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:	***2015.023a-oB***	(to be completed by ICTV officers)

Short title: To create one (1) new subfamily, *Vequintavirinae*, including three (3) new genera within 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)	Bacterial & Archaeal Virus Subcommittee

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

Please note that we have chosen to refer to the new genera as *V5virus* rather than *V5likevirus*, etc. since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" from phage genus names.

Date first submitted to ICTV: May 2015
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	***2015.023aB***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***V5virus* (new)**
Subfamily:	***Vequintavirinae* (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 V5	Escherichia phage V5	DQ832317
Escherichia virus JES2013	Escherichia phage JES2013	KC690136
Escherichia virus FV3	Escherichia phage FV3	JQ031132
Escherichia virus FFH2	Escherichia phage FFH2	KJ190158

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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

Please note that we have chosen to refer to this new genus as *V5virus* rather than *V5likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" from phage genus names.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

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

Code	***2015.023bB***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Se1virus* (new)**
Subfamily:	***Vequintavirinae* (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)**
Salmonella virus SE1	Salmonella phage SE1	GU070616
Salmonella virus SSE121	Salmonella phage SSE121	JX181824
Escherichia virus 4MG	Escherichia phage 4MG	KF550303
Cronobacter virus GAP31	Cronobacter phage vB_CsaM_GAP31	JN882284

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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

Please note that we have chosen to refer to this new genus as *Se1virus* rather than *Se1likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" from phage genus names. Since the initials PVP have been used by isolators of the type species in the names of other viruses they have chosen not to include them in the genus or species names.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

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

Code	***2015.023cB***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Cr3virus* (new)**
Subfamily:	***Vequintavirinae* (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)**
Cronobacter virus CR3	Cronobacter phage CR3	JQ691612
Cronobacter virus CR8	Cronobacter phage CR8	KC954774
Cronobacter virus CR9	Cronobacter phage CR9	JQ691611

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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

Please note that we have chosen to refer to this new genus as *Cr3virus* rather than *Cr3likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" from phage genus names.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.023dB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Vequintavirinae* (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	***2015.023eB***	(assigned by ICTV officers)

To name the new genus: *V5virus*

Assigning the type species and other species to a new genus

Code	***2015.023fB***	(assigned by ICTV officers)

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

Escherichia virus V5	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, CoreGenes and phylogenetic analyses all indicate that the proposed genus, V5virus, is cohesive and distinct from the other genera in the proposed subfamily. The next closest member is Salmonella phage PVP-SE1 which shares only 12% DNA sequence identity. The phages of this genus possess genome of approx. 138 kb (44 mol%G+C), and encode 222 proteins and 5 tRNAs. They share 88-93% DNA sequence identity and 88-91% homologous proteins (Table 1). Figure 4 derived from progressiveMauve analysis reveals the overall sequence similarity between the members of this genus.

Phage rV5 possesses "an icosahedral head of 91 nm between opposite apices. The extended tail measures 121 x 17 nm and has a sheath of 44 x 20 nm and a 7 nm-wide core in the contracted state." (1). FV3 "has an isometric head of 85 nm in apical diameter and a necked contractile tail of 120 by 18 nm in the extended form. FV3 has six slightly kinked 60-nm-long tail fibers connected to the baseplate" (5).

Origin of the new genus name:

Escherichia phage rV5; please note that the actual name of the bacteriophage is V5, and the "r" stands for "recovered" since the sequenced strain was reisolated from a phage therapy trial with V5. Therefore, we have not chosen to call the genus the *Rv5virus*.

Reasons to justify the choice of type species:

The first virus of its type that was sequenced

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. Each of the proposed species differs from the others with 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	***2015.023gB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Vequintavirinae* (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	***2015.023hB***	(assigned by ICTV officers)

To name the new genus: *Se1virus*

Assigning the type species and other species to a new genus

Code	***2015.023iB***	(assigned by ICTV officers)

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

Salmonella virus SE1

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

Phylogenetic analyses indicates a cohesive group composed of five phage, but BLASTN and CoreGenes analyses reveals only a peripheral relationship of phage Av-05. The phages of this genus possess genome of approx. 148 kb (46 mol%G+C), and encode 257 proteins and 24 tRNAs. They share 64-95% DNA sequence identity and 82-91% homologous proteins (Table 2). Other than phage Av-05 the next closest member is *Escherichia* phage rV5 which shares only 11% DNA sequence identity. Figure 5 derived from progressiveMauve analysis reveals the overall sequence similarity between the members of this genus.

The type virus *Salmonella* phage (PVP-)SE1 "is characterized by an icosahedral head with an 84-nm-diameter apex and a contractile tail of 120 by 18 nm with short tail fibers" (2); while *Escherichia* phage 4MG has been reported to possess "an isometric head with an apical diameter of 94 nm and a long contractile tail of 121 by 18 nm (n = 8) with five to six thin tail fibers." (8). *Cronobacter* phage GAP31 has "an icosahedral head 83 nm in diameter and a tail of 107 by 19 nm" (7).

Origin of the new genus name:

Salmonella phage PVP-SE1

Reasons to justify the choice of type species:

The first virus of its type to be sequenced (2)

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. Each of the proposed species differs from the others with 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	***2015.023jB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Vequintavirinae* (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	***2015.023kB***	(assigned by ICTV officers)

To name the new genus: *Cr3virus*

Assigning the type species and other species to a new genus

Code	***2015.023lB***	(assigned by ICTV officers)

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

Cronobacter virus CR3

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

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

3

Reasons to justify the creation of a new genus:

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

Phylogenetic analysis using "One click" phylogeny.fr (13) of the terminase large subunit, DNA polymerase and major capsid proteins reveals a tight cluster of three lytic *Cronobacter sakazakii* phages with the *Pectobacterium atrosepticum* generalized transducing virus, phage phiTE (Fig. 1, 2, 3).

While BLASTN and CoreGenes analyses reveals that *Cronobacter sakazakii* phages CR3, CR8 and clearly closely related (Table 3; Fig. 6). The average genome size is 150 kb (51 mol%G+C), encoding 275 proteins and 17 tRNAs. *Pectobacterium* phage phTE differs in mass, tRNA content and protein homologs (Table 3) and we have chosen, at this time, to exclude this virus from this genus. The next most closely related type species is *Salmonella* phage PVP-SE1 which only shares 8% DNA sequence identity with *Cronobacter* phage CR3.

Origin of the new genus name:

Cronobacter phage CR3

Reasons to justify the choice of type species:

The first member of this genus to be described fully

Species demarcation criteria in the new genus:

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

We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

MODULE 4: **NEW SUBFAMILY**

creating a new subfamily

A subfamily can only be created within a family.

Code	***2015.023mB***	(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	***2015.023nB***	(assigned by ICTV officers)

To name the new subfamily: *Vequintavirinae*

genera and species assigned to the new subfamily

Code	***2015.023oB***	(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

V5virus **(new)**

Se1virus **(new)**

Cr3virus **(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):**

Reasons to justify the creation of the new subfamily:

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

The authors of references 1, 2, and 4-9 all mention that their virulent phage isolates are members of the *Myoviridae* and are most closely related to coliphage rV5 or its relative, *Salmonella* phage PVP-SE1. These viruses are peripherally related to the "T4 superfamily" (10), but lack some of the members of the core genome. In the characterization of phage V5 Kropinski et al. specifically indicated that genera should be created repressing phages (r)V5, PVP-SE1 and phi92(phAPEC8).

Origin of the new subfamily name:

This subfamily is named after the first representative of the group – *Escherichia* phage rV5.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Kropinski AM, Waddell T, Meng J, Franklin K, Ackermann HW, Ahmed R, Mazzocco A, Yates J 3rd, Lingohr EJ, Johnson RP. The host-range, genomics and proteomics of *Escherichia coli* O157:H7 bacteriophage rV5. Virol J. 2013;10:76.

2. Santos SB, Kropinski AM, Ceyssens PJ, Ackermann HW, Villegas A, Lavigne R, Krylov VN, Carvalho CM, Ferreira EC, Azeredo J. Genomic and proteomic characterization of the broad-host-range *Salmonella* phage PVP-SE1: creation of a new phage genus. J Virol. 2011;85(21):11265-73.

3. Kwiatkowski B, Boschek B, Thiele H, Stirm S. Substrate specificity of two bacteriophage-associated endo-N-acetylneuraminidases. J Virol. 1983;45(1):367-74.. [phi92]

4. Shin H, Lee JH, Kim Y, Ryu S. Complete genome sequence of *Cronobacter sakazakii* bacteriophage CR3. J Virol. 2012;86(11):6367-8.

5. Truncaite L, Šimoliūnas E, Zajančkauskaite A, Kaliniene L, Mankevičiūte R, Staniulis J, Klausa V, Meškys R. Bacteriophage vB_EcoM_FV3: a new member of "rV5-like viruses". Arch Virol. 2012;157(12):2431-5.

6. Hong Y, Pan Y, Harman NJ, Ebner PD. Complete Genome Sequences of Two *Escherichia coli* O157:H7 Phages Effective in Limiting Contamination of Food Products. Genome Announc. 2014;2(5). pii: e00519-14. [vB_EcoM_FFH_2]

7. Abbasifar R, Kropinski AM, Sabour PM, Ackermann HW, Alanis Villa A, Abbasifar A, Griffiths MW. Genome sequence of *Cronobacter sakazakii* myovirus vB_CsaM_GAP31. J Virol. 2012;86(24):13830-1.
.
8. Kim M, Heu S, Ryu S. Complete genome sequence of enterobacteria phage 4MG, a new member of the subgroup "PVP-SE1-like phage" of the "rV5-like viruses". Arch Virol. 2014;159(11):3137-40.

9. Tsonos J, Adriaenssens EM, Klumpp J, Hernalsteens JP, Lavigne R, De Greve H. Complete genome sequence of the novel *Escherichia coli* phage phAPEC8. J Virol. 2012;86(23):13117-8.

10. Petrov VM, Ratnayaka S, Nolan JM, Miller ES, Karam JD. Genomes of the T4-related bacteriophages as windows on microbial genome evolution. Virol J. 2010;7:292.

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

12. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the

References:

determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013; 6:140.

13. 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.

14. Shin H, Lee JH, Kim Y, Ryu S. Complete genome sequence of *Cronobacter sakazakii* bacteriophage CR3. J Virol. 2012; 86(11):6367-8.

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.

Phylogenetic analysis of three *Vequintavirinae* proteins

Fig 1. Phylogenetic analysis of terminases of the phages which make up the *Vequintavirinae* and homologous proteins from *Pseudomonas* phages as outliers constructed using “one click” at phylogeny.fr (13). "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." 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 = *V5virus*; Green = *SE1virus*; Black = *Cr3virus*

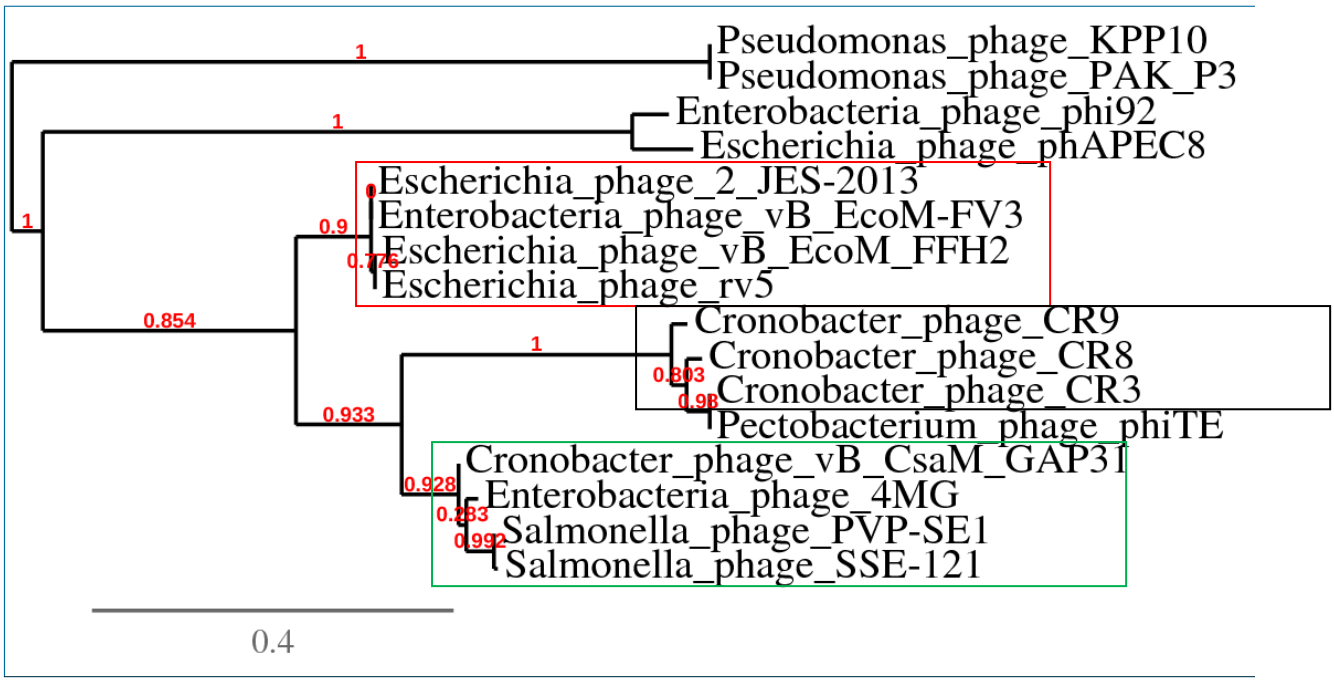


Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

Fig. 2. Phylogenetic analysis of the major capsid proteins of the phages which make up the *Vequintavirinae* and homologous proteins from two *Pseudomonas* phages as outliers constructed using "one click" at phylogeny.fr (13).

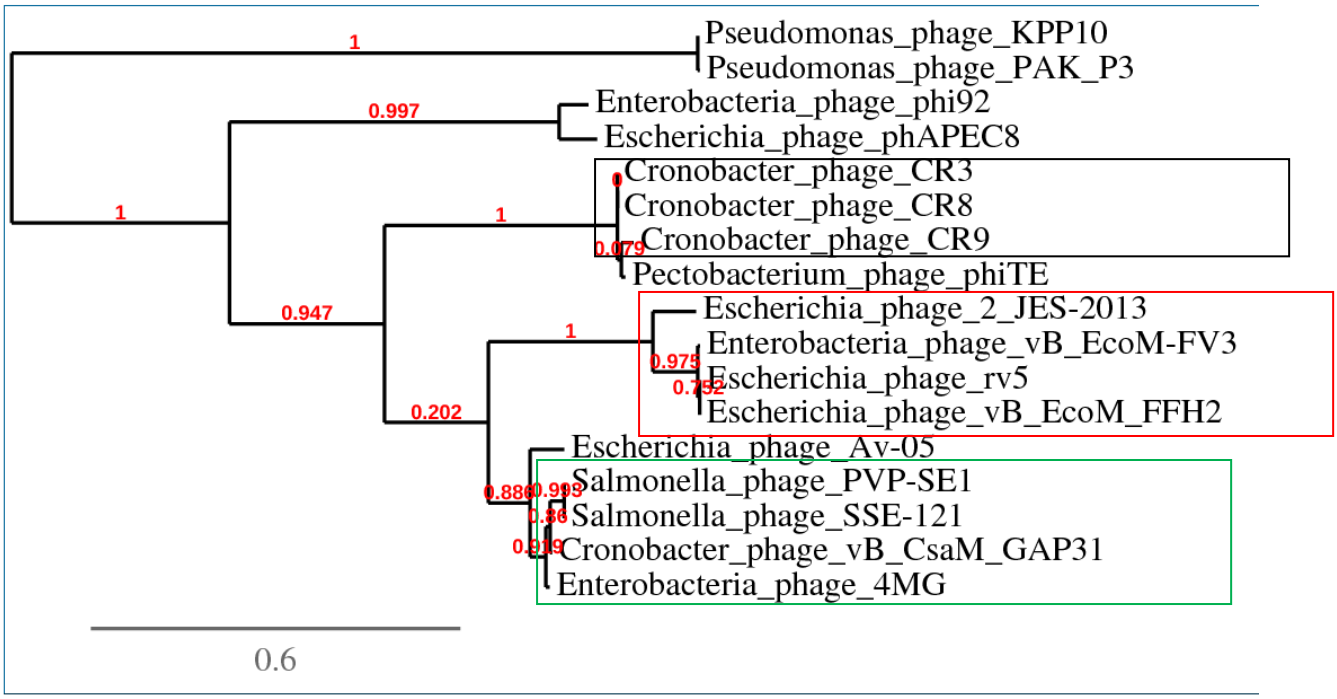


Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

Fig. 3. Phylogenetic analysis of the DNA polymerases of the phages which make up the *Vequintavirinae* and homologous proteins from two *Pseudomonas* phages as outliers constructed using "one click" at phylogeny.fr (13).

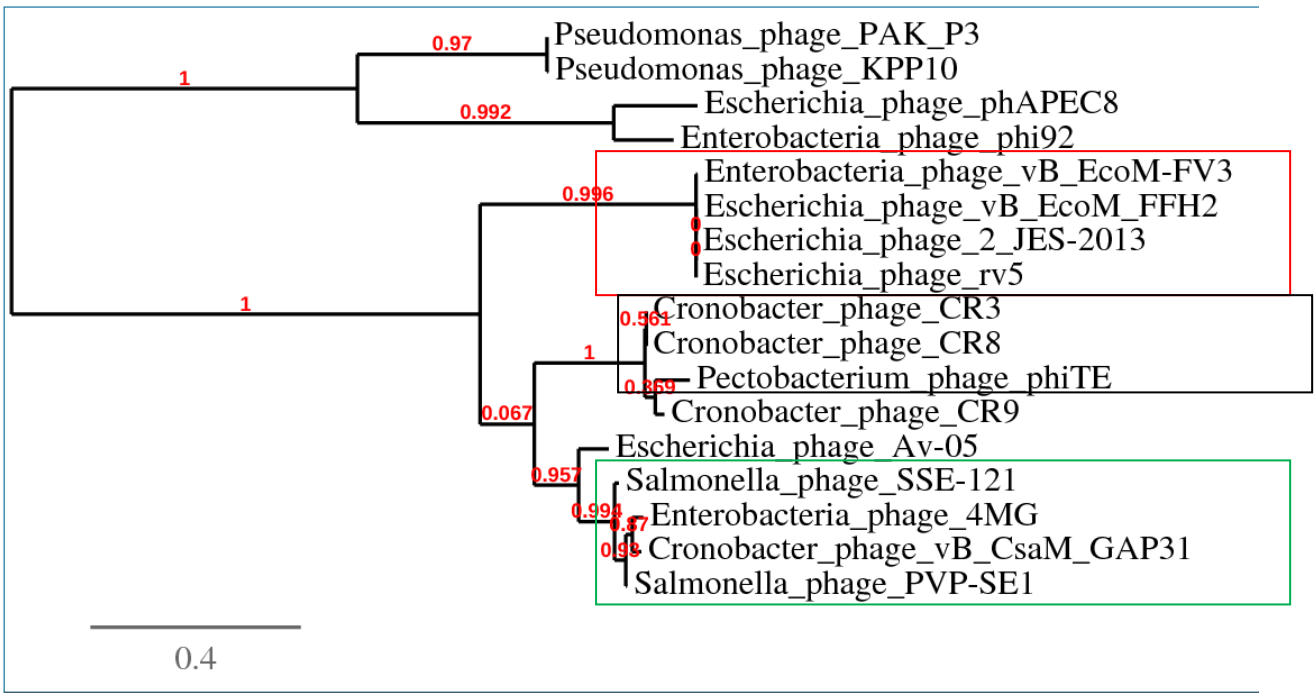


Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

A. *V5virus*

a) Electron micrograph of negatively stained rV5

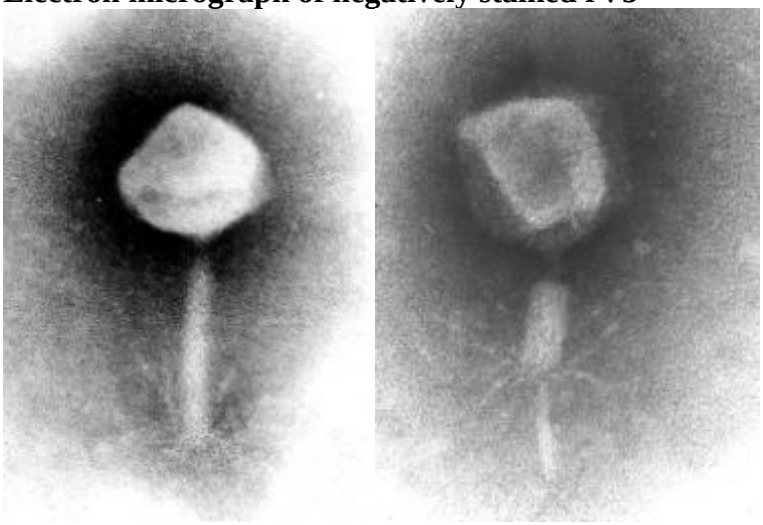
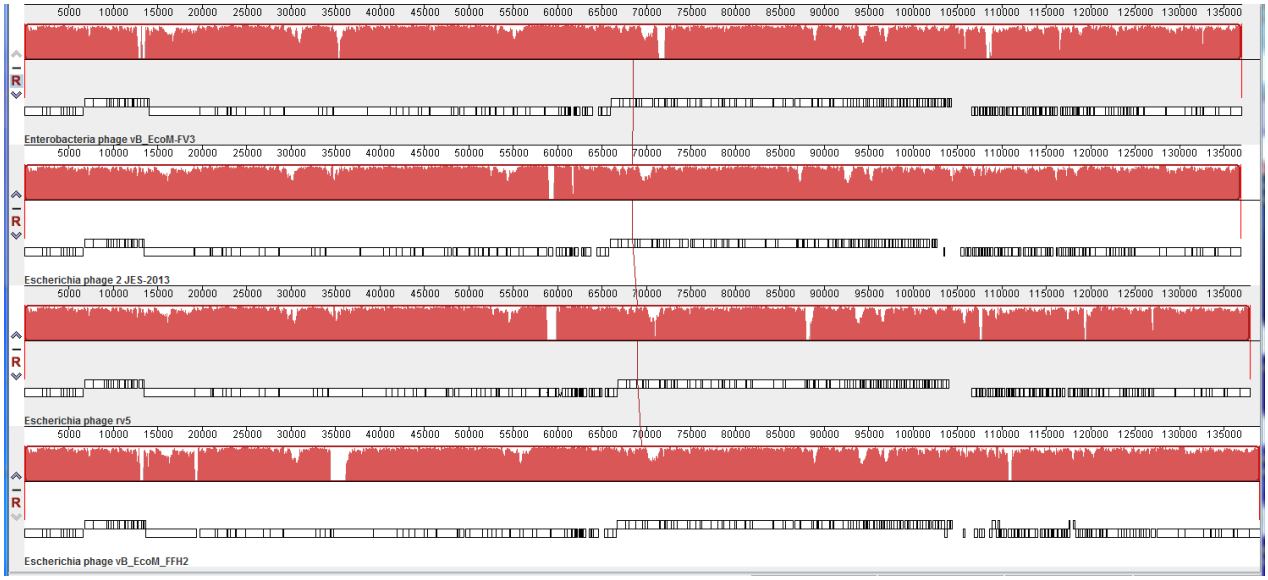


Table 1. Properties of the four phages belonging to the genus *V5virus*

Phage	GenBank accession No.	Genome length (bp)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
rV5	DQ832317	137,947	43.6	233	6	100	100
2 JES-2013	KC690136	136,910	43.6	220	4	93	91
vB_EcoM-FV3	JQ031132	136,947	43.7	218	5	88	91
vB_EcoM_FFH2	KJ190158	139,020	43.6	218	6	92	88

* Determined using BLASTN; ** Determined using CoreGenes (12)

Fig. 4. progressiveMauve alignment of the annotated genomes of members of the *V5virus* genus – top lane (FV3), upper middle (JES2013), lower middle (rV5), and bottom (FFH2) (11). 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. *Se1virus*

a) Electron micrograph of negatively stained PVP-SE1

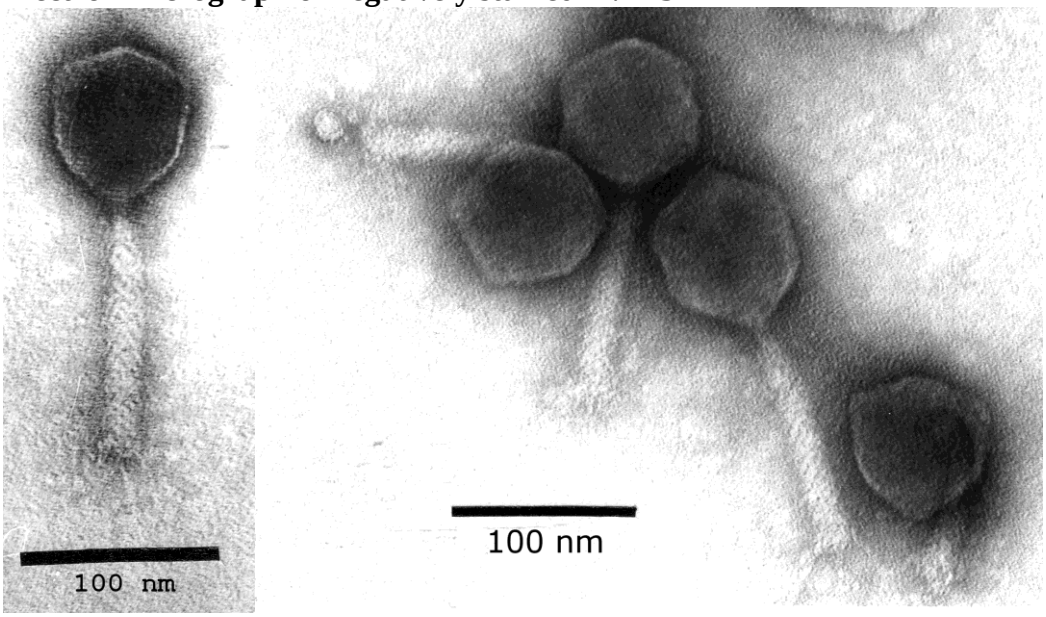
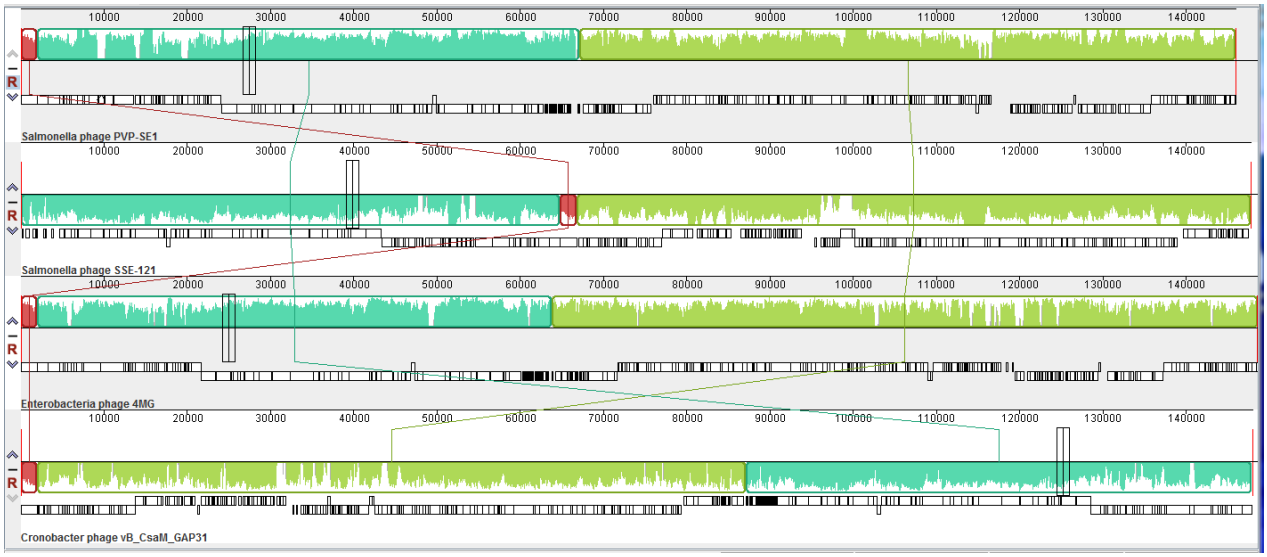


Table 2. Properties of the phages belonging to the genus *Se1virus* and the peripherally related virus Av-05.

Phage	GenBank accession No.	Genome length (bp)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
PVP-SE1	GU070616	145,964	45.6	244	24	100	100
SSE-121	JX181824	147,745	45.3	242	23	95	91
4MG	KF550303	148,567	46.3	271	21	65	82
vB_CsaM_GAP31	JN882284	147,940	46.3	269	26	64	83
Av-05	KM190144	120,938	40.0	209	0	28	48

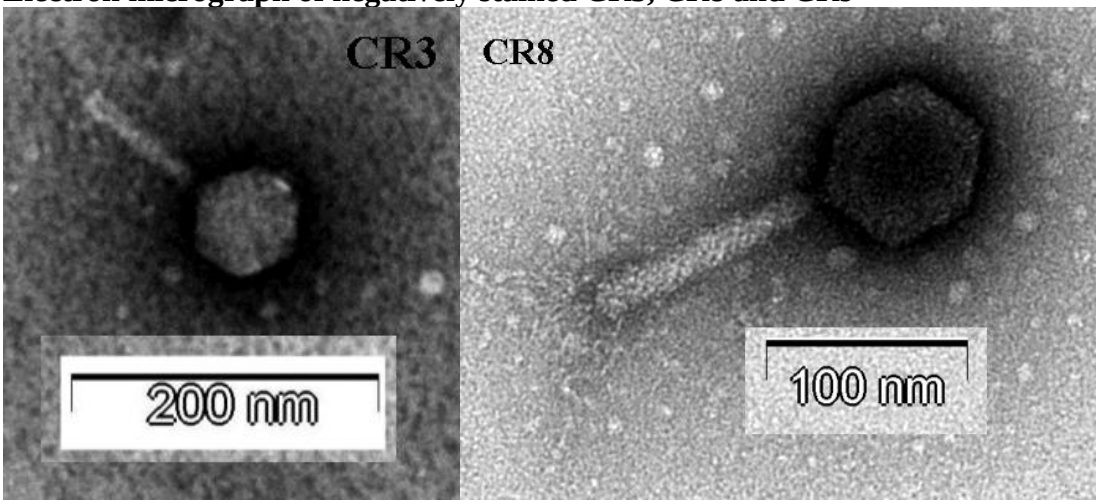
* Determined using BLASTN; ** Determined using CoreGenes (12)

Fig. 5. progressiveMauve alignment (11) of the annotated genomes of the genus *Se1virus* (from top to bottom – PVP-SE1, SSE-121, 4MG and GAP32).



C. *Cr3virus*

a) Electron micrograph of negatively stained CR3, CR8 and CR9



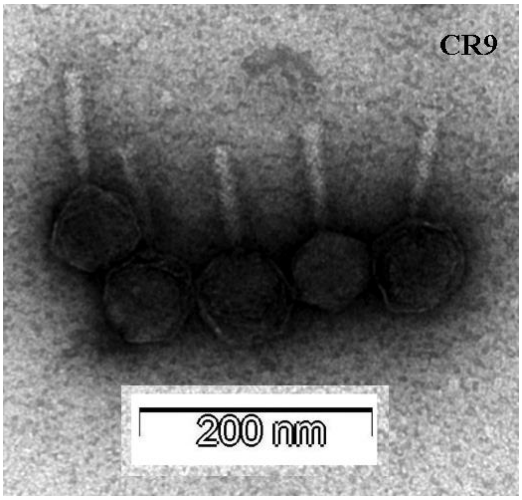


Table 3. Properties of the phages belonging to the *Cr3virus* genus plus phage phiTE as an outlier.

Phage	GenBank accession No.	Genome length (bp)	Genome (mol%G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	Proteome (% homologous proteins)**
CR3	JQ691612	149,273	50.9	265	18	100	100
CR8	KC954774	149,162	50.8	269	17	94	73
CR9	JQ691611	151,924	50.6	281	17	62	57
phiTE	JQ015307	142,349	50.1	242	2	56	41

* Determined using BLASTN; ** Determined using CoreGenes (12)

Fig. 6. progressiveMauve alignment (11) of the annotated genomes of the genus *Cr3virus* (from top to bottom – CR3, CR8, CR9).