

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

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| **Code assigned:** | ***2023.019B*** |  |
| **Short title:** To create a new subfamily *Daemsvirinae* containing two genera (*Nanditavirus* and *Elesarvirus*) [*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)** | 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 | April 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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| 2023.019B.N.v1.Daemsvirinae\_nsf.xlsx |

**Abstract**

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| We have created a new subfamily, *Daemsvirinae*, with two genera (*Nanditavirus* and *Elesarvirus*) for phages which belong to The Actinobacteriophage Database Cluster FF. |

**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 [1,2] – 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]. | |

**Supporting evidence**

**Proposals:**

1. **Create a new genus, *Nanditavirus,* with five (5) species.**
2. **Create a new single-species genus, *Elesarvirus*.**
3. **Create a new subfamily, *Daemsvirinae*, for these two genera.**

**Proposals Data:**

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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; Stre = Streptomyces

**A close-up of a graph

Description automatically generated with low confidence**

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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:**

1. **Create a new genus, *Nanditavirus,* with five (5) species.**

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

**Historical aspects:** This temperate siphophage was isolated against Arthrobacter globiformis B-2979 from soil by Kira Zack (University of Pittsburgh, Pittsburgh, PA USA) as part of the Phage Hunters Integrating Research and Education program. The genome has 12 nt 3’-cohesive termini (TCCGCCGCGTGA). The Actinobacteriophage Database considers this phage to be part of Cluster FF. We have chosen to subdivide this cluster into two genera.

A close-up of a sperm cell

Description automatically generated with low confidence

**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Nandita (<https://phagesdb.org/phages/Nandita/>). 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 Nandita | [MH834621.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834621.1) | 42.38 | 64.9 | [66](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73687/415306|Arthrobacter phage Nandita/viral segment/) | 2 | 100.0 | 100 |
| Arthrobacter phage Ryan | [MH834627.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834627.1) | 43.18 | 65.1 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73691/415310|Arthrobacter phage Ryan/viral segment/) | 1 | 83.1 | 86.4 |
| Arthrobacter phage Cole | [ON392166.1](https://www.ncbi.nlm.nih.gov/nuccore/ON392166.1) | 41.83 | 65.1 | [63](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/114332/1861590|Arthrobacter phage Cole/viral segment/) | 1 | 71.5 | 81.8 |
| Arthrobacter phage Zaheer | [MZ150784.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ150784.1) | 42.87 | 65.0 | [67](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/104023/1651746|Arthrobacter phage Zaheer/viral segment/) | 2 | 76.7 | 83.3 |
| Arthrobacter phage Popper | [MZ274308.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ274308.1) | 41.82 | 65.2 | [69](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/104884/1671043|Arthrobacter phage Popper/viral segment/) | 1 | 72.4 | 78.8 |

**(\*) 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, *Elesarvirus*.**

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

**Historical aspects:** This temperate siphophage was isolated against Arthrobacter globiformis B-2979 from Las Vagas (NV USA) soil by Leo Rule (Baylor University USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 12 nt 3’-cohesive termini (TCCGCCGCGTGA). The Actinobacteriophage Database considers this phage to be part of Cluster FF. We have chosen to subdivide this cluster into two genera.

**Electron micrograph:** An electron micrograph of negatively stained Arthrobacter phage Elesar is available at <https://phagesdb.org/phages/Elesar/>.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Elesar | [MK392368.1](https://www.ncbi.nlm.nih.gov/nuccore/MK392368.1) | 42.95 | 65.0 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75915/446573|Arthrobacter phage Elesar/viral segment/) | 1 | 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, *Daemsvirinae*, for these two genera.**

**Origin of the name of this taxon:** The taxon is named in honour of Dutch microscopist Wiggele Theodorus Daems (b. 1929; d. 2007). University of Leiden, The Netherlands. He is the first recorded person to characterize a phage against Arthrobacter [ DAEMS WT. A preliminary report on the fine structure of a bacteriophage of Arthrobacter polychromogenes Schippers-Lammertse, Muysers et Klatser-Oedekerk. Antonie Van Leeuwenhoek. 1963;29:16-21. doi: 10.1007/BF02046034. PMID: 14024588.]

**Rationale:** These two genera of temperate siphoviruses share 58.8 % DNA sequence similarity and 47 protein homologs (77.0%). On average the genomes in this subfamily possess the following characteristics: 42.7 kb (64.9 mol% G+C) and encoding 1-2 tRNAs. These characteristics are consistent with us proposing a subfamily [10].

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