

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2022.010B*** |  |
| **Short title:** Create a new subfamily (*Azeevirinae*) with four genera (*Liebevirus, Yangvirus, Manhattanvirus* and *Galvestonvirus)* (*Caudoviricetes*) | | |
|  | | |

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

|  |  |
| --- | --- |
|  |  |
| Kurtböke I, Turner D, Moraru C, Adriaenssens EM, Kropinski AM | IKurtbok@usc.edu.au; Dann2.Turner@uwe.ac.uk;liliana.cristina.moraru@uol.de; evelien.adriaenssens@quadram.ac.uk;Phage.Canada@gmail.com |

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

|  |
| --- |
| University of the Sunshine Coast, Australia [IK]  University of the West of England, Bristol, UK [DT]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  Quadram Institute Bioscience, UK [EMA]  University of Guelph, Canada [AMK] |

**Corresponding author**

|  |
| --- |
| Andrew M. Kropinski |

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

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

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

|  |
| --- |
|  |

**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) | October 2022 |

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

|  |
| --- |
| ICTV-EC: Add annotations to heatmap for subfamily membership.  Proposer: Annotations added. |

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

**Text of proposal**

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2022.010B.A.v1.Azeevirinae\_nsf.xlsx |

**Abstract**

|  |
| --- |
| In depth analysis of the members of the Actinobacteriophage Database cluster AZ reveal four potential genera, three of which are currently recognized by ICTV, which can be grouped into one subfamily. |

**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 [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 (>60% similarity when dealing with temperate phages). Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [8]  **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 (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny. [8] | |

**Supporting evidence**

**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 within a species. The blue bar indicates membership of the subfamily.

****

**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**. N/A



****

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

****

**Proposal A: To add 8 species to the genus *Yangvirus***

**Proposal B: To add 4 species to the genus *Manhattanvirus***

**Proposal C: To create a new genus, *Galvastonvirus*, with one species**

**Proposal D: To create a new subfamily for these genera and *Liebevirus***

**Proposal A: To add 8 species to the genus *Yangvirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** The genus *Yangvirus* was established via Taxonomy Proposal 2019.093B

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Yang | [NC\_048097.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048097.1) | [MH834629.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834629.1) | 43.21 | 68.4 | [68](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73693/415312|Arthrobacter phage Yang/viral segment/) | 100 | 100 |
| Arthrobacter phage Lizalica |  | OL549192.1 | 43.05 | 67.4 | 69 | 74.5 | 83.8 |
| Arthrobacter phage Phives |  | [MT889376.1](https://www.ncbi.nlm.nih.gov/nuccore/MT889376.1) | 44.2 | 67.3 | [69](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96216/1478424|Arthrobacter phage Phives/viral segment/) | 68.0 | 79.4 |
| Arthrobacter phage Amyev |  | OL549191.1 | 44.28 | 67.9 | 68 | 71.4 | 86.8 |
| Arthrobacter phage Tbone |  | [MW055910.1](https://www.ncbi.nlm.nih.gov/nuccore/MW055910.1) | 44.11 | 67.6 | [69](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97662/1533087|Arthrobacter phage Tbone/viral segment/) | 71.0 | 83.8 |
| Arthrobacter phage Warda |  | OL549188.1 | 43.79 | 67.6 | 70 | 74.5 | 85.3 |
| Arthrobacter phage Adumb2043 |  | [MT889375.1](https://www.ncbi.nlm.nih.gov/nuccore/MT889375.1) | 43.1 | 67.0 | [68](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96211/1478419|Arthrobacter phage Adumb2043/viral segment/) | 74.6 | 82.3 |
| Arthrobacter phage Elezi |  | [MT639653.1](https://www.ncbi.nlm.nih.gov/nuccore/MT639653.1) | 43.47 | 66.6 | [68](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94298/980575|Arthrobacter phage Elezi/viral segment/) | 71.5 | 82.3 |
| Arthrobacter phage Kaylissa |  | [MZ005682.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ005682.1) | 44.12 | 67.6 | [71](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/106871/1720590|Arthrobacter phage Kaylissa/viral segment/) | 73.9 | 85.3 |

**(\*) determined using VIRIDIC [2]**

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

**Proposal B: To add 4 species to the genus *Manhattanvirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** The genus *Manhattanvirus* was established via Taxonomy Proposal 2019.093B

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage DrManhattan | [MH834610.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834610.1) | 42.58 | 66.0 | [72](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73677/415296|Arthrobacter phage DrManhattan/viral segment/) | 0 | 100 | 100 |
| Arthrobacter phage KeAlii | [OK040777.1](https://www.ncbi.nlm.nih.gov/nuccore/OK040777.1) | 41.85 | 65.5 | [66](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/107503/1731374|Arthrobacter phage KeAlii/viral segment/) | 1 | 63.4 | 72.2 |
| Arthrobacter phage Reedo | OL455896.1 | 41.8 | 65.3 | 68 | 0 | 67.4 | 79.2 |
| Arthrobacter phage Crewmate | OL549189.1 | 44.4 | 68.8 | 74 | 0 | 66.3 | 75.0 |
| Arthrobacter phage DrSierra | [MN908689.1](https://www.ncbi.nlm.nih.gov/nuccore/MN908689.1) | 42.62 | 66.5 | [66](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87884/811644|Arthrobacter phage DrSierra/viral segment/) | 0 | 73.5 | 76.4 |

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

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

**Proposal C: To create a new genus, *Galvastonvirus*, with one species**

**Origin of the name of this taxon:** This taxon is named after the city in which this phage was isolated rather than after Tweety19 because there is already a *Tweetyvirus*.

**Historical aspects:** Temperate phage Tweety19 was isolated by Makayla Hillin (Texas A & M University-Galveston) on Arthrobacter globiformis B-2979 as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Tweety18 | [MT897906.1](https://www.ncbi.nlm.nih.gov/nuccore/MT897906.1) | 40.87 | 66.1 | [68](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94614/986832|Arthrobacter phage Tweety19/viral segment/) | 1 | 100 | 100 |

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

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

**Proposal D: To create a new subfamily for these genera and *Liebevirus***

**Origin of the name of this taxon:** This taxon is named after the Actinobacteriophage Database cluster (AZ) to which these phages belong.

**Historical aspects:** These are all temperate phages infecting Arthobacter. The genera *Liebevirus, Yangvirus* and *Manhattanvirus* are ICTV recognized genera. *Galvastonvirus* is proposed in this TaxoProp.

**References**

1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870
2. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. <http://kronos.icbm.uni-oldenburg.de/viridic/>
3. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. <https://www.genome.jp/viptree/>
4. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423
5. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.
6. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.
7. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.
8. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.
9. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.
10. Olsen NS, Hendriksen NB, Hansen LH and Kot W. A New High-Throughput Screening Method for Phages: Enabling Crude Isolation and Fast Identification of Diverse Phages with Therapeutic Potential. Phage (New Rochelle) 1 (3), 137-148 (2020) <https://www.liebertpub.com/doi/10.1089/phage.2020.0016>