.0	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.3	0.3
Escherichia phage vB_EcoM-VpaE1	KM657822.1	72.6	70.6	75.8	100.0	74.7	71.9	70.2	67.7	69.4	70.7	72.0	72.1	72.2	72.2	72.1	71.3	22.0	20.5	16.1	14.0	13.7	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.3	0.4
Escherichia phage vB_EcoM_AYO145A	KR014248.1	72.2	70.0	74.6	75.8	100.0	77.2	73.9	70.9	69.9	72.2	73.3	72.2	72.2	72.2	72.2	74.1	21.7	21.6	16.4	15.0	14.5	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.2	0.2
Escherichia phage UAB_Phi87	JN225449.1	74.9	72.7	75.5	73.3	77.4	100.0	75.5	72.2	71.0	71.4	71.5	70.7	70.8	70.8	70.7	76.6	20.8	19.7	15.2	15.4	15.2	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.2	0.2
Escherichia phage JH2	KF055347.1	68.9	67.0	71.8	70.9	73.5	74.7	100.0	75.3	69.7	68.7	66.9	67.0	67.1	67.1	67.0	74.5	20.2	18.8	15.3	14.4	14.3	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.3	0.3
Salmonella phage HB-2014	KP010413.1	66.5	64.7	68.7	69.2	70.9	71.7	76.1	100.0	70.3	70.3	66.6	66.3	66.4	66.4	66.3	72.1	20.2	18.1	14.3	13.3	12.8	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.3	0.3
Escherichia phage EC6	JX560968.1	66.7	64.8	68.2	70.7	70.0	71.4	70.3	71.7	100.0	73.6	72.3	73.4	73.4	73.4	73.4	69.3	21.0	19.0	12.9	12.9	12.7	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.2	0.3
Escherichia phage HY02	KM092515.1	70.4	68.7	70.5	72.7	73.1	72.0	70.2	70.9	73.8	100.0	77.2	77.0	77.1	77.1	77.0	72.3	22.1	20.3	16.0	14.5	14.6	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.2	0.2
Escherichia coli O157 typing phage 1	KP869100.1	69.0	67.2	70.4	72.8	72.9	70.2	67.2	66.1	71.1	75.6	100.0	93.1	93.2	93.2	93.1	69.6	22.3	20.4	15.6	14.5	14.6	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.2	0.2
Escherichia phage wV8	EU877232.1	68.8	66.8	70.3	72.3	71.9	69.5	66.5	65.9	72.2	75.2	92.9	100.0	100.0	100.0	99.9	69.4	21.5	20.4	15.6	14.5	14.2	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2
Escherichia coli O157 typing phage 12	KP869110.1	68.2	66.3	70.1	72.3	71.5	69.0	66.5	65.7	72.4	75.2	92.8	99.9	100.0	100.0	99.9	69.4	21.5	20.5	15.5	14.6	14.3	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2
Escherichia coli O157 typing phage 11	KP869109.1	67.7	65.6	70.0	72.0	71.2	69.5	66.2	65.8	71.7	75.2	92.8	99.9	100.0	100.0	99.9	69.3	21.8	20.6	16.3	14.5	14.3	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2
Escherichia coli O157 typing phage 8	KP869106.1	67.9	65.9	70.0	72.0	71.6	69.0	66.3	65.7	71.5	74.7	92.4	99.4	99.5	99.5	100.0	69.3	22.4	20.6	15.7	14.4	14.2	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2
Staphylococcus phage SA1	GU169904.1	45.1	43.7	44.3	42.8	43.9	45.3	44.2	42.9	40.5	42.6	41.6	41.6	41.6	41.6	41.6	100.0	13.2	12.3	9.7	8.2	8.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2
Escherichia phage phiSUSP2	KT454806.1	20.2	19.9	22.1	21.9	20.7	20.7	20.1	20.3	20.7	21.4	22.1	21.8	21.8	21.8	21.8	21.9	100.0	68.2	23.9	22.9	22.5	0.0	0.0	0.0	0.0	0.0	0.0	0.7	0.4	0.5
Escherichia phage phiSUSP1	KT454805.1	19.3	18.6	20.5	20.0	20.9	19.2	18.6	18.0	18.9	19.8	20.0	20.2	20.2	20.2	20.2	19.8	66.3	100.0	38.4	38.1	37.9	0.0	0.0	0.0	0.0	0.0	0.0	0.6	0.3	0.5
Citrobacter phage Moogle	KM236239.1	15.1	14.5	16.4	15.9	16.0	15.0	14.9	14.0	12.5	15.8	15.6	15.4	15.4	15.4	15.4	16.1	24.2	39.6	100.0	69.7	68.6	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.4	0.4
Citrobacter phage Michonne	KT001916.1	14.1	13.8	14.1	13.7	14.3	15.0	13.8	12.8	12.9	13.5	14.4	14.4	14.4	14.4	14.3	13.2	22.6	38.7	68.8	100.0	94.8	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.3	0.3
Citrobacter phage Mordin	KT363872.2	13.6	13.4	13.6	13.3	13.9	14.6	13.8	12.6	12.5	14.2	14.3	14.0	14.0	14.0	14.0	13.4	22.4	38.6	67.5	94.9	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.3	0.3
Klebsiella phage vB_KpnM_KB57	KT934943.1	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	0.0	0.0	0.0	0.0	100.0	0.0	7.7	5.8	3.8	3.6	0.0	0.0	0.0
Salmonella phage SPN3US	JN641803.1	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	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Escherichia phage 4MG	KF550303.1	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	0.0	0.0	0.0	0.0	7.4	0.0	100.0	43.3	15.3	14.4	0.0	0.0	0.0
Cronobacter phage vB_CsaM_GAP31	JN882284.1	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	0.0	0.0	0.0	0.0	5.6	0.0	43.7	100.0	16.3	15.3	0.0	0.0	0.0
Salmonella phage PVP-SE1	GU070616.1	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	0.0	0.0	0.0	0.0	3.8	0.0	15.4	16.6	100.0	87.4	0.0	0.0	0.0
Salmonella phage SSE-121	JX181824.1	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	0.0	0.0	0.0	0.0	3.6	0.0	14.6	15.4	86.1	100.0	0.0	0.0	0.0
Erwinia phage vB_EamM-M7	HQ728263.1	0.3	0.3	0.4	0.5	0.4	0.4	0.5	0.4	0.4	0.4	0.3	0.2	0.2	0.2	0.2	0.5	0.8	0.7	0.5	0.4	0.5	0.0	0.0	0.0	0.0	0.0	0.0	100.0	49.3	48.2
Erwinia phage phiEa104	FQ482083.1	0.2	0.2	0.3	0.3	0.3	0.2	0.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.4	0.4	0.3	0.4	0.3	0.3	0.0	0.0	0.0	0.0	0.0	0.0	49.7	100.0	94.4
Erwinia phage phiEa21-4	EU710883.1	0.2	0.2	0.4	0.4	0.2	0.2	0.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.5	0.5	0.4	0.3	0.3	0.0	0.0	0.0	0.0	0.0	0.0	49.0	94.3	100.0

PHAGE NAME	ACCESSION NO.	AF320576.1	JF461087.1	KP143762.1	JN225449.1	KR014248.1	KM657822.1	JX560983.1	KF055347.1	KP010413.1	KM092515.1	KP869100.1	EU877232.1	KP869109.1	KP869110.1	KP869106.1	KT454806.1	KT454805.1	KM236239.1	KT001916.1	KT363872.2	GU169904.1	HQ728263.1	FQ482083.1	EU710883.1	KT934943.1	JN882284.1	KF550303.1	GU070616.1	JX181824.1	JN641803.1
Salmonella phage FelixO1	AF320576.1	100.0	96.8	90.2	87.9	87.0	87.2	84.5	85.7	84.9	85.4	86.9	86.4	86.5	86.5	86.5	69.7	68.1	66.2	65.7	65.6	88.7	31.3	31.2	31.2	17.3	17.5	17.5	18.0	18.0	15.0
Salmonella phage FO1a	JF461087.1	99.5	100.0	90.1	87.9	86.9	87.2	84.5	86.1	85.3	85.9	87.1	86.4	86.6	86.6	86.6	69.5	67.5	65.7	65.4	65.2	88.5	31.4	31.2	31.3	17.1	17.4	17.3	17.7	17.8	15.0
Salmonella phage Mushroom	KP143762.1	89.4	87.1	100.0	86.7	86.8	87.6	83.4	86.1	85.7	84.7	85.8	85.8	86.0	86.0	86.0	69.6	68.9	66.4	65.4	65.0	87.2	31.4	31.1	31.3	17.2	17.4	17.4	17.9	18.0	15.0
Escherichia phage UAB_Phi87	JN225449.1	87.9	85.6	87.7	100.0	88.4	87.4	85.6	87.9	86.6	86.1	86.9	86.3	86.5	86.5	86.5	69.7	68.5	65.8	65.7	65.7	87.6	31.2	31.0	31.0	17.2	17.4	17.4	17.8	17.8	14.9
Escherichia phage vB_EcoM_AYO145A	KR014248.1	86.5	84.1	87.3	88.3	100.0	88.6	85.0	86.7	86.2	86.6	87.8	87.2	87.3	87.2	87.3	70.6	69.2	66.7	65.6	65.5	86.8	30.9	30.8	30.9	17.3	17.5	17.4	17.8	17.8	14.9
Escherichia phage vB_EcoM-VpaE1	KM657822.1	85.9	83.6	87.2	86.0	87.3	100.0	84.4	85.6	84.7	86.3	86.7	86.7	86.9	86.9	86.8	69.1	68.2	65.7	64.5	64.2	85.5	30.9	30.7	30.8	17.2	17.3	17.3	17.7	17.8	14.9
Escherichia phage EC6	JX560983.1	84.7	82.9	84.4	85.6	85.3	86.2	100.0	85.5	85.0	85.9	85.6	85.6	85.8	85.8	85.8	68.5	67.2	64.7	64.9	65.0	85.1	31.1	31.1	31.1	17.3	17.5	17.5	17.8	17.8	14.8
Escherichia phage JH2	KF055347.1	84.9	83.1	86.4	87.0	86.7	86.2	84.5	100.0	86.3	84.6	84.7	84.1	84.2	84.3	84.1	68.5	67.8	65.1	65.5	65.6	86.2	31.2	31.0	31.1	17.2	17.4	17.4	17.8	17.8	14.8
Salmonella phage HB-2014	KP010413.1	84.5	82.5	85.4	85.5	84.8	84.9	84.6	86.7	100.0	84.8	84.2	83.9	84.1	84.1	84.1	68.1	66.9	64.1	64.5	63.9	85.4	30.8	30.8	30.9	17.2	17.3	17.3	17.7	17.7	14.9
Escherichia phage HY02	KM092515.1	86.1	83.8	86.2	86.4	87.4	88.0	86.0	85.8	85.9	100.0	89.1	88.7	88.9	88.9	88.9	70.5	69.4	66.5	65.5	65.4	87.4	31.1	30.9	31.0	17.3	17.4	17.5	17.9	17.8	14.9
Escherichia coli O157 typing phage 1	KP869100.1	86.5	84.3	86.0	86.1	87.0	87.8	84.6	84.6	84.1	88.0	100.0	95.9	96.1	96.1	96.0	70.0	68.8	66.2	65.5	65.4	86.8	30.7	30.8	30.9	17.2	17.4	17.3	17.6	17.6	14.9
Escherichia phage wV8	EU877232.1	85.4	83.1	86.0	85.8	86.7	87.4	85.0	83.9	84.4	87.2	96.1	100.0	99.8	99.8	99.7	69.5	68.7	66.4	64.9	64.8	86.6	30.6	30.5	30.7	17.2	17.4	17.3	17.7	17.7	15.0
Escherichia coli O157 typing phage 11	KP869109.1	85.5	83.2	86.0	85.7	86.5	87.4	84.9	83.9	83.9	87.7	95.4	99.7	100.0	100.0	99.9	69.4	68.7	66.3	64.9	64.6	86.5	30.7	30.6	30.7	17.2	17.4	17.4	17.7	17.7	14.9
Escherichia coli O157 typing phage 12	KP869110.1	85.7	83.7	85.8	85.6	86.3	87.1	84.8	84.1	83.7	87.4	95.5	99.7	100.0	100.0	99.9	69.4	68.9	65.9	64.8	64.7	86.2	30.6	30.7	30.7	17.2	17.4	17.3	17.7	17.7	15.0
Escherichia coli O157 typing phage 8	KP869106.1	85.7	83.2	85.9	85.1	86.1	87.0	84.6	83.9	83.8	87.3	95.2	99.4	99.7	99.7	100.0	69.4	68.6	66.2	64.6	64.5	86.0	30.5	30.6	30.7	17.2	17.4	17.3	17.7	17.7	14.9
Escherichia phage phISUSP2	KT454806.1	67.6	66.1	68.9	68.2	69.5	69.0	66.9	67.6	67.6	68.7	69.1	69.0	69.2	69.2	69.0	100.0	86.4	69.9	68.9	68.8	68.9	31.1	30.9	31.1	17.0	17.4	17.4	17.8	17.8	14.9
Escherichia phage phISUSP1	KT454805.1	65.9	63.8	67.7	66.8	68.2	67.6	64.8	66.3	65.6	67.1	67.3	68.0	68.1	68.2	68.0	85.6	100.0	74.6	74.2	74.0	67.5	30.6	30.6	30.7	17.2	17.4	17.4	17.8	17.8	14.9
Citrobacter phage Moogle	KM236239.1	64.9	63.0	66.2	65.2	66.4	66.5	63.8	64.7	64.1	65.3	66.1	66.3	66.5	66.5	66.4	70.1	75.5	100.0	85.3	85.2	66.0	31.1	30.9	31.0	17.2	17.4	17.4	17.8	17.8	14.9
Citrobacter phage Michonne	KT001916.1	63.7	61.9	64.2	64.6	64.8	64.2	63.0	64.7	63.9	63.9	64.7	64.5	64.7	64.7	64.6	68.9	75.1	84.8	100.0	96.7	64.6	30.7	30.5	30.7	17.2	17.5	17.4	17.7	17.8	14.9
Citrobacter phage Mordin	KT363872.2	63.4	61.6	64.0	64.5	64.7	63.5	63.0	64.6	63.2	63.6	64.4	63.9	64.1	64.1	64.1	68.3	74.3	84.2	96.7	100.0	64.3	30.6	30.5	30.6	17.3	17.4	17.5	17.7	17.8	15.0
Staphylococcus phage SA1	GU169904.1	58.2	56.8	57.8	58.2	57.9	57.6	56.4	57.6	56.7	57.4	57.9	57.6	57.7	57.8	57.6	47.4	46.9	45.3	44.7	44.6	100.0	24.3	24.2	24.3	16.1	16.3	16.3	16.5	16.5	15.1
Erwinia phage vB_EamM-M7	HQ728263.1	31.2	30.7	31.3	31.3	31.3	31.1	31.1	31.3	31.1	31.0	31.0	31.1	31.1	31.1	31.1	31.7	31.5	31.4	31.5	31.5	31.6	100.0	84.8	84.7	17.5	18.5	18.6	18.7	18.7	16.7
Erwinia phage phiEa104	FQ482083.1	31.2	30.8	31.4	31.3	31.3	31.2	31.1	31.5	31.1	31.1	31.2	31.2	31.2	31.3	31.2	31.7	31.6	31.4	31.4	31.4	31.7	84.9	100.0	96.7	17.6	18.5	18.6	18.7	18.7	16.7
Erwinia phage phiEa21-4	EU710883.1	31.2	30.8	31.4	31.3	31.3	31.2	31.1	31.4	31.1	31.2	31.2	31.2	31.2	31.2	31.2	31.8	31.6	31.5	31.4	31.4	31.6	84.7	96.7	100.0	17.5	18.4	18.5	18.7	18.7	16.7
Klebsiella phage vB_KpnM_KB57	KT934943.1	15.4	15.2	15.4	15.4	15.5	15.4	15.4	15.5	15.4	15.4	15.4	15.5	15.5	15.5	15.5	15.4	15.5	15.4	15.6	15.5	15.9	15.6	15.7	15.7	100.0	50.9	52.3	48.8	48.7	14.8
Cronobacter phage vB_CsaM_GAP31	JN882284.1	15.5	15.3	15.5	15.5	15.5	15.4	15.4	15.5	15.4	15.4	15.5	15.5	15.5	15.5	15.5	15.5	15.6	15.5	15.6	15.6	16.0	16.1	16.1	16.1	49.6	100.0	79.6	63.4	62.8	15.2
Escherichia phage 4MG	KF550303.1	15.5	15.3	15.5	15.5	15.5	15.4	15.5	15.5	15.4	15.5	15.5	15.5	15.5	15.5	15.5	15.5	15.6	15.5	15.5	15.5	16.0	16.2	16.2	16.2	50.6	79.7	100.0	63.5	63.1	15.2
Salmonella phage PVP-SE1	GU070616.1	15.8	15.6	15.9	15.8	15.7	15.7	15.7	15.8	15.7	15.7	15.6	15.7	15.7	15.7	15.7	15.8	15.8	15.8	15.8	15.8	16.2	16.3	16.3	16.3	48.0	64.2	64.4	100.0	94.3	15.2
Salmonella phage SSE-121	JX181824.1	15.8	15.6	15.8	15.7	15.7	15.7	15.6	15.7	15.6	15.7	15.6	15.7	15.7	15.7	15.7	15.8	15.8	15.8	15.8	15.8	16.2	16.2	16.3	16.3	47.6	63.2	63.2	93.4	100.0	15.2
Salmonella phage SPN3US	JN641803.1	13.8	13.8	13.8	13.8	13.8	13.8	13.7	13.7	13.7	13.7	13.8	13.8	13.8	13.8	13.8	13.9	13.9	13.8	13.8	13.8	14.6	14.5	14.6	14.5	14.5	14.8	14.8	14.8	14.8	100.0

Table 1. Properties of the eleven phages belonging to the genus *Felixo1virus*.

Phage	RefSeq No.	GenBank Accession No.	Genome length (kb)	Genome (mol% G+C)	No. CDS	No. tRNAs	DNA (% sequence identity) *	% Homologous proteins **
Salmonella phage FelixO1***	NC_005282	AF320576	86.16	39.0	131	22	100	100
Salmonella phage Mushroom ***		KP143762	87.71	39.0	128	21	92	87.0
Escherichia phage vB_EcoM-VpaE1 ***	NC_027337	KM657822	88.40	38.9	132	20	91	90.1
Escherichia phage vB_EcoM_AYO145A ***	NC_028825	KR014248	87.37	39.0	131	20	89	90.8
Escherichia phage UAB_Phi87 ***	NC_027360	JN225449	87.60	38.9	147	23	91	90.8
Escherichia phage JH2***	NC_029023	KF055347	87.71	38.8	131	21#	88	87.0
Salmonella phage HB-2014***	NC_027329	KP010413	87.51	38.8	126	22	88	83.2
Escherichia phage EC6***	NC_027369	JX560968	86.23	38.9	136	22#	86	86.3
Escherichia phage HY02	NC_028872	KM092515	86.25	38.9	125	21#	86	85.5
Escherichia phage typing phage 1		KP869100	88.53	38.8	132	22	91	89.3

Escherichia phage wV8***	NC_012749	EU877232	88.49	38.9	140	23	87	92.4

* Determined using BLASTN; ** Determined using CoreGenes [2]; *** member of a species previously recognized by ICTV; # not indicated in GenBank RefSeq record; Salmonella phage FO1a (JF461087.1) and Escherichia typing phages 12, 11, and 8 (KP869110.1, KP869109.1, KP869106.1) should be considered as strains of Escherichia phage wV8 within this genus.

Table 2. Properties of the two phages belonging to the genus *Suspvirus*.

Escherichia phage	RefSeq No.	GenBank Accession No.	Genome length (kb)	Genome (mol% G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	% Homologous proteins **
phiSUSP1	NC_028808.1	KT454805.1	90.74	39.8	139	19	100	100
phiSUSP2	NC_028935.1	KT454806.1	88.7	40.2	131	19	94	91.4

* Determined using BLASTN; ** Determined using CoreGenes [2]

Table 3. Properties of the two phages belonging to the genus *Mooglevirus*.

Citrobacter phage	RefSeq No	GenBank Accession No.	Genome length (kb)	Genome (mol% G+C)	No. CDS	No tRNAs	DNA (% sequence identity)*	% Homologous proteins **
Moogle		KM236239	88.00	39.0	126	21	100	100
Mordin		KT363872	89.60	38.8	138	25	90	96.0

* Determined using BLASTN; ** Determined using CoreGenes [2]; *Salmonella* phage Michonne [KT001916] should be considered as a strain of Citrobacter phage Mordin within this genus.

Table 4. Properties of the two phages belonging to the genus *Ea214virus*.

Erwinia phage	RefSeq No.	GenBank Accession No.	Genome length (kb)	Genome (mol% G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	% Homologous proteins **
phiEa21-4	NC_011811.1	EU710883.1	84.58	43.8	118	26	100	100
vB_EamM-M7		HQ728263	85.69	43.4	117	26	87	98.3

* Determined using BLASTN; ** Determined using CoreGenes [2]; *Erwinia amylovora* phage phiEa104 (FQ482083) should be considered a strain of Erwinia phage phiEa21-4 and phiEa116 (FQ857195) should be considered a strain of Erwinia phage EamM-M7 within this genus.

Fig. 3. progressiveMauve alignment [1] of the genomes of members of the *Felixo1virus* genus – from top to bottom: Escherichia phages typing phage 1, EC6, HY02, JH2, vB_EcoM_AYO145A, vB_EcoM-VpaE1, and Salmonella phages HB-2014, Mushroom, and FelixO1. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication). N.B. the genomes of some of these phages are not collinear with that of FelixO1.

Fig. 4. progressiveMauve alignment [1] of the annotated genomes of members of the *Mooglevirus* genus – from top to bottom: Citrobacter phages Moogle and Mordin. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication).

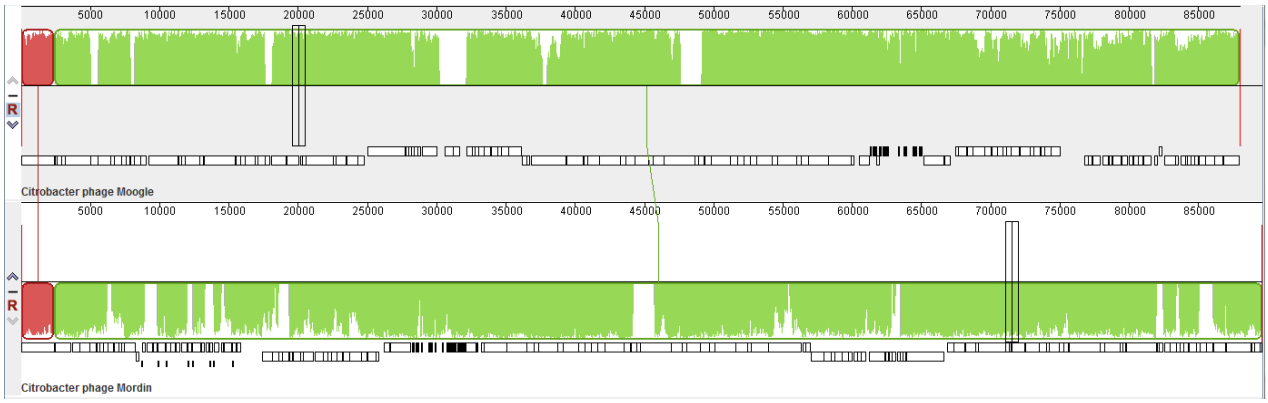


Fig. 5. progressiveMauve alignment [1] of the annotated genomes of members of the *Suspvirus* genus – from top to bottom: Escherichia phages phiSUSP1 and phiSUSP2. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication).

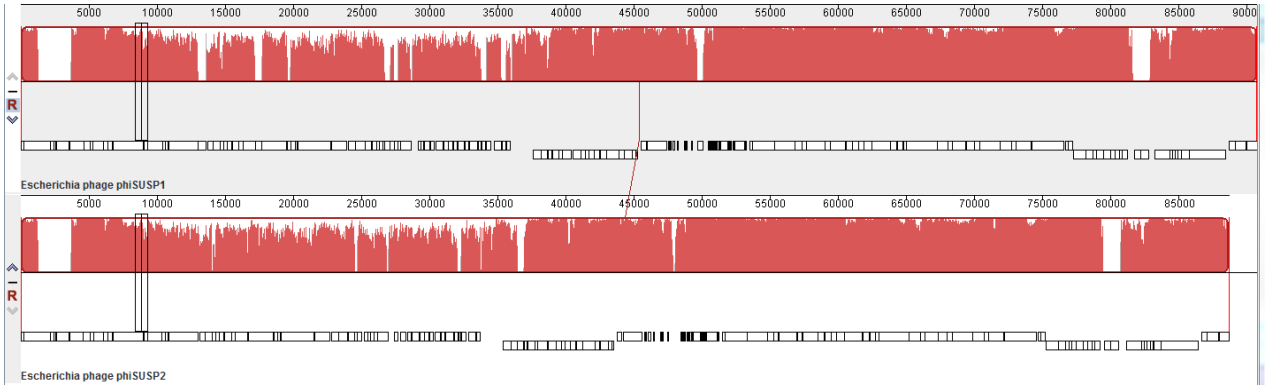


Fig. 6. progressiveMauve alignment [1] of the annotated genomes of members of the *Ea214virus* genus – from top to bottom: Erwinia phages phiEa21-4 and vB_EamM_M7. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication). N.B. The two genomes are not collinear.

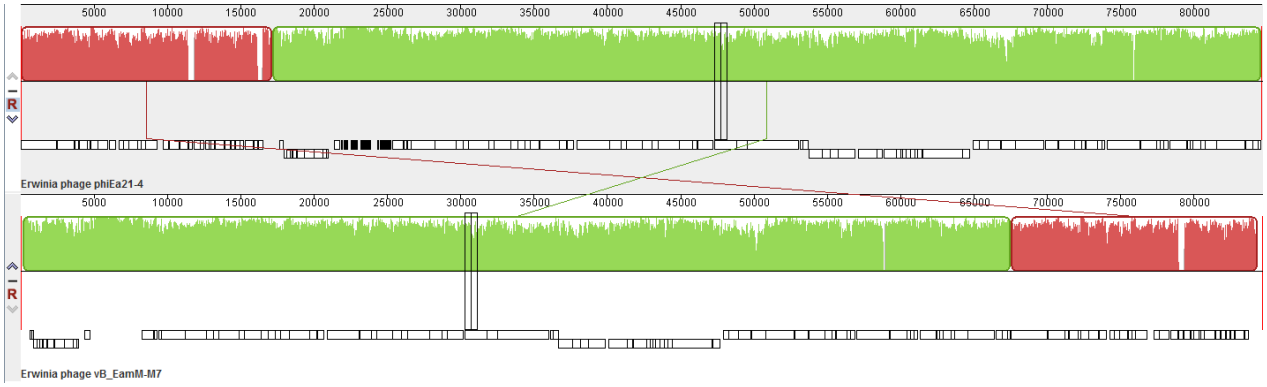
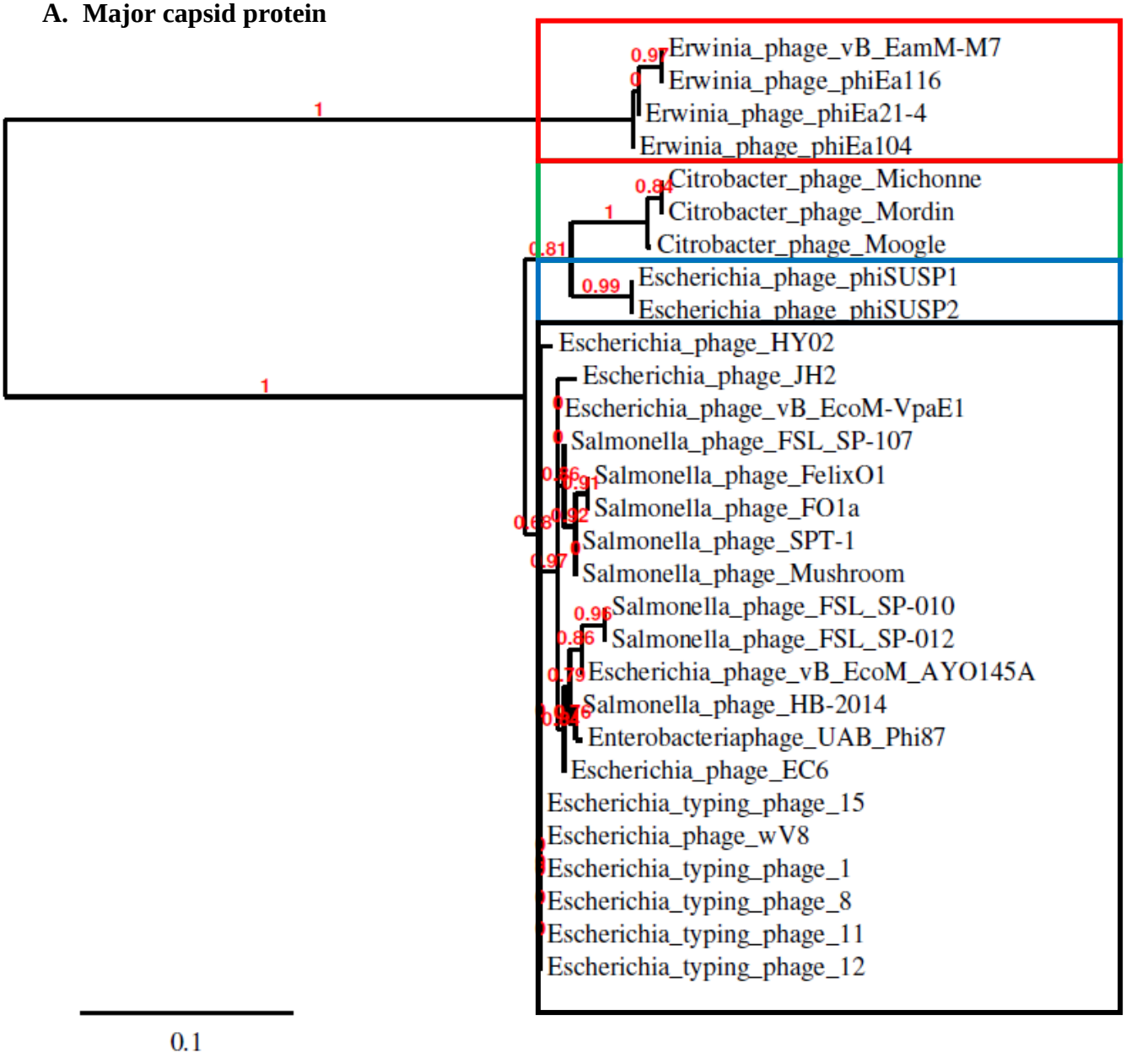
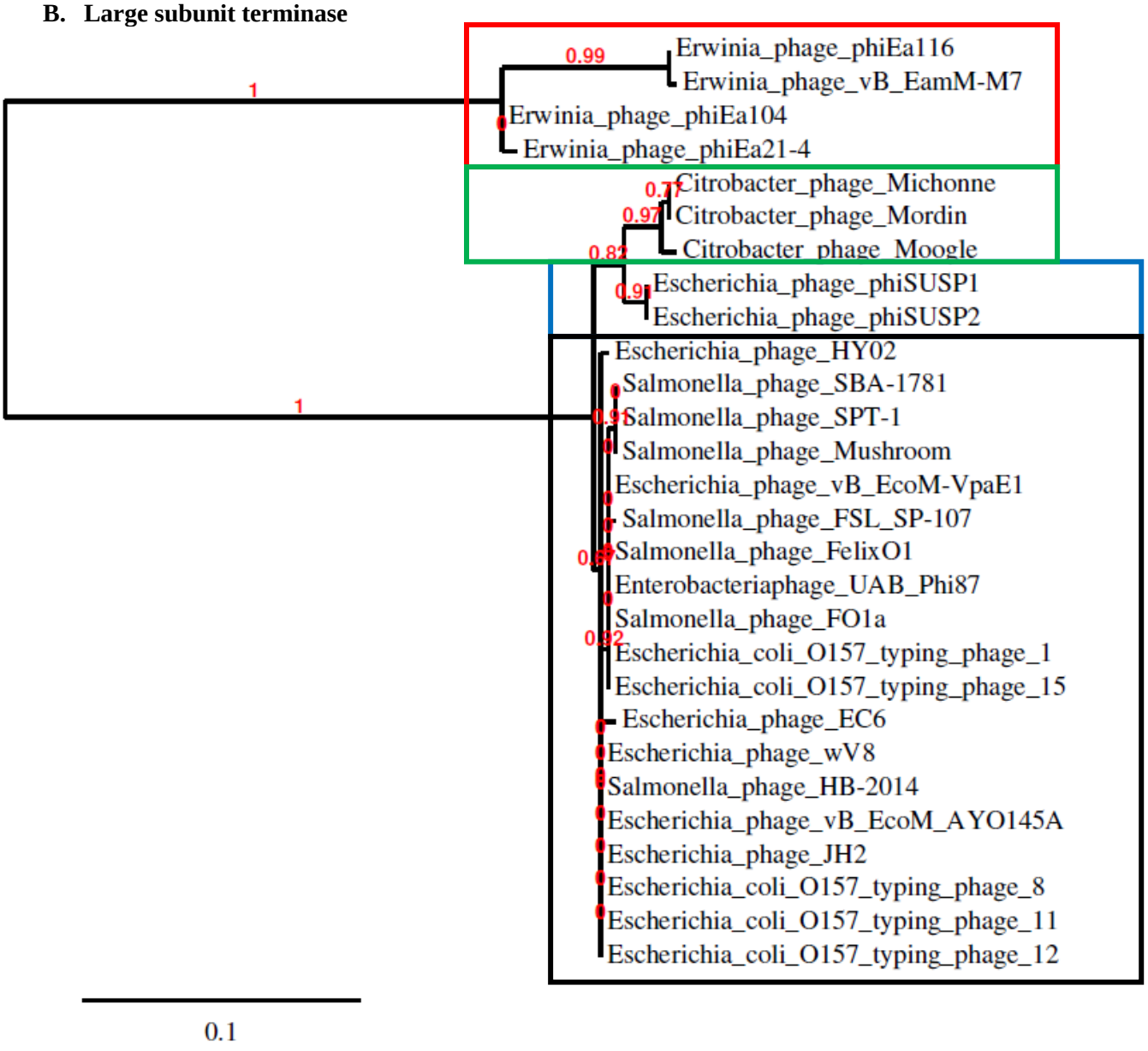


Fig. 7. Phylogenetic analysis of the (A) major capsid protein, (B) large subunit terminase proteins, (C) DNA polymerases, and (D) DNA polymerases of all phages belonging to the subfamily *Ounavirinae* constructed using “one click” at phylogeny.fr [3]. "The "One Click mode" targets users that do not wish 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." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative (Syst Biol. 2006;55(4):539-52.) for details." **Red** = *Ea214virus*, **Green** = *Mooglevirus*, **Blue** = *Suspvirus*, and **Black** = *Felixo1virus*

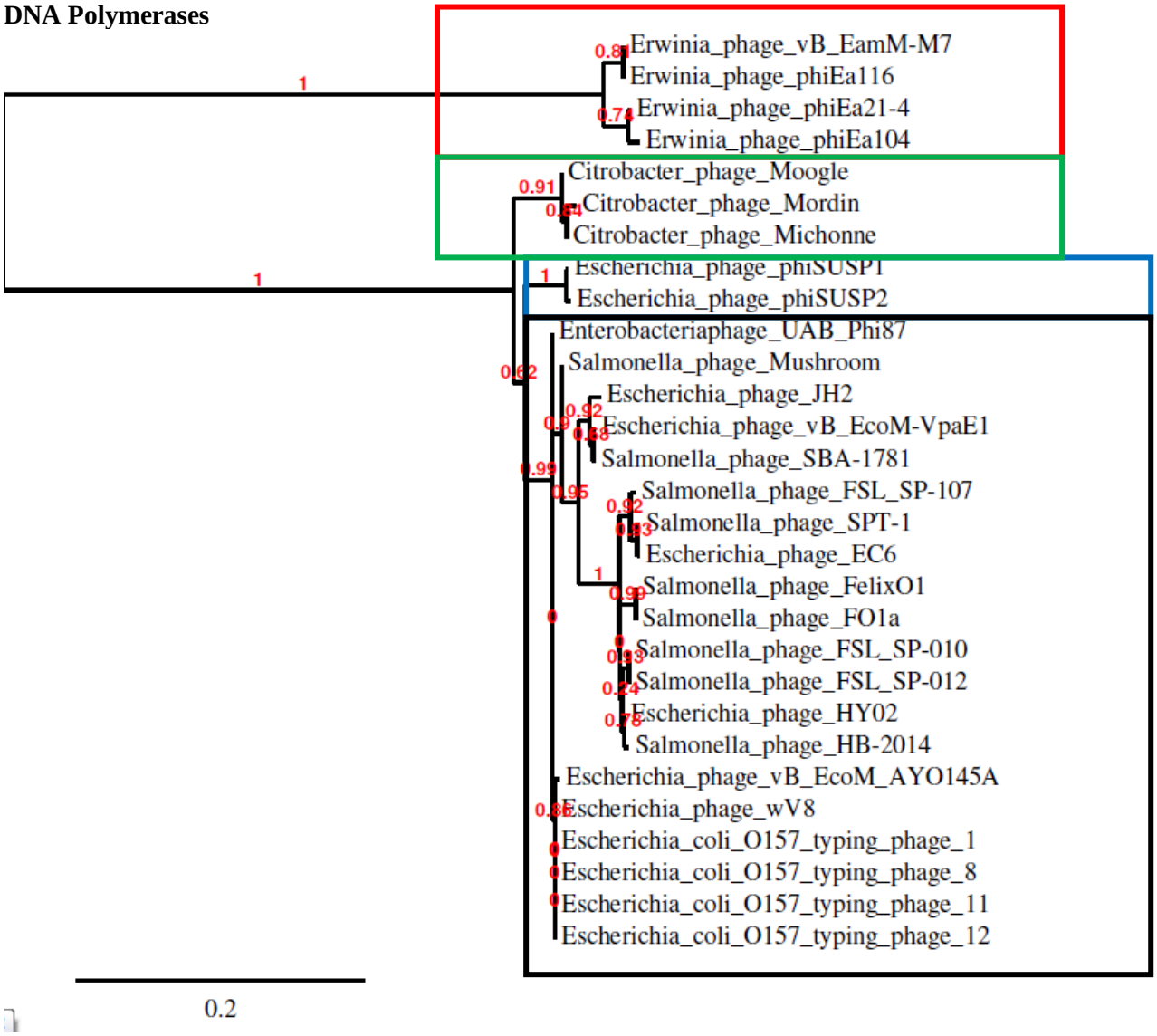
A. Major capsid protein



B. Large subunit terminase



C. DNA Polymerases



D. DNA polymerases without those of Erwinia phages

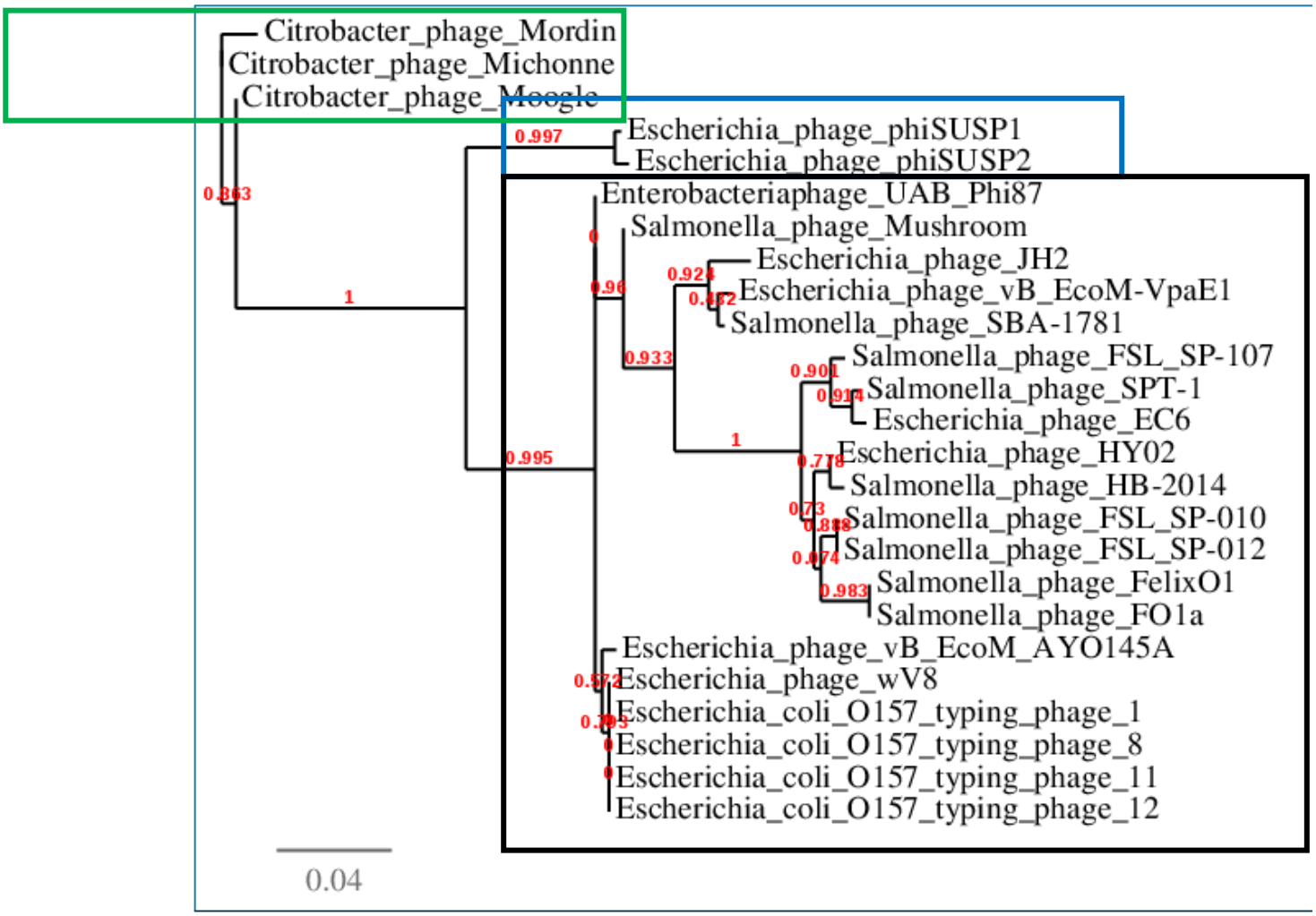


Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*