

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

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| **Code assigned:** | ***2022.081B*** |  |
| **Short title:** Create six new genera of Streptomyces phages (*Caudoviricetes*) | | |
|  | | |

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

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

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| Bacterial Viruses Subcommittee, Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**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 2022 |
| Date of this revision (if different to above) |  |

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

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

**Text of proposal**

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

**Name of accompanying Excel module**

|  |
| --- |
| 2022.081B.N.v1.Caudoviricestes\_6ng\_streptomyces.xlsx |

**Abstract**

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| We have classified phages belonging to the Actinobacteriophage Database Clusters DO and DS to six new genera. |

**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 [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **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. [8] | |

**Supporting evidence – common molecular data**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains.

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars**.







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**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from these and related phages with phylogeny.fr in “one click” mode [6]. 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 [7] for details.

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**Proposal A. Create a new genus, *Sasdunavirus*, with a single species**

**Origin of the name of this taxon:** The name of this taxon is derived from Streptomyces phage phiSASD1.

**Historical aspects:** Temperate siphophage phiSASD1 was isolated in 2009 from a failed industrial avermectin fermentation against Streptomyces avermitilis NRRL 8165. It has an isometric head (diameter approximately 52 nm) and a long, non-contractile tail (approximately 102 nm) [10]. The genome’s cos site is a 9 nt sequence (3'-GCGCCCCCTT). he Actinobacteriophage Database classified phiSASD1 to Cluster BJ. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptomyces phage phiSASD1 | [GQ379227.1](https://www.ncbi.nlm.nih.gov/nuccore/GQ379227.1) | 37.07 | 66.3 | [43](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4001/455894|Streptomyces phage phiSASD1/viral segment Unknown/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

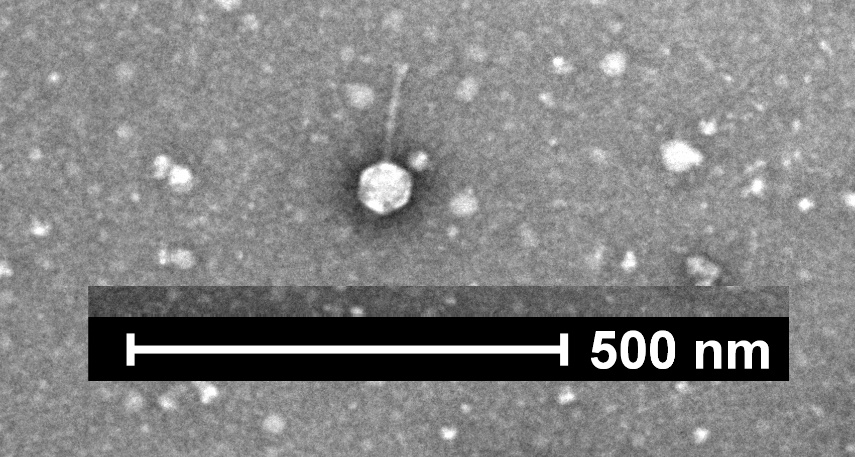
**Proposal B. Create a new genus, *Dubuvirus,* with a single species**

**Origin of the name of this taxon:** This taxon is named after the first virus of its type, Streptomyces phage Dubu.

**Historical aspects:** Temperate siphophage Dubu was isolated in 2016 by Monica Jeung (University of California, San Diego, USA) against Streptomyces platensis MJ1A1 from moist soil as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. Average of tail length was 112.5 nm and the capsid was

58.1 x 59.7 nm. The genome has 9 nt 3’-cohesive termini (CGCGGGGGA). The Actinobacteriophage Database classified Dubu to Cluster BJ, but we think that it is sufficiently different to deserve classification to a new genus. Indicated in phylogenetic tree by

**Electron micrograph:** Electron micrographs of negatively stained Streptomyces phage Dubu (https://phagesdb.org/phages/Dubu/). 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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**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptomyces phage Dubu | [MK937595.1](https://www.ncbi.nlm.nih.gov/nuccore/MK937595.1) | 39.54 | 68.7 | [47](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82576/609644|Streptomyces phage Dubu/viral segment/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal C. Create a new genus, *Veewebvirus,* with a single species**

**Origin of the name of this taxon:** The name of this taxon is derived from Streptomyces phage VWB

**Historical aspects:** Temperate siphophage VWB was isolated in 1993 J. F. C. Anne (Leuven, Belgium) using Streptomyces venezuelae ETH14630 as the host bacterium [11]. The Actinobacteriophage Database classified VWB to Cluster BA. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptomyces phage VWB | [AY320035.2](https://www.ncbi.nlm.nih.gov/nuccore/AY320035.2) | 49.22 | 71.1 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4691/892653|Streptomyces phage VWB/viral segment Unknown/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

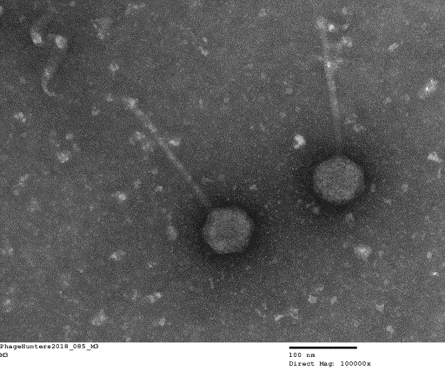
**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal D. Create a new genus, *Zukovirus,* with two species**

**Origin of the name of this taxon:** This taxon is named after Streptomyces phage Zuko.

**Historical aspects:** Probably lytic siphophage Zuko was isolated in 2018 by Jennifer Ferry and Michelle Hajdenberg (Washington University in St. Louis, MO, USA) using Streptomyces griseofuscus ATCC 23916 as the host bacterium as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome is . ircularly Permuted The Actinobacteriophage Database classified Zuko to Cluster BR. Indicated in phylogenetic tree by

**Electron micrograph:** Electron micrographs of negatively stained Streptomyces phage Zuko (https://phagesdb.org/phages/Zuko/). 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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**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptomyces phage Zuko | [MN204493.1](https://www.ncbi.nlm.nih.gov/nuccore/MN204493.1) | 82.3 | 63.7 | [115](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84628/697038|Streptomyces phage Zuko/viral segment/) | 2 | 100 | 100 |
| Streptomyces phage KimJongPhill | [MW822144.1](https://www.ncbi.nlm.nih.gov/nuccore/MW822144.1) | 82.52 | 64.0 | [115](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/103860/1646692|Streptomyces phage KimJongPhill/viral segment/) | 3 | 70.3 | 90.4 |

**(\*) determined using BLASTn [1]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal E. Create a new genus, *Sfunavirus,* with a single species**

**Origin of the name of this taxon:** This taxon is named after Streptomyces phage SF1.

**Historical aspects:** Lytic siphophage SF1 was isolated in 2015 by Sharaf,A., Marie,E., ElBaz,R., Elmaghraby,I. and Mercati,F. (Ain Shams University, Cairo, Egypt) from soil using Streptomyces flavovirens as the host bacterium. The nature of the genome termini is not known. The Actinobacteriophage Database classified SF1 as a Singleton. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptomyces phage SF1 | [KT221033.1](https://www.ncbi.nlm.nih.gov/nuccore/KT221033.1) | 43.15 | 69.1 | [52](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42514/462080|Streptomyces phage SF1/viral segment Unknown/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal F. Create new genus, *Siftrevirus* with a single species**

**Origin of the name of this taxon:** This taxon is named after Streptomyces phage SF3.

**Historical aspects:** Lytic siphophage SF3 was isolated in 2013 by Marei E., Elmaghraby I., Elbaz R. and Sharaf A. (Ain Shams University, Cairo, Egypt) from soil using Streptomyces flavovirens as the host bacterium. The nature of the genome termini is not known. The Actinobacteriophage Database classified SF1 as a Singleton. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptomyces phage SF3 | [KT221034.1](https://www.ncbi.nlm.nih.gov/nuccore/KT221034.1) | 60.93 | 69.1 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42513/462079|Streptomyces phage SF3/viral segment Unknown/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1]**

**(\*\*) determined using CoreGenes 3.5 [5]**

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