

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

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| **Code assigned:** | **2021.062B** |  |
| **Short title:** Create three new genera in the subfamily *Pclasvirinae* (*Caudoviricetes*) | | |
|  | | |

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

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| --- |
| Bacterial Viruses Subcommittee, Actinobacteriophages Study Group |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2021.062B.R.Pclasvirinae\_new\_genera |

**Abstract**

|  |
| --- |
| The subfamily *Pclasvirinae* was established through Taxonomy Proposal 2016.037a-mB and contains three genera – *Fishburnevirus* (5 species), *Bignuzvirus* (1 species) and *Phayoncevirus* (1 species). The Actinobacteriophage Database recognizes these phages as belonging to Cluster P/Subcluster P1, P4 and P5, respectively. We have employed genomic (VIRIDIC), proteomic (ViPTree, CoreGenes3.5) and phylogenetic analyses to reexamine the P-Cluster phages and propose the addition of *Tortellinivirus* (P2), *Xaviavirus* (P3), and *Purkyvirus* (P6) |

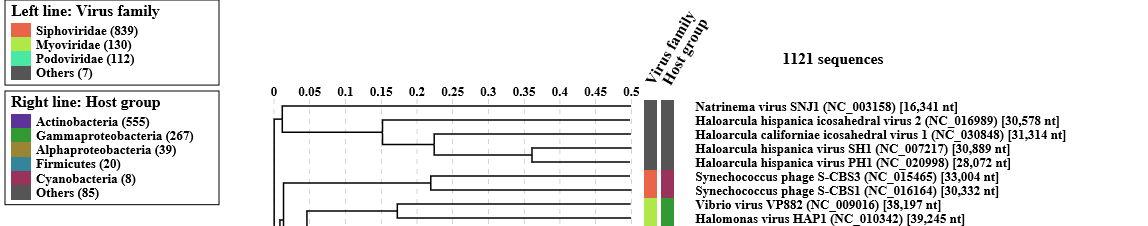
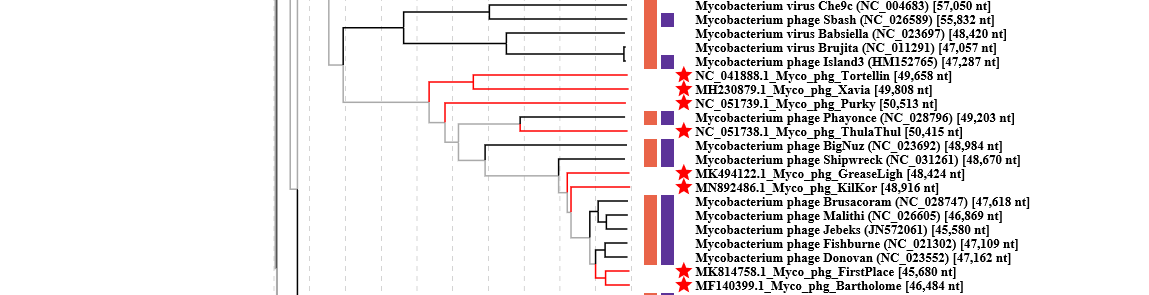
**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | **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. [17]  **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. | |

**Supporting evidence**

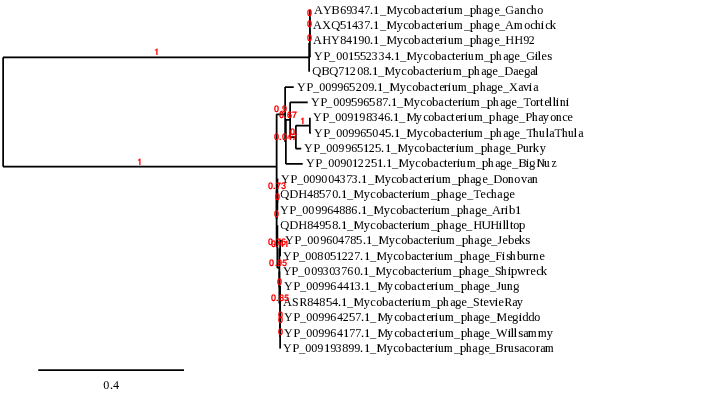
**Molecular analysis:**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5].

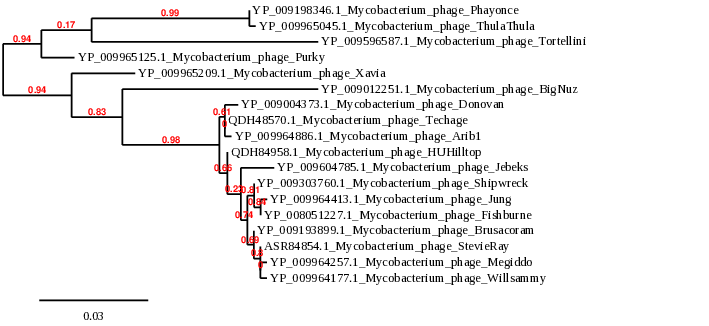
  


**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [6]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. (attached)

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of some of these phages with phylogeny.fr in “one click” mode [8]. "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 [16] for details." **A. ROOTED**

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**B. UNROOTED**



**Proposal 1: To add 11 new species to the genus *Fishburnevirus***

**Proposal 2: To add one strain to the genus *Bignuzvirus***

**Proposal 3: To add a single strain to the genus *Phayoncevirus***

**Proposal 4: To transfer the genus *Tortellinivirus* to this subfamily**

**Proposal 5: To create a new genus *Xaviavirus* with a single species**

**Proposal 6: To create a new genus *Purkyvirus* with a single species**

**Proposal 1: To add 11 new species to the genus *Fishburnevirus***

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

**History:** The genus *Fishburnevirus* was established by Taxonomy Proposal 2016.037a-mB

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Fishburne | [NC\_021302.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_021302.1) | [KC691256.1](https://www.ncbi.nlm.nih.gov/nuccore/KC691256.1) | 47.11 | 67.3 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/17847/460053%7CMycobacterium%20phage%20Fishburne/viral%20segment%20Unknown/) | 100 | 100 |
| Mycobacterium phage Arib1 | [NC\_051736.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051736.1) | [MF919492.1](https://www.ncbi.nlm.nih.gov/nuccore/MF919492.1) | 46.73 | 67.5 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64194/466601%7CMycobacterium%20phage%20Arib1/viral%20segment/) | 91.5 | 92.2 |
| Mycobacterium phage Atcoo | [NC\_051729.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051729.1) | [MN585977.1](https://www.ncbi.nlm.nih.gov/nuccore/MN585977.1) | 49.08 | 67.0 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85679/744339%7CMycobacterium%20phage%20Atcoo/viral%20segment/) | 82.8 | 90.9 |
| Mycobacterium phage Bartholomew | [NC\_051734.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051734.1) | [MF140399.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140399.1) | 46.48 | 67.2 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63721/466342%7CMycobacterium%20phage%20Bartholomew/viral%20segment/) | 92.2 | 92.2 |
| Mycobacterium phage FirstPlacePfu | [NC\_051735.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051735.1) | [MK814758.1](https://www.ncbi.nlm.nih.gov/nuccore/MK814758.1) | 45.68 | 67.3 | [82](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79549/511578%7CMycobacterium%20phage%20FirstPlacePfu/viral%20segment/) | 92.6 | 90.9 |
| Mycobacterium phage GreaseLightnin | [NC\_051731.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051731.1) | [MK494122.1](https://www.ncbi.nlm.nih.gov/nuccore/MK494122.1) | 48.42 | 67.1 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/78123/478576%7CMycobacterium%20phage%20GreaseLightnin/viral%20segment/) | 84.9 | 88.3 |
| Mycobacterium phage Jung | [NC\_051730.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051730.1) | [MT498061.1](https://www.ncbi.nlm.nih.gov/nuccore/MT498061.1) | 46.56 | 67.1 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92645/916834%7CMycobacterium%20phage%20Jung/viral%20segment/) | 83.7 | 85.7 |
| Mycobacterium phage KilKor |  | [MN892486.1](https://www.ncbi.nlm.nih.gov/nuccore/MN892486.1) | 48.92 | 67.2 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86982/760237%7CMycobacterium%20phage%20KilKor/viral%20segment/) | 87.6 | 96.1 |
| Mycobacterium phage Ksquared | [NC\_051732.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051732.1) | [MF281061.1](https://www.ncbi.nlm.nih.gov/nuccore/MF281061.1) | 48.7 | 67.1 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63681/466302%7CMycobacterium%20phage%20Ksquared/viral%20segment/) | 89.3 | 92.2 |
| Mycobacterium phage Majeke | [NC\_051737.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051737.1) | [MF472894.1](https://www.ncbi.nlm.nih.gov/nuccore/MF472894.1) | 47.61 | 67.4 | [81](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63821/466442%7CMycobacterium%20phage%20Majeke/viral%20segment/) | 93.8 | 94.8 |
| Mycobacterium phage Shipwreck | [NC\_031261.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031261.1) | [KU985090.1](https://www.ncbi.nlm.nih.gov/nuccore/KU985090.1) | 48.67 | 66.9 | [81](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46460/462789%7CMycobacterium%20phage%20Shipwreck/viral%20segment/) | 81.2 | 89.6 |
| Mycobacterium phage Willsammy | [NC\_051727.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051727.1) | [MT024866.1](https://www.ncbi.nlm.nih.gov/nuccore/MT024866.1) | 48.4 | 67.0 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/88403/838864%7CMycobacterium%20phage%20Willsammy/viral%20segment/) | 82.8 | 93.5 |
|  |  |  |  |  |  |  |  |

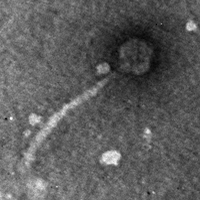
**(\*) Determined using VIRIDIC [6]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Strains:**

|  |  |  |
| --- | --- | --- |
| **Phage name** | **Accession** | **Strain of:** |
| Mycobacterium phage Bogie | MF133446.1 | *Fishburnevirus Shipwreck* |
| Mycobacterium phage Bunnies | MN096356.1 | *Fishburnevirus Ksquared* |
| Mycobacterium phage CactusJack | MN892484.1 | *Fishburnevirus KilKor* |
| Mycobacterium phage Camster | MW055902.1 | *Fishburnevirus Malithi* |
| Mycobacterium phage Glaske | MN807250.1 | *Fishburnevirus KilKor* |
| Mycobacterium phage HUHilltop | MN010757.1 | *Fishburnevirus Jebeks* |
| Mycobacterium phage Mangethe | MK016499.1 | *Fishburnevirus Majeke* |
| Mycobacterium phage Megiddo | MN807249.1 | *Fishburnevirus KilKor* |
| Mycobacterium phage Necropolis | MK937604.1 | *Fishburnevirus Jebeks* |
| Mycobacterium phage Phalm | MN807248.1 | *Fishburnevirus KilKor* |
| Mycobacterium phage Phineas | MK820639.1 | *Fishburnevirus Jebeks* |
| Mycobacterium phage StevieRay | MF373843.1 | *Fishburnevirus Brusacoram* |
| Mycobacterium phage StressBall | MN908683.1 | *Fishburnevirus KilKor* |
| Mycobacterium phage Techage | MK919480.1 | *Fishburnevirus Fishburne* |
| Mycobacterium phage Thespis | MG198785.1 | *Fishburnevirus Brusacoram* |
| Mycobacterium phage Zilizebeth | MK524508.1 | *Fishburnevirus Majeke* |

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Fishburne (https://phagesdb.org/phages/Fishburne/). 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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**Proposal 2: To add one strain to the genus *Bignuzvirus***

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

**History:** The genus *Bignuzvirus* was established by Taxonomy Proposal 2013.009a-dB

**Specific Reference:** None

**Strain:**

|  |  |  |
| --- | --- | --- |
| **Phage Name** | **Accession** | **Strain of:** |
| Mycobacterium phage Nazo | KX641262.1 | *Bignuzvirus BigNuz* |

(N.B. rename species from *Mycobacterium virus Bignuz* to *Mycobacterium virus BigNuz*)

**Electron micrograph:** None available.

**Proposal 3: To add a single species to the genus *Phayoncevirus***

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

**History:** The genus *Phayoncevirus* was established by Taxonomy Proposal 2016.037a-mB

**Specific Reference:** None

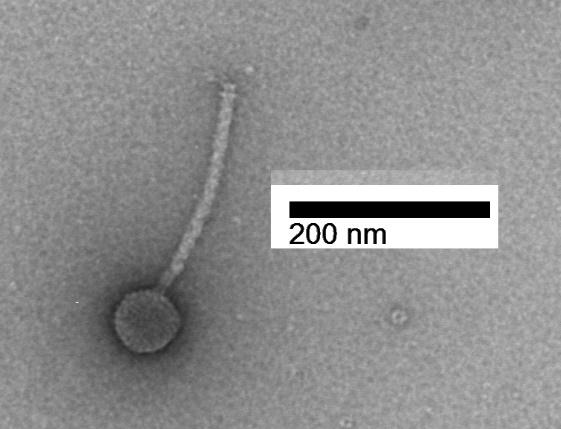
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Phayonce | [NC\_028796.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_028796.1) | [KR080195.1](https://www.ncbi.nlm.nih.gov/nuccore/KR080195.1) | 49.2 | 66.7 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42355/461938%7CMycobacterium%20phage%20Phayonce/viral%20segment%20Unknown/) | 100 | 100 |
| Mycobacterium phage ThulaThula | [NC\_051738.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051738.1) | [MN234172.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234172.1) | 50.42 | 66.5 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84805/708362%7CMycobacterium%20phage%20ThulaThula/viral%20segment/) | 71.8 | 77.9 |

**(\*) Determined using VIRIDIC [6]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage ThulaThula (https://phagesdb.org/phages/ThulaThula/). 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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**Proposal 4: To transfer the genus *Tortellinivirus* to this subfamily**

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

**History:** In 2013 Jessica Schipper and Christian Erchinger (University of Colorado at Boulder) isolated temperate phage Tortellini from soil on Mycobacterium smegmatis mc²155 as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The Actinobacteriophage Database places this virus in Cluster P/Subcluster P2. Its genome possesses 12 nt 3’-cohesive extensions (CCTGCCGCCCGC). The genus was created through Taxonomy Proposal 2018.031B. The current data reveal that it is a member of this subfamily.

**Specific Reference:** None

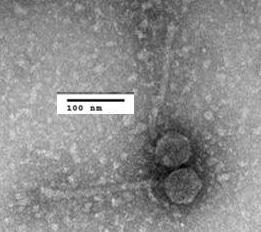
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Tortellini | [NC\_041888.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_041888.1) | [KX648391.1](https://www.ncbi.nlm.nih.gov/nuccore/KX648391.1) | 49.66 | 65.8 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63029/465652%7CMycobacterium%20phage%20Tortellini/viral%20segment/) | 100 | 100 |
|  |  |  |  |  |  |  |  |

**(\*) Determined using VIRIDIC [6]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Tortellini (https://phagesdb.org/phages/Tortellini/). 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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**Proposal 5: To create a new genus *Xaviavirus* with a single species**

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

**History:** In 2017 Stephon Scott (Morehouse College, Atlanta, GA USA) isolated temperate phage Xavia from dirty water on Mycobacterium smegmatis mc²155 as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The Actinobacteriophage Database places this virus in Cluster P/Subcluster P3. Its genome possesses 12 nt 3’-cohesive extensions (CCTGCCGCCCGA).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Xavia | [NC\_051740.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051740.1) | [MH230879.1](https://www.ncbi.nlm.nih.gov/nuccore/MH230879.1) | 49.81 | 65.9 | [71](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/69758/379956%7CMycobacterium%20phage%20Xavia/viral%20segment/) | 100 | 100 |
|  |  |  |  |  |  |  |  |

**(\*) Determined using VIRIDIC [6]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Electron micrograph:** None available.

**Proposal 6: To create a new genus *Purkyvirus* with a single species**

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

**History:** In 2013 Taylor Purks (Howard University, Washington, DC USA) isolated temperate phage Purky from dirty water on Mycobacterium smegmatis mc²155 as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The Actinobacteriophage Database places this virus in Cluster P/Subcluster P6. Its genome possesses 11 nt 3’-cohesive extensions (CCTGCCGCCCG).

**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 | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Purky | [NC\_051739.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_051739.1) | [MN096355.1](https://www.ncbi.nlm.nih.gov/nuccore/MN096355.1) | 50.51 | 66.4 | [84](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82658/614434%7CMycobacterium%20phage%20Purky/viral%20segment/) | 100 | 100 |
|  |  |  |  |  |  |  |  |

**(\*) Determined using VIRIDIC [6]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Electron micrograph:** None available

**References**

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