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:	***2012.007a-dB***	(to be completed by ICTV officers)

Short title: Create a new genus *Viunalikevirus* in the family *Myoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

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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-EC comments:

Uc; remove Greek characters and otherwise improve species names.

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

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	***2012.007aB***	(assigned by ICTV officers)

To create 7 new species within:

Genus:	***Viunalikevirus* (new)**
Subfamily:	
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write “**(new)**” after its proposed name.
- If no genus is specified, enter “**unassigned**” in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Salmonella phage ViI	FQ312032
Salmonella phage Sfp10	HQ259103
Salmonella phage Sh19	JN126049
Escherichia phage Cba120	JN593240
Escherichia phage PhaxI	JN673056
Shigella phage Ag3	FJ373894
Dickeya phage Limestone	HE600015

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

The new species described here all fall within the genus criteria described below (Module 3). For the phages to belong to different species, we propose a difference in DNA identity of more than 5% (Table 1) in combination with differences in host range (references of specific phages, Table 3).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2012.007bB***	(assigned by ICTV officers)

To create a new genus within:

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

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2012.007cB***	(assigned by ICTV officers)

To name the new genus: *Viunalikevirus*

Assigning the type species and other species to a new genus

Code	***2012.007dB***	(assigned by ICTV officers)

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

Salmonella phage ViI

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:**

7

Reasons to justify the creation of a new genus:

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

The proposed viunalikeviruses share a number of specific features which set them apart from other myoviruses.

- Morphology: The phages are nearly indistinguishable in morphology, with similar head and tail dimensions, namely an isometric head of about 90 nm and a contractile tail of about 110 x 18 nm. . Tails consist of a T4-like neck with a collar, a sheath surrounding a tail tube or core, a thin base plate and an adsorption structure. The tail sheath has 24 transverse striations and resembles that of phage T4. The adsorption organelle is complex and undergoes conformational changes. Quiescent tails show in profile 3-4 thick "prongs" with rounded ends (Figure 1). In other instances, one observes a broad, umbrella-like, fibrous structure measuring 83-90 x 70-50 nm with star-like elements. The latter consists of 4 or 5 short filaments with bulbous tips. Intermediate structures with both "prongs" and "stars" have been observed. Still other tails show, especially after tail contraction, an entangled mass of indistinct filaments. No similar tail structures have been reported in other phages.

- Gene synteny and genome organization: The phages belonging to this genus share a high degree of DNA and protein similarity (Tables 1, 2 and 3). The genome organization is also highly conserved (Figure 2). Phylogenetic analyses of highly conserved proteins such as the major capsid proteins (T4 gp23 homologues), DNA polymerases (T4 gp43 homologues), DNA ligases (T4 gp30 homologues), and terminase large subunits (T4 gp17 homologues) were carried out (Figure 3). All of these analyses substantiated the establishment of this new phage genus *Viunalikevirus* and established the same pattern of their relationship to the tevenviruses and other T4-related phages (S-PM2, P-SSM2).

The distinguishing features of this genus are described in more detail in Adriaenssens et al (2012).

Origin of the new genus name:

Named after the type species *Salmonella phage ViI*. The name *Viunalikevirus* was chosen to avoid confusion with arabic or roman numerals in the name.

Reasons to justify the choice of type species:

Salmonella phage ViI was the first phage of the new genus to be identified and is the most well-known phage of the 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.

As described in module 2, for the phages to belong to different species, we propose a difference in DNA identity of more than 5% (Table 1) in combination with differences in host range (references of specific phages, Table 3). For the phages to belong to the genus, we propose at least 40% of proteins in common, and from Table 2 it is obvious that the seven phages proposed here are well above that mark. In addition, the phages need to meet the criteria described earlier, have the same morphology and genome organization.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adriaenssens EM, Ackermann H-W, Anany H, Blasdel B, Connerton IF, Goulding D, Griffiths MW, Hooton SP, Kutter EM, Kropinski AM, Lee J-H, Maes M, Pickard D, Ryu S, Sepehrizadeh Z, Shahrbabak SS, Toribio AL, Lavigne R (2012) A suggested new bacteriophage genus: “Viunalikevirus” Arch Virol 157: 2035-2046

Adriaenssens EM, Van Vaerenbergh J, Vandenheuvel D, Dunon V, Ceyssens PJ, De Proft M, Kropinksi AM, Noben JP, Maes M, Lavigne R (2012) T4-related bacteriophage LIMEstone isolates for the control of soft rot on potato caused by 'Dickeya solani'. PLoS One 7: e33227

Anany H, Lingohr E, Villegas A, Ackermann HW, She YM, Griffiths M, Kropinski A (2011) A *Shigella boydii* bacteriophage which resembles *Salmonella* phage ViI. Virol J 8: 242

Hooton SP, Timms AR, Rowsell J, Wilson R, Connerton IF (2011) *Salmonella Typhimurium*-specific bacteriophage PhiSH19 and the origins of species specificity in the Vi01-like phage family. Virol J 8: 498

Kutter EM, Skutt-Kakaria K, Blasdel B, El-Shibiny A, Castano A, Bryan D, Kropinski AM, Villegas A, Ackermann HW, Toribio AL, Pickard D, Anany H, Callaway T, Brabban AD (2011) Characterization of a ViI-like phage specific to *Escherichia coli* O157:H7. Virol J 8: 430

Park M, Lee JH, Shin H, Kim M, Choi J, Kang DH, Heu S, Ryu S (2011) Characterization and comparative genomic analysis of a novel bacteriophage SFP10 simultaneously inhibiting both *Salmonella* and *Escherichia coli* O157:H7. Appl Environ Microbiol AEM.06231-11

Pickard D, Toribio AL, Petty NK, van TA, Yu L, Goulding D, Barrell B, Rance R, Harris D, Wetter M, Wain J, Choudhary J, Thomson N, Dougan G (2010) A conserved acetyl esterase domain targets diverse bacteriophages to the Vi capsular receptor of *Salmonella enterica* serovar Typhi. J Bacteriol 192: 5746-5754 JB.

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.

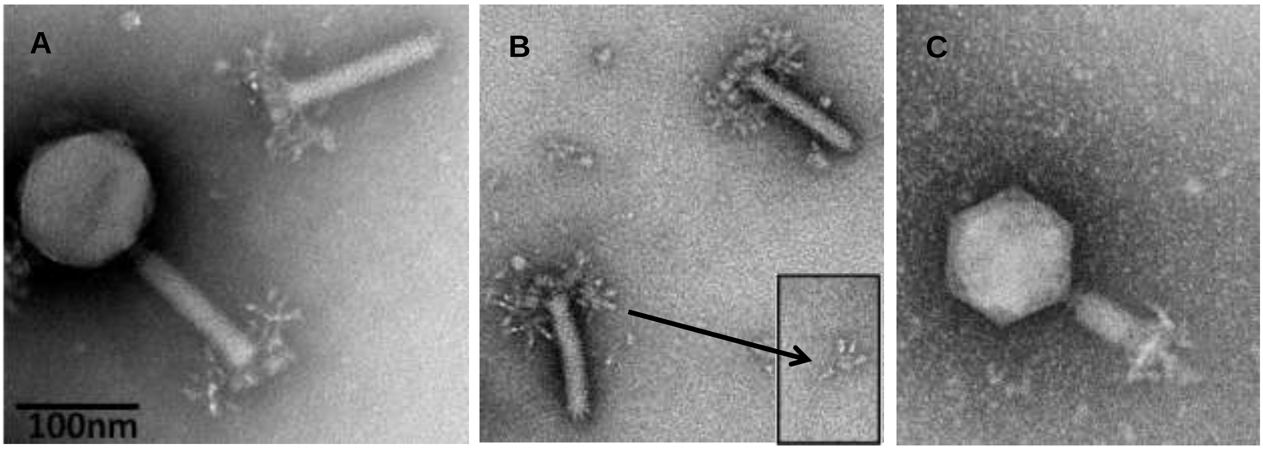

Figure 1: Electron micrographs of *Salmonella phage ViI*. A) Complete phage ViI with quiescent tail and severed tail; B) ViI tails with unfolded tail entities, displaying an umbrella-like structure; C) ViI with contracted tail. (copyright Springer Archives of Virology, Adriaenssens et al 2012, A suggested new bacteriophage genus: "Viunalikevirus", Figure 1, with kind permission from Springer Science+Business Media B.V.)

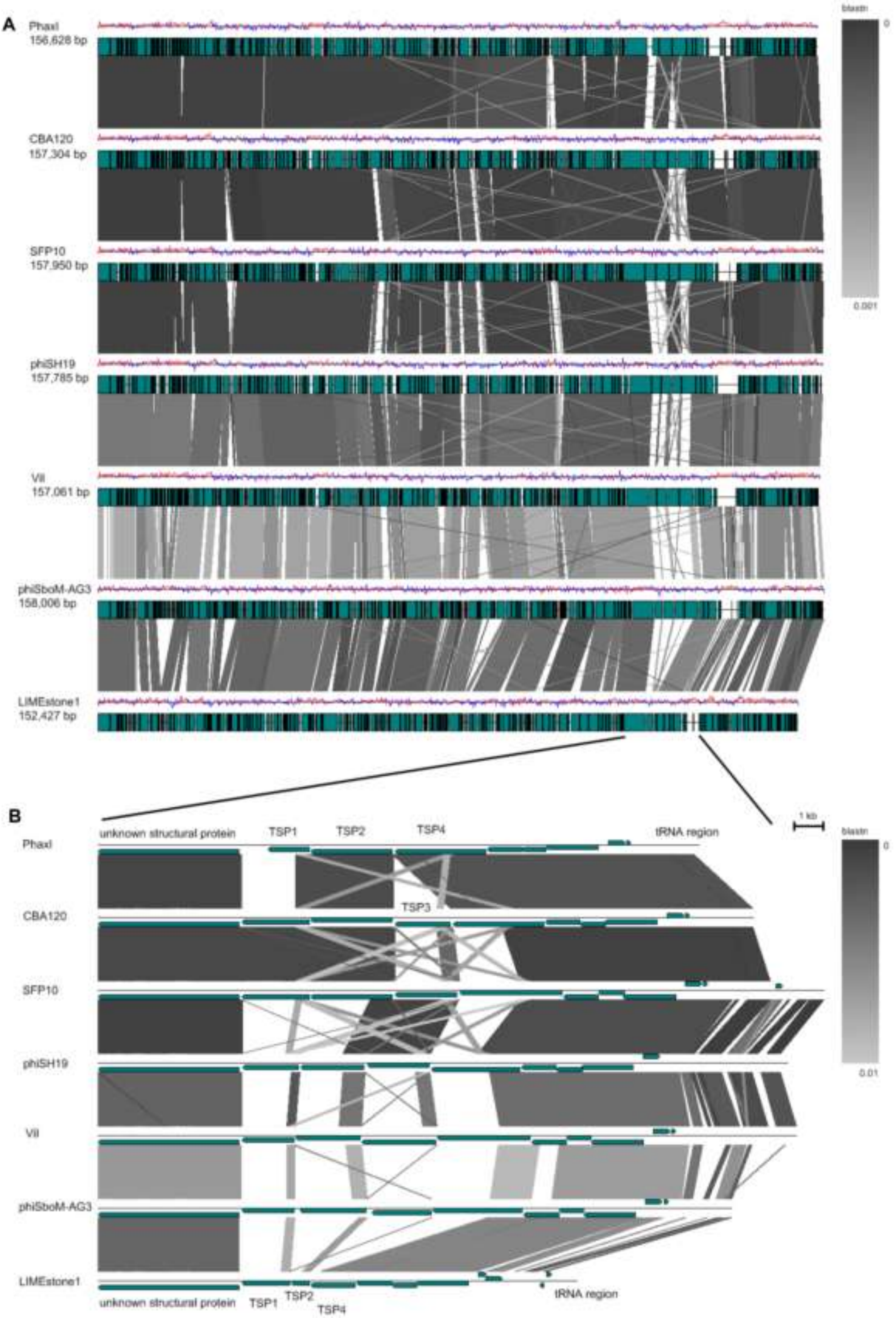

Figure 2: BLASTN comparison of the phages belonging to the suggested genus "Viunalikevirus". Phages are compared pair-wised with their neirest neighbours on the figure. A) Genomes are represented by a GC skew plot (top line per phage) and annotated ORFs are depicted as boxes (bottom line per phage). B) Subregion pair-wise comparison. ORFs are depicted as arrows according to frame. (copyright Springer Archives of Virology, Adriaenssens et al 2012, A suggested new bacteriophage genus: "Viunalikevirus", Figure 3, with kind permission from Springer Science+Business Media B.V.)

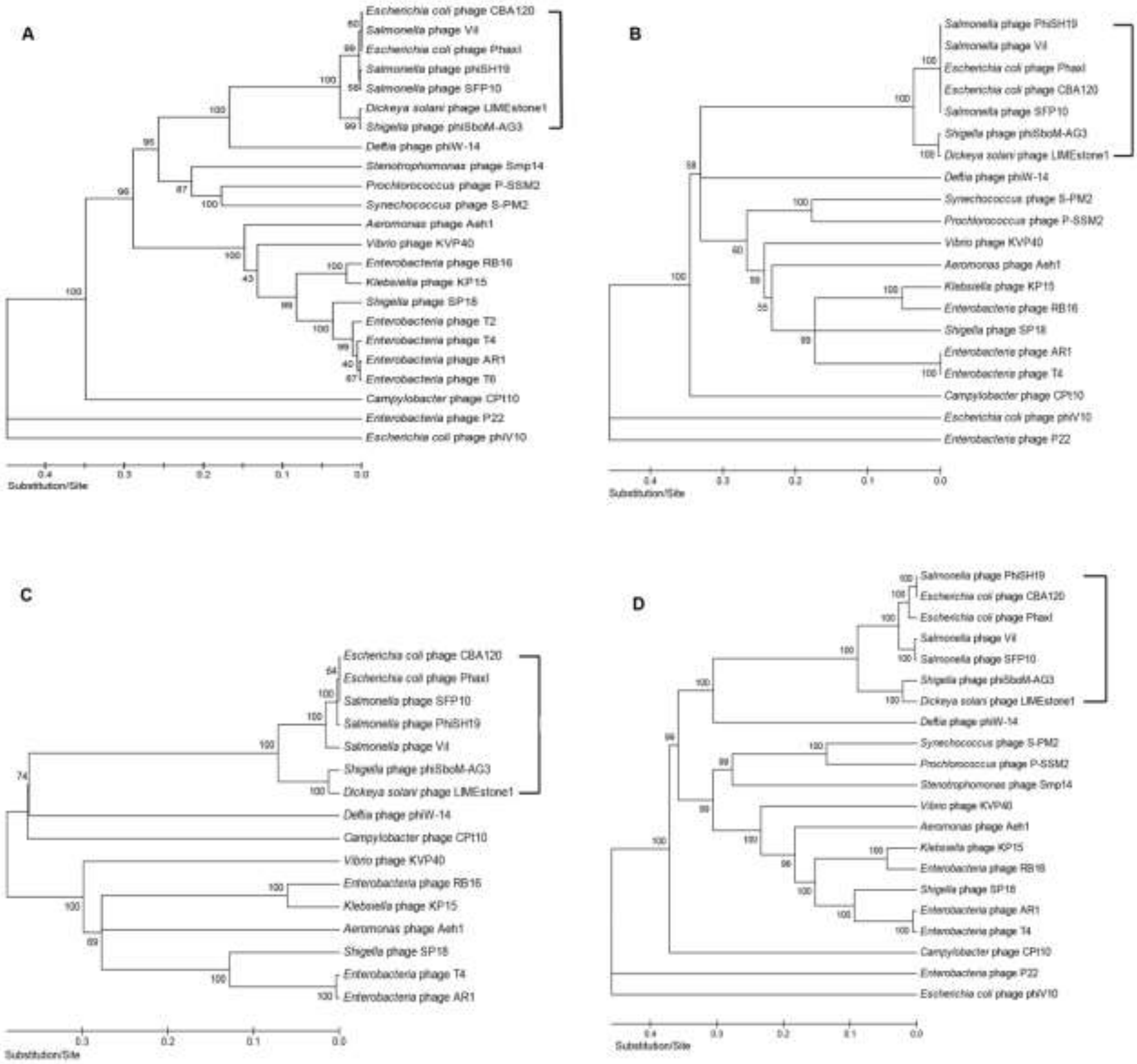

Figure 3: Phylogenetic trees. Comparisons of A) major capsid proteins (T4 gp23 homologues), B) DNA polymerases (T4 gp43 homologues), C) DNA ligases (T4 gp30 homologues), and D) terminase large subunits (T4 gp17 homologues). Square brackets indicate the genus *Viunalikevirus*. (copyright copyright Springer Archives of Virology, Adriaenssens et al 2012, A suggested new bacteriophage genus: "Viunalikevirus", Figure 6, with kind permission from Springer Science+Business Media B.V.)

Table 1: Percentages DNA identity between the reference isolate phages of the genus *Viunalikevirus* as calculated with the EMBOSS Stretcher algorithm.

	ViI	SFP10	phiSH19	CBA120	PhaxI	phiSboM-AG3
Salmonella phage ViI						
Salmonella phage Sfp10	81.1					
Salmonella phage Sh19	80.6	87.9				
Escherichia phage Cba120	81	93.1	88.5			
Escherichia phage PhaxI	80.7	89.2	86.6	91.9		
Shigella phage Ag3	66.1	66.2	65.6	65.5	64.7	
Dickeya phage Limestone	58.8	59	58.6	59.4	60.2	69.1

Table 2: Percentages protein similarity between the reference isolate phages of the genus *Viunalikevirus* calculated with CoreGenes 3.0.

	ViI	SFP10	phiSH19	CBA120	PhaxI	phiSboM-AG3	LIMEstone1
Salmonella phage ViI	100	90.9	76.9	88.5	90.9	86.1	77.4
Salmonella phage Sfp10	94.0	100	79.1	94.5	95.5	88.6	78.6
Salmonella phage Sh19	96.4	95.8	100	95.2	96.4	91.0	83.7
Escherichia phage Cba120	90.2	93.1	77.5	100	95.1	85.3	76.0
Escherichia phage PhaxI	90.4	91.9	76.6	92.8	100	86.1	77.5
Shigella phage Ag3	82.9	82.4	69.9	80.6	83.3	100	79.6
Dickeya phage Limestone	80.1	78.6	69.2	77.1	80.6	85.6	100

Table 3: General features of the viunalikeviruses.

Phage isolate name	Host	Head dimensions (nm)	Tail dimensions (nm)	Genome size (bp)	Mol%G+C	Number of ORFs	Number of tRNAs	Number of HEases	Reference
ViI (syn. Vi1, Vi01)	*Salmonella* Typhimurium	90-9*	105-115 x 17	157,061	45	208	6		Pickard et al. 2010
SFP10	*S.* Typhimurium	69	131 x 13	157,950	44.5	201	4		Park et al 2011
phiSH19	*S.* Typhimurium	83	110 x 14	157,785	44.7	166	5	2	Hooton et al 2011
CBA120	*Escherichia coli*	90	105 x 17	157,304	44.5	202	4		Kutter et al 2011
PhaxI	*E. coli*	86	109x18	156,628	44.5	209	4	1	Shahrbabak et al, unpublished
LIMEstone1	“Dickeya solani”	91	114 x 17	152,427	44.9	201	1	14	Adriaenssens et al 2012
phiSboM-AG3	*Shigella boydii*	83	110 x 14	158,006	50.4	216	4		Anany et al 2011