

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

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| **Code assigned:** | **2021.007B** |  |
| **Short title:** Create seven new genera in the subfamily *Bclasvirinae* (*Caudoviricetes*) | | |
|  | | |

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

|  |
| --- |
| Caudoviricetes 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)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

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

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

|  |
| --- |
| 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 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2021.007B.R.Bclasvirinae |

**Abstract**

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| We have reexamined the *Bclasvirinae* which now has >300 isolates, and define seven new genera, most with only a single isolate. |

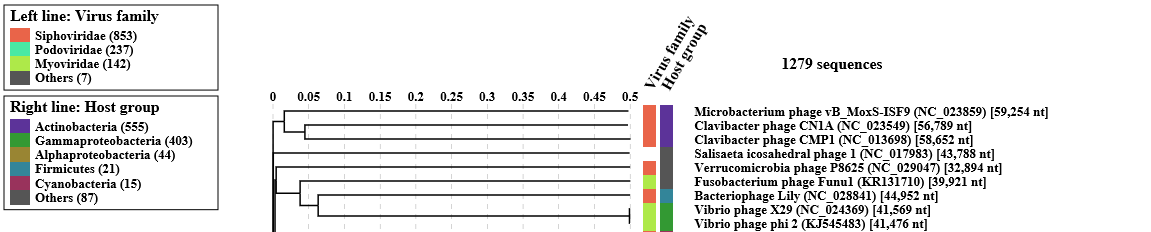
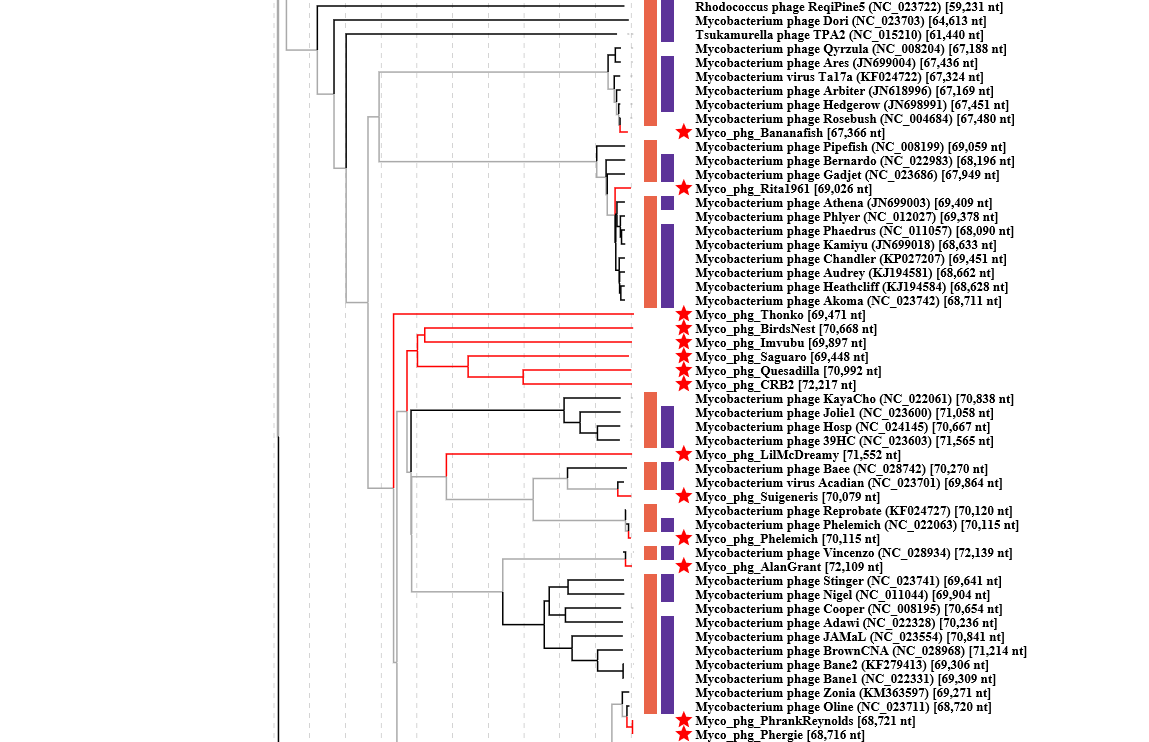
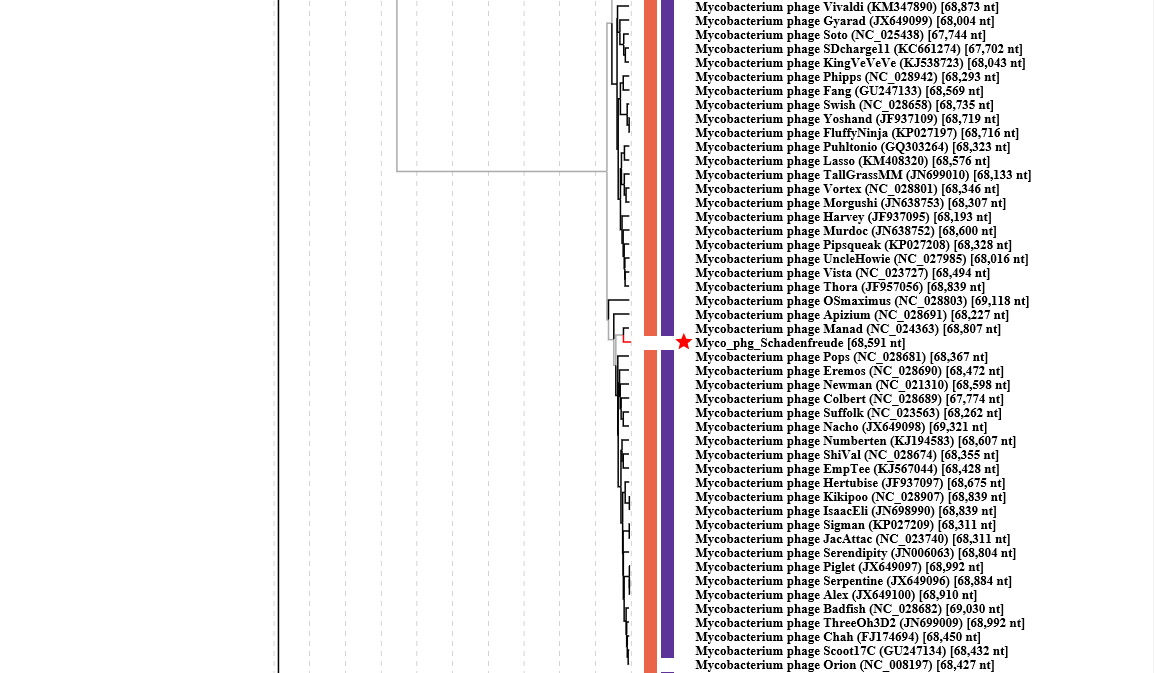
**Text of proposal**

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| --- | --- |
| |  | | --- | | **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:** Members of the subfamily share a low degree of sequence similarity (e.g. VIRIDIC) and the genera form a clade in a marker tree phylogeny. | |

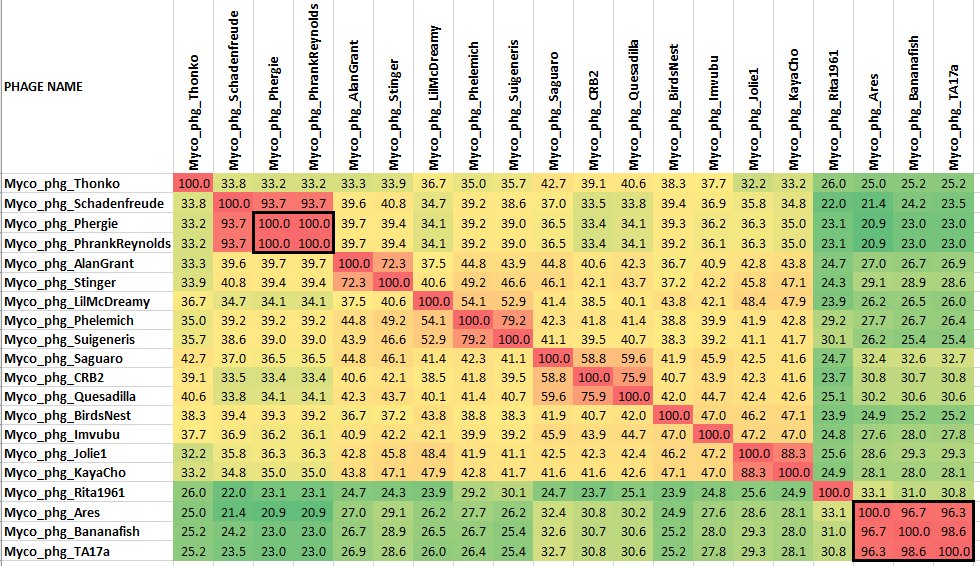
**Supporting molecular evidence**

**History:** The subfamily *Bclasvirinae* was established through Taxonomy Proposal 2016.005a-yB. Since that time more than a hundred new isolates have been isolated and sequenced. They all fall within the Actinobacteriophage Database Cluster B, which now has 13 subclusters.

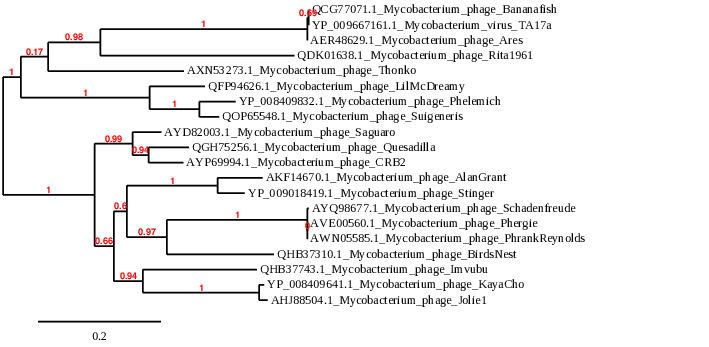
**ViPTree analysis of select *Bclasvirinae* phages:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. Newly analyzed members are indicated with **red stars**.

  
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**VIRIDIC heat map of select *Bclasvirinae*:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates species with multiple strains. For the complete VIRIDIC analysis see attached appendices.



**Phylogeny of select *Bclasvirinae* TerL proteins:** The phylogenetic tree was constructed using the terminase large subunit of a select group of *Bclasvirinae* 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."



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

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

**History:** Lytic Mycobacterium phage Thonko was isolated from Empangeni, South Africa soil by Nomusa Christina Mzimela (University of Kwazulu-Natal) as part of the Mycobacterial Genetics Course, Durban, South Africa program in 2017. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is Circularly Permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B8.(<https://phagesdb.org/phages/Thonko/>).

**Specific Reference:** None

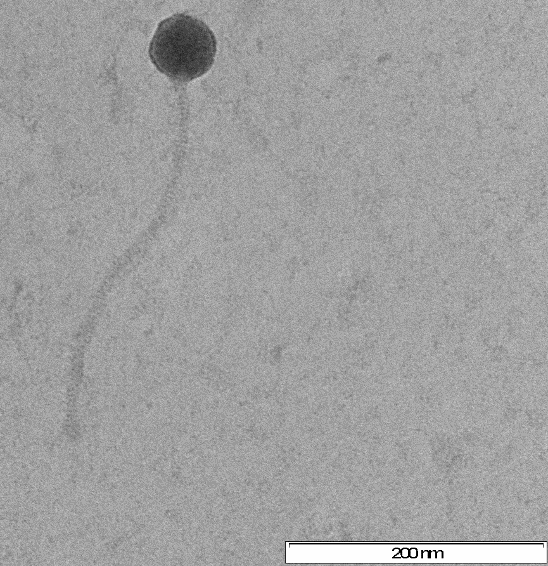
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Thonko |  | [MH632120.1](https://www.ncbi.nlm.nih.gov/nuccore/MH632120.1) | 69.47 | 68.6 | [108](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71587/396798%7CMycobacterium%20phage%20Thonko/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 Thonko (https://phagesdb.org/phages/Thonko/). 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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**2. Proposal B: To create a new genus *Birdsnestvirus***

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

**History:** Lytic Mycobacterium phage BirdsNest was isolated from Kruger National Park in South Africa soil by Christian Gauthier (University of Pittsburgh) as part of the Phage Hunters Integrating Research and Education program in 2018. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permutted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B13 (<https://phagesdb.org/phages/Birdsnest/>).

**Specific Reference:** None

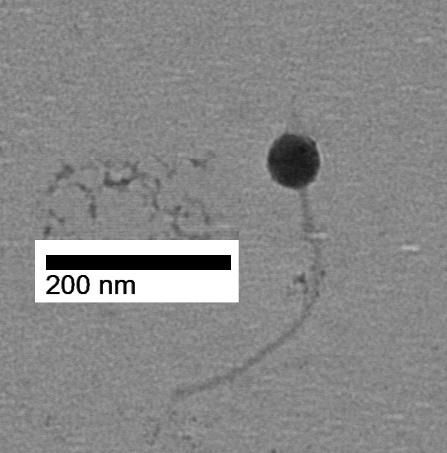
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| BirdsNest |  | [MN813686.1](https://www.ncbi.nlm.nih.gov/nuccore/MN813686.1) | 70.67 | 70.1 | [105](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86727/755992%7CMycobacterium%20phage%20BirdsNest/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 BirdsNest (https://phagesdb.org/phages/BirdsNest/). 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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**3. Proposal C: To create a new genus *Lilmcdreamyvirus***

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

**History:** Lytic Mycobacterium phage LilMcDreamy was isolated from Spokane, WA USA drainpipe by Madeline Marlatt and Annaliese Lippold (Gonzaga University) 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 is Circularly Permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B12 ([https://phagesdb.org/phages/LilMcDreamy/](https://phagesdb.org/phages/xxx/)).

**Specific Reference:** None

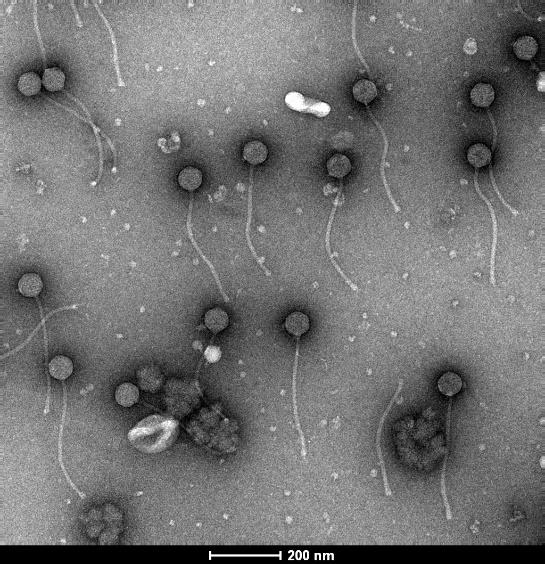
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| LilMcDreamy |  | [MN284893.1](https://www.ncbi.nlm.nih.gov/nuccore/MN284893.1) | 71.55 | 69.3 | [99](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84954/717015%7CMycobacterium%20phage%20LilMcDreamy/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 LilMcDreamy (https://phagesdb.org/phages/LilMcDreamy/). 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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**4. Proposal D: To create a new genus *Saguarovirus***

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

**History:** Lytic Mycobacterium phage Saguaro was isolated from Tucson, AZ USA soil by Jacqueline Washington (Nyack College) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2015. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/ B7(<https://phagesdb.org/phages/Saguaro/>).

**Specific Reference:** None

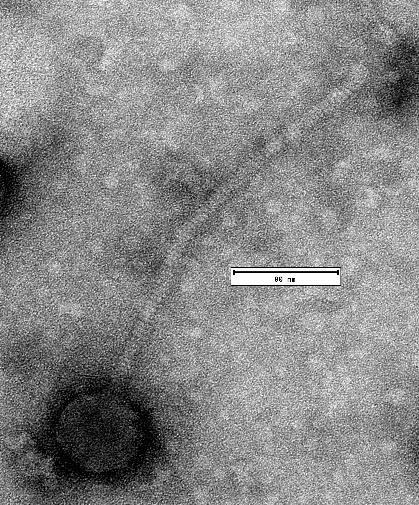
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Saguaro |  | [MH744423.1](https://www.ncbi.nlm.nih.gov/nuccore/MH744423.1) | 69.45 | 69.5 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72796/409417%7CMycobacterium%20phage%20Saguaro/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 Saguaro (https://phagesdb.org/phages/Saguaro/). 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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**5. Proposal E: To create a new genus *Quesadillavirus***

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

**History:** Lytic Mycobacterium phage Quesadilla was isolated from Mason City, IA USA soil by Hannah Jorgensen (Northwestern College) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2018. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/ B9 (<https://phagesdb.org/phages/Quesadilla/>).

**Specific Reference:** Suarez CA, Franceschelli JJ, Morbidoni HR. Mycobacteriophage CRB2 defines a new subcluster in mycobacteriophage classification. PLoS One. 2019 Feb 27;14(2):e0212365. doi: 10.1371/journal.pone.0212365. PMID: 30811481; PMCID: PMC6392294.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Quesadilla |  | [MN617843.1](https://www.ncbi.nlm.nih.gov/nuccore/MN617843.1) | 70.99 | 69.9 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85601/743760%7CMycobacterium%20phage%20Quesadilla/viral%20segment/) | 100 | 100 |
| CRB2 |  | [MK059749.1](https://www.ncbi.nlm.nih.gov/nuccore/MK059749.1) | 72.22 | 69.7 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76374/468429%7CMycobacterium%20phage%20CRB2/viral%20segment/) | 75.9 | 89.8 |

**(\*) 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]**

**Electron micrograph:** None available

**6. Proposal F: To create a new genus *Imvubuvirus***

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

**History:** Lytic Mycobacterium phage Imvubu was isolated from Mpumalanga, South Africa soil by Deborah Jacobs-Sera as part of the Phage Hunters Integrating Research and Education program in 2018. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/ B10 (https://phagesdb.org/phages/Imvubu/).

**Specific Reference:** None

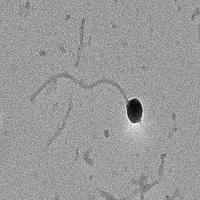
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Imvubu |  | [MN813693.1](https://www.ncbi.nlm.nih.gov/nuccore/MN813693.1) | 69.9 | 70.5 | [102](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86729/755994%7CMycobacterium%20phage%20Imvubu/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 Imvubu (https://phagesdb.org/phages/Imvubu/). 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 *Julieunavirus***

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Julie1

**History:** Lytic Mycobacterium phage Julie1 was isolated from Argentinian soil by Franceschelli,J.J., Suarez,C.A., Teran,L., and Raya,R. (Universidad Nacional de Rosario) in 2014. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted . The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B6 (<https://phagesdb.org/phages/Julie1/>).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Julie1 | [NC\_023600.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023600.1) | [KJ433976.1](https://www.ncbi.nlm.nih.gov/nuccore/KJ433976.1) | 71.06 | 69.9 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/24338/460442%7CMycobacterium%20phage%20Jolie1/viral%20segment%20Unknown/) | 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 Julie1(https://phagesdb.org/phages/Julie1/). 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.

**8. Proposal H: To create a new species in the genus *Acadianvirus***

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

**History:** This genus was established by Taxonomy Proposal 2016.005a-yB. Lytic Mycobacterium phage Serendipitous was isolated from High Shoals, NC USA soil by Lindsey Farris (Western Carolina University) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2015. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B5 (https://phagesdb.org/phages/Serendipitous/).

**Specific Reference:** None

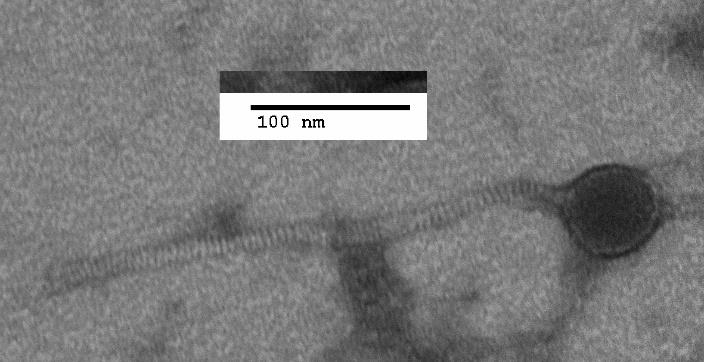
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Acadian | [NC\_023701.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023701.1) | [JN699007.1](https://www.ncbi.nlm.nih.gov/nuccore/JN699007.1) | 69.86 | 68.4 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62381/464956%7CMycobacterium%20virus%20Acadian/viral%20segment%20Unknown/) | 100 | 100 |
| Serendipitous |  | [MH727561.1](https://www.ncbi.nlm.nih.gov/nuccore/MH727561.1) | 69.87 | 68.0 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72684/408812%7CMycobacterium%20phage%20Serendipitous/viral%20segment/) | 85.9 | 96.9 |

**(\*) 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 Serendipitous (https://phagesdb.org/phages/Serendipitous/). 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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**9. Proposal I: To create two new species in the genus *Coopervirus***

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

**History:** This genus was established by Taxonomy Proposal 2016.005a-yB. Lytic Mycobacterium phage Heath was isolated from soil by Macy Clevenger and Taylor McIntosh (LeTourneau University, Longview, TX USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2019. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B4 (https://phagesdb.org/phages/Heath/).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Cooper | [NC\_008195.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_008195.1) | [DQ398044.1](https://www.ncbi.nlm.nih.gov/nuccore/DQ398044.1) | 70.65 | 69.1 | [99](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/5783/891173%7CMycobacterium%20phage%20Cooper/viral%20segment%20Unknown/) | 100 | 100 |
| Heath |  | [MT639648.1](https://www.ncbi.nlm.nih.gov/nuccore/MT639648.1) | 69.26 | 68.7 | [91](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94309/980586%7CMycobacterium%20phage%20Heath/viral%20segment/) | 81.2 | 84.8 |
| Fortunato |  | [KX589269.1](https://www.ncbi.nlm.nih.gov/nuccore/KX589269.1) | 70.68 | 69.0 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62995/465618%7CMycobacterium%20phage%20Fortunato/viral%20segment/) | 82.7 | 90.9 |

**(\*) 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:** NA

**10. Proposal J: To create one new species in the genus *Pipefishvirus***

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

**History:** This genus was established by Taxonomy Proposal 2016.005a-yB. Lytic Mycobacterium phage Obutu was isolated from soil by Quentin Ray (Morehouse College. Atlanta, GA, USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2018. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B3 (https://phagesdb.org/phages/Heath/).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Pipefish | [NC\_008199.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_008199.1) | [DQ398049.1](https://www.ncbi.nlm.nih.gov/nuccore/DQ398049.1) | 69.06 | 67.3 | [102](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/5790/891178%7CMycobacterium%20phage%20Pipefish/viral%20segment%20Unknown/) | 100 | 100 |
| Obutu |  | [MN096359.1](https://www.ncbi.nlm.nih.gov/nuccore/MN096359.1) | 69.02 | 67.4 | [104](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82662/614438%7CMycobacterium%20phage%20Obutu/viral%20segment/) | 92.9 | 93.1 |
|  |  |  |  |  |  |  |  |

**(\*) 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:** None available

**11. Proposal K: To create one new species in the genus *Pegunavirus***

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage PG1

**History:** This genus was established by Taxonomy Proposal 2016.005a-yB. Lytic Mycobacterium phage KingTut was isolated from soil by Lauren Filippidis and Erin Kuisti (The Ohio State University, Columbus, OH USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2015. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B1 (https://phagesdb.org/phages/KingTut/).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| PG1 | [NC\_005259.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_005259.1) | [AF547430.1](https://www.ncbi.nlm.nih.gov/nuccore/AF547430.1) | 69 | 66.5 | [100](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4564/890822%7CMycobacterium%20phage%20PG1/viral%20segment/) | 100 | 100 |
| KingTut |  | [MH450122.1](https://www.ncbi.nlm.nih.gov/nuccore/MH450122.1) | 64.83 | 66.5 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71873/399745%7CMycobacterium%20phage%20KingTut/viral%20segment/) | 92.7 | 87.0 |
|  |  |  |  |  |  |  |  |

**(\*) 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]**

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage KingTut (https://phagesdb.org/phages/KingTut/). 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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**11. Proposal L: To create one new species in the genus *Rosebushvirus***

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

**History:** This genus was established by Taxonomy Proposal 2016.005a-yB. Lytic Mycobacterium phage Laurie was isolated from soil by Tyler Williams (University of Maine, Machias) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2013. The host bacterium was Mycobacterium smegmatis mc²155. Its genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster/Subcluster B/B2 (https://phagesdb.org/phages/Laurie/).

**Specific Reference:** None

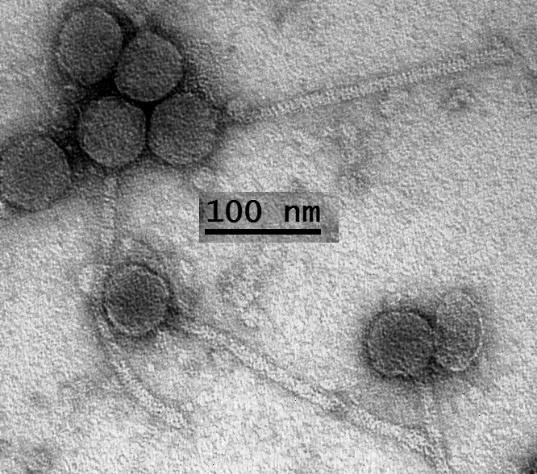
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Rosebush | [NC\_004684.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_004684.1) | [AY129334.1](https://www.ncbi.nlm.nih.gov/nuccore/AY129334.1) | 67.48 | 69.0 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4513/892557%7CMycobacterium%20phage%20Rosebush/viral%20segment%20Unknown/) | 100 | 100 |
| Laurie |  | KX443696.1 | 66.51 | 69.0 | 90 | 93.0 | 96.7 |
|  |  |  |  |  |  |  |  |

**(\*) 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 Laurie (https://phagesdb.org/phages/Laurie/). 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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