

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

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| **Code assigned:** | ***2023.002B*** |  |
| **Short title:** To resolve the Actinobacteriophage database cluster FE into five (5) genera [*Caudoviricetes*] | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Actinophage Study Group |

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

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**ICTV Study Group votes on proposal**

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

|  |  |  |
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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 2023 |
| 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**

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| 2023.002B.N.v1.Actinobacteriophage\_Database\_Cluster\_FE\_1nsf\_5ng.xlsx |

**Abstract**

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| We have resolved the Actinobacteriophage Database Cluster FE phages into five genera – *Whytuvirus, Bluefeathervirus, Idahovirus, Corgivirus* and *Noelyvirus*. The latter three genera have been placed in the subfamily *Feeclasvirinae*. |

**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 [1,2] – 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 [10].  **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 [10]. | |

**Supporting evidence**

**Proposals Data:**

1. **Create a new genus, *Whytuvirus,* with two species**
2. **Create a new single-species genus, *Bluefeathervirus***
3. **Create a new single-species genus, *Idahovirus***
4. **Create a new single-species genus, *Corgivirus***
5. **Create a new single-species genus, *Noelyvirus***
6. **Create a new subfamily, *Feeclasvirinae* comprising the genera *Idahovirus*, *Corgivirus* and *Noelyvirus***

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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; Arth = Arthrobacter

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**Figure 2. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages of interest are indicated with **red lines and stars**.

**Taxonomic Proposals:**

**Preamble:** According The Actinobacteriophage Database the following phages belong to a single cluster (FE) - Arthrobacter phage Idaho, Arthrobacter phage Corgi, Arthrobacter phage Noely, Arthrobacter phage BlueFeather, Arthrobacter phage Whytu, and Arthrobacter phage Yavru. The VIRIDIC and ViPTree analysis shown above clearly indicates that they belong to one subfamily, and two unrelated genera.

**A. Create a new genus, *Whytuvirus,* with two species**

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Arthrobacter phage Whytu.

**Historical aspects:** This lytic siphophage was isolated against Arthrobacter globiformis B-2979 from Marina del Rey, CA soil by Lucy Nakashima (University of California, Los Angeles, CA USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 15 nt 3’-cohesive termini (CCACGGTCCCCGTCC). The Actinobacteriophage Database considers this phage to be part of Cluster FE. We have chosen to subdivide this Cluster into several genera/species.

A close-up of a microscope

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**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Whytu (<https://phagesdb.org/phages/Whytu/>). 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.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Whytu | [MT024870.1](https://www.ncbi.nlm.nih.gov/nuccore/MT024870.1) | 15.37 | 64.8 | [22](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/88395/838856|Arthrobacter phage Whytu/viral segment/) | 0 | 100.0 | 100 |
| Arthrobacter phage Yavru | [MT889364.1](https://www.ncbi.nlm.nih.gov/nuccore/MT889364.1) | 15.19 | 64.3 | [23](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96217/1478425|Arthrobacter phage Yavru/viral segment/) | 0 | 81.1 | 95.4 |

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

**(\*\*) determined using CoreGenes 3.5 [6]**

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive genus.

1. **Create a new single-species genus, *Bluefeathervirus***

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Arthrobacter phage BlueFeather

**Historical aspects:** This lytic siphophage was isolated against Arthrobacter globiformis B-2979 from soil by Kimberly Hoh (University of California, Los Angeles, CA USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome 15 nt 3’-cohesive termini (CCACGGTTCCCGTCC). The Actinobacteriophage Database considers this phage to be part of Cluster FE.

A close-up of a microscope

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**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage BlueFeather (<https://phagesdb.org/phages/BlueFeather/>). 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.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage BlueFeather | [MT024867.1](https://www.ncbi.nlm.nih.gov/nuccore/MT024867.1) | 16.3 | 64.3 | [25](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/88393/838854|Arthrobacter phage BlueFeather/viral segment/) | 0 | 100.0 | 100 |

**Conclusion:** A genus comprised of a single species is proposed based on DNA (Fig. 1) and protein (Fig. 2) similarity.

1. **Create a new single-species genus, *Idahovirus***

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Arthrobacter phage Idaho

**Historical aspects:** This lytic siphophage was isolated against Arthrobacter sp. ATCC 21022 from soil by Madison Biasin and Jess Matsuoka (Smith College, Northampton, MA USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 15 nt 3’-cohesive termini (CCACGTATACCGTCC). The Actinobacteriophage Database considers this phage to be part of Cluster FE.

A close-up of a cell

Description automatically generated with low confidence

**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Idaho (<https://phagesdb.org/phages/Idaho/>). 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.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Idaho | [MK757448.1](https://www.ncbi.nlm.nih.gov/nuccore/MK757448.1) | 15.68 | 63.6 | [22](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79538/511567|Arthrobacter phage Idaho/viral segment/) | 0 | 100.0 | 100 |

**Conclusion:** A genus comprised of a single species is proposed based on DNA (Fig. 1) and protein (Fig. 2) similarity.

1. **Create a new single-species genus, *Corgivirus***

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Arthrobacter phage Corgi

**Historical aspects:** This lytic siphophage was isolated against Arthrobacter globiformis B-2979 from soil by Patrick Rimple (University of Pittsburgh, PA USA) as part of the Phage Hunters Integrating Research and Education program. The genome has 15 nt 3’-cohesive termini (CCACGTATACCGTCC). The Actinobacteriophage Database considers this phage to be part of Cluster FE.

**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Corgi are available at <https://phagesdb.org/phages/Corgi/>.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Corgi | [MH834607.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834607.1) | 15.77 | 67.6 | [26](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73674/415293|Arthrobacter phage Corgi/viral segment/) | 0 | 100.0 | 100 |

**Conclusion:** A genus comprised of a single species is proposed based on DNA (Fig. 1) and protein (Fig. 2) similarity.

1. **Create a new single-species genus, *Noelyvirus***

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of the first virus of its type Arthrobacter phage Noely

**Historical aspects:** This lytic siphophage was isolated against Arthrobacter globiformis B-2979 from soil by Kira Zack (University of Pittsburgh, PA USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome 15 nt 3’-cohesive termini (CCACGTATACCGTCC). The Actinobacteriophage Database considers this phage to be part of Cluster FE.

A close-up of a microscope

Description automatically generated with low confidence

**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Noely (<https://phagesdb.org/phages/Noely/>). 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.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Noely | [MH834622.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834622.1) | 15.01 | 68.3 | [23](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73658/415277|Arthrobacter phage Noely/viral segment/) | 0 | 100.0 | 100 |

**Conclusion:** A genus comprised of a single species is proposed based on DNA (Fig. 1) and protein (Fig. 2) similarity.

1. **Create a new subfamily, *Feeclasvirinae*, for the latter three genera**

**Origin of the name of this taxon:** The name of this taxon derives directly from The Actinobacteriophage Database Cluster to which these phages belong (FE).

**Rationale:** Members of the three genera described immediately above share ≥51.6 % DNA sequence similarity and 65.4% protein sequence similarity (17 homologs).These values are well within the parameters established for the creation of a subfamily.

**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. 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.

3. 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/

4. 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/

5. 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

6. 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.

7. Davis P, Seto D, Mahadevan P. CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. Viruses. 2022 Nov 16;14(11):2534. doi: 10.3390/v14112534. PMID: 36423143; PMCID: PMC9693508.

8. 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.

9. 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.

10. 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.