

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

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| **Code assigned:** | **2021.089B** |  |
| **Short title:** Create one new family (*Vilmaviridae*) including one new subfamily (*Lclasvirinae*) and one subfamily (*Mclasvirinae*) moved from the family *Siphoviridae* (*Caudoviricetes*) | | |
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**Corresponding author**

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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**

|  |
| --- |
| 2021.089B.R.Vilmaviridae |

**Abstract**

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| --- |
| As the number and diversity of phages increase in the Actinobacteriophage Database and the molecular taxonomic tools available to us also increases we are beginning to see new families of viruses. The members of the taxon *Vilmaviridae* possess the following average features: 76.3 kb (59.3 mol%G+C) and encode 132 proteins and 14 tRNAs. They are usually temperate, though members of the genus *Wildcatvirus* are lytic. The genomes all possess 10-11 nt 3’-cohesive termini. This taxon is cohesive as shown by VIRIDIC, ViPTree, Symbet and phylogenetic analyses. CoreGenes5 analysis (https://coregenes.ngrok.io/) with representatives from each taxon reveals 16 shared protein homologs (12.1%) which include TerL, portal, minor and major capsid proteins, head-to-tail adaptor, major tail, tail terminator, tail assembly chaperone, tail tapemeasure protein, two minor tail proteins, lysin B, DnaB-like helicase, ssDNA-binding protein and DNA polymerase III subunit. |

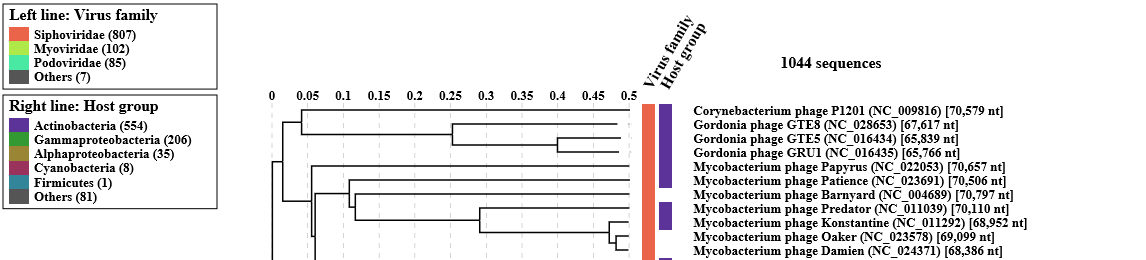
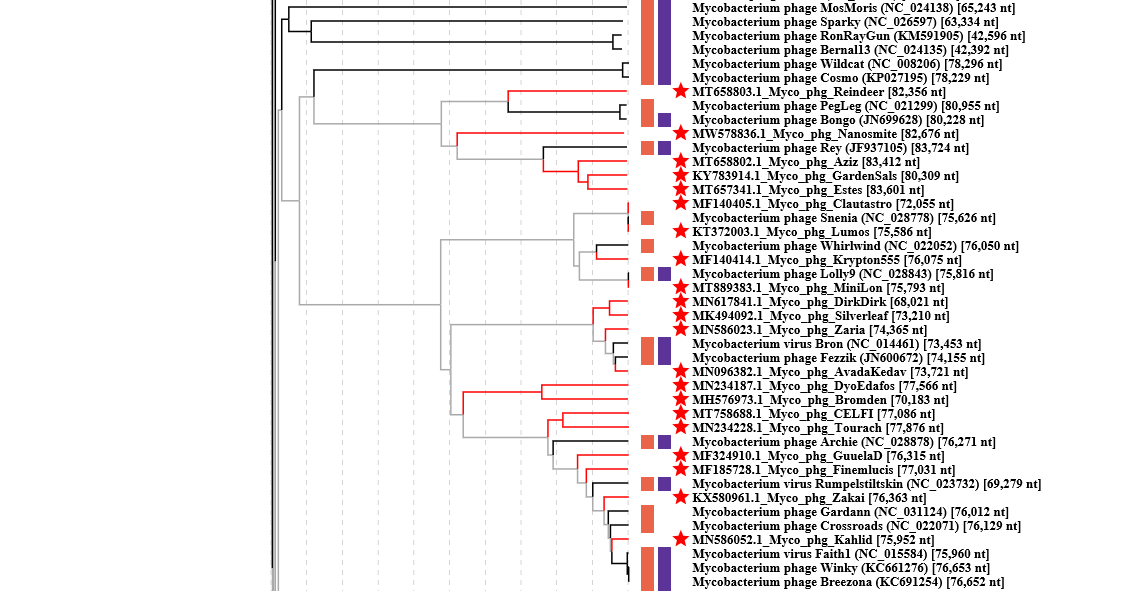
**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | **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.  **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 [11]) | |

**Supporting evidence**

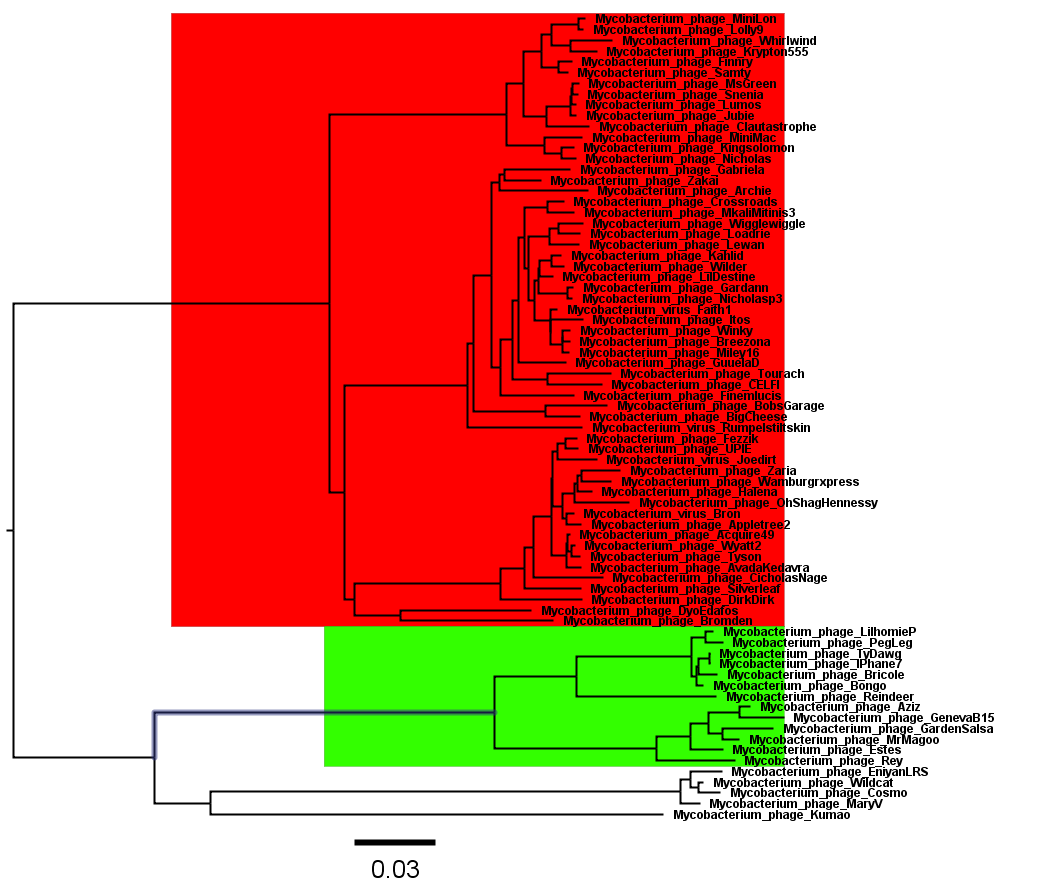
**Molecular analysis:**

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

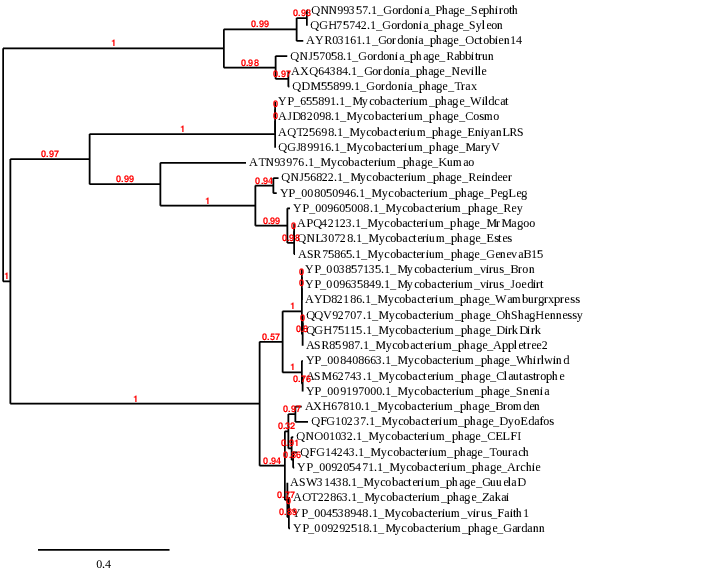
  


**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. (attached)

**Symbet analysis:** Symmetrical best hits were identified between all pairs of phage genomes [17]. For each pair of phage genomes (A and B), the lengths of ORFs were summed for both genomes (ORFs\_A and ORFS\_B) for each symbet. A dissimilarity matrix was constructed using the formula 1 - (ORFs\_A + ORFs\_B) / (Length\_A + Length\_B) where Length\_A and Length\_B represent the genome size of phages A and B, respectively. The PH.26.asm file from <ftp://ftp.ncbi.nlm.nih.gov/genomes/Viruses/FamilyPhylogeneticTree/> was downloaded and opened in NCBI Genome Workshop. The tree of interest was exported and opened and edited in FigTree (<http://tree.bio.ed.ac.uk/software/figtree/>). The two subfamilies are coloured (red *Lclasvirinae*, green *Mclasvirinae*).

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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 [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."

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**PROPOSALS:**

**Proposal A: To create a new subfamily, *Lclasvirinae* with three new genera – *Lumosvirus, Bromdenvirus* and *Faithunavirus***

**Proposal B: To create five (5) new species in the genus *Bronvirus***

**Proposal C: To add three (3) new strains to the genus *Wildcatvirus***

**Proposal D: To create a new genus *Kumaovirus* with a single species**

**Proposal E: To add three (3) new species to the genus *Reyvirus*, subfamily *Mclasvirinae***

**Proposal F: To add one (1) new species to the genus *Bongovirus,* subfamily *Mclasvirinae***

**Proposal G: To create a new family *Vilmaviridae***

**--------------------------------------------------------------------------------------------------------------------------**

**Proposal A: To create a new subfamily, *Lclasvirinae* with three new genera – *Lumosvirus, Bromdenvirus* and *Faithunavirus***

**Source of the name of this taxon:** This subfamily is named after the Actinobacteriophage Database Cluster (L) in which all these phages are classified. The name stands for **L Cl**uster of **A**ctinobacteriophage database **S**iphovirus.

**Rationale:** Our VIRIDIC analysis (attached) indicate that the Actinobacteriophage Database L Cluster phages (<https://phagesdb.org/clusters/L/>) fall into four subgroups, confirming the AbDb classification.This grouping is confirmed by ViPTree, Symbets and phylogenetic analyses.

**Proposal A1: To create a new genus *Lumosvirus* with four (4) species in the subfamily *Lclasvirinae*.**

**Source of the name of this taxon:** This genus is named after Mycobacterium phage Lumos.

**History:** Temperate Mycobacterium phage Lumos was isolated in 2014 by Laura Molina (Indian River State College, Stuart, FL USA) from soil on Mycobacterium smegmatis mc²155, as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. It's genome possesses 10 nt 3'-cohesive termini (TCGATCAGCC). This phage is classified by the Actinobacteriophage Database into Cluster L/Subcluster L3 (<https://phagesdb.org/phages/Lumos/>).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Lumos | [KT372003.1](https://www.ncbi.nlm.nih.gov/nuccore/KT372003.1) | 75.59 | 59.3 | [128](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76477/468965%7CMycobacterium%20phage%20Lumos/viral%20segment/) | 10 | 100 | 100 |
| Mycobacterium phage Lolly9 | [KT281791.1](https://www.ncbi.nlm.nih.gov/nuccore/KT281791.1) | 75.82 | 59.3 | [130](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42500/462066%7CMycobacterium%20phage%20Lolly9/viral%20segment%20Unknown/) | 11 | 86.7 | 90.6 |
| Mycobacterium phage Whirlwind | [KF024725.1](https://www.ncbi.nlm.nih.gov/nuccore/KF024725.1) | 76.05 | 59.3 | [128](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/22403/460200%7CMycobacterium%20phage%20Whirlwind/viral%20segment%20Unknown/) | 11 | 86.5 | 91.4 |
| Mycobacterium phage Krypton555 | [MF140414.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140414.1) | 76.08 | 59.3 | [130](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63731/466352%7CMycobacterium%20phage%20Krypton555/viral%20segment/) | 11 | 88.5 | 91.4 |

**(\*) 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:**

|  |  |  |
| --- | --- | --- |
| **Accession No.** | **Phage Name** | **Strain of:** |
| MF140405.1 | Mycobacterium phage Clautastrophe | *Lumosvirus Lumos* |
| MW291024.1 | Mycobacterium phage Jubie | *Lumosvirus Lumos* |
| MK878900.1 | Mycobacterium phage MsGreen | *Lumosvirus Lumos* |
| KT281794.1 | Mycobacterium phage Snenia | *Lumosvirus Lumos* |
| MF140413.1 | Mycobacterium phage Kingsolomon | *Lumosvirus Lumos* |
| MF140421.1 | Mycobacterium phage Nicholas | *Lumosvirus Lumos* |
| MH727559.1 | Mycobacterium phage Samty | *Lumosvirus Lumos* |
| MN096377.1 | Mycobacterium phage Finnry | *Lumosvirus Lumos* |
| MT889391.1 | Mycobacterium phage MiniMac | *Lumosvirus Lolly9* |
| MT889383.1 | Mycobacterium phage MiniLon | *Lumosvirus Lolly9* |

**Electron micrograph:** None available

**Proposal A2: To create a new genus *Faithunavirus* with seven (7) species**

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Faith1

**History:** Temperate Mycobacterium phage Faith1 was isolated in 2009 by Jazmyn McCloud (Spelman College, Atlanta, GA USA) from soil on Mycobacterium smegmatis mc²155, as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. Its genome possesses 10 nt 3'-cohesive termini (TCGATCAGCC). This phage is classified by the Actinobacteriophage Database into Cluster L/Subcluster L2 (https://phagesdb.org/phages/Faith1/).

**Specific Reference:** Hatfull GF; Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science Program; KwaZulu-Natal Research Institute for Tuberculosis and HIV Mycobacterial Genetics Course Students; Phage Hunters Integrating Research and Education Program. Complete genome sequences of 138 mycobacteriophages. J Virol. 2012 Feb;86(4):2382-4. doi: 10.1128/JVI.06870-11. PMID: 22282335; PMCID: PMC3302410. **[Faith1]**

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Faith1 | JF744988.1 | 76.49 | 58.9 | 132 | 12 | 100 | 100 |
| Mycobacterium phage Archie | [KT591489.1](https://www.ncbi.nlm.nih.gov/nuccore/KT591489.1) | 76.27 | 58.7 | [128](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42486/462051%7CMycobacterium%20phage%20Archie/viral%20segment%20Unknown/) | 12 | 82.4 | 90.7 |
| Mycobacterium phage CELFI | [MT758688.1](https://www.ncbi.nlm.nih.gov/nuccore/MT758688.1) | 77.09 | 59.0 | [122](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94630/986848%7CMycobacterium%20phage%20CELFI/viral%20segment/) | 11 | 83.0 | 86.0 |
| Mycobacterium phage Finemlucis | [MF185728.1](https://www.ncbi.nlm.nih.gov/nuccore/MF185728.1) | 77.03 | 58.9 | [131](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64159/466567%7CMycobacterium%20phage%20Finemlucis/viral%20segment/) | 10 | 89.7 | 92.2 |
| Mycobacterium phage GuuelaD | [MF324910.1](https://www.ncbi.nlm.nih.gov/nuccore/MF324910.1) | 76.32 | 58.9 | [129](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63667/466288%7CMycobacterium%20phage%20GuuelaD/viral%20segment/) | 11 | 92.2 | 91.5 |
| Mycobacterium phage Tourach | [MN234228.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234228.1) | 77.88 | 58.8 | [132](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84855/708412%7CMycobacterium%20phage%20Tourach/viral%20segment/) | 11 | 84.0 | 89.9 |

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

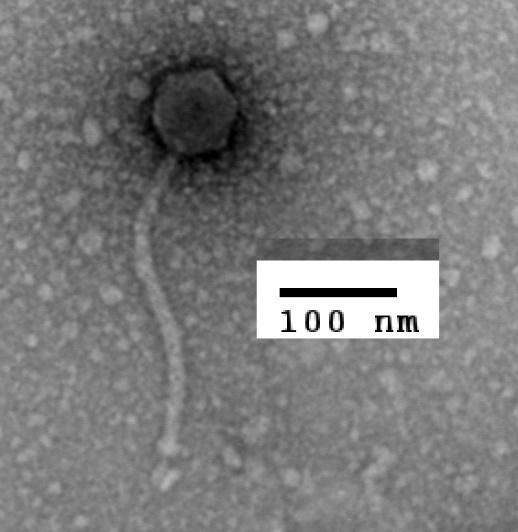
**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Transfer *Mycobacterium virus Rumpelstiltskin* (JN680858.1) from *Bronvirus* to *Faithunavirus*.**

**Strains:**

|  |  |  |
| --- | --- | --- |
| **Accession No.** | **Phage Name** | **Strain of:** |
| MH834600.1 | Mycobacterium phage BigCheese | *Faithunavirus Faith1* |
| MN586030.1 | Mycobacterium phage BobsGarage | *Faithunavirus Faith1* |
| KC691254.1 | Mycobacterium phage Breezona | *Faithunavirus Faith1* |
| KF024731.1 | Mycobacterium phage Crossroads | *Faithunavirus Faith1* |
| MN703406.1 | Mycobacterium phage Gabriela | *Faithunavirus Faith1* |
| KX507361.1 | Mycobacterium phage Gardann | *Faithunavirus Faith1* |
| MN703410.1 | Mycobacterium phage Itos | *Faithunavirus Faith1* |
| MN586052.1 | Mycobacterium phage Kahlid | *Faithunavirus Faith1* |
| MN096380.1 | Mycobacterium phage Lewan | *Faithunavirus Faith1* |
| MH779511.1 | Mycobacterium phage LilDestine | *Faithunavirus Faith1* |
| KU997639.1 | Mycobacterium phage Loadrie | *Faithunavirus Faith1* |
| MF185730.1 | Mycobacterium phage Miley16 | *Faithunavirus Faith1* |
| KU234099.1 | Mycobacterium phage MkaliMitinis3 | *Faithunavirus Faith1* |
| MF140422.1 | Mycobacterium phage Nicholasp3 | *Faithunavirus Faith1* |
| MK937600.1 | Mycobacterium phage Wigglewiggle | *Faithunavirus Faith1* |
| KX580962.1 | Mycobacterium phage Wilder | *Faithunavirus Faith1* |
| KC661276.1 | Mycobacterium phage Winky | *Faithunavirus Faith1* |
| KX580961.1 | Mycobacterium phage Zakai | *Faithunavirus Faith1* |

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Faith1 (https://phagesdb.org/phages/MooMoo/). 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.



**Proposal A3: To create a new genus *Bromdenvirus*  with two (2) species**

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

**History:** Temperate Mycobacterium phage Bromden was isolated in 2017 by Hannah E Cizauskas (Hope College, Westland, MI USA) from soil on Mycobacterium smegmatis mc²155, as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. It's genome possesses 10 nt 3'-cohesive termini (TCGATCAGCC). This phage is classified by the Actinobacteriophage Database into Cluster L/Subcluster L4 (https://phagesdb.org/phages/Bromden/).

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Bromden | [MH576973.1](https://www.ncbi.nlm.nih.gov/nuccore/MH576973.1) | 70.18 | 58.2 | [118](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71967/399839%7CMycobacterium%20phage%20Bromden/viral%20segment/) | 13 | 100 | 100 |
| Mycobacterium phage DyoEdafos | [MN234187.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234187.1) | 77.57 | 58.5 | [142](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84819/708376%7CMycobacterium%20phage%20DyoEdafos/viral%20segment/) | 14 | 74.8 | 84.7 |

**(\*) 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 B: To create five (5) new species in the genus *Bronvirus***

**Source of the name of this taxon:** This genus is named after Mycobacterium phage Bron

**History:** The genus *Bronlikevirus* was proposed in Taxonomy Proposal 2013.017a-dB to contain four species *Mycobacterium virus Bron, Mycobacterium virus Faith1, Mycobacterium virus JoeDirt*, and *Mycobacterium virus Rumpelstiltskin*. Faith1 and Rumpelstiltskin have now been transferred to *Faithunavirus*.

**Specific Reference:** Pope WH, Jacobs-Sera D, Russell DA, Peebles CL, Al-Atrache Z, Alcoser TA, Alexander LM, Alfano MB, Alford ST, Amy NE, Anderson MD, Anderson AG, Ang AA, Ares M Jr, Barber AJ, Barker LP, Barrett JM, Barshop WD, Bauerle CM, Bayles IM, Belfield KL, Best AA, Borjon A Jr, Bowman CA, Boyer CA, Bradley KW, Bradley VA, Broadway LN, Budwal K, Busby KN, Campbell IW, Campbell AM, Carey A, Caruso SM, Chew RD, Cockburn CL, Cohen LB, Corajod JM, Cresawn SG, Davis KR, Deng L, Denver DR, Dixon BR, Ekram S, Elgin SC, Engelsen AE, English BE, Erb ML, Estrada C, Filliger LZ, Findley AM, Forbes L, Forsyth MH, Fox TM, Fritz MJ, Garcia R, George ZD, Georges AE, Gissendanner CR, Goff S, Goldstein R, Gordon KC, Green RD, Guerra SL, Guiney-Olsen KR, Guiza BG, Haghighat L, Hagopian GV, Harmon CJ, Harmson JS, Hartzog GA, Harvey SE, He S, He KJ, Healy KE, Higinbotham ER, Hildebrandt EN, Ho JH, Hogan GM, Hohenstein VG, Holz NA, Huang VJ, Hufford EL, Hynes PM, Jackson AS, Jansen EC, Jarvik J, Jasinto PG, Jordan TC, Kasza T, Katelyn MA, Kelsey JS, Kerrigan LA, Khaw D, Kim J, Knutter JZ, Ko CC, Larkin GV, Laroche JR, Latif A, Leuba KD, Leuba SI, Lewis LO, Loesser-Casey KE, Long CA, Lopez AJ, Lowery N, Lu TQ, Mac V, Masters IR, McCloud JJ, McDonough MJ, Medenbach AJ, Menon A, Miller R, Morgan BK, Ng PC, Nguyen E, Nguyen KT, Nguyen ET, Nicholson KM, Parnell LA, Peirce CE, Perz AM, Peterson LJ, Pferdehirt RE, Philip SV, Pogliano K, Pogliano J, Polley T, Puopolo EJ, Rabinowitz HS, Resiss MJ, Rhyan CN, Robinson YM, Rodriguez LL, Rose AC, Rubin JD, Ruby JA, Saha MS, Sandoz JW, Savitskaya J, Schipper DJ, Schnitzler CE, Schott AR, Segal JB, Shaffer CD, Sheldon KE, Shepard EM, Shepardson JW, Shroff MK, Simmons JM, Simms EF, Simpson BM, Sinclair KM, Sjoholm RL, Slette IJ, Spaulding BC, Straub CL, Stukey J, Sughrue T, Tang TY, Tatyana LM, Taylor SB, Taylor BJ, Temple LM, Thompson JV, Tokarz MP, Trapani SE, Troum AP, Tsay J, Tubbs AT, Walton JM, Wang DH, Wang H, Warner JR, Weisser EG, Wendler SC, Weston-Hafer KA, Whelan HM, Williamson KE, Willis AN, Wirtshafter HS, Wong TW, Wu P, Yang Yj, Yee BC, Zaidins DA, Zhang B, Zúniga MY, Hendrix RW, Hatfull GF. Expanding the diversity of mycobacteriophages: insights into genome architecture and evolution. PLoS One. 2011 Jan 27;6(1):e16329. doi: 10.1371/journal.pone.0016329. PMID: 21298013; PMCID: PMC3029335.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Bron | [HM152763.1](https://www.ncbi.nlm.nih.gov/nuccore/HM152763.1) | 73.45 | 58.8 | [123](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4035/455904%7CMycobacterium%20virus%20Bron/viral%20segment%20Unknown/) | 9 | 100 | 100 |
| Mycobacterium phage Silverleaf | [MK494092.1](https://www.ncbi.nlm.nih.gov/nuccore/MK494092.1) | 73.21 | 58.8 | [116](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/78095/478548%7CMycobacterium%20phage%20Silverleaf/viral%20segment/) | 11 | 89.3 | 89.4 |
| Mycobacterium phage DirkDirk | [MN617841.1](https://www.ncbi.nlm.nih.gov/nuccore/MN617841.1) | 68.02 | 58.7 | [110](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85600/743759%7CMycobacterium%20phage%20DirkDirk/viral%20segment/) | 9 | 89.7 | 85.4 |
| Mycobacterium phage OhShagHennessy | [MW435855.1](https://www.ncbi.nlm.nih.gov/nuccore/MW435855.1) | 72.62 | 58.9 | [118](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98293/1553530%7CMycobacterium%20phage%20OhShagHennessy/viral%20segment/) | 7 | 93.7 | 92.7 |
| Mycobacterium phage CicholasNage | M[K310144.1](https://www.ncbi.nlm.nih.gov/nuccore/MK310144.1) | 71.06 | 58.6 | [118](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75925/446583%7CMycobacterium%20phage%20CicholasNage/viral%20segment/) | 5 | 93.2 | 92.7 |

**(\*) 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:**

|  |  |  |
| --- | --- | --- |
| **Accession No.** | **Phage Name** | **Strain of:** |
| MN586023.1 | Mycobacterium phage Zaria | *Bronvirus Bron* |
| JF704113.1 | Mycobacterium phage UPIE | *Bronvirus Bron* |
| JN600672.1 | Mycobacterium phage Fezzik | *Bronvirus Bron* |
| MN096382.1 | Mycobacterium phage AvadaKedavra | *Bronvirus Bron* |
| MT771349.1 | Mycobacterium phage Tyson | *Bronvirus Bron* |
| MK279905.1 | Mycobacterium phage Acquire49 | *Bronvirus Bron* |
| MN586018.1 | Mycobacterium phage Wyatt2 | *Bronvirus Bron* |
| MF185726.1 | Mycobacterium phage Appletree2 | *Bronvirus Bron* |
| MK494100.1 | Mycobacterium phage Halena | *Bronvirus Bron* |
| MH744425.1 | Mycobacterium phage Wamburgrxpress | *Bronvirus Bron* |

**Electron micrograph:** Not available

**Proposal C: To add three (3) new strains to the genus *Wildcatvirus***

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

**History:** The genus Wildcatvirus was established through Taxonomy Proposal 2016.053a-dB. This lytic phages belongs to The Actinobacteriophage Database Cluster V.

**Specific Reference:** None

**Strains:**

|  |  |  |
| --- | --- | --- |
| **Accession No.** | **Phage name** | **Strain of:** |
| KY385381.1 | Mycobacterium phage EniyanLRS | *Wildcatvirus Wildcat* |
| KP027195.1 | Mycobacterium phage Cosmo | *Wildcatvirus Wildcat* |
| MN585992.1 | Mycobacterium phage MaryV | *Wildcatvirus Wildcat* |

**Electron micrograph:** None added

**Proposal D: To create a new genus *Kumaovirus* with a single species**

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

**History:** Temperate Mycobacterium phage Kumao was isolated in 2015 by Lisa Sako-Glover (Lehigh University, Easton, PA USA) from soil on Mycobacterium smegmatis mc²155, as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. This phage is classified by the Actinobacteriophage Database as a singleton (https://phagesdb.org/phages/Kumao/)

**Specific Reference:** None

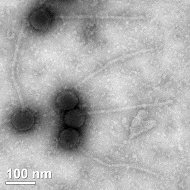
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Kumao |  | [MG009575.1](https://www.ncbi.nlm.nih.gov/nuccore/MG009575.1) | 70.37 | 62.1 | [115](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64179/466587%7CMycobacterium%20phage%20Kumao/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 Kumao (https://phagesdb.org/phages/Kumao/). 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.



**Proposal E: To add three (3) new species to the genus *Reyvirus*, subfamily *Mclasvirinae***

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

**History:** This genus was proposed in Taxonomy Proposal 2013.021a-dB to contain a single species. It is classified by the Actinobacteriophage Database into Cluster M/Subcluster M2. It is temperate.

**Specific Reference:** Pope WH, Ferreira CM, Jacobs-Sera D, Benjamin RC, Davis AJ, DeJong RJ, Elgin SC, Guilfoile FR, Forsyth MH, Harris AD, Harvey SE, Hughes LE, Hynes PM, Jackson AS, Jalal MD, MacMurray EA, Manley CM, McDonough MJ, Mosier JL, Osterbann LJ, Rabinowitz HS, Rhyan CN, Russell DA, Saha MS, Shaffer CD, Simon SE, Sims EF, Tovar IG, Weisser EG, Wertz JT, Weston-Hafer KA, Williamson KE, Zhang B, Cresawn SG, Jain P, Piuri M, Jacobs WR Jr, Hendrix RW, Hatfull GF. Cluster K mycobacteriophages: insights into the evolutionary origins of mycobacteriophage TM4. PLoS One. 2011;6(10):e26750. doi: 10.1371/journal.pone.0026750. Epub 2011 Oct 28. PMID: 22053209; PMCID: PMC3203893. **[Rey]**

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Rey | [JF937105.1](https://www.ncbi.nlm.nih.gov/nuccore/JF937105.1) | 83.72 | 60.9 | [153](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63588/466209%7CMycobacterium%20phage%20Rey/viral%20segment/) | 21 | 100 | 100 |
| Mycobacterium phage Aziz | [MT658802.1](https://www.ncbi.nlm.nih.gov/nuccore/MT658802.1) | 83.41 | 60.7 | [150](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94269/980546%7CMycobacterium%20phage%20Aziz/viral%20segment/) | 21 | 81.0 | 86.3 |
| Mycobacterium phage Estes | [MT657341.1](https://www.ncbi.nlm.nih.gov/nuccore/MT657341.1) | 83.6 | 60.9 | [151](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94455/985784%7CMycobacterium%20phage%20Estes/viral%20segment/) | 21 | 82.0 | 87.6 |
| Mycobacterium phage MrMagoo | [KY223999.1](https://www.ncbi.nlm.nih.gov/nuccore/KY223999.1) | 84.3 | 60.8 | [155](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63264/465887%7CMycobacterium%20phage%20MrMagoo/viral%20segment/) | 21 | 80.8 | 84.3 |

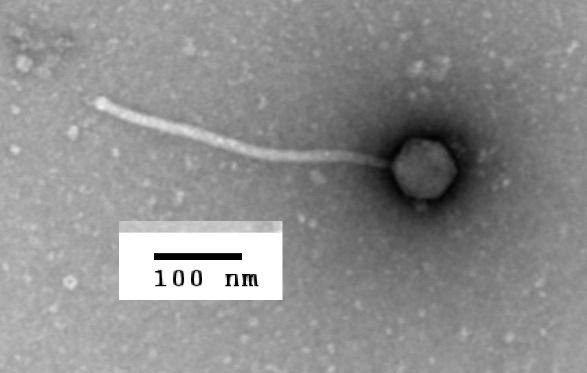
**(\*) Determined using VIRIDIC [6]**

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

**Strains:**

|  |  |  |
| --- | --- | --- |
| **Accession No.** | **Phage Name** | **Strain of:** |
| KY783914.1 | Mycobacterium phage GardenSalsa | *Reyvirus MrMagoo* |
| MF319184.1 | Mycobacterium phage GenevaB15 | *Reyvirus Aziz* |

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Rey (https://phagesdb.org/phages/Rey/). 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.



**Proposal F: To add one (1) new species to the genus *Bongovirus,* subfamily *Mclasvirinae***

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

**History:** This genus was proposed in Taxonomy Proposal 2016.028a-jB to contain a single species. It is classified by the Actinobacteriophage Database into Cluster M/Subcluster M1. It is temperate.

**Specific Reference:** None

**GenBank Summary:**

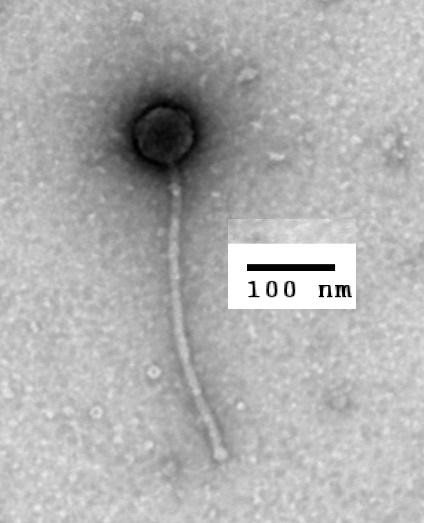
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Bongo | [JN699628.3](https://www.ncbi.nlm.nih.gov/nuccore/JN699628.3) | 80.23 | 61.6 | [132](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63587/466208%7CMycobacterium%20phage%20Bongo/viral%20segment%20Unknown/) | 20 | 100 | 100 |
| Mycobacterium phage Reindeer | [MT658803.1](https://www.ncbi.nlm.nih.gov/nuccore/MT658803.1) | 82.36 | 60.3 | [140](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94271/980548%7CMycobacterium%20phage%20Reindeer/viral%20segment/) | 19 | 72.4 | 84.8 |

**(\*) 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]**

|  |  |  |
| --- | --- | --- |
| **Accession No.** | **Phage Name** | **Strain of:** |
| KC900379.1 | Mycobacterium phage PegLeg | *Bongovirus Bongo* |
| MK937612.1 | Mycobacterium phage LilhomieP | *Bongovirus Bongo* |
| KT591491.1 | Mycobacterium phage Bricole | *Bongovirus Bongo* |
| MH697587.1 | Mycobacterium phage IPhane7 | *Bongovirus Bongo* |
| MN586024.1 | Mycobacterium phage TyDawg | *Bongovirus Bongo* |

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Bongo (https://phagesdb.org/phages/Bongo/). 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 G: To create a new family *Vilmaviridae* for the above described taxa**

**Source of the name of this taxon:** This taxon is named after **V** and **L** and **M** Clusters on the Actinobacteriophage Database.

**Rationale:** The members of this taxon possess the follow average features 76.3 kb (59.3 mol%G+C) and encode 132 proteins and 14 tRNAs. They are usually temperate, though members of the *Wildcatvirus* are lytic. The genome all possess 10-11 nt 3’-cohesive termini. This taxon is cohesive as shown by VIRIDIC, ViPTree, Symbet and phylogenetic analyses. CoreGenes5 analysis (<https://coregenes.ngrok.io/>) of representatives from each taxon reveals 16 protein homologs (12.1%) which include TerL, portal, minor and major capsid proteins, head-to-tail adaptor, major tail, tail terminator, tail assembly chaperone, tail tapemeasure protein, two minor tail proteins, lysin B, DnaB-like helicase, ssDNA-binding protein and DNA polymerase III subunit.

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