

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

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| **Code assigned:** | ***2022.091B*** |  |
| **Short title:** Create three new genera of actinophages (*Caudoviricetes*) | | |
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**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**

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| --- | --- | --- | --- |
| **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)** |
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|  |  |  |
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**Submission dates**

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| --- | --- |
| 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**

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| --- |
| 2022.091B.N.v1.Caudoviricetes\_3ng\_actinophages.xlsx |

**Abstract**

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| We have classified phages belonging to the Actinobacteriophage Database Cluster AE to a new genus, *Onyinyevirus,* and have split Cluster AX into the genera *Atraxavirus* and *Adaiavirus*. |

**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, *Onyinyevirus*, with a single species**

**Origin of the name of this taxon:** The name of this taxon is derived from Mycobacterium phage Onyinye.

**Historical aspects:** Lytic siphophage Onyinye was isolated in 2018 by Esther Nwozo (Howard University, Washington, DC USA) against Mycobacterium smegmatis mc²155as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. Its genome is Circularly Permuted. The Actinobacteriophage Database classified Skog to Cluster AE. 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 (\*\*) |
| Mycobacterium phage Onyinye | [MN813687.1](https://www.ncbi.nlm.nih.gov/nuccore/MN813687.1) | 71.42 | 58.8 | [107](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86731/755996|Mycobacterium phage Onyinye/viral segment/) | 0 | 100 | 100 |

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

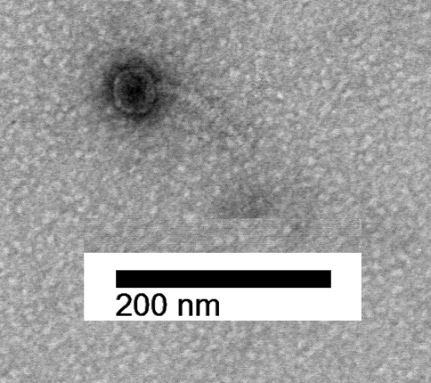
**(\*\*) determined using CoreGenes 3.5 [5]**

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

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

**Historical aspects:** Lytic siphophage Adaia was isolated in 2017 by Patrick Rimple (University of Pittsburgh, PA, USA) against Arthrobacter sulfureus NRRL B-14730 from Saylorsburg, PA compost pile as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 10 nt 3’-cohesive termini (CCCGCGCCCC). The Actinobacteriophage Database classified Adaia to Cluster AX. Indicated in phylogenetic tree by

**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Adaia (https://phagesdb.org/phages/Adaia/). 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 Adaia | [MH834594.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834594.1) | 15.84 | 56.1 | [28](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73665/415284|Arthrobacter phage Adaia/viral segment/) | 0 | 100 | 100 |

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

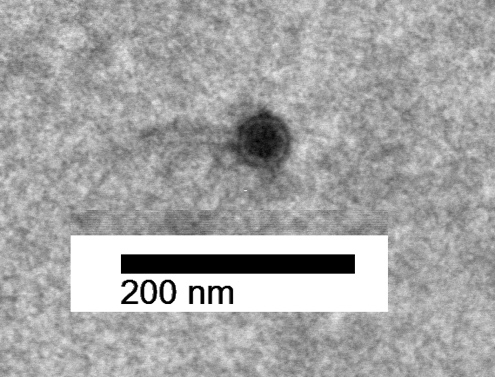
**(\*\*) determined using CoreGenes 3.5 [5]**

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

**Origin of the name of this taxon:** The name of this taxon is derived from Arthrobacter phage Atraxa

**Historical aspects:** Lytic siphophage Atraxa was isolated in 2017 by Patrick Rimple (University of Pittsburgh, PA, USA) against Arthrobacter sulfureus NRRL B-14730 from Saylorsburg, PA compost pile as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 10 nt 3’-cohesive termini (CCCGCGCCCC). The Actinobacteriophage Database classified Adaia to Cluster AX, but we consider that this cluster could be subdivided. Indicated in phylogenetic tree by

**Electron micrograph:** Electron micrographs of negatively stained Arthrobacter phage Atraxa (https://phagesdb.org/phages/Atraxa/). 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 (\*\*) |
| Arthrobacter phage Atraxa | [MH834597.1](https://www.ncbi.nlm.nih.gov/nuccore/MH834597.1) | 14.93 | 58.0 | [23](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73667/415286|Arthrobacter phage Atraxa/viral segment/) | 0 | 100 | 100 |

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

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

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