

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

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| **Code assigned:** | **2020.105B** |  |
| **Short title:** Create one new genus (*Mufasoctovirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew Kropinski |

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

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| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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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 | July 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.105B.R.Mufasoctvirus .xlsx |

**Abstract**

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| We propose to create a single species genus, *Musfasoctovirus,* for temperate Arthrobacter siphovirus Mufasa8. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm | |

**Supporting evidence**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [1]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The colour codes in columns 1 indicate ICTV recognized species.

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**History:** Temperate Arthrobacter phage Mufasa8 was isolated in 2018 by Aminata Khan and Alisha Shrestha (Smith College) as part of Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science Program. It was isolated from soil ( Northampton, MA USA) using Arthrobacter globiformis B-2979 as the host. Its genome is circularly permuted. The Actinobacteriophage Database places it in Cluster FJ.

**Source of the name of this taxon:** The name of this genus is derived from Arthrobacter phage Mufasa8.

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Arthrobacter phage Mufasa8 | [MN586027.1](https://www.ncbi.nlm.nih.gov/nuccore/MN586027.1) | 60.21 | 66.1 | [104](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85728/744388|Arthrobacter phage Mufasa8/viral segment/) | 0 |

**BLASTN homologs:** The next most related phage is Arthrobacter phage Sonali but this only shares 35.5% DNA sequence identity with Mufasa8. This suggests a subfamily relationship which we do not intend to formally recognize at this time. Interestingly The Actinobacteriophage Database places these two phages in the same Cluster, FG

**Electron micrograph:** Electron micrograph of negatively stained Arthrobacter phage Mufasa8 (<https://phagesdb.org/phages/Mufasa8/>). Limited permission was granted by The

Actinobacteriophages Database, 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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**References**

1. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>