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:	***2009.007a-rB***	(to be completed by ICTV officers)

Short title: : Create new subfamily *Tevenvirinae* containing the new genus *Schizot4likevirus*, in the family *Myoviridae*, order *Caudovirales*
(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** ☒	

Author(s) with e-mail address(es) of the proposer:

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Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

ICTV-EC or Study Group comments and response of the proposer:

[previous (EC41) decision: the genus name is inconsistent with naming rules and "Tquatrovirinae" is not easily pronouncible.]

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

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.007aB***	(assigned by ICTV officers)

To create 10 new species with the name(s):

Escherichia phage JS98
Escherichia phage RB14
Escherichia phage RB16
Escherichia phage RB32
Escherichia phage RB43
Escherichia phage RB49
Escherichia phage RB69
Escherichia phage phi1
Aeromonas phage 31
Aeromonas phage 25

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.007bB***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***T4likevirus*** (proposed name for "T4-like viruses")
Subfamily:	***Tevenvirinae*** (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.

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Members of the genus *T4likevirus* (proposed name for "T4-like viruses") listed above are morphologically indistinguishable and have moderately elongated heads of about 110 nm in length, 114 nm long tails with a collar, base plates with short spikes, and six long kinked tail fibers. Within this assemblage we identified four distinct subtypes with >70% protein similarity (average percentage of shared proteins with various levels of similarity), or a 0.2 dissimilarity on the cluster dendrogram) (Genome references have been addedd in Table 2). These are the T4-type phages (phages T4, JS98, RB14, RB32, RB69), 44RR-type (phages 44RR2.8t, 31, 25), RB43-type (RB43, RB16), and the RB49-type viruses (RB49, phi1). They can be subdivided by the presence of specific encoded proteins as outlined in Table 1. For the type T4-type phages, three specific proteins with defined functions (Pin, MotB, ModA) were found. Pin is an inhibitor of the host's Lon protease (Noguchi & Takahashi, 1991; Skorupski et al., 1988), while the other two proteins function to modulate transcription (Tiemann et al., 2004; Pulitzer et al., 1985).

Heteroduplex analyses indicate that coliphages T2, T4 and T6 share >85% sequence similarity (Kim & Davidson, 1974)**,** warranting their inclusion, in spite of lack of detailed sequence data for T2 and T6, into the T4-type subgroup. The DNA of the T-even phages contains 5-hydroxymethylcytosine (5-HMC). While this modified nucleotide is common in T4-related phages (Ackermann & Krisch, 1997)**,** its presence has not been ascertained biochemically in the other phages (JS98, RB14, RB32, RB69) included in this subgroup. T4 gp*42* dCMP hydroxymethylase and Alc that blocks transcription from cytosine containing DNA are required for the incorporation of 5-HMC rather than cytosine into T-even DNA. Genes specifying homologs of the T4 gp*42* and Alc proteins are also present in the 44RR2.8t-type phages.

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.007cB***	(assigned by ICTV officers)

To create 1 new species with the name(s):

Vibrio phage KVP40

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.007dB***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***Schizot4likevirus*** (new)
Subfamily:	***Tevenvirinae*** (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.

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

there are morphological differences between phage T4 and KVP40. For example, the head of KVP40 is longer (140 nm long and 70 nm wide) than that of T4. Due to the constraints of head size on DNA packaging, this observation suggested that the genome of KVP40 is larger than the 168,903-bp genome of T4.

Indeed, the genome sequence is 244,835 bp, with an overall G+C content of 42.6%. It encodes 386 putative protein-encoding open reading frames (CDSs), 30 tRNAs, 33 T4-like late promoters, and 57 potential rho-independent terminators. 65% of the CDSs were unique to KVP40 and had no known function, the genome sequence and organization show specific regions of extensive conservation with phage T4. At least 99 KVP40 CDSs have homologs in the T4 genome (Blast alignments of 45 to 68% amino acid similarity). The shared CDSs represent 36% of all T4 CDSs but only 26% of those from KVP40. There are 26 CDSs that have no viral homolog, and many did not necessarily originate from *Vibrio* spp., suggesting an even broader host range for KVP40.

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	***2009.007eB***	(assigned by ICTV officers)
To create a new genus to contain the species listed below		

Code	***2009.007fB***	(assigned by ICTV officers)
To name the new genus: *Schizot4likevirus*		

assigning a new genus to higher taxa

Code	***2009.007gB***	(assigned by ICTV officers)

To assign the new genus as follows: Ideally, a genus should be placed within a higher taxon, but if not, write "**unassigned**" in the box below.

Subfamily:	***Tevenvirinae*** (new)
Family:	***Myoviridae***
Order:	***Caudovirales***

If any of these taxa has yet to be created (in module 4, 5 or 6) please write "**(new)**" after its proposed name.

assigning type species and other species to a new genus

Code	***2009.007hB***	(assigned by ICTV officers)

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

Vibrio phage KVP40

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

Code	***2009.007iB***	(assigned by ICTV officers)

To assign the following as additional species of the new genus:

Vibrio phage nt-1

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 *Schizot4likevirus* comprise two marine vibriophages**,** KVP40 and nt-1**,** with genomes of approximately 246 kb. KVP40 infects *Vibrio parahaemolytius* and was isolated from seawater. Phage nt-1 infects *Vibrio natriegens* and originates from a coastal marsh. The phages differ from T4 in head length (137 nm vs. 111 nm), but are identical to phage T4 in tail morphology. KVP40 has a feather of decoration proteins on its head (Ackermann & DuBow, 1987; Ackermann et al., 1984).

Origin of the new genus name:

In historical literature, these phages were named "schizo T-even phages"

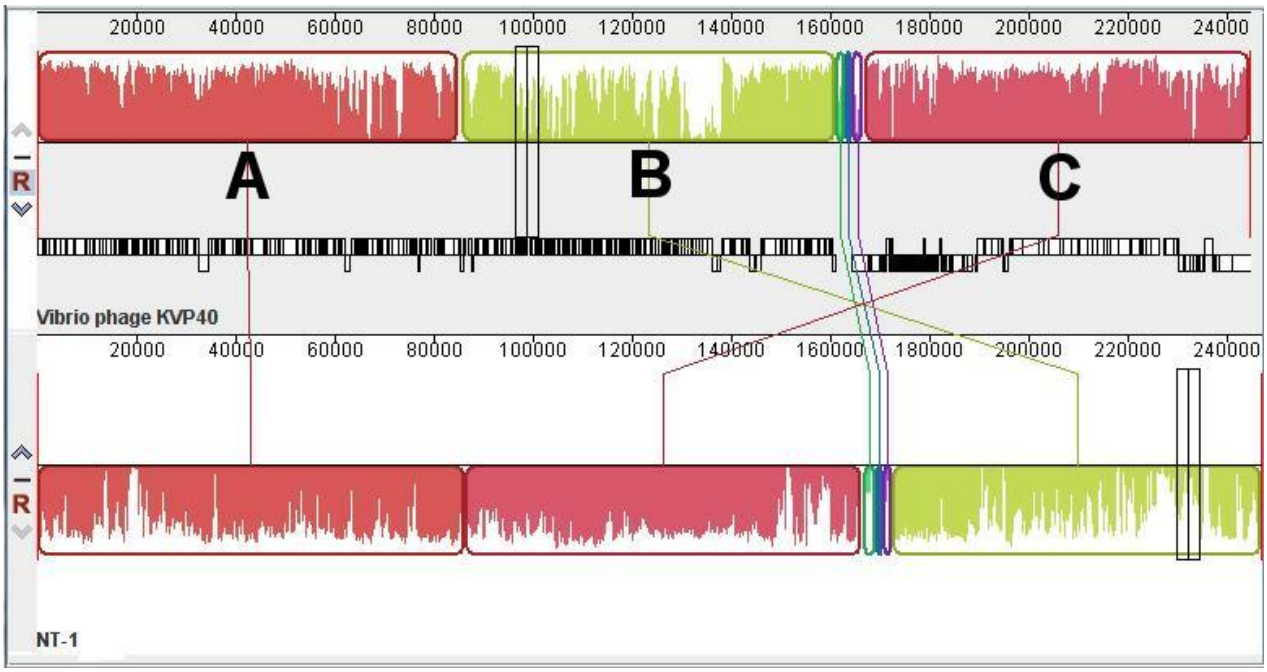
Reasons to justify the choice of type species:

This is the first sequenced phage 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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

KVP40 infects *Vibrio parahaemolytius*. Phage nt-1 infects *Vibrio natriegens*. Apart from host range differences, significant variation exists at the proteome level.



Alignment (based upon DNA sequence relatedness using Mauve) of KVP40 RefSeq versus draft sequence of NT-1 from Tulane T4-like Genomes Website (http://phage.bioc.tulane.edu/). Three major blocks of sequence similarity (ABC) can be ready seen. In the draft sequence these are currently arranged in inverted orientation and in the order ACB.

MODULE 4: **NEW SUBFAMILY**

creating and naming a new subfamily

Code	***2009.007jB***	(assigned by ICTV officers)

To create a new subfamily containing the genera listed below

Code	***2009.007kB***	(assigned by ICTV officers)

To name the new subfamily: *Tevenvirinae*

assigning a new subfamily to a family

Code	***2009.007lB***	(assigned by ICTV officers)

To assign the new subfamily as follows:

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.

genera and species assigned to the new subfamily

Code	***2009.007mB***	(assigned by ICTV officers)

genera assigned 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

T4likevirus (proposed name for "T4-like viruses")

Schizot4likevirus (new)

Code	***2009.007nB***	(assigned by ICTV officers)

unassigned species in the new subfamily (i.e. within the subfamily but not assigned to any genus):

You may list several species here. For each species, please state whether it is new or existing. If the species is new, it must be created in Module 2

Acinetobacter phage 133,
Aeromonas phage Aeh1
Aeromonas phage 65.

Morphologically, phage 133 is identical to T4, whereas Aeh1 and 65 have the same heads of 133 nm in length as *Vibrio* phages KVP40 and nt-1. They were considered to be part of the schizo-T-even group (Tetart et al., 2001) and have a T4-type tail structure (Ackermann & Krisch, 1997). CoreGenes and our supplementary phylogenetical analyses indicate that these phages are too dissimilar to be included into one of the genera listed above (Figure 1).

Reasons to justify the creation of the new subfamily: Additional material in support of this proposal may be presented in the Appendix, Module 9
See module 9
Origin of the new subfamily name:
named after the best-studied of these phages, coliphage T4.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2009.007oB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Vibrio phage nt-1

The present taxonomic position of these taxon/taxa:

Genus:	***T4likevirus***
Subfamily:	***Tevenvirinae*** (new)
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Part (b) re-assign to a higher taxon

Code	***2009.007pB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Schizot4likevirus***
Subfamily:	***Tevenvirinae*** (new)
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please 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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Cfr module 9

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2009.007qB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Acinetobacter phage 133
Aeromonas phage Aeh1
Aeromonas phage 65

The present taxonomic position of these taxon/taxa:

Genus:	***T4likevirus***
Subfamily:	***Tevenvirinae*** (new)
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Part (b) re-assign to a higher taxon

Code	***2009.007rB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

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

Fill in all that apply.

- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Cfr module 9

-

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Jia Z, Ishihara R, Nakajima Y, Asakawa S, Kimura M: Molecular characterization of T4-type bacteriophages in a rice field. Environmental Microbiology 2007, 9: 1091-1096.

Filée J, Bapteste E, Susko E, Krisch HM: A selective barrier to horizontal gene transfer in the T4-type bacteriophages that has preserved a core genome with the viral replication and structural genes. Molecular Biology & Evolution 2006, 23: 1688-1696.

Filée J, Tétart F, Suttle CA, Krisch HM: Marine T4-type bacteriophages, a ubiquitous component of the dark matter of the biosphere. Proceedings of the National Academy of Sciences of the United States of America 2005, 102: 12471-12476.

Klausa V, Piesiniene L, Staniulis J, Nivinskas R: Abundance of T4-type bacteriophages in municipal wastewater and sewage . Ekologija (Vilnius) 2003, 1: 47-50.

Zuber S, Ngom-Bru C, Barretto C, Bruttin A, Brüssow H, Denou E: Genome analysis of phage JS98 defines a fourth major subgroup of T4-like phages in Escherichia coli. Journal of Bacteriology 2007, 189: 8206-8214.

Comeau AM, Bertrand C, Letarov A, Tétart F, Krisch HM: Modular architecture of the T4 phage superfamily: a conserved core genome and a plastic periphery. Virology 2007, 362: 384-396.

Nolan JM, Petrov V, Bertrand C, Krisch HM, Karam JD: Genetic diversity among five T4-like bacteriophages. Virology Journal 2006, 3: 30.

Petrov VM, Nolan JM, Bertrand C, Levy D, Desplats C, Krisch HM et al.: Plasticity of the gene functions for DNA replication in the T4-like phages. Journal of Molecular Biology 2006, 361: 46-68.

Desplats C, Dez C, Tétart F, Eleaume H, Krisch HM: Snapshot of the genome of the pseudo-T-even bacteriophage RB49. Journal of Bacteriology 2002, 184: 2789-2804.

Monod C, Repoila F, Kutateladze M, Tétart F, Krisch HM: The genome of the pseudo T-even bacteriophages, a diverse group that resembles T4. Journal of Molecular Biology 1997, 267: 237-249.

Miller ES, Heidelberg JF, Eisen JA, Nelson WC, Durkin AS, Ciecko A et al.: Complete genome sequence of the broad-host-range vibriophage KVP40: comparative genomics of a T4-related bacteriophage. Journal of Bacteriology 2003, 185: 5220-5233.

Noguchi T, Takahashi H: A novel expression system for production of a labile protein in Escherichia coli by infection with cytosin-substituting T4 phage. Agricultural and Biological Chemistry 1991, 55: 2507-2513.

Skorupski K, Tomaschewski J, Rüger W, Simon LD: A bacteriophage T4 gene which functions to inhibit Escherichia coli Lon protease. Journal of Bacteriology 1988, 170: 3016-3024.

References:

Tiemann B, Depping R, Gineikiene E, Kaliniene L, Nivinskas R, Ruger W: ModA and ModB, two ADP-ribosyltransferases encoded by bacteriophage T4: catalytic properties and mutation analysis. Journal of Bacteriology 2004, 186: 7262-7272.

Pulitzer JF, Colombo M, Ciaramella M: New control elements of bacteriophage T4 pre-replicative transcription. Journal of Molecular Biology 1985, 182: 249-263.

Kim JS, Davidson N: Electron microscope heteroduplex study of sequence relations of T2, T4, and T6 bacteriophage DNAs. Virology 1974, 57: 93-111.

Ackermann H-W, Krisch HM: A catalogue of T4-type bacteriophages. Archives of Virology 1997, 142: 2329-2345.

Ackermann H-W, DuBow MS: Viruses of Prokaryotes. Boca Raton, FL: CRC Press; 1987.

Ackermann H-W, Kasatiya SS, Kawata T, Koga T, Lee JV, Mbiguino A et al.: Classification of Vibrio bacteriophages. Intervirology 1984, 22: 61-71.

Tetart F, Desplats C, Kutateladze M, Monod C, Ackermann H-W, Krisch HM: Phylogeny of the major head and tail genes of the wide-ranging T4-type bacteriophages. Journal of Bacteriology 2001, 183: 358-366.

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.

The ICTV currently lists only six sequenced viruses as members of the T4 phage genus**,** namely enterobacterial phage T4, *Acinetobacter* phage 133, *Aeromonas* phages Aeh1, 65 and 44RR2.8t, and *Vibrio* phage nt-1. However, the scientific literature and public databases are abound with descriptions of "T4-like" phages and the analysis of complete genome sequences indicates that the T4-related phages constitute one of the largest groups of bacterial viruses. This corroborates ecogenomic studies on the diversity of these viruses as apparent in the heterogeneity of capsid (gp*23*) genes in isolates from Japanese rice fields (Jia et al., 2007), marine systems (Filée et al., 2006; 2005), and from Lithuania, Bangladesh and Switzerland (Klausa et al., 2003; Zuber et al., 2007). These studies suggest that the fully sequenced T4 phages are but a small fraction of the T4-related genomes in nature. Nevertheless, there are clear commonalities among all sequenced "T4-like" genomes from different host groups, including the cyanophages, namely a set of 33-35 genes that have persisted during the evolution of genomes with sizes from 160 to 250 kb (Comeau et al., 2007). This core of genes seems to have resisted division throughout evolution. Nevertheless, these horizontal substitutions do not erase the evidence of the global relationship between phages and clear hybrid phages within this group have not been identified to date. Work done at Tulane University (Nolan et al., 2006; Petrov et al., 2006), led to the tentative conclusion that it takes about 33 T4 genes to determine a genetic program that controls lytic phage development in the host cell.

Based on the *Myoviridae* cluster dendrogram (Figure 1), the current ICTV genus "T4 viruses" can be subdivided into two genera and several subgroups. By raising it to the rank of subfamily, the *Tevenvirinae*, named after the best-studied of these phages, coliphage T4. The first genus, the *T4likevirus***,** includes what were previously termed the T-even and pseudo-T-even phages (Desplats et al., 2002; Monod et al., 1997) and which can be subdivided further as listed in Table 1. Our name perpetuates the old ICTV nomenclature, but is now limited to enterobacterial

and *Aeromonas* phages. The *Schizot4likevirus*, consisting of two former members of the "schizo-T-evens" (Miller et al., 2003) form the other genus.

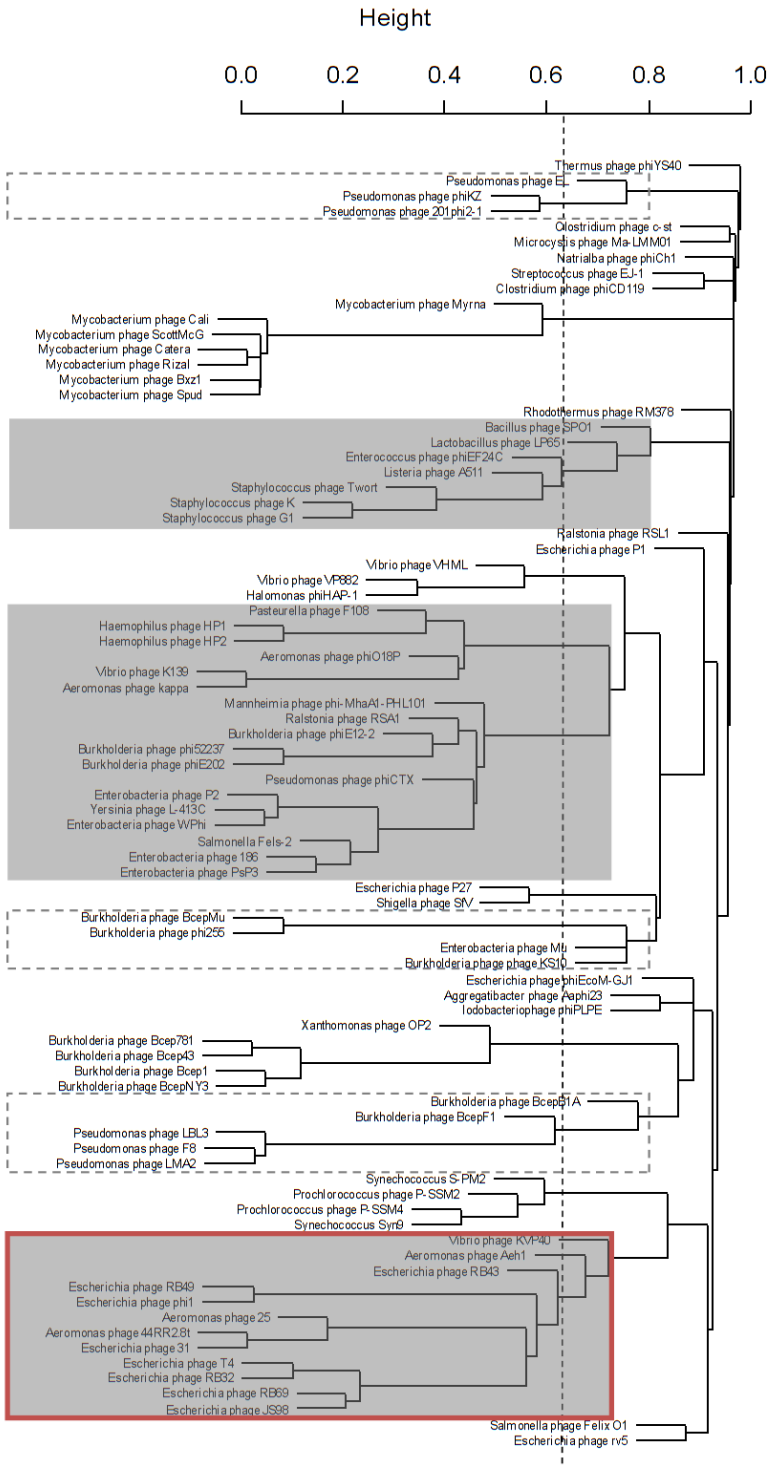


Figure 1: Hierarchical cluster dendrogram of the *Myoviridae*
The relative dissimilarity between the phage proteomes (between 0.0 and 1.0) forms the basis for the proposed groupings. The dotted lines reflects the cut-off value used for the establishement of genera, used consistently for all *Myoviridae* and the previously defined *Podoviridae* (Lavigne et al., 2008). Subfamily and tentative subfamily groupings are indicated in the grey and dotted boxes, respectively. The *Tevenvirinae* are within the red box.

Table 1: Type-specific proteins in T4 phages

Type (host)	Genome size (in kb)	Type-specific proteins
T4 (*E.coli*)	165.9-170.5	NP_049650, 049704, 049747, 049694 (Pin), 049626 (MotB), 049635 (ModA)
44RR2.8t (*Aeromonas*)	161.5-173.6	NP_932430, 932451, 932460, 932567, 932569, 932577
RB49 (*E. coli*)	164.1	NP_891619, 891621, 891622, 891626, 891736, 891753, 891760, 891800, 891816
RB43 (*E. coli*)	178.7	YP_239033, 239034, 239054, 239086, 239094, 239097, 239130, 239215, 239216, 239241

Table 2: Listing of the accession numbers of available *Tevenvirinae* genomes

Escherichia phage T4	NC_000866
Escherichia phage JS98	NC_010105
Escherichia phage RB14	not available in public database
Escherichia phage RB32	NC_008515
Escherichia phage RB69	NC_004928
Aeromonas phage 44RR2.8t	NC_005135
Aeromonas phage 31	NC_007022
Aeromonas phage 25	NC_008208
Escherichia phage RB43	NC_007023
Escherichia phage RB16	not available in public database
Escherichia phage RB49	NC_005066
Escherichia phage φ1	NC_009821
Vibrio phage KVP40	NC_005083
Vibrio phage nt-1	not available in public database
Acinetobacter phage 133	not available in public database
Aeromonas phage Aeh1	NC_005260
Aeromonas phage 65	not available in public database