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:** | ***2016.077a-pB*** | (to be completed by ICTV officers) |

**Short title:** To create one (1) new subfamily, *Arquatrovirinae*, containing three (3) new genera and fourteen (14) new species within the family *Siphoviridae*
(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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**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) | ICTV Bacterial and Archaeal Virus Subcommittee |

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

Date first submitted to ICTV: July 2016
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 | ***2016.077aB*** | (assigned by ICTV officers) |
|---|---|---|

**To create 2 new species within:**

| | |
|---|---|
| Genus: | ***R4virus* (new)** |
| Subfamily: | ***Arquatrovirinae* (new)** |
| Family: | ***Siphoviridae*** |
| 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)** |
|---|---|---|
| *Streptomyces virus R4* | Streptomyces phage R4 | JX262370 |
| *Streptomyces virus ELB20* | Streptomyces phage phiELB20 | JX262376 |

**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. The members of each of the proposed species differ from those of other species by 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 | ***2016.077bB*** | (assigned by ICTV officers) |
|---|---|---|

**To create a new genus within:**

| | |
|---|---|
| Subfamily: | ***Arquatrovirinae* (new)** |
| Family: | ***Siphoviridae*** |
| 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 | ***2016.077cB*** | (assigned by ICTV officers) |
|---|---|---|

**To name the new genus: *R4virus***

Assigning the type species and other species to a new genus

| Code | ***2016.077dB*** | (assigned by ICTV officers) |
|---|---|---|

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

| |
|---|
| ***Streptomyces virus R4*** |

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

The type species of this genus, *Streptomyces virus R4*, has a capsid of 64 nm in diameter and a laterally striated tail of 190 nm in length by 12.5 nm in diameter [6]. The genome is 51.1 kb in length, terminated by 11 bp cohesive termini [7]. Streptomyces phage ELB20 [8] shared 92.5% DNA similarity with Streptomyces phage R4 as calculated with Gegenees BLASTN [4]. Gegenees BLASTN/X [4] (Fig. 2,3), CoreGenes (Fig. 4) [2], and phylogenetic analyses (Fig. 1) [3] all indicate that the proposed genus, *R4virus*, is cohesive and distinct from other genera. The creation of this genus was proposed previously, but never formally submitted to ICTV [9].

**Origin of the new genus name:**

*Streptomyces* phage R4

**Reasons to justify the choice of type species:**

The first phage of its type to be 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. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.

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 | ***2016.077eB*** | (assigned by ICTV officers) |
|---|---|---|

**To create 9 new species within:**

| | |
|---|---|
| Genus: | ***Likavirus* (new)** |
| Subfamily: | ***Arquatrovirinae* (new)** |
| Family: | ***Siphoviridae*** |
| 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)** |
|---|---|---|
| *Streptomyces virus Lika* | Streptomyces phage Lika | KC700556 |
| *Streptomyces virus Sujidade* | Streptomyces phage Sujidade | KC700557 |
| *Streptomyces virus Zemlya* | Streptomyces phage Zemlya | KC700558 |
| *Streptomyces virus Danzina* | Streptomyces phage Danzina | KC124228 |
| *Streptomyces virus Hydra* | Streptomyces phage Hydra | KT124229 |
| *Streptomyces virus Izzy* | Streptomyces phage Izzy | KT184390 |
| *Streptomyces virus Caliburn* | Streptomyces phage Caliburn | KT152029 |
| *Streptomyces virus Aaronocolus* | Streptomyces phage Aaronocolus | KT124227 |
| *Streptomyces virus Lannister* | Streptomyces phage Lannister | KT184391 |

**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. The members of each of the proposed species differ from those of other species by 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 | ***2016.077fB*** | (assigned by ICTV officers) |
|---|---|---|

**To create a new genus within:**

| | |
|---|---|
| Subfamily: | ***Aquatrovirinae* (new)** |
| Family: | ***Siphoviridae*** |
| 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 | ***2016.077gB*** | (assigned by ICTV officers) |
|---|---|---|

**To name the new genus: *Likavirus***

Assigning the type species and other species to a new genus

| Code | ***2016.077hB*** | (assigned by ICTV officers) |
|---|---|---|

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

| | |
|---|---|
| ***Streptomyces virus Lika*** | 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:**

***9***

**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 phages belonging to the proposed genus *Likavirus* were isolated as part of the Phage Hunters Integrating Research and Education or Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science programs on several *Streptomyces* sp. as the hosts [8]. These phages were assigned to cluster BD, subcluster BD1.
Gegenees BLASTN/X [4] (Fig. 2,3), CoreGenes (Fig. 4) [2], and phylogenetic analyses (Fig. 1) [3] all indicate that the proposed genus, *Likavirus*, is cohesive and distinct from other genera. While the DNA-based analysis showed two subgroups within this genus (Fig. 2,3), these phages shared more than 85% of their proteome, warranting their inclusion in the same genus. The phages belonging to this genus have an average genome length of 50.5 kb and an average GC content of 66%. The creation of this genus was proposed previously, but never formally submitted to ICTV [9].

**Origin of the new genus name:**

Streptomyces phage Lika

**Reasons to justify the choice of type species:**

The first sequenced phage of its type

**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. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm. |

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 | ***2016.077iB*** | (assigned by ICTV officers) |
|---|---|---|

**To create 2 new species within:**

| | |
|---|---|
| Genus: | ***Camvirus* (new)** |
| Subfamily: | ***Arquatrovirinae* (new)** |
| Family: | ***Siphoviridae*** |
| 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)** |
|---|---|---|
| *Streptomyces virus phiCAM*<br>*Streptomyces virus Amela* | Streptomyces phage phiCAM<br>Streptomyces phage Amela | JX889246<br>KT186228 |

**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. The members of each of the proposed species differ from those of other species by 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 | ***2016.077jB*** | (assigned by ICTV officers) |
|---|---|---|

**To create a new genus within:**

| | |
|---|---|
| Subfamily: | ***Arquatrovirinae* (new)** |
| Family: | ***Siphoviridae*** |
| 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 | ***2016.077kB*** | (assigned by ICTV officers) |
|---|---|---|

**To name the new genus: *Camvirus***

Assigning the type species and other species to a new genus

| Code | ***2016.077lB*** | (assigned by ICTV officers) |
|---|---|---|

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

| |
|---|
| ***Streptomyces virus phiCAM*** |

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

The phages belonging to the proposed genus *Camvirus* were isolated as part of the Phage Hunters Integrating Research and Education or Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science programs on several *Streptomyces* sp. as the hosts [10]. These phages were assigned to cluster BD, subcluster BD3.
Gegenees BLASTN/X [4] (Fig. 2,3), CoreGenes (Fig. 4) [2], and phylogenetic analyses (Fig. 1) [3] all indicate that the proposed genus, *Camvirus*, is cohesive and distinct from other genera. The phages belonging to this genus have an average genome length of 50kb and an average GC content of 65.6%. Based on DNA homology greater than 95%, Streptomyces phage Verse (KT186229) is considered a strain of Streptomyces phage Amela.

**Origin of the new genus name:**

*Streptomyces* phage phiCAM

**Reasons to justify the choice of type species:**

The first phage of its type to be 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. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm. |

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 | ***2016.077mB*** | (assigned by ICTV officers) |
|---|---|---|

**To create 1 new species within:**

| | |
|---|---|
| Genus: | ***unassigned*** |
| Subfamily: | ***Arquatrovirinae* (new)** |
| Family: | ***Siphoviridae*** |
| 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)** |
|---|---|---|
| *Streptomyces virus phiHau3* | Streptomyces phage phiHau3 | JX182369 |

**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. The members of each of the proposed species differ from those of other species by 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 | ***2016.077nB*** | (assigned by ICTV officers) |
|---|---|---|

**To create a new subfamily within:**

| | |
|---|---|
| Family: | ***Siphoviridae*** |
| 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 | ***2016.077oB*** | (assigned by ICTV officers) |
|---|---|---|

**To name the new subfamily: *Arquatrovirinae***

genera and species assigned to the new subfamily

| Code | ***2016.077pB*** | (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

***Likavirus* (new)**

***R4virus* (new)**

***Camvirus* (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):**

***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

Genomic and proteomic analyses showed that the genera presented here are related, yet distinct from other siphovirus genera. This has been recognized previously by the Actinobacteriophage database (phagesdb.org) since these phages are all assigned to the same cluster. Previous publications have also recognized the evolutionary relationship [8,9].

**Origin of the new subfamily name:**

***Named after Streptomyces virus R4, the first sequenced isolate of this subfamily.***

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

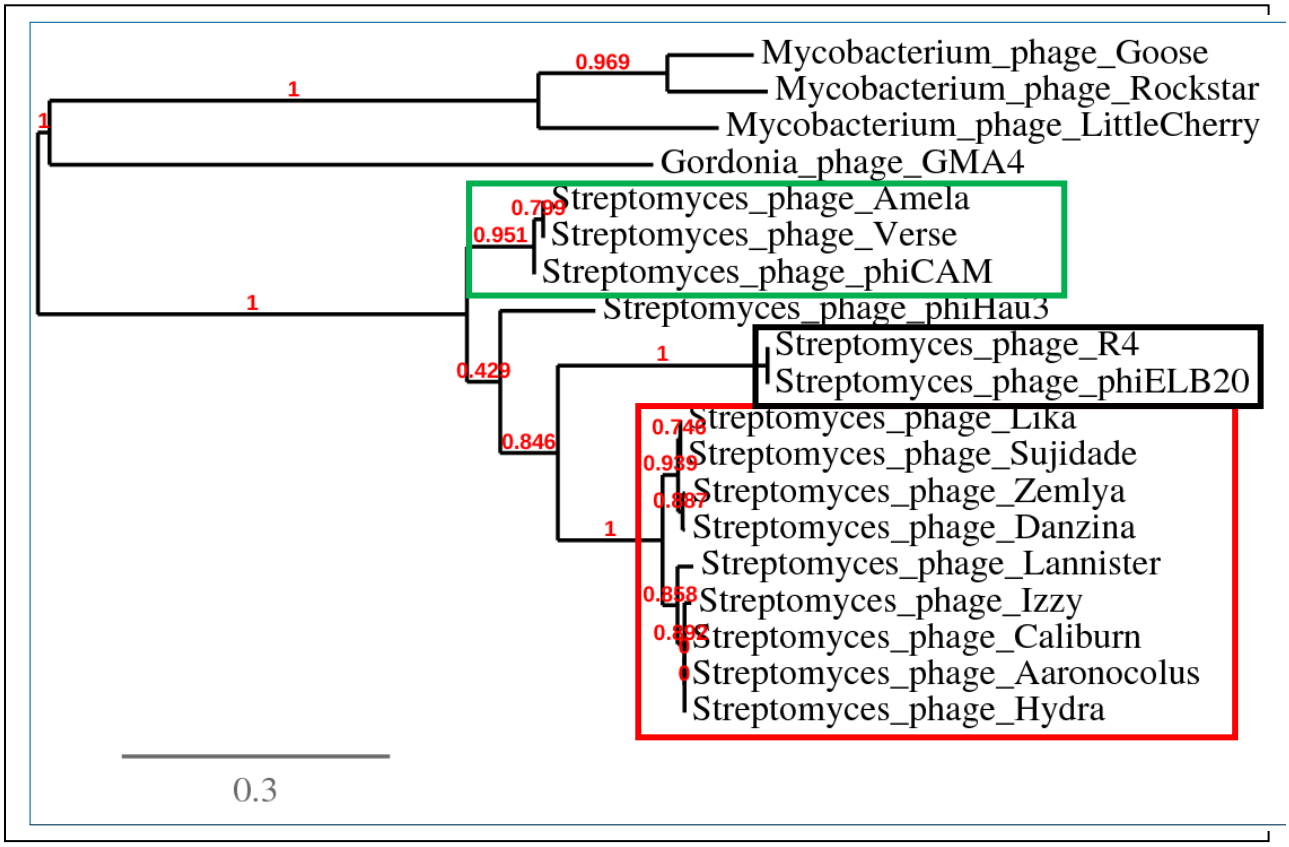

1. Darling AE, Mau B, Perna NT. (2010) progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One; 5(6):e11147.
2. Turner D, Reynolds D, Seto D, Mahadevan P. (2013) CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes; 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. Agren J et al. (2012) Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One.;7(6):e39107
5. Huson DH & Bryant D (2006) Application of phylogenetic networks in evolutionary studies. Mol Biol Evol. 23: 254-67.
6. Chater, K.F., Carter, A.T., 1979. A new, wide host-range, temperate bacteriophage (R4) of Streptomyces and its interaction with some restriction-modification systems. J. Gen. Microbiol. 115, 431–442.
7. Mitsui, H., Takahashi, H., 1992. Cohesive single-stranded ends of Streptomyces temperate bacteriophage R4. Mol. Gen. Genet. 231, 360–362.
8. Smith, M.C.M., Hendrix, R.W., Dedrick, R., Mitchell, K., Ko, C.-C., Russell, D., Bell, E., Gregory,M., Bibb,M.J., Pethick, F., Jacobs-Sera,D., Herron, P., Buttner,M.J.,Hatfull, G.F., 2013. Evolutionary relationships among actinophages and a putative adaptation for growth in Streptomyces spp. J. Bacteriol. 195, 4924–4935. http://dx.doi.org/10.1128/
9. Adriaenssens, E.M., Edwards, R., Nash, J.H.E., Mahadevan, P., Seto, D., Ackermann, H-W, Lavigne, R., Kropinski, A.M (2015) Integration of genomic and proteomic analyses in the classification of the *Siphoviridae* family. Virol. 477:144-154.
10. Monson R, Salmond GP. Genome sequence of a new *Streptomyces coelicolor* generalized transducing bacteriophage, ΦCAM. J Virol. 2012 Dec;86(24):13860


**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.** Phylogenetic analysis of terminases (A) and repressor proteins (B) of the phages which make up the *Arquatrovirinae* and homologous proteins from *Mycobacterium* phages as outliers 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." *Likavirus* in **red**; *R4virus* in **black** and *Camvirus* in **green**.

**A. Terminase, large subunit**



**B. Repressor proteins**

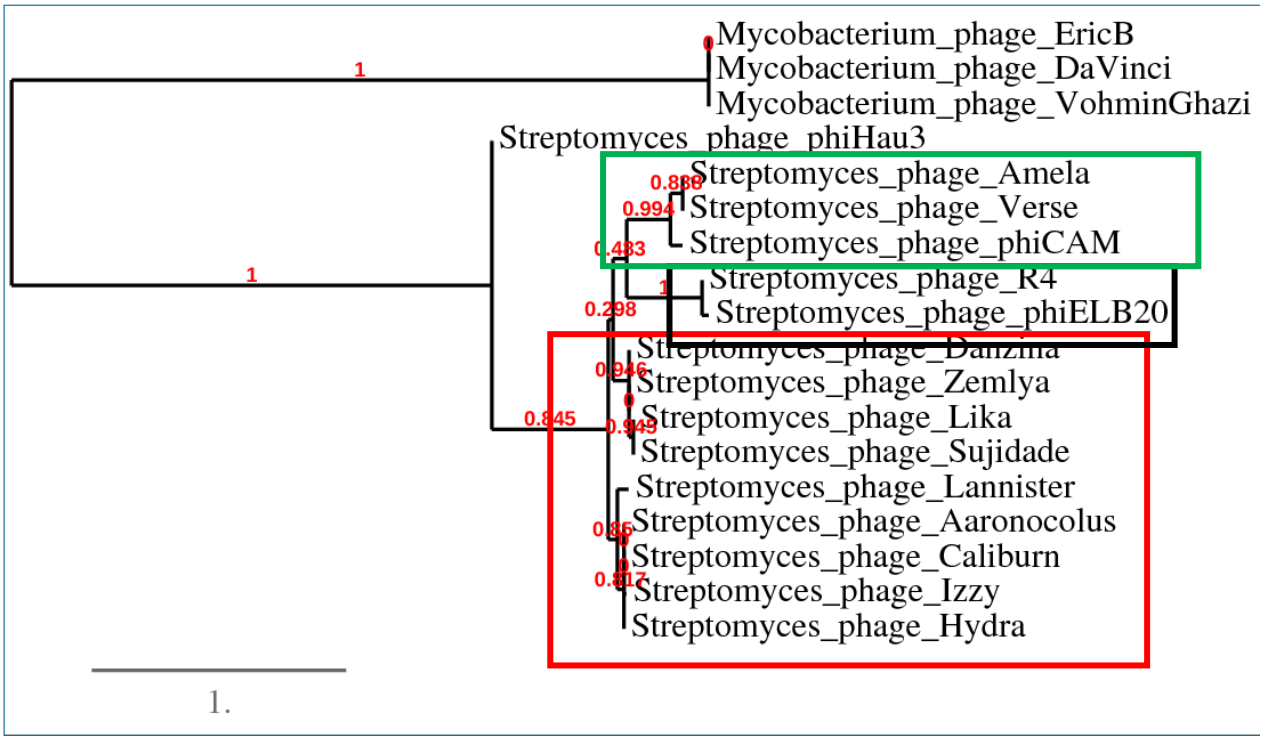



**Figure 1:** *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

**Fig 2.** Genomic comparison of *Streptomyces* bacteriophages. Similarity values were calculated using Gegenees 2.2.1 based on pairwise comparisons of the analyzed sequences (BLASTN method with "custom" settings of fragmenting algorithm – window size: 100 bp, shift 50 bp) [4]. The results were exported to Excel.

| PHAGE | ACCESSION NO. | aj006589.3 | kt221033.1 | ay320035.2 | dq372923.1 | gq379227.1 | jx182371.1 | km652554.1 | JX182372.1 | aj550940.2 | JX182369.1 | kp876466.1 | kp876465.1 | kt186229.1 | kt186228.1 | jx889246.1 | jx262376.1 | jx182370.1 | kt184391.1 | kc700557.1 | kc700556.1 | kc700558.1 | kt124228.1 | kt184390.1 | kt124229.1 | kt152029.1 | kt124227.1 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| phiC31 | aj006589.3 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 4.6 | 15.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| SF1 | kt221033.1 | 0.0 | 100.0 | 1.5 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| VWB | ay320035.2 | 0.0 | 1.3 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| mu1/6 | dq372923.1 | 0.0 | 0.0 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| phiSASD1 | gq379227.1 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| SV1 | jx182371.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Jay2Jay | km652554.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| TG1 | JX182372.1 | 4.9 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 2.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| phi-BT1 | aj550940.2 | 15.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 2.3 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| phiHau3 | JX182369.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 0.0 | 0.0 | 1.1 | 1.2 | 0.8 | 2.5 | 2.6 | 1.0 | 1.1 | 1.3 | 0.9 | 0.7 | 0.8 | 1.0 | 1.3 | 1.2 |
| TP1604 | kp876466.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 50.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| YDN12 | kp876465.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 51.0 | 100.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Verse | kt186229.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.1 | 0.0 | 0.0 | 100.0 | 95.5 | 37.3 | 1.4 | 1.2 | 5.2 | 4.6 | 4.5 | 4.7 | 4.6 | 3.8 | 5.7 | 5.3 | 5.4 |
| Amela | kt186228.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.1 | 0.0 | 0.0 | 95.5 | 100.0 | 37.5 | 1.6 | 1.5 | 5.1 | 4.7 | 4.7 | 4.8 | 4.6 | 4.2 | 5.8 | 5.4 | 5.4 |
| phiCAM | jx889246.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.9 | 0.0 | 0.0 | 36.3 | 36.9 | 100.0 | 2.0 | 1.9 | 4.8 | 4.2 | 4.5 | 4.8 | 4.5 | 4.5 | 5.3 | 5.4 | 4.8 |
| phiELB20 | jx262376.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 2.6 | 0.0 | 0.0 | 1.4 | 1.5 | 2.0 | 100.0 | 92.5 | 3.9 | 2.1 | 2.4 | 2.4 | 2.2 | 3.1 | 3.4 | 3.4 | 3.5 |
| R4 | jx182370.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 2.6 | 0.0 | 0.0 | 1.3 | 1.5 | 1.8 | 92.2 | 100.0 | 3.9 | 1.9 | 2.2 | 2.3 | 2.1 | 3.0 | 3.4 | 3.5 | 3.5 |
| Lannister | kt184391.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.1 | 0.0 | 0.0 | 5.4 | 5.2 | 5.1 | 4.2 | 4.3 | 100.0 | 36.4 | 36.2 | 34.0 | 33.1 | 27.6 | 29.7 | 29.5 | 29.7 |
| Sujidade | kc700557.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 4.5 | 4.3 | 4.1 | 2.0 | 2.2 | 35.2 | 100.0 | 85.7 | 63.7 | 63.4 | 22.1 | 23.5 | 23.1 | 22.9 |
| Lika | kc700556.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.3 | 0.0 | 0.0 | 4.3 | 4.3 | 4.4 | 2.5 | 2.7 | 34.9 | 86.6 | 100.0 | 64.1 | 63.2 | 22.0 | 23.6 | 23.3 | 23.1 |
| Zemlya | kc700558.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 4.4 | 4.4 | 4.5 | 2.5 | 2.7 | 33.3 | 64.0 | 64.4 | 100.0 | 90.4 | 22.2 | 23.8 | 23.4 | 23.9 |
| Danzina | kt124228.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.0 | 0.0 | 4.5 | 4.4 | 4.5 | 2.2 | 2.4 | 32.6 | 63.9 | 63.5 | 90.9 | 100.0 | 22.3 | 23.9 | 23.7 | 23.6 |
| Izzy | kt184390.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.9 | 0.0 | 0.0 | 3.8 | 4.1 | 4.8 | 3.3 | 3.4 | 28.1 | 22.6 | 22.5 | 23.5 | 23.5 | 100.0 | 71.0 | 73.4 | 76.2 |
| Hydra | kt124229.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 5.3 | 5.1 | 5.0 | 3.2 | 3.4 | 29.6 | 23.6 | 23.9 | 24.0 | 23.9 | 70.0 | 100.0 | 92.6 | 88.8 |
| Caliburn | kt152029.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.3 | 0.0 | 0.0 | 5.2 | 4.9 | 5.4 | 3.2 | 3.4 | 30.5 | 23.3 | 23.9 | 24.2 | 24.0 | 73.3 | 94.1 | 100.0 | 93.6 |
| Aaronocolus | kt124227.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.3 | 0.0 | 0.0 | 5.9 | 5.5 | 5.2 | 3.6 | 3.7 | 30.9 | 23.7 | 24.7 | 24.9 | 24.4 | 77.1 | 90.8 | 94.1 | 100.0 |

**Fig. 3.** Genomic comparison of *Streptomyces* bacteriophages. Similarity values were calculated using Gegenees 2.2.1 based on pairwise translated comparison of the analyzed sequences (TBLASTX method, "custom" settings of fragmenting algorithm – window size: 100 bp, shift 50 bp) [4]. The results were exported to Excel.

| PHAGE | ACCESS-ION NO. | aj006589.3 | aj550940.2 | JX182372.1 | kt221033.1 | ay320035.2 | dq372923.1 | jx182371.1 | gq379227.1 | kp876466.1 | kp876465.1 | km652554.1 | JX182369.1 | jx262376.1 | jx182370.1 | jx889246.1 | kt186229.1 | kt186228.1 | kt184391.1 | kc700557.1 | kc700556.1 | kc700558.1 | kt124228.1 | kt184390.1 | kt124227.1 | kt152029.1 | kt124229.1 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| phiC31 | aj006589.3 | 100.0 | 65.8 | 58.3 | 30.2 | 30.1 | 29.6 | 30.2 | 31.7 | 29.3 | 29.2 | 27.1 | 30.7 | 30.5 | 30.6 | 29.5 | 29.8 | 29.8 | 29.9 | 30.0 | 30.2 | 30.0 | 30.0 | 29.9 | 29.9 | 29.9 | 30.0 |
| phi-BT1 | aj550940.2 | 65.0 | 100.0 | 55.7 | 29.6 | 29.6 | 28.9 | 29.7 | 31.4 | 28.9 | 28.8 | 26.9 | 30.0 | 29.9 | 29.9 | 29.2 | 29.3 | 29.3 | 29.4 | 29.4 | 29.4 | 29.6 | 29.5 | 29.6 | 29.4 | 29.4 | 29.5 |
| TG1 | JX182372.1 | 58.9 | 56.7 | 100.0 | 30.6 | 30.8 | 29.9 | 30.9 | 32.4 | 29.8 | 29.8 | 27.2 | 31.2 | 30.9 | 31.0 | 30.0 | 30.0 | 30.1 | 30.3 | 30.4 | 30.3 | 30.4 | 30.3 | 30.3 | 30.5 | 30.4 | 30.4 |
| SF1 | kt221033.1 | 29.7 | 29.4 | 30.4 | 100.0 | 41.7 | 31.7 | 32.9 | 30.7 | 31.6 | 31.7 | 27.4 | 32.0 | 31.9 | 31.7 | 31.1 | 31.2 | 31.3 | 31.4 | 31.2 | 31.4 | 31.3 | 31.4 | 31.3 | 31.6 | 31.5 | 31.7 |
| VWB | ay320035.2 | 29.8 | 29.5 | 30.5 | 40.6 | 100.0 | 33.7 | 33.4 | 29.9 | 32.2 | 32.2 | 27.7 | 32.6 | 32.5 | 32.5 | 31.5 | 31.5 | 31.5 | 31.8 | 31.8 | 31.9 | 32.0 | 32.1 | 31.9 | 32.1 | 32.0 | 32.0 |
| mu1/6 | dq372923.1 | 29.0 | 28.5 | 29.8 | 31.7 | 34.0 | 100.0 | 33.5 | 30.5 | 32.2 | 32.2 | 27.3 | 32.6 | 32.2 | 32.3 | 31.2 | 31.5 | 31.5 | 31.6 | 31.5 | 31.5 | 31.7 | 31.6 | 31.4 | 31.6 | 31.7 | 31.6 |
| SV1 | jx182371.1 | 30.3 | 30.0 | 31.5 | 33.7 | 34.1 | 34.0 | 100.0 | 30.9 | 33.2 | 33.2 | 27.9 | 33.3 | 32.9 | 32.8 | 31.9 | 32.2 | 32.3 | 32.4 | 32.3 | 32.5 | 32.5 | 32.5 | 32.3 | 32.5 | 32.6 | 32.6 |
| phiSASD1 | gq379227.1 | 31.4 | 31.3 | 32.1 | 31.0 | 30.2 | 30.5 | 30.3 | 100.0 | 30.3 | 30.6 | 26.7 | 30.6 | 30.7 | 30.6 | 29.9 | 30.1 | 30.0 | 30.0 | 30.1 | 30.1 | 30.3 | 30.2 | 30.3 | 30.3 | 30.4 | 30.4 |
| TP1604 | kp876466.1 | 27.8 | 27.7 | 28.4 | 30.6 | 31.1 | 31.1 | 31.5 | 29.4 | 100.0 | 78.8 | 27.2 | 31.1 | 31.1 | 31.0 | 30.3 | 30.4 | 30.5 | 30.5 | 30.5 | 30.5 | 30.4 | 30.5 | 30.5 | 30.7 | 30.7 | 30.8 |
| YDN12 | kp876465.1 | 27.9 | 27.7 | 28.6 | 30.7 | 31.1 | 31.3 | 31.6 | 29.6 | 79.4 | 100.0 | 27.0 | 31.3 | 31.1 | 31.2 | 30.6 | 30.5 | 30.5 | 30.7 | 30.6 | 30.7 | 30.7 | 30.6 | 30.8 | 30.8 | 30.8 | 30.8 |
| Jay2Jay | km652554.1 | 24.3 | 24.3 | 24.3 | 24.8 | 24.8 | 24.7 | 24.5 | 24.3 | 25.2 | 25.1 | 100.0 | 24.9 | 24.9 | 24.9 | 25.0 | 25.0 | 24.9 | 25.2 | 25.2 | 25.2 | 25.2 | 25.2 | 25.2 | 25.1 | 25.1 | 25.1 |
| phiHau3 | JX182369.1 | 29.8 | 29.4 | 30.5 | 31.7 | 32.2 | 32.2 | 32.4 | 30.3 | 32.0 | 32.1 | 27.6 | 100.0 | 50.7 | 50.5 | 47.1 | 47.5 | 47.5 | 48.5 | 48.0 | 47.9 | 48.2 | 48.1 | 48.6 | 48.6 | 48.6 | 48.6 |
| phiELB20 | jx262376.1 | 29.7 | 29.3 | 30.2 | 31.6 | 32.4 | 32.1 | 32.3 | 30.3 | 31.8 | 31.8 | 27.7 | 50.3 | 100.0 | 96.2 | 48.2 | 48.1 | 48.0 | 50.4 | 50.4 | 50.5 | 50.4 | 50.2 | 50.9 | 50.7 | 50.8 | 50.9 |
| R4 | jx182370.1 | 29.6 | 29.3 | 30.3 | 31.6 | 32.3 | 32.1 | 32.3 | 30.3 | 31.8 | 31.8 | 27.8 | 50.4 | 96.2 | 100.0 | 48.4 | 48.2 | 48.2 | 50.4 | 50.4 | 50.5 | 50.3 | 50.2 | 51.0 | 50.8 | 50.9 | 51.0 |
| phiCAM | jx889246.1 | 28.4 | 28.4 | 29.1 | 30.7 | 31.0 | 30.8 | 31.0 | 29.3 | 30.7 | 30.9 | 27.5 | 47.1 | 48.1 | 48.1 | 100.0 | 70.9 | 70.7 | 52.6 | 51.3 | 51.4 | 51.5 | 51.3 | 52.7 | 53.2 | 53.3 | 53.4 |
| Verse | kt186229.1 | 28.7 | 28.6 | 29.5 | 30.9 | 31.1 | 30.9 | 31.2 | 29.6 | 31.0 | 31.0 | 27.5 | 47.7 | 48.5 | 48.6 | 71.8 | 100.0 | 96.8 | 53.0 | 52.4 | 52.4 | 51.9 | 51.8 | 53.8 | 54.6 | 54.6 | 54.7 |
| Amelia | kt186228.1 | 28.8 | 28.7 | 29.5 | 31.0 | 31.2 | 31.0 | 31.3 | 29.6 | 31.1 | 31.0 | 27.6 | 47.7 | 48.4 | 48.6 | 71.6 | 96.8 | 100.0 | 52.7 | 52.1 | 52.2 | 51.8 | 51.6 | 53.9 | 54.5 | 54.6 | 54.7 |
| Lannister | kt184391.1 | 29.1 | 28.8 | 29.7 | 31.0 | 31.4 | 31.2 | 31.3 | 29.6 | 31.1 | 31.2 | 27.8 | 48.5 | 50.5 | 50.5 | 52.8 | 52.7 | 52.5 | 100.0 | 72.9 | 72.4 | 71.9 | 71.7 | 68.5 | 68.8 | 69.0 | 68.7 |
| Sujidade | kc700557.1 | 29.1 | 28.8 | 29.6 | 31.0 | 31.5 | 31.3 | 31.4 | 29.7 | 31.0 | 31.0 | 27.8 | 47.5 | 50.0 | 50.1 | 51.0 | 51.5 | 51.2 | 71.9 | 100.0 | 92.8 | 83.7 | 83.7 | 65.9 | 65.6 | 65.9 | 65.5 |
| Lika | kc700556.1 | 29.1 | 28.8 | 29.5 | 31.0 | 31.5 | 31.1 | 31.4 | 29.5 | 31.0 | 31.2 | 27.9 | 47.6 | 50.3 | 50.3 | 51.3 | 51.7 | 51.4 | 71.6 | 93.2 | 100.0 | 84.3 | 84.0 | 65.9 | 65.6 | 65.8 | 65.6 |
| Zemlya | kc700558.1 | 29.1 | 28.8 | 29.5 | 31.0 | 31.5 | 31.2 | 31.3 | 29.6 | 31.2 | 31.2 | 28.0 | 47.7 | 50.1 | 50.1 | 51.2 | 51.2 | 51.0 | 71.2 | 84.2 | 84.5 | 100.0 | 95.4 | 66.8 | 66.2 | 65.6 | 65.5 |
| Danzina | kt124228.1 | 28.9 | 28.8 | 29.5 | 30.9 | 31.5 | 31.2 | 31.4 | 29.6 | 31.0 | 31.3 | 28.0 | 47.7 | 50.0 | 50.1 | 51.3 | 51.1 | 50.9 | 71.2 | 84.5 | 84.4 | 95.7 | 100.0 | 67.1 | 66.6 | 65.9 | 65.6 |
| Izzy | kt184390.1 | 28.9 | 28.9 | 29.6 | 30.9 | 31.3 | 31.1 | 31.3 | 29.8 | 31.1 | 31.2 | 27.9 | 48.6 | 51.1 | 51.1 | 53.1 | 53.5 | 53.5 | 68.6 | 67.0 | 66.8 | 67.3 | 67.5 | 100.0 | 87.6 | 86.1 | 84.6 |
| Aaronocolus | kt124227.1 | 29.2 | 29.0 | 29.7 | 31.1 | 31.7 | 31.4 | 31.8 | 29.9 | 31.4 | 31.4 | 28.1 | 48.9 | 51.2 | 51.2 | 53.8 | 54.5 | 54.5 | 69.3 | 67.2 | 67.0 | 67.5 | 67.7 | 88.5 | 100.0 | 96.4 | 94.4 |
| Hydra | kt152029.1 | 29.3 | 28.8 | 29.9 | 31.3 | 31.8 | 31.5 | 31.7 | 30.1 | 31.5 | 31.5 | 28.1 | 48.8 | 51.1 | 51.2 | 53.8 | 54.3 | 54.4 | 69.4 | 67.2 | 66.9 | 66.6 | 66.6 | 86.6 | 95.9 | 100.0 | 96.4 |
| Caliburn | kt124229.1 | 29.3 | 29.0 | 29.8 | 31.2 | 31.9 | 31.6 | 31.8 | 30.2 | 31.5 | 31.6 | 28.0 | 48.5 | 51.1 | 51.1 | 53.5 | 54.1 | 54.1 | 68.6 | 66.3 | 66.2 | 65.9 | 65.8 | 84.2 | 93.0 | 95.4 | 100.0 |

**Fig. 4.** CoreGenes 3.5 analysis of selected members of the subfamily *Arquatrovirinae*. The three genera and singleton species are boxed in black.

| Phage | Accession | R4 | phiELB20 | Izzy | Hydra | Caliburn | Aaronocu | Lika | Sujidade | Zemlya | Danzina | Lannister | phiHau3 | phiCAM | Amela | Verse |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Streptomyces virus R4* | JX182370 | 100 | 96.3 | 78.67 | 77.63 | 80.56 | 82.19 | 80 | 77.92 | 78.97 | 78.95 | 79.45 | 73.61 | 76.39 | 76 | 76 |
| *Streptomyces virus phiELB20* | JX262376 | 90.7 | 100 | 78.67 | 77.63 | 80.56 | 82.19 | 80 | 77.92 | 78.95 | 78.95 | 80.82 | 72.22 | 76.39 | 76 | 76 |
| *Streptomyces virus Izzy* | KT184390 | 68.6 | 72.84 | 100 | 92.11 | 97.22 | 98.63 | 92 | 89.61 | 90.79 | 90.79 | 90.41 | 73.61 | 83.33 | 84 | 84 |
| *Streptomyces virus Hydra* | KT124229 | 68.6 | 72.84 | 93.33 | 100 | 98.61 | 97.26 | 93.33 | 89.61 | 92.11 | 90.79 | 90.41 | 72.22 | 83.33 | 85.33 | 85.33 |
| *Streptomyces virus Caliburn* | KT152029 | 67.44 | 71.6 | 93.33 | 93.42 | 100 | 97.26 | 90.67 | 88.31 | 89.47 | 89.47 | 89.04 | 70.83 | 83.33 | 84 | 84 |
| *Streptomyces virus Aaronocolu* | KT124227 | 69.77 | 74.07 | 96 | 93.42 | 98.6 | 100 | 93.33 | 90.91 | 92.11 | 92.11 | 91.78 | 71.23 | 84.72 | 85.33 | 85.33 |
| *Streptomyces virus Lika* | KC700556 | 69.77 | 74.07 | 92 | 92.11 | 94.44 | 95.89 | 100 | 94.81 | 97.37 | 96.05 | 91.78 | 72.22 | 84.72 | 85.33 | 85.33 |
| *Streptomyces virus Sujidade* | KC700557 | 69.77 | 74.07 | 92 | 90.79 | 94.44 | 95.89 | 97.33 | 100 | 94.74 | 96.05 | 91.78 | 69.44 | 83.33 | 86.67 | 86.67 |
| *Streptomyces virus Zemlya* | KC700558 | 69.77 | 74.07 | 92 | 92.11 | 94.44 | 95.89 | 98.67 | 93.51 | 100 | 97.37 | 91.78 | 70.83 | 83.33 | 86.67 | 86.67 |
| *Streptomyces virus Danzina* | KT124228 | 69.77 | 74.07 | 92 | 90.79 | 94.44 | 95.89 | 97.33 | 94.81 | 97.37 | 100 | 93.15 | 69.44 | 83.33 | 86.67 | 86.67 |
| *Streptomyces virus Lannister* | KT184391 | 67.44 | 72.84 | 88 | 86.84 | 90.28 | 91.78 | 89.33 | 87.01 | 88.16 | 89.47 | 100 | 72.22 | 83.33 | 84 | 84 |
| *Streptomyces virus Hau3* | JX182369 | 61.63 | 64.2 | 70.67 | 68.42 | 70.83 | 71.23 | 69.33 | 64.94 | 67.11 | 65.79 | 71.23 | 100 | 65.28 | 65.33 | 65.33 |
| *Streptomyces virus phiCAM* | JX889246 | 63.95 | 67.9 | 80 | 78.95 | 83.33 | 83.56 | 81.33 | 77.92 | 78.95 | 78.95 | 82.19 | 65.28 | 100 | 89.33 | 89.33 |
| *Streptomyces virus Amela* | KT186228 | 66.28 | 70.37 | 84 | 84.21 | 87.5 | 87.67 | 85.33 | 84.42 | 85.53 | 85.53 | 86.3 | 68.06 | 93.06 | 100 | 100 |
| *Streptomyces phage Verse* | KT186229 | 66.28 | 66.28 | 84 | 84.21 | 87.5 | 87.67 | 85.33 | 84.42 | 85.53 | 85.53 | 86.3 | 68.06 | 93.06 | 100 | 100 |

**Table 1.** Properties of the type virus for each of the above mentioned genera.

| Streptomyces phage | RefSeq No | GenBank Accession No. | Genome length (kb) | GC % | Protein | tRNA |
|---|---|---|---|---|---|---|
| Lika* | NC_021298 | KC700556 | 51.25 | 65.8 | 75 | 0 |
| R4 | NC_019414 | JX182370 | 51.07 | 67.0 | 86 | 1 |
| phiCAM | - | JX889246 | 50.35 | 65.6 | 72 | 0 |

* 3' overhang (length of sequence not given) ** 11 bp 3' overhang (CGGGCAGTGAT),

**Fig. 5.** Electron micrographs of negatively stained phage Lika (http://phagesdb.org/phages/Lika/) - Limited permission was granted by The Actinobacteriophages Database, funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.