

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2021.091B** |  |
| **Short title:** Create one new subfamily (*Weiservirinae*)including eight genera (*Caudoviricetes*) | | |
|  | | |

**Author(s) and email address(es)**

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**Corresponding author**

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| --- |
| Andrew Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

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| Actinobacteriophages Study Group, Bacterial Viruses Subcommittee |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2021 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2021.091B.R.Weiservirinae |

**Abstract**

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| The taxon *Tm4likevirus* (ultimately renamed *Timquatrovirus*) was established through Taxonomy Proposal 2013.022a-dB with nine species. Subsequent analysis by the Actinobacteriophage Database reveals that this is a heterogeneous group of phages. The current proposal which relies on the Actinobacteriophage Database, VIRIDIC, ViPTree and phylogenetic analyses proposes the creation of eight genera within a new subfamily named *Weiservirinae* in honour of Russell S. Weiser (1906-2000) who together with Grace M. Gardner (1924-2007) characterized the first phages against Mycobacterium smegmatis in 1947 in the Department of Microbiology, School of Medicine, University of Washington, Seattle (USA).  The average properties of members of this subfamily are genome size 59.78 kb (66.9 mol%G+C) encoding 97 proteins and 0-2 tRNA.  CoreGenes 5.0 analysis at <https://coregenes.ngrok.io/> revealed 34 homologous proteins (35%) including the large subunit terminase, portal protein, MuF-like minor capsid protein, scaffolding protein, major capsid protein, head-to-tail adaptor, head-to-tail stopper, tail terminator protein, two tail assembly chaperones, tape measure protein, six minor tail proteins, lysin B, double-strand break endo/exonuclease, Cas4 family exonuclease, NrdH-like glutaredoxin and seven hypothetical proteins. |

**Text of proposal**

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**Supporting evidence**

**Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.

These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic distance calculator VIRIDIC [3].

**Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree.

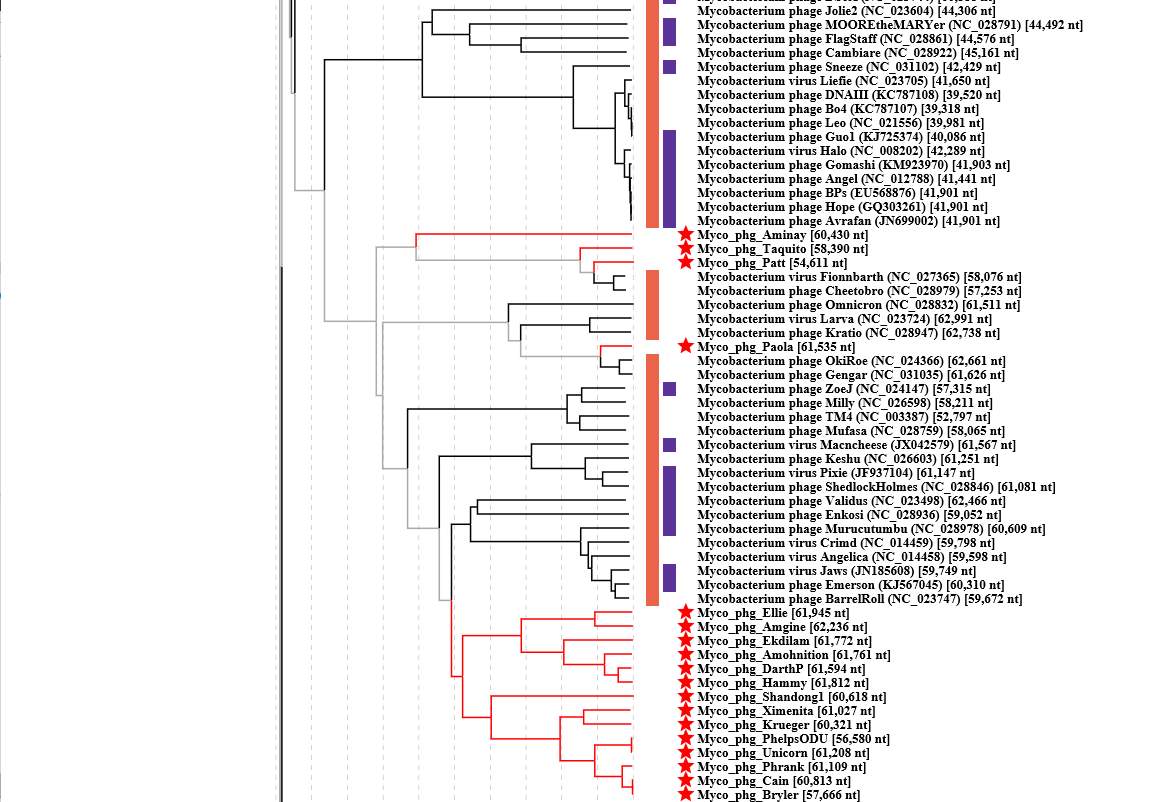
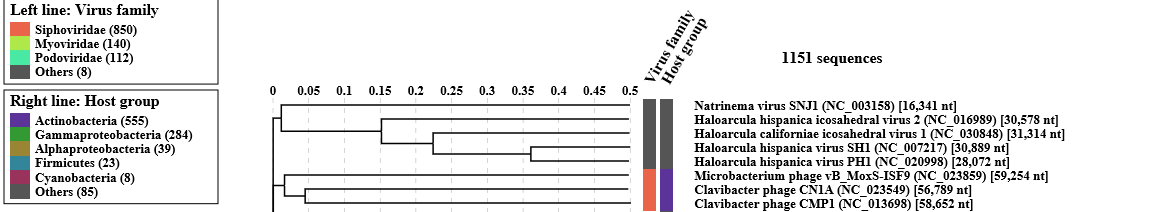
**Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity and that the genera form a clade in a marker tree phylogeny.

**Family demarcation criteria: -** The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (VipTree, GRAViTy, vConTACT2). Members of the family share a significant number of orthologous genes (more than 10% of the genome).

(Taken from: Turner D et al. [9] )

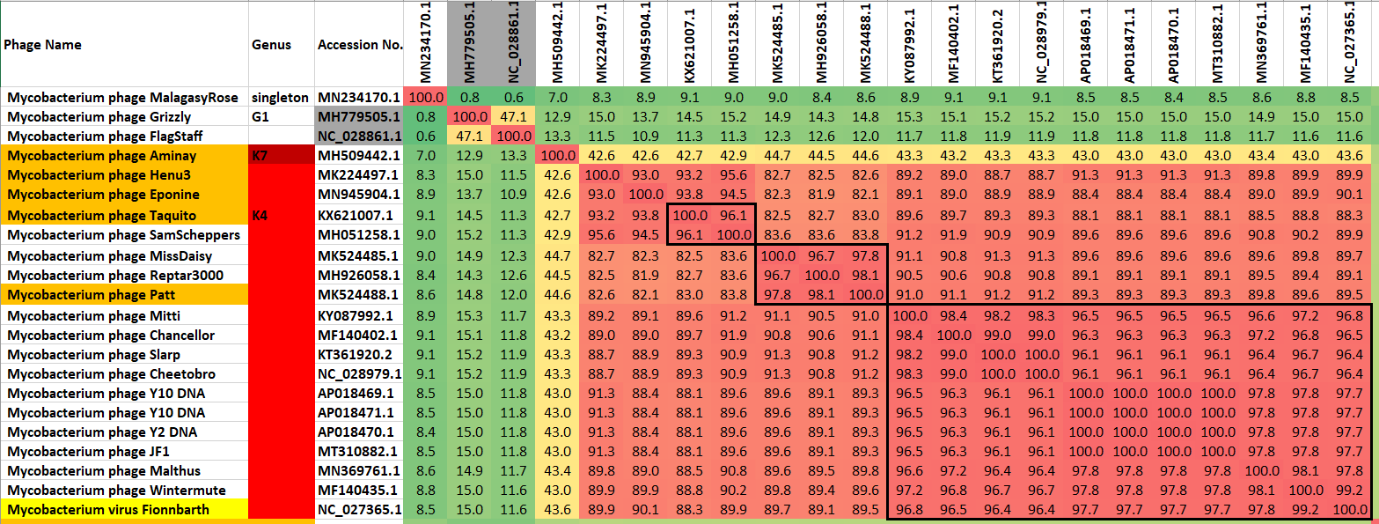
**Molecular analysis:**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. Phages under consideration are marked with a **blue bar**.

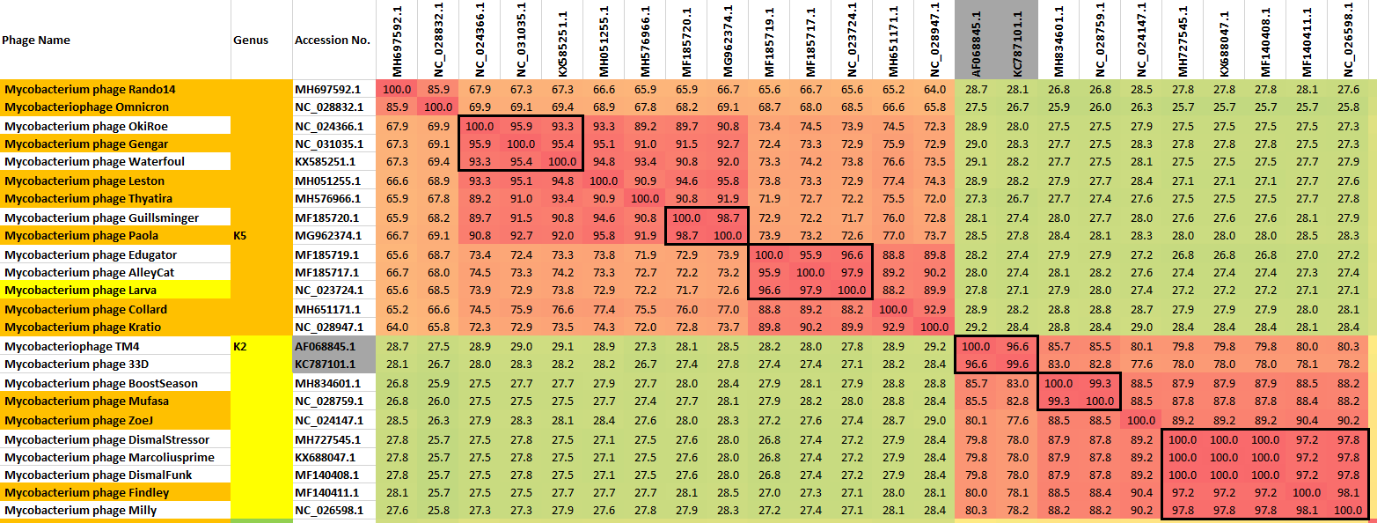
  


**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. Because of the huge number of isolates the *Anayavirus* heat map is attached as a separate file. Yellow coloured names correspond to currently defined *Timquatrovirus* species, the golden names correspond to new species. (file attached).

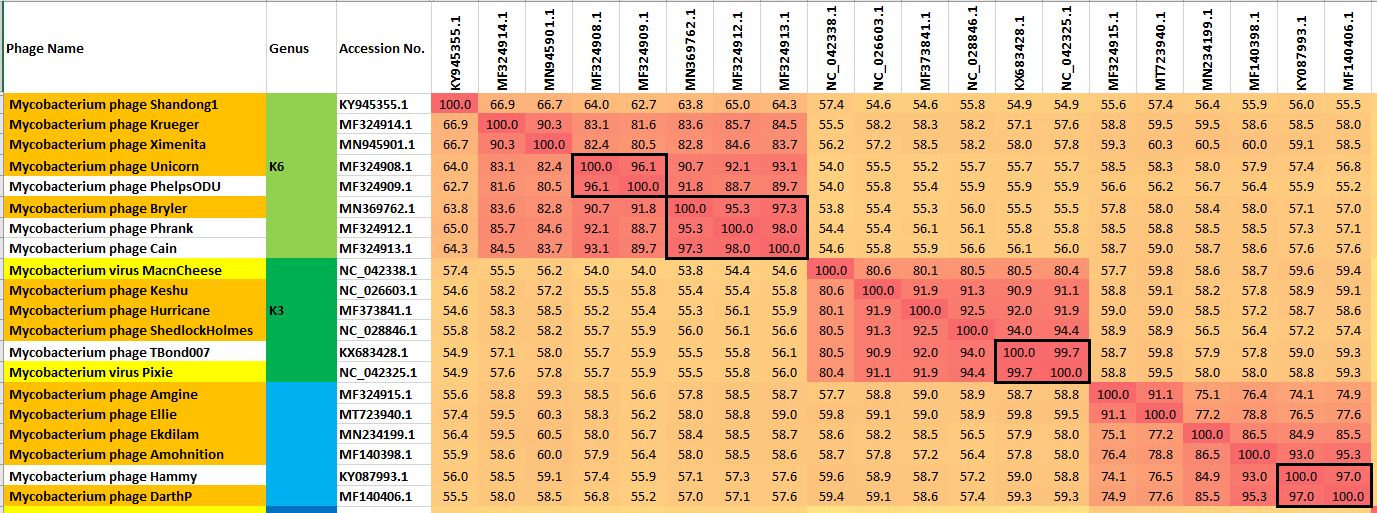
1. ***Aminayvirus* and *Fionnbharthvirus***

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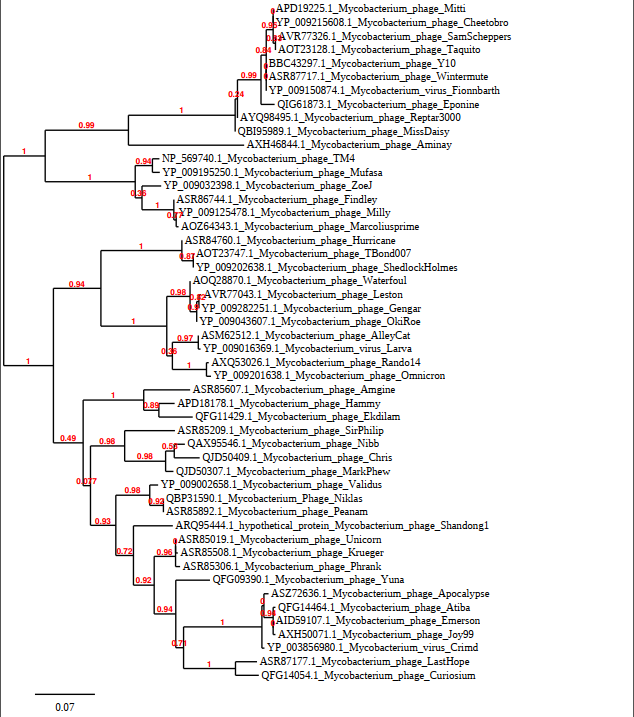
1. ***Kratiovirus* and *Timquatrovirus***

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1. ***Unicornvirus*, *Keshuvirus* and *Ellievirus***

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**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of some of these phages with phylogeny.fr in “one click” mode [5]. "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 [6] for details."

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**Proposals:**

**Proposal A: To create a new genus *Aminayvirus***

**Proposal B: To create a new genus *Fionnbharthvirus***

**Proposal C: T create a new genus *Kratiovirus***

**Proposal D: To update the genus *Timquatrovirus***

**Proposal E: To create a new genus *Unicornvirus***

**Proposal F: To create a new genus *Keshuvirus***

**Proposal G: To create a new genus *Amginevirus***

**Proposal H: To create a new genus *Anayavirus***

**Proposal I: To create a new subfamily *Weiservirinae* containing these seven genera**

**1. Proposal A: To create a new genus *Aminayvirus***

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Aminay

**History:** Temperate Mycobacterium phage Aminay was isolated from Bangor, ME USA soil by Alejandro Casillas and Arabella Sillsby (University of Maine, Honors College) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2016. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 12 nt 3'-cohesive termini (CTCATCGTGGGT). The Actinobacteriophage Database places this phage in Cluster/Subcluster K/K7 (<https://phagesdb.org/phages/Aminay/>).

**Specific Reference:** None

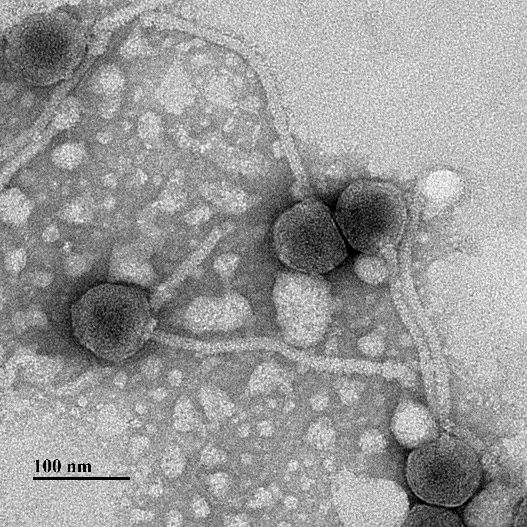
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Aminay |  | [MH509442.1](https://www.ncbi.nlm.nih.gov/nuccore/MH509442.1) | 60.43 | 67.8 | [105](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71901/399773%7CMycobacterium%20phage%20Aminay/viral%20segment/) | 100 | 100 |
|  |  |  |  |  |  |  |  |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Aminay (https://phagesdb.org/phages/Aminay/). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), 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.



**2. Proposal B: To create a new genus *Fionnbharthvirus* containing five species**

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Fionnbharth

**History:** Temperate Mycobacterium phage Fionnbharth was isolated from La Jolla, CA USA soil by Garrett Brooks (University of California, San Diego) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2010. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 1 nt 3'-cohesive termini (CTCGCGGCCAT). The Actinobacteriophage Database places this phage in Cluster/Subcluster K/K4 (<https://phagesdb.org/phages/Fionnbharth/>).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Fionnbharth | [NC\_027365.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_027365.1) | [JN831653.1](https://www.ncbi.nlm.nih.gov/nuccore/JN831653.1) | 58.08 | 68.0 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/38650/461558%7CMycobacterium%20virus%20Fionnbarth/viral%20segment%20Unknown/) | 1 | 100 | 100 |
| Mycobacterium phage Henu3 |  | [MK224497.1](https://www.ncbi.nlm.nih.gov/nuccore/MK224497.1) | 58.9 | 67.6 | [86](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75768/445145%7CMycobacterium%20phage%20Henu3/viral%20segment/) | 1 (\*\*\*) | 89.9 | 54.3 |
| Mycobacterium phage Eponine |  | [MN945904.1](https://www.ncbi.nlm.nih.gov/nuccore/MN945904.1) | 58.68 | 67.4 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87897/811657%7CMycobacterium%20phage%20Eponine/viral%20segment/) | 1 | 90.1 | 100 |
| Mycobacterium phage Taquito |  | [KX621007.1](https://www.ncbi.nlm.nih.gov/nuccore/KX621007.1) | 58.39 | 67.5 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63032/465655%7CMycobacterium%20phage%20Taquito/viral%20segment/) | 1 | 88.3 | 94.7 |
| Mycobacterium phage Patt |  | [MK524488.1](https://www.ncbi.nlm.nih.gov/nuccore/MK524488.1) | 54.61 | 67.6 | [88](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76380/468435%7CMycobacterium%20phage%20Patt/viral%20segment/) | 1\*\*\* | 89.5 | 91.5 |
|  |  |  |  |  |  |  |  |  |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**(\*\*\*) None indicated in NCBI genome records. One discovered using tRNAscan-SE [7] at http://lowelab.ucsc.edu/tRNAscan-SE/**

**Strains:**

|  |  |  |
| --- | --- | --- |
| **PHAGE NAME** | **ACCESSION NO.** | **Strain of:** |
| Mycobacterium phage Chancellor | MF140402.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage Cheetobro | NC\_028979.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage JF1 | MT310882.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage Malthus | MN369761.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage MissDaisy | MK524485.1 | *Fionnbharthvirus Patt* |
| Mycobacterium phage Mitti | KY087992.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage Reptar3000 | MH926058.1 | *Fionnbharthvirus Patt* |
| Mycobacterium phage SamScheppers | MH051258.1 | *Fionnbharthvirus Taquito* |
| Mycobacterium phage Slarp | KT361920.2 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage Wintermute | MF140435.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage Y10 DNA | AP018469.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage Y10 DNA | AP018471.1 | *Fionnbharthvirus Fionnbharth* |
| Mycobacterium phage Y2 DNA | AP018470.1 | *Fionnbharthvirus Fionnbharth* |

**Electron micrograph:** None available

**3. Proposal C: To create a new genus *Kratiovirus* with nine species**

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Kratio.

**History:** Temperate Mycobacterium phage Kratio was isolated from Arroyo, PR USA soil by Natalia Maldonado-Vazquez (University of Puerto Rico at Cayey) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2011. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 11 nt 3'-cohesive termini (CTCAGTGGCAT). The Actinobacteriophage Database places this phage in Cluster/Subcluster K/K5 (<https://phagesdb.org/phages/Kratio/>).

**Specific Reference:** Pope WH, Bowman CA, Russell DA, Jacobs-Sera D, Asai DJ, Cresawn SG, Jacobs WR, Hendrix RW, Lawrence JG, Hatfull GF; Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science; Phage Hunters Integrating Research and Education; Mycobacterial Genetics Course. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. Elife. 2015 Apr 28;4:e06416. doi: 10.7554/eLife.06416. PMID: 25919952; PMCID: PMC4408529.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Kratio |  | KM923971.1 |  |  |  |  | 100 | 100 |
| Mycobacterium phage Collard |  | [MH651171.1](https://www.ncbi.nlm.nih.gov/nuccore/MH651171.1) | 61.4 | 65.6 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72139/400275%7CMycobacterium%20phage%20Collard/viral%20segment/) | 1 | 92.9 | 90.9 |
| Mycobacterium phage Gengar | N[C\_031035.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031035.1) | [KX636165.1](https://www.ncbi.nlm.nih.gov/nuccore/KX636165.1) | 61.63 | 65.0 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46281/462677%7CMycobacterium%20phage%20Gengar/viral%20segment/) | 1 | 72.9 | 83.8 |
| Mycobacterium phage Larva Δ | [NC\_023724.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023724.1) | [JN243855.1](https://www.ncbi.nlm.nih.gov/nuccore/JN243855.1) | 62.99 | 65.3 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/24528/460528%7CMycobacterium%20virus%20Larva/viral%20segment%20Unknown/) | 1 | 89.9 | 90.9 |
| Mycobacterium phage Leston |  | [MH051255.1](https://www.ncbi.nlm.nih.gov/nuccore/MH051255.1) | 61.81 | 64.9 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/69049/373033%7CMycobacterium%20phage%20Leston/viral%20segment/) | 1 | 74.3 | 83.4 |
| Mycobacterium phage Omnicron | [NC\_028832.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028832.1) | [KM363596.1](https://www.ncbi.nlm.nih.gov/nuccore/KM363596.1) | 61.51 | 64.0 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42324/461906%7CMycobacterium%20phage%20Omnicron/viral%20segment%20Unknown/) | 1 | 65.9 | 78.8 |
| Mycobacterium phage Paola |  | [MG962374.1](https://www.ncbi.nlm.nih.gov/nuccore/MG962374.1) | 61.54 | 65.0 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68666/369815%7CMycobacterium%20phage%20Paola/viral%20segment/) | 1 | 73.7 | 80.8 |
| Mycobacterium phage Rando14 |  | [MH697592.1](https://www.ncbi.nlm.nih.gov/nuccore/MH697592.1) | 59.93 | 64.3 | [91](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72113/400249%7CMycobacterium%20phage%20Rando14/viral%20segment/) | 1 | 64.0 | 75.8 |
| Mycobacterium phage Thyatira |  | [MH576966.1](https://www.ncbi.nlm.nih.gov/nuccore/MH576966.1) | 63.87 | 64.6 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71960/399832%7CMycobacterium%20phage%20Thyatira/viral%20segment/) | 1 | 72.0 | 83.8 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Δ – indicates an existing species in the genus *Timquatrovirus*.**

**Strains:**

|  |  |  |
| --- | --- | --- |
| **PHAGE NAME** | **ACCESSION NO.** | **Strain of:** |
| Mycobacterium phage AlleyCat | MF185717.1 | *Kratiovirus Larva* |
| Mycobacterium phage Edugator | MF185719.1 | *Kratiovirus Larva* |
| Mycobacterium phage Guillsminger | MF185720.1 | *Kratiovirus Paola* |
| Mycobacterium phage OkiRoe | KJ567042.1 | *Kratiovirus Gengar* |
| Mycobacterium phage Waterfoul | KX585251.1 | *Kratiovirus Gengar* |

**Electron micrograph:** None available

**4. Proposal D: To update the genus *Timquatrovirus* with three new species**

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage TM4

**History:** The genus *Tm4likevirus* (*Timquatrovirus*) was established by Taxonomy Proposal 2013.022a-dB with nine species. Our current analysis reveals that many of these belong to new genera.

**Specific Reference:** Ford ME, Stenstrom C, Hendrix RW, Hatfull GF (1998) Mycobacteriophage TM4: genome structure and gene expression. Tuber lung Dis 79: 63–73. doi:10.1054/tuld.1998.0007.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage TM4 | [NC\_003387.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_003387.1) | [AF068845.1](https://www.ncbi.nlm.nih.gov/nuccore/AF068845.1) | 52.8 | 68.1 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4368/892453%7CMycobacterium%20phage%20TM4/viral%20segment%20Unknown/) | 100 | 100 |
| Mycobacterium phage Findley |  | [MF140411.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140411.1) | 58.15 | 68.3 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63728/466349%7CMycobacterium%20phage%20Findley/viral%20segment/) | 80.0 | 91.3 |
| Mycobacterium phage Mufasa | [NC\_028759.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028759.1) | [KT591490.1](https://www.ncbi.nlm.nih.gov/nuccore/KT591490.1) | 58.07 | 68.2 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42485/462050%7CMycobacterium%20phage%20Mufasa/viral%20segment%20Unknown/) | 85.5 | 93.5 |
| Mycobacterium phage ZoeJ | [NC\_024147.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_024147.1) | [KJ510412.1](https://www.ncbi.nlm.nih.gov/nuccore/KJ510412.1) | 57.32 | 68.5 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/33335/460678%7CMycobacterium%20phage%20ZoeJ/viral%20segment%20Unknown/) | 80.1 | 91.3 |
|  |  |  |  |  |  |  |  |

**(\*) Determined using VIRIDIC [3]**

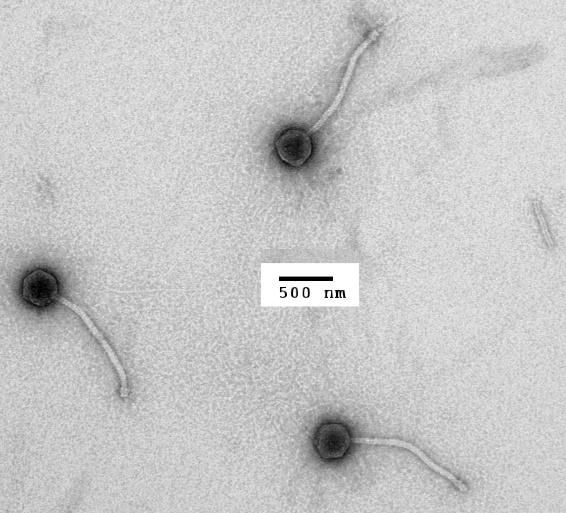
**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Strains:**

|  |  |  |
| --- | --- | --- |
| **PHAGE NAME** | **ACCESSION NO.** | **Strain of:** |
| Mycobacterium phage 33D | KC787101.1 | *Timquatrovirus TM4* |
| Mycobacterium phage BoostSeason | MH834601.1 | *Timquatrovirus Mufasa* |
| Mycobacterium phage DismalFunk | MF140408.1 | *Timquatrovirus Findley* |
| Mycobacterium phage DismalStressor | MH727545.1 | *Timquatrovirus Findley* |
| Mycobacterium phage Marcoliusprime | KX688047.1 | *Timquatrovirus Findley* |
| Mycobacterium phage Milly | KP027206.1 | *Timquatrovirus Findley* |

|  |  |
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**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage TM4(https://phagesdb.org/phages/TM4/). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), 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.



**5. Proposal E: To Create a new genus** ***Unicornvirus* with five species**

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Unicorn

**History:** Temperate Mycobacterium phage Unicorn was isolated by Sabrina Richards and Mary Ellen Sclafani (Old Dominium University) from Suffolk, VA USA soil as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2016. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 10 nt 3'-cohesive termini (CTCGGGGCAT). The Actinobacteriophage Database places this phage in Cluster/Subcluster K/K6 (<https://phagesdb.org/phages/Unicorn/>).

**Specific Reference:** Anders KR, Barekzi N, Best AA, Frederick GD, Mavrodi DV, Vazquez E; SEA-PHAGES, Amoh NYA, Baliraine FN, Buchser WJ, Cast TP, Chamberlain CE, Chung HM, D'Angelo WA, Farris CT, Fernandez-Martinez M, Fischman HD, Forsyth MH, Fortier AG, Gallo KF, Held GJ, Lomas MA, Maldonado-Vazquez NY, Moonsammy CH, Namboote P, Paudel S, Polley SM, Reyes GM, Rubin MR, Saha MS, Stukey J, Tobias TD, Garlena RA, Stoner TH, Cresawn SG, Jacobs-Sera D, Pope WH, Russell DA, Hatfull GF. Genome Sequences of Mycobacteriophages Amgine, Amohnition, Bella96, Cain, DarthP, Hammy, Krueger, LastHope, Peanam, PhelpsODU, Phrank, SirPhilip, Slimphazie, and Unicorn. Genome Announc. 2017 Dec 7;5(49):e01202-17. doi: 10.1128/genomeA.01202-17. PMID: 29217790; PMCID: PMC5721135.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Mycobacterium phage Unicorn | [MF324908.1](https://www.ncbi.nlm.nih.gov/nuccore/MF324908.1) | 61.21 | 66.2 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63673/466294%7CMycobacterium%20phage%20Unicorn/viral%20segment/) | 2 | 100 | 100 |
| Mycobacterium phage Bryler | [MN369762.1](https://www.ncbi.nlm.nih.gov/nuccore/MN369762.1) | 57.67 | 66.1 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85567/743726%7CMycobacterium%20phage%20Bryler/viral%20segment/) | 2 | 90.7 | 90.0 |
| Mycobacterium phage Krueger | [MF324914.1](https://www.ncbi.nlm.nih.gov/nuccore/MF324914.1) | 60.32 | 66.5 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63668/466289%7CMycobacterium%20phage%20Krueger/viral%20segment/) | 1 | 83.1 | 87.0 |
| Mycobacterium phage Shandong1 | [KY945355.1](https://www.ncbi.nlm.nih.gov/nuccore/KY945355.1) | 60.62 | 67.5 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63561/466183%7CMycobacterium%20phage%20Shandong1/viral%20segment/) | 0 | 64.0 | 80.0 |
| Mycobacterium phage Ximenita | [MN945901.1](https://www.ncbi.nlm.nih.gov/nuccore/MN945901.1) | 61.03 | 66.7 | [102](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87899/811659%7CMycobacterium%20phage%20Ximenita/viral%20segment/) | 1 | 82.4 | 89.0 |
|  |  |  |  |  |  |  |  |

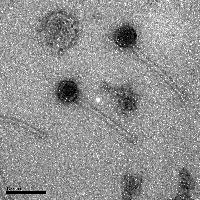
**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Strains:**

|  |  |  |
| --- | --- | --- |
| **PHAGE** | **ACCESSION NO.** | **Strains of:** |
| Mycobacterium phage Cain | MF324913.1 | *Unicornvirus Bryler* |
| Mycobacterium phage PhelpsODU | MF324909.1 | *Unicornvirus Unicorn* |
| Mycobacterium phage Phrank | MF324912.1 | *Unicornvirus Bryler* |

**Electron micrograph:** None available for Unicorn.Electron micrographs of negatively stained Mycobacterium phage Krueger (https://phagesdb.org/phages/Krueger/). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), 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.

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**6. Proposal F: To create a new genus *Keshuvirus* with five species**

**Source of the name of this taxon:** This genus is named after a virus of this type, Mycobacterium phage Keshuvirus

**History:** Temperate Mycobacterium phage Keshu was isolated by Navisha Dookie (University of Kwazulu-Natal) from Durban, South Africa soil as part of the Mycobacterial Genetics Course, Durban, South Africa program in 2009. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 11 nt 3'-cohesive termini (CTCGATGGCAT). The Actinobacteriophage Database places this phage in Cluster/Subcluster K/K3 (<https://phagesdb.org/phages/Keshu/>). From our analysis two existing members of the Timquatrovirus should be move to this taxon - *Mycobacterium virus MacnCheese* and *Mycobacterium virus Pixie.*

**Specific Reference:** Pope WH, Bowman CA, Russell DA, Jacobs-Sera D, Asai DJ, Cresawn SG, Jacobs WR, Hendrix RW, Lawrence JG, Hatfull GF; Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science; Phage Hunters Integrating Research and Education; Mycobacterial Genetics Course. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. Elife. 2015 Apr 28;4:e06416. doi: 10.7554/eLife.06416. PMID: 25919952; PMCID: PMC4408529.

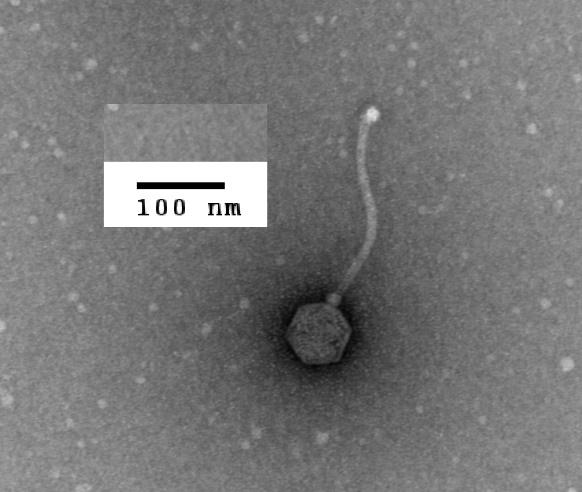
**GenBank Summary:** The **yellow** highly phages are existing species.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Mycobacterium phage Keshu | [NC\_026603.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_026603.1) | [KP027199.1](https://www.ncbi.nlm.nih.gov/nuccore/KP027199.1) | 61.25 | 67.3 | [101](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/36446/461181%7CMycobacterium%20phage%20Keshu/viral%20segment%20Unknown/) | 100 | 100 |
| Mycobacterium phage Hurricane |  | [MF373841.1](https://www.ncbi.nlm.nih.gov/nuccore/MF373841.1) | 61.32 | 67.1 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63659/466280%7CMycobacterium%20phage%20Hurricane/viral%20segment/) | 91.0 | 95.0 |
| Mycobacterium phage ShedlockHolmes | [NC\_028846.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028846.1) | [KR080206.1](https://www.ncbi.nlm.nih.gov/nuccore/KR080206.1) | 61.08 | 67.3 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42350/461933%7CMycobacterium%20phage%20ShedlockHolmes/viral%20segment%20Unknown/) | 91.3 | 97.0 |
| Mycobacterium virus MacnCheese | [NC\_042338.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_042338.1) | [JX042579.1](https://www.ncbi.nlm.nih.gov/nuccore/JX042579.1) | 61.57 | 67.3 | [99](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62610/465234%7CMycobacterium%20virus%20Macncheese/viral%20segment/) | 80.6 | 94.1 |
| Mycobacterium virus Pixie | [NC\_042325.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_042325.1) | [JF937104.1](https://www.ncbi.nlm.nih.gov/nuccore/JF937104.1) | 61.15 | 67.3 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62567/465182%7CMycobacterium%20virus%20Pixie/viral%20segment/) | 91.1 | 95.0 |

**Strains:**

|  |  |  |
| --- | --- | --- |
| **PHAGE NAME** | **ACCESSION NO.** | **Strain of:** |
| Mycobacterium phage TBond007 | KX683428.1 | *Keshuvirus ShedlockHolmes* |

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Keshu (https://phagesdb.org/phages/Keshu/). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), 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.

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**7. Proposal G: To create a new genus *Amginevirus* with five species**

**Source of the name of this taxon:** This genus is named after a virus of this type, Mycobacterium phage Amgine

**History:** Temperate Mycobacterium phage Amgine was isolated by Carmen Chamberlain (Hope College) from MI USA soil as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2016. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 11 nt 3'-cohesive termini (CTCGTAGGCAT). The Actinobacteriophage Database places this phage in Cluster/Subcluster K/K6 (<https://phagesdb.org/phages/Amgine/>).

**Specific Reference:** Anders KR, Barekzi N, Best AA, Frederick GD, Mavrodi DV, Vazquez E; SEA-PHAGES, Amoh NYA, Baliraine FN, Buchser WJ, Cast TP, Chamberlain CE, Chung HM, D'Angelo WA, Farris CT, Fernandez-Martinez M, Fischman HD, Forsyth MH, Fortier AG, Gallo KF, Held GJ, Lomas MA, Maldonado-Vazquez NY, Moonsammy CH, Namboote P, Paudel S, Polley SM, Reyes GM, Rubin MR, Saha MS, Stukey J, Tobias TD, Garlena RA, Stoner TH, Cresawn SG, Jacobs-Sera D, Pope WH, Russell DA, Hatfull GF. Genome Sequences of Mycobacteriophages Amgine, Amohnition, Bella96, Cain, DarthP, Hammy, Krueger, LastHope, Peanam, PhelpsODU, Phrank, SirPhilip, Slimphazie, and Unicorn. Genome Announc. 2017 Dec 7;5(49):e01202-17. doi: 10.1128/genomeA.01202-17. PMID: 29217790; PMCID: PMC5721135.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Mycobacterium phage Amgine |  | [MF324915.1](https://www.ncbi.nlm.nih.gov/nuccore/MF324915.1) | 62.24 | 66.4 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63665/466286%7CMycobacterium%20phage%20Amgine/viral%20segment/) | 0 | 100 | 100 |
| Mycobacterium phage Amohnition |  | [MF140398.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140398.1) | 61.76 | 67.2 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63720/466341%7CMycobacterium%20phage%20Amohnition/viral%20segment/) | 1 | 91.1 | 90.7 |
| Mycobacterium phage DarthP |  | [MF140406.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140406.1) | 61.59 | 67.2 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63725/466346%7CMycobacterium%20phage%20DarthP/viral%20segment/) | 1 | 75.1 | 90.7 |
| Mycobacterium phage Ekdilam |  | [MN234199.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234199.1) | 61.77 | 67.4 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84830/708387%7CMycobacterium%20phage%20Ekdilam/viral%20segment/) | 0 | 76.4 | 85.6 |
| Mycobacterium phage Ellie |  | [MT723940.1](https://www.ncbi.nlm.nih.gov/nuccore/MT723940.1) | 61.95 | 67.0 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94293/980570%7CMycobacterium%20phage%20Ellie/viral%20segment/) | 0 | 74.9 | 92.8 |

**Strains:**

|  |  |  |
| --- | --- | --- |
| **PHAGE NAME** | **ACCESSION NO.** | **Strain of:** |
| Mycobacterium phage Hammy | KY087993.1 | *Amginevirus DarthP* |

**Electron micrograph:** NA

**8. Proposal H: To create a new genus *Anayavirus* with 28 species**

**Source of the name of this taxon:** This genus is named after a virus of this type, Mycobacterium phage Anaya

**History:** Temperate Mycobacterium phage Anaya was isolated by Ariangela Joy Davis (Calvin University) from Grand Rapids, MI USA soil as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2009. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 11 nt 3'-cohesive termini (no sequence given). The Actinobacteriophage Database places this phage in Cluster/Subcluster K/K1 (<https://phagesdb.org/phages/Anaya/>). From our analysis these existing members of the Timquatrovirus should be move to this taxon - *Mycobacterium virus Anaya, Mycobacterium virus Angelica, Mycobacterium virus CrimD and Mycobacterium virus JAWS*

**Specific Reference:** Pope WH, Bowman CA, Russell DA, Jacobs-Sera D, Asai DJ, Cresawn SG, Jacobs WR, Hendrix RW, Lawrence JG, Hatfull GF; Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science; Phage Hunters Integrating Research and Education; Mycobacterial Genetics Course. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. Elife. 2015 Apr 28;4:e06416. doi: 10.7554/eLife.06416. PMID: 25919952; PMCID: PMC4408529.

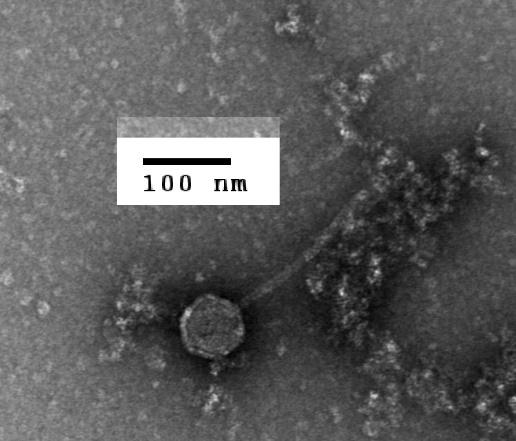
**VIRIDIC Summary: new species.** The **yellow** highly phages are existing species.

|  |  |
| --- | --- |
| **PHAGE NAME** | **ACCESSION NO.** |
| Mycobacterium phage Anaya | JF704106.1 |
| Mycobacterium phage Adephagia | JF704105.1 |
| Mycobacterium phage Adonis | MH001453.1 |
| Mycobacterium phage AlishaPH | MH077577.1 |
| Mycobacterium phage Amelie | KX808132.1 |
| Mycobacterium phage Angelica | HM152764.1 |
| Mycobacterium phage Apocalypse | MF668267.1 |
| Mycobacterium phage Beezoo | MH371113.1 |
| Mycobacterium phage Bella96 | MF377440.1 |
| Mycobacterium phage Chris | MT310860.1 |
| Mycobacterium phage CrimD | HM152767.2 |
| Mycobacterium phage Curiosium | MN234226.1 |
| Mycobacterium phage JAWS | JN185608.1 |
| Mycobacterium phage KiSi | MK376955.1 |
| Mycobacterium phage LastHope | MF140416.1 |
| Mycobacterium phage LaterM | MG962371.1 |
| Mycobacterium phage MarkPhew | MT310859.1 |
| Mycobacterium phage Marshawn | MN284895.1 |
| Mycobacterium phage Murucutumbu | KM677211.1 |
| Mycobacterium phage Nibb | MK460246.1 |
| Mycobacterium Phage Niklas | MK494119.1 |
| Mycobacterium phage Prithvi | MK016503.1 |
| Mycobacterium phage SirPhilip | MF324911.1 |
| Mycobacterium phage Urkel | KX657796.1 |
| Mycobacterium phage Validus | KF713486.1 |
| Mycobacterium phage Yuna | MN234176.1 |
| Mycobacterium phage Yunkel11 | MN234165.1 |
| Mycobacterium phage Zavala | MN234198.1 |

**Strains:**

|  |  |  |
| --- | --- | --- |
| **PHAGE** | **ACCESSION NO.** | **Strain of:** |
| Mycobacterium phage ActinUp | MH051246.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Atiba | MN234230.1 | *Anayavirus Adephagia* |
| Mycobacterium phage BarrelRoll | JN643714.1 | *Anayavirus Adephagia* |
| Mycobacterium phage BEEST | MH509444.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Belladonna | MH697578.1 | *Anayavirus Adephagia* |
| Mycobacterium Phage BGlluviae | MN908692.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Biglebops | MH399770.1 | *Anayavirus Amelie* |
| Mycobacterium Phage Capricorn | MK112537.1 | *Anayavirus Adephagia* |
| Mycobacterium phage CREW | KY380102.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Dalmuri | MH727544.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Deby | MG962364.1 | *Anayavirus Angelica* |
| Mycobacterium phage DrHayes | KX657795.1 | *Anayavirus Urkel* |
| Mycobacterium phage Efra2 | MN234174.1 | *Anayavirus Yunkel11* |
| Mycobacterium phage Emerson | KJ567045.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Enkosi | KT281789.1 | *Anayavirus Amelie* |
| Mycobacterium phage Geraldini | MN234182.1 | *Anayavirus Beezoo* |
| Mycobacterium phage Guanica15 | MN234201.1 | *Anayavirus Yunkel11* |
| Mycobacterium phage HedwigODU | KX585253.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Homura | MH536821.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Inky | MN369746.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Jeckyll | MF140412.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Joy99 | MH536822.1 | *Anayavirus Adephagia* |
| Mycobacterium phage LeMond | MH910038.1 | *Anayavirus KiSi* |
| Mycobacterium phage LilPharaoh | MF919518.1 | *Anayavirus Amelie* |
| Mycobacterium phage LindNT | KX641264.1 | *Anayavirus Prithvi* |
| Mycobacterium phage Mdavu | MN586025.1 | *Anayavirus Amelie* |
| Mycobacterium phage Mynx | MH513977.1 | *Anayavirus Zavala* |
| Mycobacterium phage Oscar | MH910039.1 | *Anayavirus KiSi* |
| Mycobacterium phage Peanam | MF185722.1 | *Anayavirus Niklas* |
| Mycobacterium phage Ramen | MN234197.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Rapunzel97 | MN234231.1 | *Anayavirus Adephagia* |
| Mycobacterium phage SamuelLPlaqson | KX657794.1 | *Anayavirus Urkel* |
| Mycobacterium phage Scarlett | MH910042.1 | *Anayavirus KiSi* |
| Mycobacterium phage SgtBeansprout | MH020245.1 | *Anayavirus Amelie* |
| Mycobacterium phage Shaobing | MK310138.1 | *Anayavirus Niklas* |
| Mycobacterium phage Slimphazie | MF140428.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Spock | MN369742.1 | *Anayavirus Adephagia* |
| Mycobacterium phage Sulley | MF919532.1 | *Anayavirus Angelica* |
| Mycobacterium phage Tachez | MF140430.1 | *Anayavirus Adephagia* |
| Mycobacterium phage TreyKay | MF472892.1 | *Anayavirus Prithvi* |
| Mycobacterium phage Veliki | MN234205.1 | *Anayavirus Adephagia* |
| Mycobacterium phage YoureAdopted | MK460247.1 | *Anayavirus Beezoo* |

**Electron micrograph:** NA



**9. Proposal I: To create a new subfamily *Weiservirinae* containing these eight genera**

**Source of the name of this taxon:** This genus is in honour of Russell S. Weiser (1906-2000) who together with Grace M. Gardner (1924-2007) characterized the first phages against Mycobacterium smegmatis in 1947 in the Department of Microbiology, School of Medicine, University of Washington, Seattle (USA). Dr. Russell Weiser was born in Grimes, Iowa (USA) and obtained his PhD in bacteriology from the University of Washington in 1934. He was one of the founders of the University of Washington School of Medicine, retired in 1977 after teaching there for 43 years, he set up an annual lectureship at the medical school in his speciality, immunology. He was a co-author on Fundamentals of Medical Bacteriology and Mycology and Fundamentals of Immunology.

**Evidence:** Phylogenetic, genomic (VIRIDIC) and proteomic (ViPTree) analysis reveals that all these phages belong to a single group.

**References:**

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