



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:	2015.017a-dB	(to be completed by ICTV officers)			
Short title: To create one (1) new genus, <i>Sextaevirus</i> , including two (2) new species within the family <i>Siphoviridae</i> . (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

Author(s):

Andrew M. Kropinski – University of Guelph (Canada)
Luis D.R. de Melo – Universidade do Minho (Portugal)
Joana Azeredo – Universidade do Minho (Portugal)
Vijay Aswani – Marshfield Clinic (U.S.A.)
Jens Kuhn – NIH (U.S.A.)
Evelien M. Adriaenssens – University of Pretoria (South Africa)

Corresponding author with e-mail address:

Andrew M. Kropinski Phage.Canada@gmail.com

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 *Sextaevirus* rather than *Sextaevirus*, 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:

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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	2015.017aB	(assigned by ICTV officers)
To create 2 new species within:		
Genus:	<i>Sextaevirus</i> (<i>new</i>)	Fill in all that apply. <ul style="list-style-type: none"> • 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.
Subfamily:		
Family:	<i>Siphoviridae</i>	
Order:	<i>Caudovirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Staphylococcus virus Sextaec</i>	Staphylococcus phage 6ec	KJ804259
<i>Staphylococcus virus SEP9</i>	Staphylococcus phage vB_SepS_SEP9	KF929199

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 *Sextaevirus* rather than *Sextaeclikevirus* 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	2015.017bB	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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
Family:	<i>Podoviridae</i>	
Order:	<i>Caudovirales</i>	

naming a new genus

Code	2015.017cB	(assigned by ICTV officers)
To name the new genus: <i>Sextaecvirus</i>		

Assigning the type species and other species to a new genus

Code	2015.017dB	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Staphylococcus virus Sextaec</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
2		

Reasons to justify the creation of a new genus:

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

BLASTN, CoreGenes (Table 1), progressiveMauve (Fig. 2) and phylogenetic analyses (Fig. 3) all indicate that the proposed genus, *Sextaecvirus*, is cohesive and distinct from the other genera of viruses. The next closest related phage is *Staphylococcus* phage phiIBB-SEP1 (KF021268) which shares 7% DNA sequence identity.

These two virulent *Staphylococcus epidermidis* phages possess elongated tails. The morphology of SEP9 possesses a “head of 64 nm in diameter and a very long flexible tail of 375 × 10 nm, conspicuous transverse striations and a six-sided star-like baseplate (Fig. 1). Heads were icosahedra, as shown by the observation of both hexagonal and pentagonal capsids.” (5) By comparison phage 6ec has an icosahedral capsid (69 in diameter) and 362 nm long noncontractile tail (4).

The phages of this genus possess genome of approx. 93.1 kb (29.4 mol%G+C), and encode 135 proteins and 1 tRNAs. The genome of 6ec possesses 10 bp 3’ cohesive termini. In interesting feature is that they both appear to encode a nonfunctional integrase (4, 5).e

Origin of the new genus name:

Staphylococcus phage 6ec

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 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.
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. Aswani VH, Tremblay DM, Moineau S, Shukla SK. Complete Genome Sequence of a *Staphylococcus epidermidis* Bacteriophage Isolated from the Anterior Nares of Humans. Genome Announc. 2014; 2(4). pii: e00549-14.
5. Melo LD, Sillankorva S, Ackermann HW, Kropinski AM, Azeredo J, Cerca N. Characterization of *Staphylococcus epidermidis* phage vB_SepS_SEP9 - a unique member of the Siphoviridae family. Res Microbiol. 2014; 165(8):679-85.

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 micrographs of negatively stained SEP9.

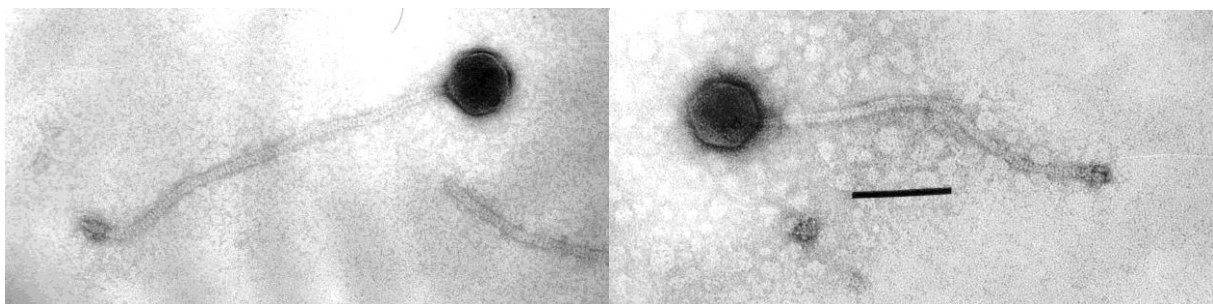


Table 1. Properties of the member of the *Sextaevirus* genus.

Phage	Accession Number	Genome length in bp	Mol%G+C	Termini	DNA sequence relatedness(*)	Protein sequence relatedness(**)
SEP9	KF929199	92417	29.57	Not determined	100%	100%
6ec	KJ804259	93794	29.30	10 bp 3' cohesive	75.9	82.9

* Determined using BLASTN; ** Determined using CoreGenes (2)

Fig. 2. progressiveMauve alignment of the annotated genomes of members of the *Sextaevirus* genus – top (SEP9), and bottom (6ec) (1). 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).

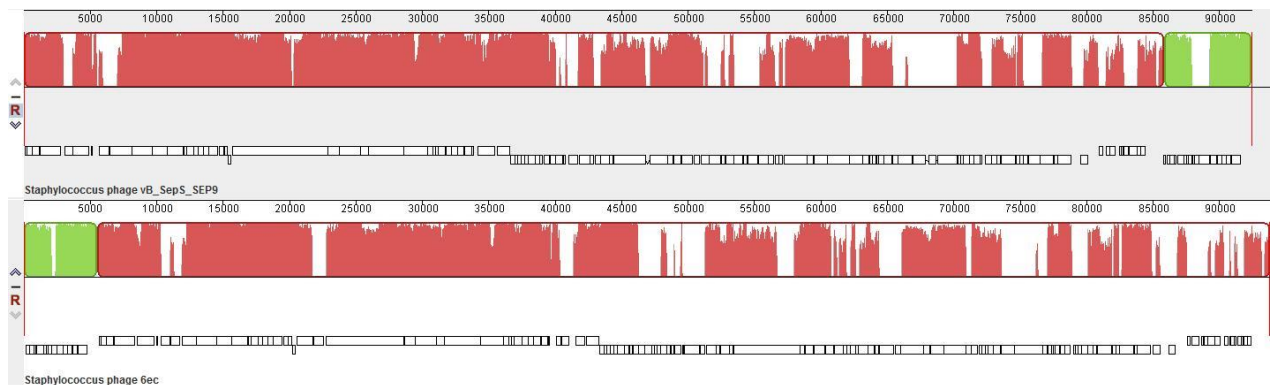


Fig. 3. Phylogenetic analysis of major capsid proteins of sextaeviruses and peripherally related *Lactobacillus* and *Streptococcus* phages constructed using “one click” at phylogeny.fr (3). "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, 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."

