

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2021.005B** |  |
| **Short title:** Create eight new genera in the subfamily *Arquatrovirinae* (*Caudoviricetes*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Turner D, Moraru C, Tolstoy I, Adriaenssens EM, Kropinski AM | dann2.turner@uwe.ac.uk;  liliana.cristina.moraru@uni-oldenburg.de; tolstoy@ncbi.nlm.nih.gov;  evelien.adriaenssens@quadram.ac.uk;  Phage.Canada@gmail.com |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| University of the West of England at Bristol, UK [DT]  Institute for Chemistry and Biology of the Marine Environment, Germany [CM]  NCBI, USA [IT]  Quadram Institute Bioscience, UK [EMA]  University of Guelph, Canada [AMK] |

**Corresponding author**

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| --- |
| Andrew M. 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)** |
|  |  |  |
|  |  |  |
|  |  |  |

**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**

|  |
| --- |
| 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**

|  |
| --- |
| 2021.005B.R.Arquatrovirinae |

**Abstract**

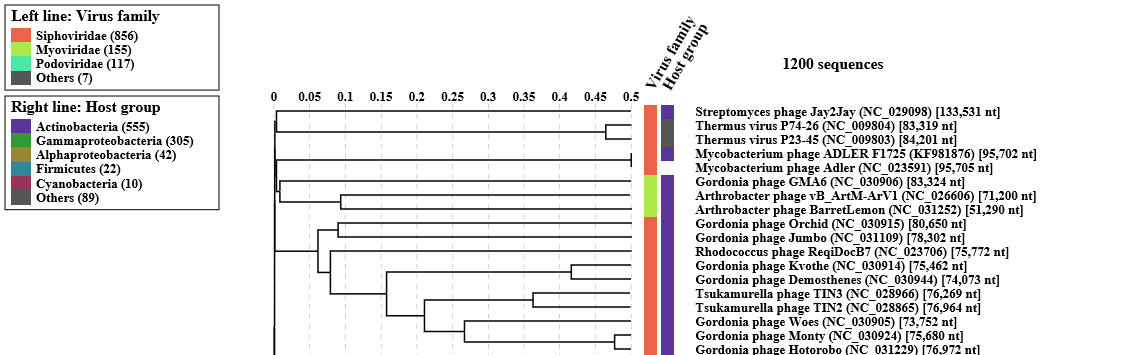
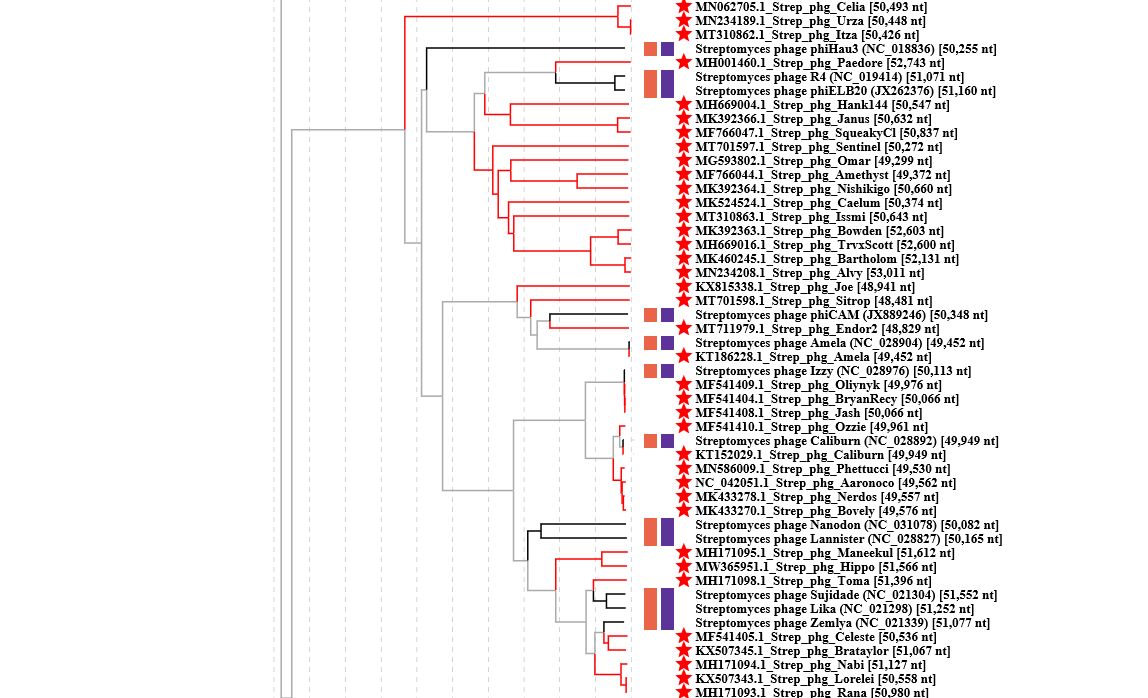
|  |
| --- |
| The subfamily *Arquatrovirinae* was established through Taxonomy Proposal 2016.077a-pB. According to the Actinobacteriophage Database these and related phages belong to Cluster DB, on which there are now six subclusters. Our reexamination of these phages in GenBank results in recognition of eight new genera. These genera all fit within a single subfamily the members of which possess, on average, genomes of 50.50 kb (66.5 mol%G+C) and encode for 79 proteins and 0-1 tRNA. At the DNA level these phages share at least 34.0% DNA similarity. |

**Text of proposal**

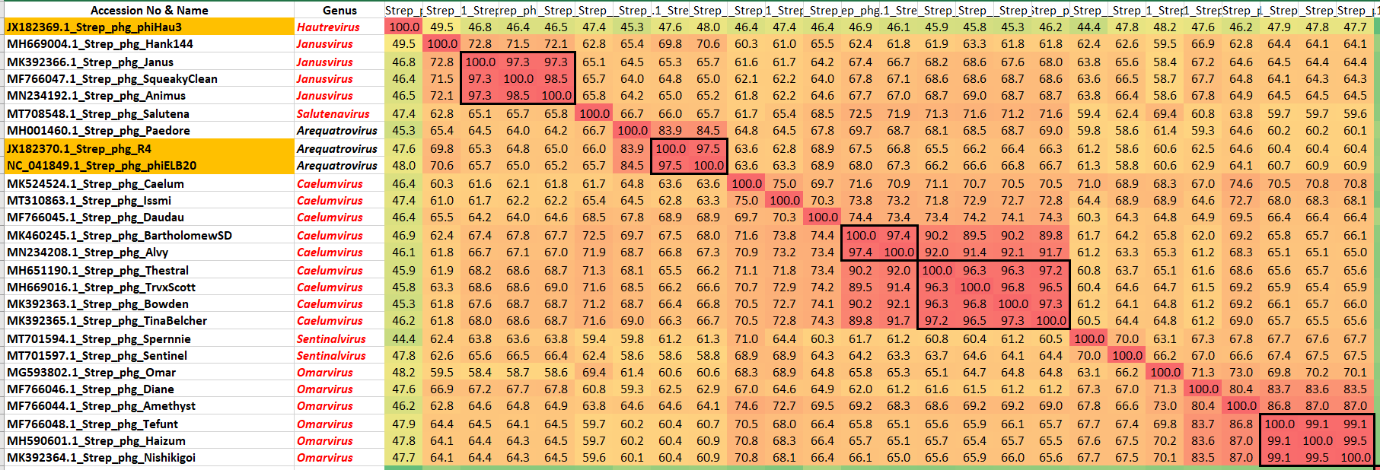
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic 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 (here minimum 34%) and that the genera form a clade in a marker tree phylogeny. [9] | |

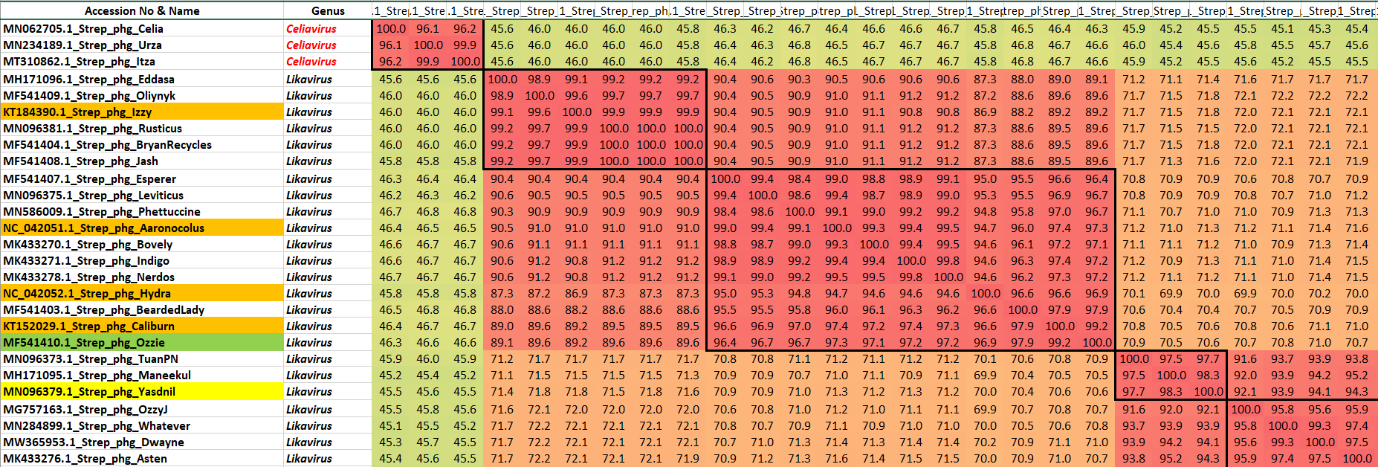
**Supporting evidence**

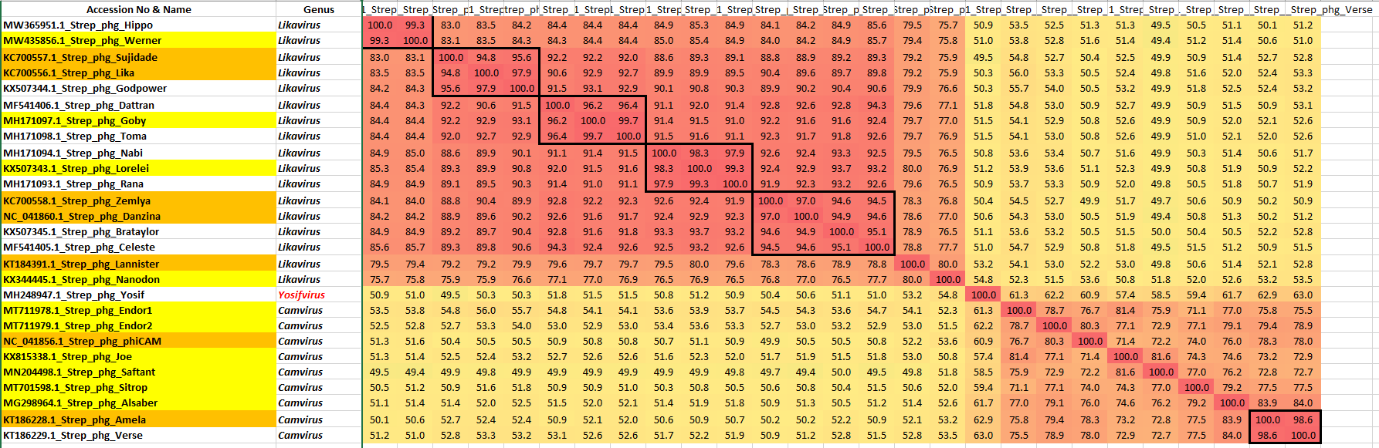
**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. The phages of interest are indicated with **red lines**.

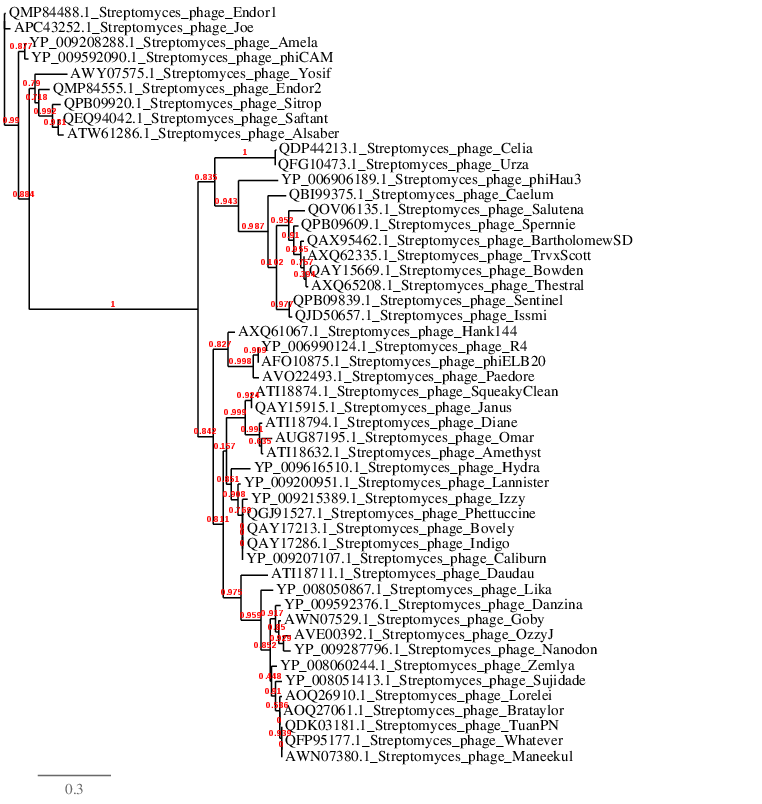
**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. Strains are indicated in black boxes.







**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins of phages belonging to the subfamily *Arquatrovirinae* 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." The new genera are indicated with arrows or boxes.

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**Proposals:**

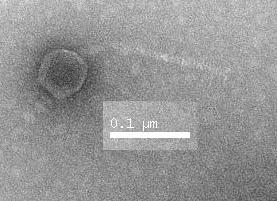
1. **To create a new genus, *Celiavirus* with a single species**
2. **To create a new genus, *Hautrevirus* with single species**
3. **To create a new genus, *Yosifvirus* with a single species**
4. **To create a new genus, *Salutenavirus* with one species**
5. **To create a new genus, *Sentinelvirus* with two species**
6. **To create a new genus, *Janusvirus* with two species**
7. **To create a new genus *Omarvirus* with four species**
8. **To create a new genus, *Caelumvirus* with five species**
9. **To add one new species to the genus *Arquatrovirus***
10. **To add five (5) new species to the genus *Likavirus***
11. **To add six (6) new species to the genus *Camvirus***

**To create a new genus, *Celiavirus* with a single species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage Celia.

**History:** Temperate Streptomyces phage Celia was isolated in 2018 by Julia Lopez (University of North Texas, Denton, TX, USA) from soil using Streptomyces xanthochromogenes NRRL B-5410 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (CGCTGCGTCAT). The Actinobacteriophage Database places this phage in Cluster BD, Subcluster BD6.

**Electron micrograph:** Electron micrographs of negatively stained Streptomyces phage Celia (https://phagesdb.org/phages/Celia/). 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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**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Celia | [MN062705.1](https://www.ncbi.nlm.nih.gov/nuccore/MN062705.1) | 50.49 | 68.6 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83104/639495%7CStreptomyces%20phage%20Celia/viral%20segment/) | 1 | 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]**

**To create a new genus, *Hautrevirus* with single species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage phiHau3.

**History:** Temperate Streptomyces phage phiHau3 was isolated in 2012 by Xiufen Zhou using Streptomyces coelicolor A3(2) as the host bacterium. The Actinobacteriophage Database places this phage in Cluster BD, Subcluster BD4.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage phiHau3 | [JX182369.1](https://www.ncbi.nlm.nih.gov/nuccore/JX182369.1) | 50.26 | 67.8 | [72](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/15249/459717%7CStreptomyces%20phage%20phiHau3/viral%20segment%20Unknown/) | 1 | 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]**

**To create a new genus, *Yosifvirus* with a single species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage Yosif.

**History:** Temperate Streptomyces phage Yosif was isolated in 2016 by Hessah Alzaid (University of North Texas, Denton, TX, USA) from soil using Streptomyces toxytricini NRRL B-5426 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (CGCCATGTGAT). The Actinobacteriophage Database places this phage in Cluster BD, Subcluster BD3.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Yosif | [MH248947.1](https://www.ncbi.nlm.nih.gov/nuccore/MH248947.1) | 50.13 | 66.1 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/70921/388828%7CStreptomyces%20phage%20Yosif/viral%20segment/) | 0 | 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]**

**To create a new genus, *Salutenavirus* with one species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage Salutena.

**History:** Temperate Streptomyces phage Salutena was isolated in 2017 by Tyler Higbee (Texas A&M, College Station, TX, USA) from South Jordan (UT USA) soil using a Streptomyces strain as the host bacterium. The Actinobacteriophage Database does not classify this phage.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Salutena | [MT708548.1](https://www.ncbi.nlm.nih.gov/nuccore/MT708548.1) | 51.96 | 67.5 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96581/1483820%7CStreptomyces%20phage%20Salutena/viral%20segment/) | 1 | 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]**

**To create a new genus, *Sentinelvirus* with two species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage Sentinel.

**History:** Temperate Streptomyces phage Sentinel was isolated in 2019 by Russell Moreland (Texas A&M, College Station, TX, USA) from Houston, TX soil using a Streptomyces strain as the host bacterium. The Actinobacteriophage Database does not classify this phage.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Sentinel | [MT701597.1](https://www.ncbi.nlm.nih.gov/nuccore/MT701597.1) | 50.27 | 66.9 | [81](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96739/1493964%7CStreptomyces%20phage%20Sentinel/viral%20segment/) | 0 | 100 | 100 |
| Streptomyces phage Spernnie | [MT701594.1](https://www.ncbi.nlm.nih.gov/nuccore/MT701594.1) | 50.83 | 65.7 | [83](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96743/1493968%7CStreptomyces%20phage%20Spernnie/viral%20segment/) | 0 | 70.0 | 79.0 |

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

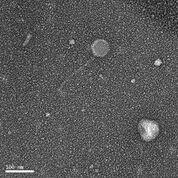
**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**To create a new genus, *Janusvirus* with two species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage Janus.

**History:** Temperate Streptomyces phage Janus was isolated in 2016 by Jose Molina (University of North Texas, Dallas, TX, USA) from soil using Streptomyces xanthochromogenes NRRL B-5410 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (CGCCGTGTCTT). The Actinobacteriophage Database places this phage in Cluster BD, Subcluster BD2.

**Electron micrograph:** Electron micrographs of negatively stained Streptomyces phage Janus (https://phagesdb.org/phages/Janus/). 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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**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Janus | [MK392366.1](https://www.ncbi.nlm.nih.gov/nuccore/MK392366.1) | 50.63 | 67.0 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76023/446681%7CStreptomyces%20phage%20Janus/viral%20segment/) | 0 | 100 | 100 |
| Streptomyces phage Hank144 | [MH669004.1](https://www.ncbi.nlm.nih.gov/nuccore/MH669004.1) | 50.55 | 66.3 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72119/400255%7CStreptomyces%20phage%20Hank144/viral%20segment/) | 0 | 72.8 | 85.9 |

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

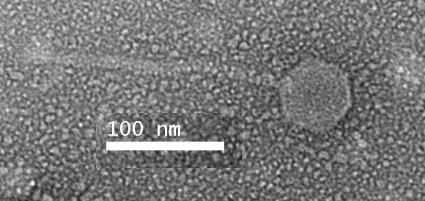
**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**To create a new genus *Omarvirus* with four species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage Omar.

**History:** Temperate Streptomyces phage Omar was isolated in 2018 by Ahmad Sulaiman (University of North Texas, Denton, TX, USA) from Denton TX soil using Streptomyces azureus NRRL B-2655 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (CGCCACGTCTT). The Actinobacteriophage Database places this phage in Cluster BD, Subcluster BD2.

**Electron micrograph:** Electron micrographs of negatively stained Streptomyces phage Omar (https://phagesdb.org/phages/Omar/). 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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**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Omar | [MG593802.1](https://www.ncbi.nlm.nih.gov/nuccore/MG593802.1) | 49.3 | 67.3 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68311/369458%7CStreptomyces%20phage%20Omar/viral%20segment/) | 1 | 100 | 100 |
| Streptomyces phage Diane | [MF766046.1](https://www.ncbi.nlm.nih.gov/nuccore/MF766046.1) | 50.48 | 66.7 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64170/466578%7CStreptomyces%20phage%20Diane/viral%20segment/) | 0 | 71.3 | 83.7 |
| Streptomyces phage Amethyst | [MF766044.1](https://www.ncbi.nlm.nih.gov/nuccore/MF766044.1) | 49.37 | 67.2 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64168/466576%7CStreptomyces%20phage%20Amethyst/viral%20segment/) | 0 | 73.0 | 83.7 |
| Streptomyces phage Tefunt | [MF766048.1](https://www.ncbi.nlm.nih.gov/nuccore/MF766048.1) | 50.57 | 66.8 | [81](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64172/466580%7CStreptomyces%20phage%20Tefunt/viral%20segment/) | 0 | 69.8 | 83.7 |

**(\*) 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]**

**To create a new genus, *Caelumvirus* with five species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Streptomyces phage Caelum.

**History:** Temperate Streptomyces phage Caelum was isolated in 2014 by Samantha Reinhardt (Wilkes University, Scranton, PA USA) from soil using Streptomyces lividans JI 1326 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (CGCCACGTCTT). The Actinobacteriophage Database places this phage in Cluster BD, Subcluster BD2.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Caelum | [MK524524.1](https://www.ncbi.nlm.nih.gov/nuccore/MK524524.1) | 50.37 | 67.0 | [84](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76414/468469%7CStreptomyces%20phage%20Caelum/viral%20segment/) | 0 | 100 | 100 |
| Streptomyces phage Issmi | [MT310863.1](https://www.ncbi.nlm.nih.gov/nuccore/MT310863.1) | 50.64 | 67.6 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89548/893410%7CStreptomyces%20phage%20Issmi/viral%20segment/) | 0 | 75.0 | 89.3 |
| Streptomyces phage Daudau | [MF766045.1](https://www.ncbi.nlm.nih.gov/nuccore/MF766045.1) | 50.6 | 67.1 | [83](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64169/466577%7CStreptomyces%20phage%20Daudau/viral%20segment/) | 0 | 69.7 | 84.5 |
| Streptomyces phage Alvy | [MN234208.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234208.1) | 53.01 | 67.5 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84838/708395%7CStreptomyces%20phage%20Alvy/viral%20segment/) | 1 | 70.9 | 88.1 |
| Streptomyces phage Thestral | [MH651190.1](https://www.ncbi.nlm.nih.gov/nuccore/MH651190.1) | 52.63 | 67.7 | [82](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72158/400294%7CStreptomyces%20phage%20Thestral/viral%20segment/) | 1 | 71.1 | 89.3 |

**(\*) 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]**

**To add one new species to the genus *Arequatrovirus***

**Source of the name of this taxon:** NA

**History:** The genus *R4virus* (renamed *Arequatrovirus*) was established by Taxonomy Proposal 2016.077a-pB to contain two species R4 and ELB20. Temperate Streptomyces phage Paedore was isolated in 2013 by Michael Ward and Rebekah Dedrick (University of Pittsburgh, PA USA) from Glenshaw, PA USA soil using Streptomyces lividans JI 1326 as the host bacterium. This was part of the Phage Hunters Integrating Research and Education program. The Actinobacteriophage Database places this phage in Cluster BD, Subcluster BD2.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage R4 | [JX182370.1](https://www.ncbi.nlm.nih.gov/nuccore/JX182370.1) | 51.07 | 67.0 | [86](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/15406/459743%7CStreptomyces%20phage%20R4/viral%20segment%20Unknown/) | 1 | 100 | 100 |
| Streptomyces phage Paedore | [MH001460.1](https://www.ncbi.nlm.nih.gov/nuccore/MH001460.1) | 52.74 | 67.0 | [84](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68633/369782%7CStreptomyces%20phage%20Paedore/viral%20segment/) | 0 | 83.9 | 87.2 |
|  |  |  |  |  |  |  |  |

**(\*) 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]**

**To add six (6) new species to the genus *Camvirus***

**Source of the name of this taxon:** NA

**History:** The genus *R4virus* (renamed *Arequatrovirus*) was established by Taxonomy Proposal 2016.077a-pB to contain two species phiCAM and Amela. The Actinobacteriophage Database places phage phiCAM in Cluster BD, Subcluster BD3.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage phiCAM | [JX889246.1](https://www.ncbi.nlm.nih.gov/nuccore/JX889246.1) | 50.35 | 65.6 | [72](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62635/465259%7CStreptomyces%20phage%20phiCAM/viral%20segment/) | 0 | 100 | 100 |
| Streptomyces phage Endor1 | [MT711978.1](https://www.ncbi.nlm.nih.gov/nuccore/MT711978.1) | 49.40 | 65.8 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94260/980537%7CStreptomyces%20phage%20Endor1/viral%20segment/) | 0 | 76.7 | 90.3 |
| Streptomyces phage Endor2 | [MT711979.1](https://www.ncbi.nlm.nih.gov/nuccore/MT711979.1) | 48.83 | 65.1 | [74](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94261/980538%7CStreptomyces%20phage%20Endor2/viral%20segment/) | 1 | 80.3 | 93.1 |
| Streptomyces phage Joe | [KX815338.1](https://www.ncbi.nlm.nih.gov/nuccore/KX815338.1) | 48.94 | 65.5 | [81](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63122/465745%7CStreptomyces%20phage%20Joe/viral%20segment/) | 0 | 71.4 | 93.1 |
| Streptomyces phage Saftant | [MN204498.1](https://www.ncbi.nlm.nih.gov/nuccore/MN204498.1) | 48.88 | 65.6 | [74](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84633/697043%7CStreptomyces%20phage%20Saftant/viral%20segment/) | 0 | 72.2 | 93.1 |
| Streptomyces phage Sitrop | [MT701598.1](https://www.ncbi.nlm.nih.gov/nuccore/MT701598.1) | 48.48 | 65.6 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96742/1493967%7CStreptomyces%20phage%20Sitrop/viral%20segment/) | 1 | 74.0 | 90.3 |
| Streptomyces phage Alsaber | [MG298964.1](https://www.ncbi.nlm.nih.gov/nuccore/MG298964.1) | 48.80 | 65.9 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68284/369431%7CStreptomyces%20phage%20Alsaber/viral%20segment/) | 0 | 76.0 | 90.3 |

**(\*) 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]**

**To add five (5) new species to the genus *Likavirus***

**Source of the name of this taxon:** NA

**History:** This genus was established by Taxonomy Proposal 2016.077a-pB to contain nine species. The Actinobacteriophage Database places phage Lika in Cluster BD, Subcluster BD1.

**Electron micrograph:** None available

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Streptomyces phage Lika | [KC700556.1](https://www.ncbi.nlm.nih.gov/nuccore/KC700556.1) | 51.25 | 65.8 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/17851/460057%7CStreptomyces%20phage%20Lika/viral%20segment%20Unknown/) | 0 | 100 | 100 |
| Streptomyces phage Yasdnil | [MN096379.1](https://www.ncbi.nlm.nih.gov/nuccore/MN096379.1) | 51.63 | 65.7 | [73](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82681/614457%7CStreptomyces%20phage%20Yasdnil/viral%20segment/) | 0 | 83.5 | 89.3 |
| Streptomyces phage Werner | [MW435856.1](https://www.ncbi.nlm.nih.gov/nuccore/MW435856.1) | 51.57 | 65.7 | [73](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98296/1553533%7CStreptomyces%20phage%20Werner/viral%20segment/) | 0 | 83.5 | 90.7 |
| Streptomyces phage Goby | [MH171097.1](https://www.ncbi.nlm.nih.gov/nuccore/MH171097.1) | 51.39 | 65.8 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/69794/379992%7CStreptomyces%20phage%20Goby/viral%20segment/) | 0 | 92.9 | 100.0 |
| Streptomyces phage Lorelei | [KX507343.1](https://www.ncbi.nlm.nih.gov/nuccore/KX507343.1) | 50.56 | 65.8 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62987/465610%7CStreptomyces%20phage%20Lorelei/viral%20segment/) | 0 | 91.5 | 97.3 |
| Streptomyces phage Nanodon | [KX344445.1](https://www.ncbi.nlm.nih.gov/nuccore/KX344445.1) | 50.08 | 65.7 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46226/462614%7CStreptomyces%20phage%20Nanodon/viral%20segment/) | 0 | 77.0 | 92.0 |
|  |  |  |  |  |  |  |  |

**(\*) 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]**

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