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:	***2015.027aB***	(to be completed by ICTV officers)

Short title: To amend the description of the *Viunalikevirus* (proposed new name *Vi1virus*) and create seven (7) new species
(e.g. 6 new species in the genus *Zetavirus*)

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

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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 the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

Date first submitted to ICTV: June 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	***2015.027aB***	(assigned by ICTV officers)

To create 7 new species within:

Genus:	***Viunalikevirus*** (to be renamed ***Vi1virus***)
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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Escherichia virus ECML4	Escherichia phage ECML-4	JX128257
Salmonella virus Marshall	Salmonella phage Marshall	KF669653
Salmonella virus STML131	Salmonella phage STML-13-1	JX181828
Salmonella virus SJ3	Salmonella phage vB_SalM_SJ3	KJ174318
Salmonella virus Maynard	Salmonella phage Maynard	KF669654
Salmonella virus Det7	Salmonella phage Det7	KP797973
Salmonella virus SJ2	Salmonella phage vB_SalM_SJ2	KJ174317

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

Several new Vi1-like phage genomes have recently been deposited to GenBank. This proposal recognizes the fact that they are part of the *Viunalikevirus* genus (new proposed name: *Vi1virus*) (1,2,3,4).

Please note that we have chosen to refer to this new genus as *Vi1virus* rather than *Viunalikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

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 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Casjens SR, Jacobs-Sera D, Hatfull GF, Hendrix RW. Genome Sequence of *Salmonella enterica* Phage Det7. Genome Announc. 2015;3(3). pii: e00279-15.
2. Tatsch CO, Wood TL, Chamakura KR, Kuty Everett GF. Complete Genome of *Salmonella enterica* Serovar Typhimurium Myophage Maynard. Genome Announc. 2013;1(6). pii: e00866-13.
3. Zhang J, Hong Y, Harman NJ, Das A, Ebner PD. Genome sequence of a salmonella phage used to control salmonella transmission in Swine. Genome Announc. 2014;2(5). pii: e00521-14. [vB_SalM_SJ_3]
4. Luna AJ, Wood TL, Chamakura KR, Kuty Everett GF. Complete Genome of *Salmonella enterica* Serovar Enteritidis Myophage Marshall. Genome Announc. 2013;1(6). pii: e00867-13.

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.

Note: Whole genome analysis reveals that these seven phages are distinct, and clearly fall into the ICTV ratified genus *Viunalikevirus*. Therefore, the only supplementary data that we will present is the DNA and proteome homology (Table 1)

Table 1. Properties of the seven phages belonging to the genus *Vi1virus*

Phage	DNA (% sequence identity)*	Proteome (% homologous proteins)**
Vi1	100	100
ECML-4	91	88.9
Marshall	88	88.0
STML-13-1	88	90.4
vB_SalM_SJ3	81	88.5
Maynard	86	86.1
Det7	78	89.9
vB_SalM_SJ2	84	87.0

* Determined using BLASTN relative to Vi1; ** Determined using CoreGenes (2) relative to Vi1.