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:	***2016.045a-oB***	(to be completed by ICTV officers)

Short title: To create one (1) new subfamily, *Sepvirinae* containing three (3) new genera, in the family *Podoviridae*.
(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	***2016.045aB***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Nona33virus* (new)**
Subfamily:	***Sepvirinae* (new)**
Family:	***Podoviridae***
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 PA28	Escherichia phage PA28	KP682381.1
Escherichia virus 24B	Escherichia phage vB_EcoP_24B	HM208303.1
Escherichia virus Min27	Escherichia phage Min27	EU311208.1
Escherichia virus 933W	Escherichia phage 933W	AF125520.1
Escherichia virus Stx2 II	Escherichia phage Stx2 II	AP005154.1

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	***2016.045bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Sepvirinae* (new)**
Family:	***Podoviridae***
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	***2016.045cB***	(assigned by ICTV officers)

To name the new genus: *Nona33virus*

Assigning the type species and other species to a new genus

Code	***2016.045dB***	(assigned by ICTV officers)

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

Escherichia virus 933W

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:**

5

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 (Fig. 2), CoreGenes (Table 1) [2], and progressiveMauve alignment (Fig. 3) [1] all indicate that the proposed genus, *Nona33virus*, is cohesive and distinct from other genera. Common proteins shared by members of this genus are listed in Table 5. Diagnostic proteins present only in members of this genus are listed in (Table 6). Phylogenetic analyses (Fig. 7) [3] reveals a problem associated with the subclassification of this group of viruses, since most of the commonly used phylogenetic proteins occur in the conserved region of the phage genomes. On average, the genomes of members of this genus are 61.2 kb in length (49.6 mol% G+C), and encode 85 proteins and 3 tRNAs.

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	***2016.045eB***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Tl2011virus*** **(new)**
Subfamily:	***Sepvirinae*** **(new)**
Family:	***Podoviridae***
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 TL2011	Escherichia phage TL-2011c	JQ011318.1
Escherichia virus 191	Escherichia phage phi191	KF971864.1
Shigella phage VASD	Shigella phage Ss-VASD	KR781488.1
Escherichia virus PA2	Escherichia phage PA2	KP682371.1

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	***2016.045fB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Sepvirinae***
Family:	***Podoviridae***
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	***2016.045gB***	(assigned by ICTV officers)

To name the new genus: *Tl2011virus*

Assigning the type species and other species to a new genus

Code	***2016.045hB***	(assigned by ICTV officers)

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

Escherichia virus TL2011

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

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

4

Reasons to justify the creation of a new genus:

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

BLASTN (Fig. 2), CoreGenes (Table 2) [2], and progressiveMauve alignment (Fig. 4) [1] all indicate that the proposed genus, *TL2011virus*, is cohesive and distinct from other genera. Common proteins shared by members of this genus are listed in Table 5. Diagnostic proteins present only in members of this genus are listed in (Table 6). Phylogenetic analyses (Fig. 7) [3] reveals a problem associated with the subclassification of this group of viruses, since most of the commonly used phylogenetic proteins occur in the conserved region of the phage genomes. On average, the genomes of this genus are 62.0 kb in length (50.2 mol% G+C), and encode 79 proteins and 2.25 tRNAs.

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	***2016.045iB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Pocjvirus* (new)**
Subfamily:	***Sepvirinae* (new)**
Family:	***Podoviridae***
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)**
Shigella virus POCJ13 *Shigella virus 7502Stx*	Shigella phage POCJ13 Shigella phage 75/02 Stx	KJ603229.1 KF766125.2

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	***2016.045jB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Sepvirinae* (new)**
Family:	***Podoviridae***
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	***2016.045kB***	(assigned by ICTV officers)

To name the new genus: *Pocjvirus*

Assigning the type species and other species to a new genus

Code	***2016.045lB***	(assigned by ICTV officers)

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

Shigella virus POCJ13

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 (Fig. 2), CoreGenes (Table 3) [2], and progressiveMauve alignment (Fig. 5) [1] all indicate that the proposed genus, *Pocjvirus*, is cohesive and distinct from other genera. Common proteins shared by members of this genus are listed in Table 5. Diagnostic proteins present only in members of this genus are listed in (Table 6). Phylogenetic analyses (Fig. 7) [3] reveals a problem associated with the subclassification of this group of viruses, since most of the commonly used phylogenetic proteins occur in the conserved region of the phage genomes. On average, the genomes of this genus are 61.8 kb in length (49.2 mol% G+C), and encode 77 proteins and 0 tRNAs.

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 4: **NEW SUBFAMILY**

creating a new subfamily

A subfamily can only be created within a family.

Code	***2016.045mB***	(assigned by ICTV officers)

To create a new subfamily within:

Family:	***Podoviridae***
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	***2016.045nB***	(assigned by ICTV officers)

To name the new subfamily: *Sepvirinae*

genera and species assigned to the new subfamily

Code	***2016.045oB***	(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

***Nona33virus* (new)**

***Tl2011virus* (new)**

***Pocjvirus* (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

Shigatoxin-encoding phages belong to the three families included in the *Caudovirales*. An analysis of the 933W-like phages identified using BLASTN revealed that while they possessed very similar genome lengths and overall G+C contents they could be resolved into three DNA-sequence based clusters, which we have assigned to three genera, named after the first isolated type virus, respectively: *Nona33virus, T2011virus*, and *Pocjvirus*. Inter-genus global alignments using progressiveMauve [1] revealed that the members of the type species of each of these genera showed significant DNA sequence identity largely restricted to the right two-thirds of their genomes (Figure 6). For members of each of these proposed genera we have been able to identify

diagnostic proteins (Table 6).

It has been noted for some time that there is a phylogenetic relationship between the 933W-like members of the *Podoviridae* and Escherichia phage lambda, which is a member of the *Siphoviridae*. Based upon the total proteome [2], what we observed that phages 933W, TL-2011c, and POCJ13 share 23 (28.7%), 12 (16.7%) and 12 (16.7%) protein homologs with Escherichia phage lambda, respectively. These numbers are similar to the proteomic relationship between Escherichia phages lambda and P22 (*Podoviridae*) – 16 homologs (24.2%) [5]. The latter two phages have long been considered members of the lambdoid supergroup.

Origin of the new subfamily name:

Sepvirinae includes the Sigil "SEP" for Shigatoxin-Encoding Podovirus.

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.

5. Lavigne R, Seto D, Mahadevan P, Ackermann HW, Kropinski AM. Unifying classical and molecular taxonomic classification: analysis of the *Podoviridae* using BLASTP-based tools. Res Microbiol. 2008;159(5):406-14.

6. Plunkett G 3rd, Rose DJ, Durfee TJ, Blattner FR. Sequence of Shiga toxin 2 phage 933W from *Escherichia coli* O157:H7: Shiga toxin as a phage late-gene product. J Bacteriol. 1999;181(6):1767-78. [933W]

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 negatively stained Escherichia phage 933W (Journal of Bacteriology, with permission). Bar: 200 nm.

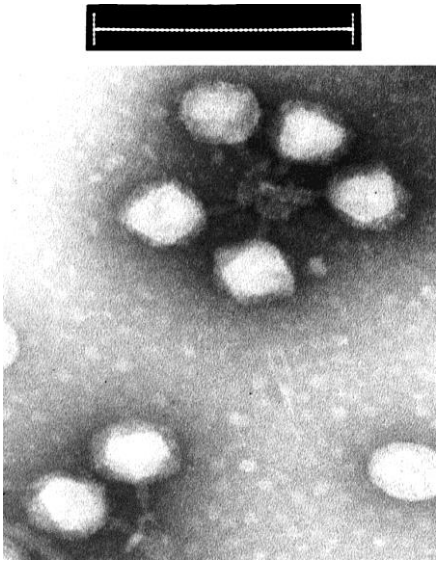


Fig. 2. BLASTN heat map analysis of Escherichia 933W-like phages using Gegenees [4] with the following settings: fragment size - 200 bp; step size: 100 bp.

PHAGE	ACCESSION NO.	AB255436	KJ603229.	KF766125.	JQ011318.1	HG792104.	HG792102.	HG792103.	KF971864.	HE664024.	HG792105.	KR781488.	KP682371.	KP682374.	HQ424691.	KP682381.	HM208303	EU311208.1	AP004402	AF125520	AP000363	KP682389.	KP682392.	KP682380.	KP682387.	KP682379.	KP682384.	KP682373.	KP682375.	KP682372.	KP682378.	KP682383.	KP682385.	KP682388.	KP682382.	KP682390.	KP682377.	AP005154.	KP682376.	KP682391.	KP682386.	KJ909655.	AP005153.	FJ188381.1	FM180578.	AJ556162.	FJ184280.1	JQ347801.	EU078592.	KT232076.
86	AB255436.1	100.0	42.0	40.0	43.2	43.3	42.6	42.6	42.1	42.6	42.5	38.5	47.5	47.5	47.5	59.6	59.1	60.4	60.8	60.2	56.5	57.5	57.4	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.4	57.5	57.5	57.5	53.7	52.9	13.0	13.1	17.3	14.9	19.5	6.7	7.8
POCJ13	KJ603229.1	40.4	100.0	77.8	40.8	40.8	40.2	40.2	39.5	40.2	41.1	46.9	40.0	40.0	39.9	39.1	40.9	41.7	41.7	41.5	42.4	42.2	42.1	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.2	42.3	42.3	42.2	44.7	44.7	8.8	9.6	11.2	9.8	2.8	2.0	2.0
75/02 Stx	KF766125.2	39.5	80.1	100.0	53.1	55.6	53.4	53.4	52.9	53.4	54.3	57.9	52.0	52.0	51.9	52.4	52.0	53.2	54.3	53.5	52.7	54.0	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.0	54.1	54.1	54.1	55.9	55.4	8.3	9.0	11.9	10.4	2.7	3.1	3.1
TL-2001c	JQ011318.1	43.6	42.1	53.5	100.0	91.6	89.8	89.8	89.2	89.8	90.8	83.3	83.9	84.0	83.9	58.4	57.8	62.2	62.4	62.4	61.4	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.6	62.7	62.7	62.6	58.7	58.2	9.0	10.7	8.5	5.1	2.4	1.2	1.6
P13771	HG792104.1	42.5	41.6	55.3	89.9	100.0	94.3	94.4	93.8	94.3	95.4	85.3	81.2	81.2	81.2	56.4	54.3	58.6	59.5	58.5	58.2	58.7	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.9	58.9	58.8	55.1	55.2	6.5	8.2	7.8	4.4	1.5	1.3	1.7
P13803	HG792102.1	42.2	41.3	53.4	89.0	95.3	100.0	100.0	99.4	99.9	99.8	84.0	80.5	80.5	80.5	55.5	53.4	58.2	58.4	58.0	58.5	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.3	58.2	54.3	54.4	7.2	9.0	7.6	3.8	1.6	0.2	0.6
P8983	HG792103.1	41.8	41.0	53.0	89.0	95.2	99.9	100.0	99.3	99.8	99.7	84.0	80.0	80.0	80.0	55.2	53.1	58.4	58.6	58.2	58.7	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	58.3	58.5	58.5	58.3	54.5	54.7	7.2	8.9	7.6	3.8	1.6	0.2	0.6
phi191	KF971864.1	42.1	40.6	52.8	88.3	94.6	99.3	99.3	100.0	99.2	99.1	83.2	79.9	79.9	79.9	55.2	52.7	57.4	58.0	57.3	57.8	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.4	53.6	53.9	7.2	8.9	7.5	3.6	1.6	0.2	0.6
P13374	HE664024.1	42.5	41.4	53.5	89.0	95.3	99.9	99.9	99.3	100.0	99.7	83.8	80.5	80.5	80.5	55.5	53.3	58.0	58.2	57.7	58.4	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	57.9	58.0	58.0	57.9	54.1	54.3	7.2	9.0	7.7	3.8	1.6	0.2	0.6
P14437	HG792105.1	41.8	41.7	54.2	89.2	95.5	98.9	98.9	98.3	98.9	100.0	84.6	80.0	80.0	80.0	55.0	53.0	57.5	57.8	57.3	58.0	57.7	57.6	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.6	57.8	57.8	57.6	53.9	54.0	7.3	9.0	7.4	3.9	1.5	0.2	0.5
Ss-VASD	KR781488.1	36.7	46.5	56.4	80.2	83.6	81.8	81.8	81.2	81.8	82.8	100.0	75.3	75.3	75.3	48.6	49.1	51.1	51.3	50.9	51.5	51.1	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	53.8	53.8	6.5	8.1	10.2	7.6	2.5	0.3	0.9
PA2	KP682371.1	45.3	39.0	49.9	79.4	78.4	77.1	77.1	76.6	77.1	77.1	74.2	100.0	99.7	99.7	65.3	57.1	59.7	60.2	59.5	59.0	61.6	61.6	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.6	59.6	59.6	61.6	56.0	55.9	10.9	11.7	10.8	6.3	4.6	1.4	1.9
PA8	KP682374.1	45.1	39.3	50.0	79.4	78.5	77.1	77.1	76.7	77.1	77.1	74.3	99.7	100.0	99.9	65.3	56.9	59.4	60.1	59.3	58.8	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	59.4	59.4	61.3	55.8	55.7	10.9	11.6	10.6	6.2	4.5	1.4	1.9
VT2phi_272	HQ424691.1	43.6	37.6	48.2	76.4	75.4	74.0	74.0	73.5	73.9	74.0	71.3	96.2	96.4	100.0	63.3	55.1	57.3	57.9	57.3	56.7	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.2	57.5	57.5	59.2	53.9	53.8	10.4	11.2	10.1	6.0	4.2	1.2	1.7
PA28	KP682381.1	59.0	39.9	52.4	57.9	56.6	55.3	55.3	54.8	55.2	55.1	50.0	69.6	69.6	69.6	100.0	67.2	68.8	73.4	72.5	68.5	73.3	73.4	73.4	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.4	69.9	69.9	73.4	65.7	64.4	25.1	24.2	26.5	16.7	20.5	10.0	10.5
vB_EcoP_24B	HM208303.1	62.0	44.2	55.1	60.4	57.9	56.3	56.3	55.8	56.3	56.3	53.5	63.0	63.0	62.9	71.3	100.0	91.3	81.4	82.5	74.0	75.3	75.3	75.4	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.4	75.5	75.5	75.4	73.2	70.7	18.5	18.6	24.9	19.0	22.4	7.9	8.6
Min27	EU311208.1	58.4	41.0	51.2	59.1	57.0	55.9	55.9	55.4	55.9	55.9	51.0	60.3	60.2	60.2	66.9	84.0	100.0	89.5	90.6	83.4	84.0	84.0	84.0	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.0	84.2	84.2	84.0	80.0	78.4	19.6	19.6	23.8	18.3	21.9	7.5	8.2
Stx2 I	AP004402.1	60.2	42.0	53.8	61.1	59.2	57.7	57.7	57.4	57.6	57.6	52.3	62.3	62.2	62.2	72.9	77.0	92.1	100.0	98.8	84.0	85.2	85.2	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.4	85.4	85.4	85.4	81.3	80.0	20.0	20.2	29.7	17.3	25.1	10.2	11.1
933W	AF125520	59.7	41.8	53.0	61.1	58.3	57.2	57.2	56.9	57.2	57.2	52.2	61.8	61.7	61.7	72.3	78.2	93.2	98.8	100.0	85.1	86.3	86.3	86.4	86.5	86.5	86.5	86.5	86.5	86.5	86.5	86.5	86.5	86.5	86.5	86.5	86.4	86.5	86.5	86.4	82.2	80.8	19.9	20.2	30.7	18.3	25.0	10.5	11.3
VT2-Sakai	AP000363.1	57.1	43.9	52.8	60.9	58.8	58.4	58.4	57.9	58.4	58.4	53.3	61.9	61.9	61.9	69.1	70.8	86.7	84.9	86.0	100.0	99.0	99.0	99.1	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.1	99.2	99.2	99.1	95.0	92.3	27.1	27.4	23.0	24.5	15.4	6.8	8.1
PA45	KP682389.1	54.1	40.1	50.5	57.9	55.5	54.3	54.3	53.8	54.2	54.2	49.2	64.3	64.3	64.2	71.5	67.3	81.6	80.5	81.5	92.6	100.0	99.5	99.6	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.6	93.9	93.9	99.6	89.9	86.7	31.2	31.5	26.4	22.7	19.4	7.3	8.6
PA52	KP682392.1	53.9	40.2	50.4	57.9	55.4	54.3	54.3	53.8	54.3	54.2	49.3	64.3	64.3	64.3	71.5	67.4	81.6	80.5	81.6	92.6	99.5	100.0	99.8	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.6	94.0	94.0	99.6	89.9	86.7	31.2	31.5	26.7	22.6	19.5	7.3	8.5
PA27	KP682380.1	55.1	40.9	51.5	59.2	56.6	55.4	55.4	54.8	55.4	55.4	50.5	63.7	63.6	63.6	71.0	68.8	83.3	82.2	83.3	94.5	99.7	99.9	100.0	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.7	95.9	95.9	99.8	91.8	88.5	29.8	30.1	25.3	23.1	18.1	7.4	8.7
PA42	KP682387.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA21	KP682379.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA32	KP682384.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA5	KP682373.1	56.1	42.0	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA11	KP682375.1	56.1	42.0	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.7	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA4	KP682372.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA18	KP682378.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA30	KP682383.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA33	KP682385.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA44	KP682388.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA29	KP682382.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA50	KP682390.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.8	24.1	23.6	16.8	7.6	8.9
PA16	KP682377.1	56.1	42.1	52.7	60.5	57.9	56.8	56.8	56.2	56.8	56.8	51.6	62.9	62.9	62.9	70.4	70.3	85.1	83.9	85.0	96.4	99.8	99.8	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	97.9	97.9	99.9	93.7	90.3	28.4	28.7	24.1	23.6	16.8	7.6	8.9
Stx2 II	AP005154.1	56.2	42.1	52.9	60.6	57.9	56.8	56.8	56.4	56.8	56.8	51.6	62.6	62.6	62.6	70.3	70.2	85.1	84.0	85.0	96.4	99.8	99.7	99.8	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	100.0	97.8	97.8	99.8	93.7	90.4	28.5	28.7	24.2	23.6	16.8	7.5	8.9
PA12	KP682376.1	57.5	42.9	54.0	61.8	59.1	58.1	58.1	57.5	58.0	58.0	52.8	62.0	62.0	62.0	69.7	71.8	86.9	85.6	86.8	98.5	99.7	99.8	99.8	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.8	100.0	100.0	99.8	95.6	92.2	27.1	27.4	22.9	24.2	15.4	7.7	9.0
PA51	KP682391.1	57.5	42.9	54.0	61.8	59.1	58.1	58.1	57.5	58.0	58.0	52.8	62.0	62.0	62.0	69.7	71.8	86.9	85.6	86.8	98.5	99.7	99.8	99.8	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.8	100.0	100.0	99.8	95.6	92.2	27.1	27.4	22.9	24.2	15.4	7.7	9.0
PA36	KP682386.1	54.8	41.2	51.4	59.2	56.7	55.6	55.6	55.0	55.6	55.6	50.4	63.5	63.5	63.5	70.9	68.8	83.3	82.1	83.3	94.5	99.7	99.7	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.7	95.9	95.9	100.0	91.7	88.5	29.9	30.2	25.5	23.1	18.2	7.4	8.7
HUN/2013	KJ909655.1	54.0	45.2	55.5	58.1	55.4	54.0	54.0	53.5	53.9	53.9	55.4	58.7	58.7	58.7	66.2	69.8	82.9	81.8	82.8	94.8	95.9	95.9	96.0	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.0	100.0	96.5	24.9	25.2	25.3	26.7	15.2	7.8	9.1
Sx1	AP005153.1	54.3	46.6	56.8	58.9	56.9	55.6	55.6	55.3	55.6	55.6	56.6	59.7	59.7	59.6	66.0	68.9	83.0	82.2	83.2	94.0	94.4	94.5	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.5	98.5	100.0	22.7	23.0	24.6	25.8	14.1	7.9	9.3
Stx2 1717	FJ188381.1	12.5	8.9	8.2	8.6	6.5	7.1	7.1	7.0	7.1	7.1	6.4	11.1	11.1	11.1	23.1	17.2	19.1	19.1	19.0	26.1	28.2	28.2	28.2	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	28.3	26.3	26.3	28.3	24.2	21.4	100.0	84.9	50.9	59.2	50.0	8.8	10.1
2851	FM180578.1	13.7	10.7	9.8	10.9	8.5	9.1	9.1	9.0	9.1	9.1	8.5	12.8	12.8	12.8	24.2	19.1	21.1	21.0	20.9	28.8	31.1	31.1	31.1	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	29.0	29.0	29.0	31.2	26.5	23.4	92.4	100.0	55.6	66.6	56.8	9.1	10.6
BP-4795	AJ556162.1	18.1	12.1	12.7	8.9	8.6	8.0	8.0	7.8	8.0	8.0	11.3	13.5	13.5	13.4	28.3	24.8	25.1	30.8	31.8	23.5	27.1	27.1	27.1	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	23.5	23.5	27.2	26.1	24.7	56.4	57.2	100.0	59.3	65.4	11.0	11.6
YYZ-2008	FJ184280.1	16.6	11.3	11.6	5.8	5.1	4.5	4.5	4.3	4.5	4.5	8.7	7.2	7.2	7.2	18.6	20.5	20.5	18.8	19.8	26.9	26.4	26.5	26.5	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	26.6	29.2	27.6	67.2	69.7	62.3	100.0	59.0	8.9	10.5
JLK-2012	JQ347801.1	20.6	3.3	3.1	2.6	1.6	1.7	1.7	1.7	1.7	1.7	2.9	5.0	5.0	5.0	20.0	22.9	23.5	26.2	26.1	15.8	17.7	17.6	17.6	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	15.8	15.8	17.7	15.7	14.0	54.4	56.8	64.3	56.3	100.0	11.8	12.8
DE3	EU078592.1	9.5	3.1	4.3	1.7	1.8	0.3	0.3	0.3	0.3	0.3	0.4	1.9	1.9	1.9	14.3	10.4	10.6	14.3	14.6	9.4	10.8	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	12.8	12.4	14.7	11.4	15.5	100.0	84.9
Lambda	KT232076.1	9.7	2.7	3.9	1.9	2.0	0.6	0.6	0.6	0.6	0.6	1.0	2.4	2.4	2.4	13.0	10.2	10.4	13.6	13.8	10.0	11.3	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.3	11.3	11.4	11.4	11.4	11.1	11.3	12.8	12.5	13.8	11.6	14.6	75.3	100.0

Table 1. Properties of the two phages belonging to the genus *Nona33virus*.

Escherichia phage	RefSeq No.	GenBank Accession No.	Genome length (kb)	Genome (mol% G+C)	No. tRNAs	No. CDS	DNA (% sequence identity)*	% Homologous proteins **
933W	NC_000924	AF125520	61.67	49.4	3	80	100	100
PA28		KP682381	61.29	49.7	3	90	79	73.8
vB_EcoP_24B	NC_027984	HM208303	57.68	49.7	3	88	79	77.5
Min27	NC_010237	EU311208	63.40	49.5	3	83	93	87.5
Stx2 II	NC_004914	AP005154	61.71	49.9	3***	#	87	86.3
TL-2011c****							65	50.0

* Determined using BLASTN; ** Determined using CoreGenes [2]; *** none indicated in GenBank; # overannotated; **** type phage of another genus within this subfamily

Table 2. Properties of the three phages belonging to the genus *TL2011virus*.

Phage	RefSeq No.	GenBank Accession No.	Genome length (kb)	Genome (mol% G+C)	No. tRNAs	No. CDS	DNA (% sequence identity)*	% Homologous proteins **
Escherichia phage TL-2011c	NC_019442	JQ011318.1	60.52	50.3	3***	72	100	100
Escherichia phage phi191		KF971864.1	61.03	50.2	3	87	93	88.3
Shigella phage Ss-VASD		KR781488.1	62.85	50.1	0	74	91	84.7
Escherichia phage PA2		KP682371.1	63.57	50.2	3	84	86	81.9
933W****							67	55.6

* Determined using BLASTN; ** Determined using CoreGenes [2]; *** none indicated in GenBank; **** type phage of another genus within this subfamily

Table 3. Properties of the two phages which belong to the *Pocjvirus* genus.

Shigella phage	RefSeq No.	GenBank Accession No.	Genome length (kb)	Genome (mol% G+C)	No. tRNAs	No. CDS	DNA (% sequence identity)*	% Homologous proteins **
POCJ13	NC_025434.1	KJ603229.1	62.70	49.3	0	79	100	100
75/02 Stx		KF766125.2	60.88	49.1	0	76	91	91.1
933W***							58	54.4

* Determined using BLASTN; ** Determined using CoreGenes [2]; *** type phage of another genus within this subfamily

Table 4. Phages which should be considered strains within the subfamily *Sepvirinae*.

Phage	**Accession No.**	**Strain of**
P13771	HG792104.1	Escherichia phage phi191
P13803	HG792102.1	Escherichia phage phi191
P8983	HG792103.1	Escherichia phage phi191
P13374	HE664024.1	Escherichia phage phi191
P14437	HG792105.1	Escherichia phage phi191
PA8	KP682374.1	Escherichia phage PA2
Stx2 I	AP004402.1	Escherichia phage Stx2 II
VT2-Sakai	AP000363.1	Escherichia phage Stx2 II
PA45	KP682389.1	Escherichia phage Stx2 II
PA52	KP682392.1	Escherichia phage Stx2 II
PA27	KP682380.1	Escherichia phage Stx2 II
PA42	KP682387.1	Escherichia phage Stx2 II
PA21	KP682379.1	Escherichia phage Stx2 II
PA32	KP682384.1	Escherichia phage Stx2 II
PA5	KP682373.1	Escherichia phage Stx2 II
PA11	KP682375.1	Escherichia phage Stx2 II
PA4	KP682372.1	Escherichia phage Stx2 II
PA18	KP682378.1	Escherichia phage Stx2 II
PA30	KP682383.1	Escherichia phage Stx2 II
PA33	KP682385.1	Escherichia phage Stx2 II
PA44	KP682388.1	Escherichia phage Stx2 II
PA29	KP682382.1	Escherichia phage Stx2 II
PA50	KP682390.1	Escherichia phage Stx2 II
PA16	KP682377.1	Escherichia phage Stx2 II
PA12	KP682376.1	Escherichia phage Stx2 II
PA51	KP682391.1	Escherichia phage Stx2 II
PA36	KP682386.1	Escherichia phage Stx2 II
HUN/2013	KJ909655.1	Escherichia phage Stx2 II
Stx1	AP005153.1	Escherichia phage Stx2 II

Table 5. Common proteins of members of each of the genera. These were discovered using CoreGenes 3.1 (CGUG; http://binf.gmu.edu:8080/CoreGenes3.1/).

A. *Nona33virus*

Enterobacteria phage 933W	Escherichia phage PA28	Stx2 converting phage vB_EcoP_24B	Enterobacteria phage Min27	Stx2 converting phage II
AF125520	KP682381	HM208303	EU311208	AP005154
GI:4585387	GI:824464774	GI:307604087	GI:163955714	GI:32128278
GI:4585388	GI:824464761	GI:307604088	GI:163955715	GI:32128279
GI:4585390	GI:824464776	GI:307604091	GI:163955717	GI:32128282
GI:4585391	GI:824464777	GI:307604092	GI:163955718	GI:32128285
GI:4585392	GI:824464778	GI:307604093	GI:163955719	GI:32128289
GI:4585393	GI:824464779	GI:307604094	GI:163955720	GI:32128290
GI:4585394	GI:824464780	GI:307604095	GI:163955721	GI:32128291
GI:4585404	GI:824464787	GI:307604105	GI:163955731	GI:32128303
GI:4585410	GI:824464795	GI:307604112	GI:163955737	GI:32128312
GI:4585411	GI:824464796	GI:307604113	GI:163955738	GI:32128313
GI:4585413	GI:824464800	GI:307604117	GI:163955740	GI:32128317
GI:4585414	GI:824464801	GI:307604118	GI:163955741	GI:32128319
GI:4585415	GI:824464802	GI:307604119	GI:163955742	GI:32128320
GI:4585416	GI:824464803	GI:307604120	GI:163955743	GI:32128321
GI:4585417	GI:824464805	GI:307604121	GI:163955744	GI:32128324
GI:4585419	GI:824464809	GI:307604125	GI:163955746	GI:32128326
GI:4585420	GI:824464813	GI:307604127	GI:163955748	GI:32128336
GI:4585421	GI:824464814	GI:307604128	GI:163955749	GI:32128337
GI:4585422	GI:824464815	GI:307604129	GI:163955750	GI:32128339
GI:4585423	GI:824464816	GI:307604130	GI:163955751	GI:32128341
GI:4585424	GI:824464818	GI:307604131	GI:163955752	GI:32128343
GI:4585426	GI:824464819	GI:307604133	GI:163955753	GI:32128347
GI:4585427	GI:824464821	GI:307604135	GI:163955754	GI:32128349
GI:4585428	GI:824464822	GI:307604136	GI:163955755	GI:32128351
GI:4585429	GI:824464823	GI:307604137	GI:163955756	GI:32128181
GI:4585430	GI:824464824	GI:307604139	GI:163955758	GI:32128185
GI:4585431	GI:824464825	GI:307604140	GI:163955759	GI:32128187
GI:4585432	GI:824464826	GI:307604142	GI:163955760	GI:32128190
GI:4585433	GI:824464827	GI:307604144	GI:163955761	GI:32128193
GI:4585434	GI:824464828	GI:307604145	GI:163955762	GI:32128194
GI:4585435	GI:824464829	GI:307604147	GI:163955763	GI:32128196
GI:4585436	GI:824464830	GI:307604148	GI:169412289	GI:32128199
GI:4585437	GI:824464831	GI:307604150	GI:163955765	GI:32128207
GI:4585438	GI:824464835	GI:307604151	GI:163955766	GI:32128208

GI:4585439	GI:824464837	GI:307604152	GI:163955767	GI:32128209
GI:4585440	GI:824464838	GI:307604153	GI:163955769	GI:32128212
GI:4585442	GI:824464840	GI:307604155	GI:163955770	GI:32128216
GI:4585443	GI:824464841	GI:307604156	GI:163955771	GI:32128217
GI:4585444	GI:824464842	GI:307604157	GI:163955772	GI:32128219
GI:4585445	GI:824464843	GI:307604158	GI:163955773	GI:32128221
GI:4585446	GI:824464844	GI:307604159	GI:163955774	GI:32128224
GI:4585447	GI:824464845	GI:307604160	GI:163955775	GI:32128225
GI:4585448	GI:824464846	GI:307604161	GI:169412290	GI:32128227
GI:4585449	GI:824464847	GI:307604162	GI:163955777	GI:32128229
GI:4585456	GI:824464773	GI:307604086	GI:163955785	GI:32128257
GI:4585457	GI:824464765	GI:307604116	GI:163955739	GI:32128259

N.B. GI = GenInfo Identifier

B. *T2011virus*

Escherichia phage TL-2011c	**Escherichia phage phi191**	**Shigella phage Ss-VASD**	**Escherichia phage PA2**
JQ011318	KF971864	KR781488	KP682371
GI:363498319	GI:584590932	GI:857292479	GI:824463360
GI:363498320	GI:584590931	GI:857292480	GI:824463361
GI:363498296	GI:584590930	GI:857292481	GI:824463362
GI:363498321	GI:584590929	GI:857292482	GI:824463366
GI:363498323	GI:584590927	GI:857292485	GI:824463373
GI:363498327	GI:584590923	GI:857292491	GI:824463382
GI:363498298	GI:584590921	GI:857292492	GI:824463383
GI:363498328	GI:584590920	GI:857292493	GI:824463384
GI:363498329	GI:584590918	GI:857292494	GI:824463385
GI:363498299	GI:584590917	GI:857292495	GI:824463386
GI:363498365	GI:584590916	GI:857292496	GI:824463387
GI:363498330	GI:584590915	GI:857292497	GI:824463388
GI:363498331	GI:584590914	GI:857292498	GI:824463389
GI:363498300	GI:584590913	GI:857292499	GI:824463390
GI:363498332	GI:584590911	GI:857292500	GI:824463367
GI:363498301	GI:584590886	GI:857292501	GI:824463391
GI:363498302	GI:584590909	GI:857292502	GI:824463392
GI:363498303	GI:584590908	GI:857292503	GI:824463393
GI:363498304	GI:584590906	GI:857292504	GI:824463394

GI:363498333	GI:584590905	GI:857292505	GI:824463395
GI:363498334	GI:584590904	GI:857292506	GI:824463397
GI:363498305	GI:584590903	GI:857292507	GI:824463398
GI:363498306	GI:584590902	GI:857292508	GI:824463399
GI:363498335	GI:584590901	GI:857292509	GI:824463400
GI:363498336	GI:584590899	GI:857292510	GI:824463401
GI:363498307	GI:584590898	GI:857292511	GI:824463402
GI:363498308	GI:584590897	GI:857292512	GI:824463403
GI:363498309	GI:584590896	GI:857292513	GI:824463405
GI:363498310	GI:584590895	GI:857292514	GI:824463406
GI:363498337	GI:584590893	GI:857292516	GI:824463407
GI:363498340	GI:584590892	GI:857292517	GI:824463410
GI:363498311	GI:584590891	GI:857292518	GI:824463411
GI:363498312	GI:584590890	GI:857292519	GI:824463412
GI:363498341	GI:584590887	GI:857292522	GI:824463414
GI:363498314	GI:584590885	GI:857292526	GI:824463417
GI:363498316	GI:584590970	GI:857292528	GI:824463419
GI:363498342	GI:584590969	GI:857292529	GI:824463420
GI:363498344	GI:584590967	GI:857292530	GI:824463421
GI:363498345	GI:584590966	GI:857292531	GI:824463422
GI:363498346	GI:584590965	GI:857292532	GI:824463423
GI:363498347	GI:584590964	GI:857292533	GI:824463424
GI:363498348	GI:584590962	GI:857292534	GI:824463425
GI:363498350	GI:584590961	GI:857292535	GI:824463426
GI:363498353	GI:584590959	GI:857292537	GI:824463430
GI:363498354	GI:584590958	GI:857292538	GI:824463431
GI:363498355	GI:584590956	GI:857292540	GI:824463433
GI:363498317	GI:584590955	GI:857292541	GI:824463434
GI:363498357	GI:584590953	GI:857292542	GI:824463436
GI:363498358	GI:584590951	GI:857292543	GI:824463437
GI:363498359	GI:584590950	GI:857292544	GI:824463438
GI:363498360	GI:584590949	GI:857292545	GI:824463439
GI:363498361	GI:584590946	GI:857292546	GI:824463440
GI:363498363	GI:584590938	GI:857292547	GI:824463441

N.B. GI = GenInfo Identifier

C. *Pocj13virus*

Shigella phage POCJ13	Shigella phage 75/02 Stx
KJ603229	KF766125
GI:636483635	GI:873278923
GI:636483636	GI:564271506
GI:636483637	GI:564271505
GI:636483638	GI:564271504
GI:636483639	GI:564271503
GI:636483640	GI:564271502
GI:636483641	GI:564271501
GI:636483642	GI:564271500
GI:636483643	GI:564271499
GI:636483644	GI:564271498
GI:636483646	GI:564271497
GI:636483647	GI:873278924
GI:636483648	GI:564271495
GI:636483649	GI:564271494
GI:636483650	GI:564271493
GI:636483651	GI:564271492
GI:636483652	GI:564271491
GI:636483713	GI:564271490
GI:636483653	GI:564271489
GI:636483654	GI:564271488
GI:636483655	GI:564271487
GI:636483656	GI:564271486
GI:636483657	GI:564271485
GI:636483658	GI:564271484
GI:636483659	GI:873278925
GI:636483660	GI:564271481
GI:636483661	GI:564271480
GI:636483662	GI:564271479
GI:636483663	GI:564271478
GI:636483664	GI:564271477
GI:636483665	GI:564271476
GI:636483666	GI:564271475
GI:636483667	GI:564271474
GI:636483668	GI:564271473

GI:636483670	GI:873278926
GI:636483671	GI:564271549
GI:636483672	GI:564271548
GI:636483673	GI:873278927
GI:636483674	GI:564271546
GI:636483675	GI:564271544
GI:636483676	GI:564271543
GI:636483679	GI:873278929
GI:636483680	GI:564271540
GI:636483681	GI:873278930
GI:636483682	GI:564271538
GI:636483683	GI:564271537
GI:636483684	GI:564271536
GI:636483685	GI:564271535
GI:636483686	GI:873278931
GI:636483687	GI:564271533
GI:636483688	GI:564271532
GI:636483689	GI:564271531
GI:636483690	GI:873278932
GI:636483693	GI:564271528
GI:636483694	GI:564271527
GI:636483695	GI:564271526
GI:636483696	GI:564271525
GI:636483697	GI:564271524
GI:636483698	GI:564271523
GI:636483699	GI:564271522
GI:636483700	GI:564271521
GI:636483701	GI:564271520
GI:636483702	GI:564271519
GI:636483703	GI:564271518
GI:636483704	GI:564271517
GI:636483705	GI:564271516
GI:636483707	GI:564271515
GI:636483708	GI:564271514
GI:636483709	GI:564271513
GI:636483710	GI:564271512
GI:636483711	GI:564271510
GI:636483712	GI:564271509

N.B. GI = GenInfo Identifier

Table 6. Genus-specific proteins i.e. the indicated proteins are restricted to the genus indicated within the subfamily *Sepvirinae*. In a number of cases, such as with the Kil protein, homologs are found outside of this subfamily.

Genus	**Diagnostic proteins of member viruses**
Pocjvirus	exodeoxyribonuclease VIII (YP_009100228), DNA replication protein (YP_009100239), Kil protein (YP_009100230), Holliday junction resolvase (YP_009100252), hypothetical protein (YP_009100232) and LygF (YP_009100241)
T2011virus	hypothetical proteins (YP_007001437, YP_007001436, YP_007001434, YP_007001427, YP_007001435), primase (YP_006906854), helicase (YP_006906853), DNA methylase (YP_006906848, YP_007001426), type II restriction endonuclease (YP_007001445), phage regulatory protein, Rha family (YP_007001444)
Nona33virus	hypothetical proteins (NP_049470, NP_049539), Kil protein (NP_049476), regulatory protein CIII (NP_049477), NinB protein (NP_613010), DNA N-6-adenine methyltransferase (NP_049494), DNA-binding protein Roi (NP_049496)

Fig. 3. progressiveMauve alignment [1] of the genomes of members of the *Nona33virus* genus – from top to bottom: Escherichia phage 933W, Escherichia phage PA28, Escherichia phage vB_EcoP_24B, Escherichia phage Min27 and Escherichia phage Stx2 II. 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. Not all the genomes are co-linear.

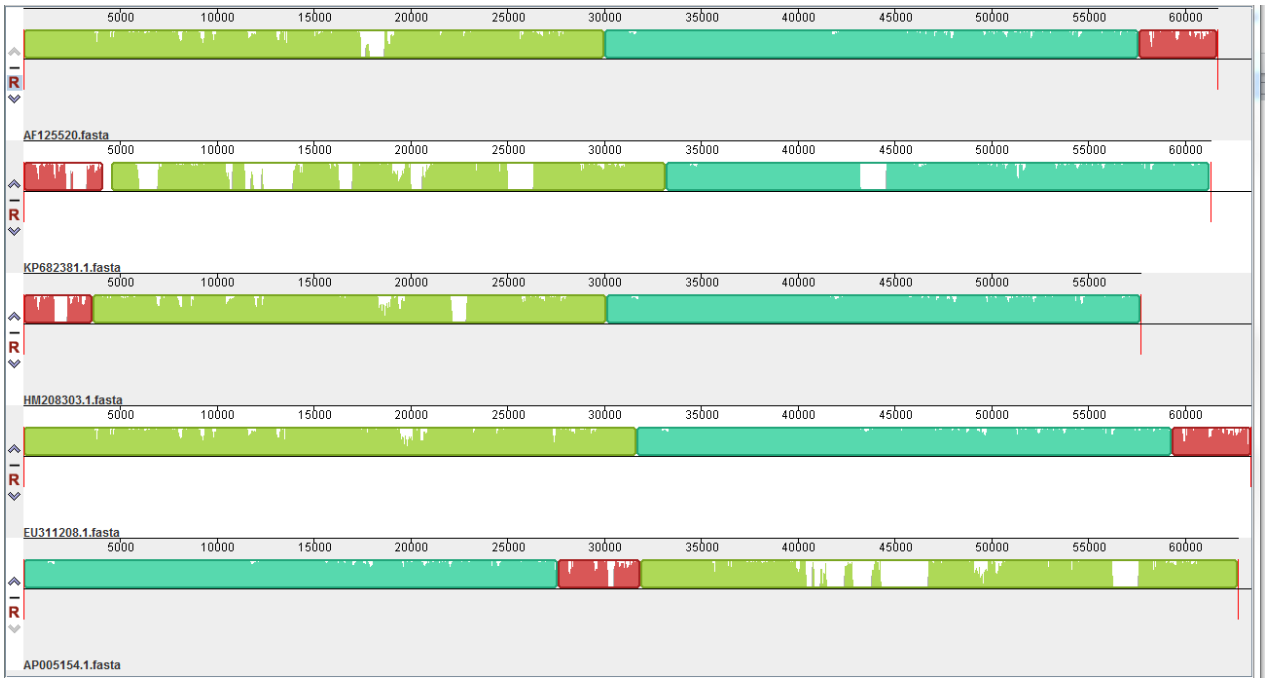


Fig. 4. progressiveMauve alignment [1] of the genomes of members of the *T2011virus* genus – from top to bottom: Escherichia phage TL-2011c, Escherichia phage phi191, Shigella phage Ss-VASD, and Escherichia phage PA2. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints 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). Please note that the second sequence is inverted relative to the others.

Fig. 5. progressiveMauve alignment [1] of the genomes of Shigella phage POCJ13 (TOP) compared with Shigella phage 75/02 Stx (BOTTOM). 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).

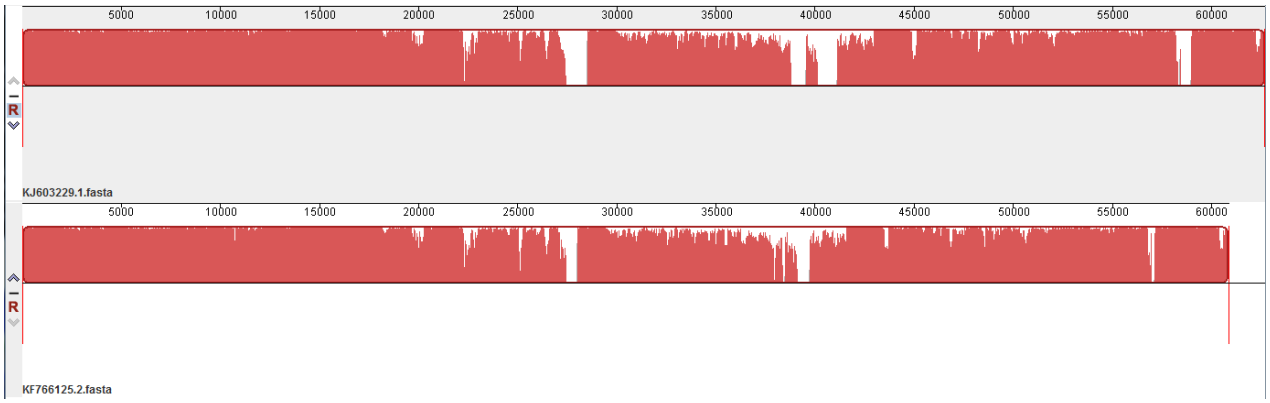
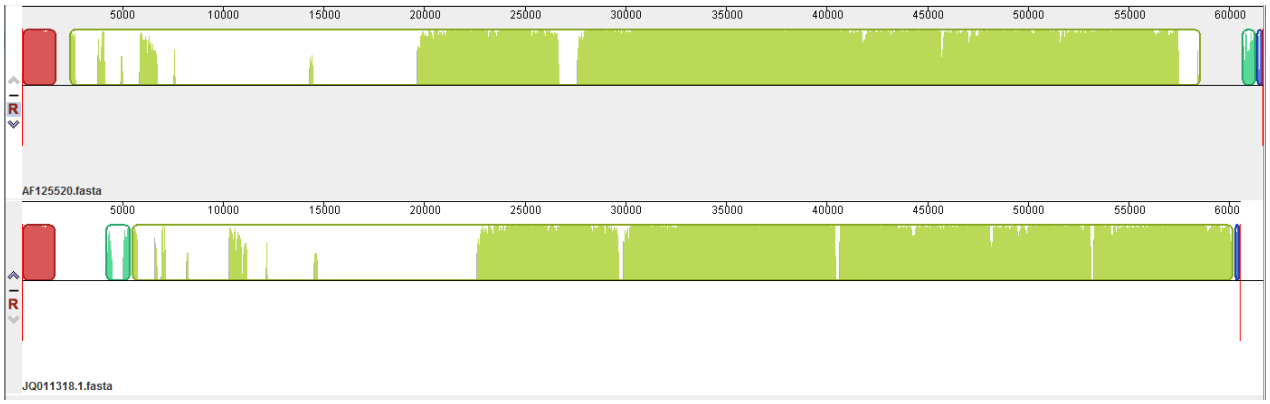


Fig. 6. COMPARATIVE GENOMICS A. progressiveMauve alignment [1] of the genomes of Escherichia phage 933W (TOP) compared with Escherichia phage TL-2011c (BOTTOM) indicating that only the right end of the genome, which encodes TerL and the major capsid protein, is conserved. Colored blocks indicate the 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).



B. progressiveMauve alignment [1] of the genomes of Shigella phage POCJ13 (TOP) compared with Escherichia phage 933W (BOTTOM).

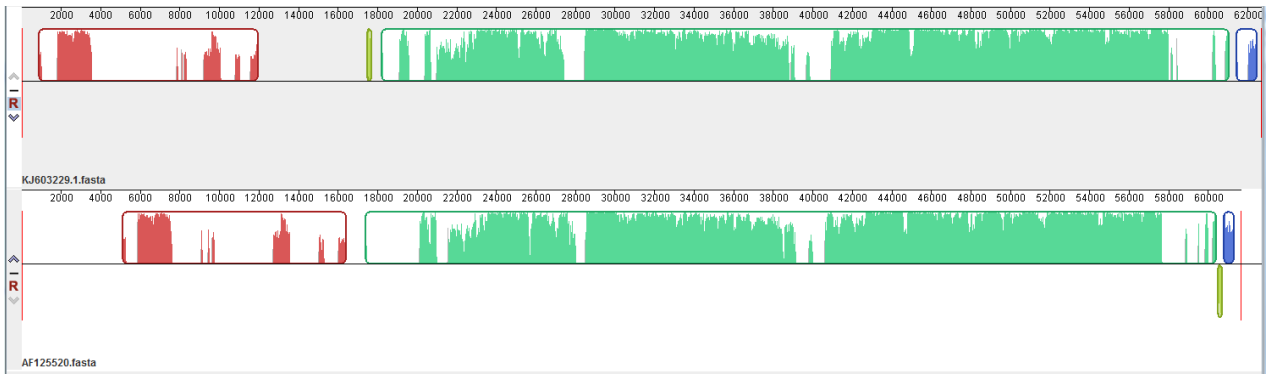
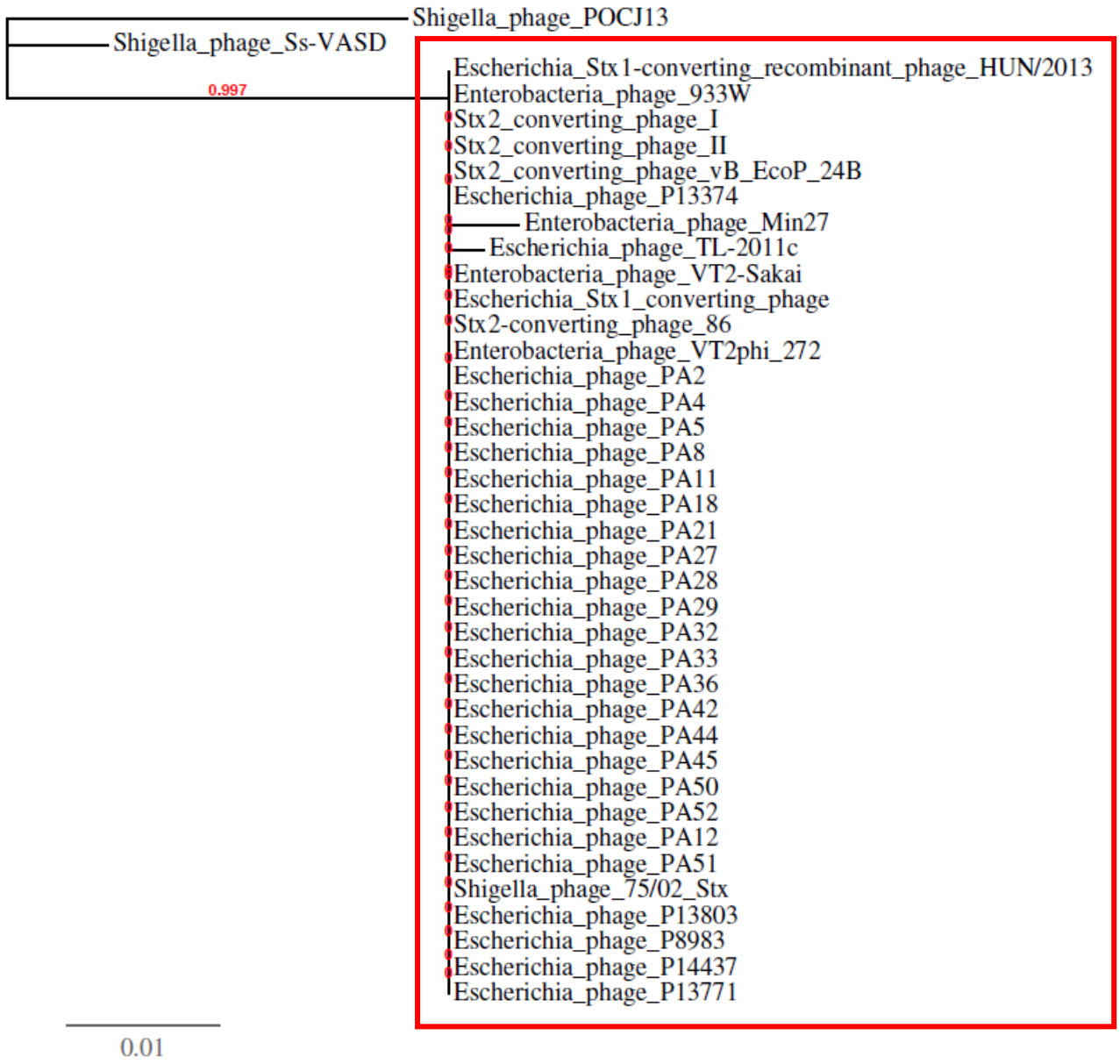


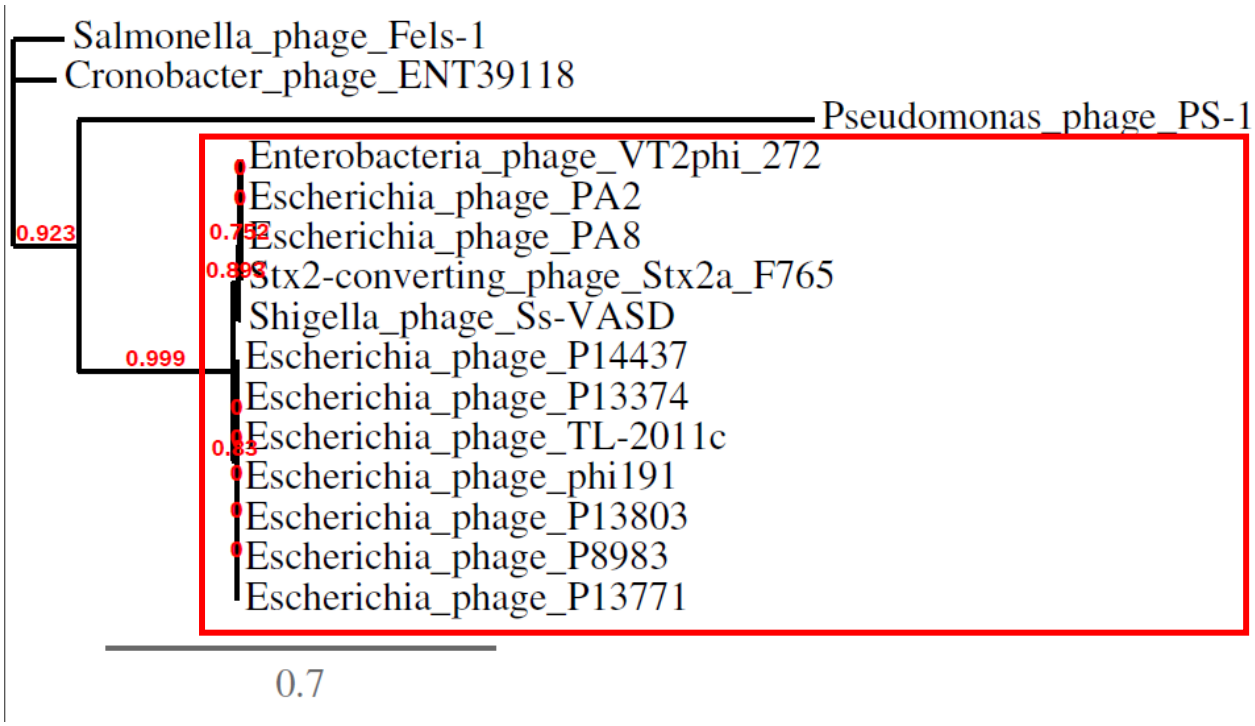
Fig. 7. Phylogenetic analysis of the large subunit terminase (A) major coat (B) and helicase proteins (C) of Escherichia 933W-like viruses and homologous proteins from a variety of other phages constructed using “one click” at phylogeny.fr [3]. "The "One Click mode" targets users that do not wish to 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."

A. TerL



B. Major capsid protein

C. Helicase


Salmonella_phage_Fels-1
Cronobacter_phage_ENT39118
Pseudomonas_phage_PS-1
Enterobacteria_phage_VT2phi_272
Escherichia_phage_PA2
Escherichia_phage_PA8
Stx2-converting_phage_Stx2a_F765
Shigella_phage_Ss-VASD
Escherichia_phage_P14437
Escherichia_phage_P13374
Escherichia_phage_TL-2011c
Escherichia_phage_phi191
Escherichia_phage_P13803
Escherichia_phage_P8983
Escherichia_phage_P13771
0.923
0.999
0.7