

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

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| **Code assigned:** | ***2022.054B*** |  |
| **Short title:** Create ten new species in the genus *Mudcatvirus* and rename two species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew M. Kropinski |

**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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|  |  |  |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 2022 |
| Date of this revision (if different to above) | September 2022 |

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

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| ICTV-EC: Two renamed species were previously renamed. Check overlap with proposed family “Riverfallsviridae”.  Proposer: Renamed species removed from proposal. Addition clarification added in support of genus. |

**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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| 2022.054B.A.v2.Mudcatvirus\_10nsp.xlsx |

**Abstract**

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| Using nucleic acid identity and phylogenetics, we have identified ten new species in the genus *Mudcatvirus*. |

**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**

**Origin of the name of this taxon:** This taxon is named after Arthrobacter phage Mudcat

**Historical aspects:** This taxon was created through Taxonomy Proposal 2016.074a-dB

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Mudcat | [KU647628.2](about:blank) | 59.44 | 45.1 | [95](about:blank#!/proteins/46430/462760|Arthrobacter phage Mudcat/viral segment Unknown/) | 100 | 100 |
| Arthrobacter phage Arcadia | [MF189170.1](about:blank) | 58.06 | 45.2 | [97](about:blank#!/proteins/63799/466420|Arthrobacter phage Arcadia/viral segment/) | 83.2 | 90.5 |
| Arthrobacter phage Tribby | [MF189175.1](about:blank) | 59.08 | 45.2 | [102](about:blank#!/proteins/63804/466425|Arthrobacter phage Tribby/viral segment/) | 82.1 | 90.5 |
| Arthrobacter phage Cheesy | [MF324906.1](about:blank) | 58.74 | 45.2 | [101](about:blank#!/proteins/63664/466285|Arthrobacter phage Cheesy/viral segment/) | 83.7 | 94.7 |
| Arthrobacter phage Correa | [MF189171.1](about:blank) | 57.4 | 45.2 | [96](about:blank#!/proteins/63800/466421|Arthrobacter phage Correa/viral segment/) | 79.3 | 88.4 |
| Arthrobacter phage Xenomorph | [MK919473.1](about:blank) | 58.69 | 45.4 | [95](about:blank#!/proteins/82461/604124|Arthrobacter phage Xenomorph/viral segment/) | 80.3 | 88.4 |
| Arthrobacter phage Heisenberger | [MF189173.1](about:blank) | 58.21 | 45.1 | [100](about:blank#!/proteins/63802/466423|Arthrobacter phage Heisenberger/viral segment/) | 92.6 | 98.9 |
| Arthrobacter phage JEGGS | [MK967398.1](about:blank) | 58.29 | 45.1 | [100](about:blank#!/proteins/82928/624801|Arthrobacter phage JEGGS/viral segment/) | 91.4 | 100.0 |
| Arthrobacter phage Kardesai | [MZ209300.1](about:blank) | 57.87 | 44.9 | [100](about:blank#!/proteins/106942/1720661|Arthrobacter phage Kardesai/viral segment/) | 81.8 | 89.5 |
| Arthrobacter phage Dynamite | [MZ747520.1](about:blank) | 57.85 | 45.3 | [99](about:blank#!/proteins/106816/1720534|Arthrobacter phage Dynamite/viral segment/) | 82.6 | 89.5 |
| Arthrobacter phage KeaneyLin | [MH450120.1](about:blank) | 57.85 | 45.4 | [95](about:blank#!/proteins/71871/399743|Arthrobacter phage KeaneyLin/viral segment/) | 82.1 | 87.4 |

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

**(\*\*) determined using CoreGenes 5.0 [https://coregenes.ngrok.io/coregenes3\_5/]**

**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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**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from Mudcat 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." The members of the *Mudcatvirus* are indicated with a **blue rectangle**.

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**References**

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