

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

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| **Code assigned:** | **2020.106B** |  |
| **Short title:** Create one new genus (*Muldoonvirus*) including two new species (*Caudovirales*: *Myoviridae*) | | |
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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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| 2020.106B.R.Muldoonvirus.xlsx |

**Abstract**

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| To create a new genus for Serratia T4-type phages. |

**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**

**Source of the name of this taxon:** This genus is named after Serratia phage Muldoon.

**History:** Lytic Serratia phage Muldoon was isolated from wastewater treatment plant samples collected in College Station, TX, by growth on Serratia marcescens D1. Phage PS2 was isolated in China. The authors recognized the relation between their phages and coliphage T4.

**Specific Reference:** Campbell S, Atkison C, Moreland R, Liu M, Ramsey J, Leavitt J. Complete Genome Sequence of Serratia Phage Muldoon. Microbiol Resour Announc. 2020;9(1):e01418-19. Published 2020 Jan 2. doi:10.1128/MRA.01418-19

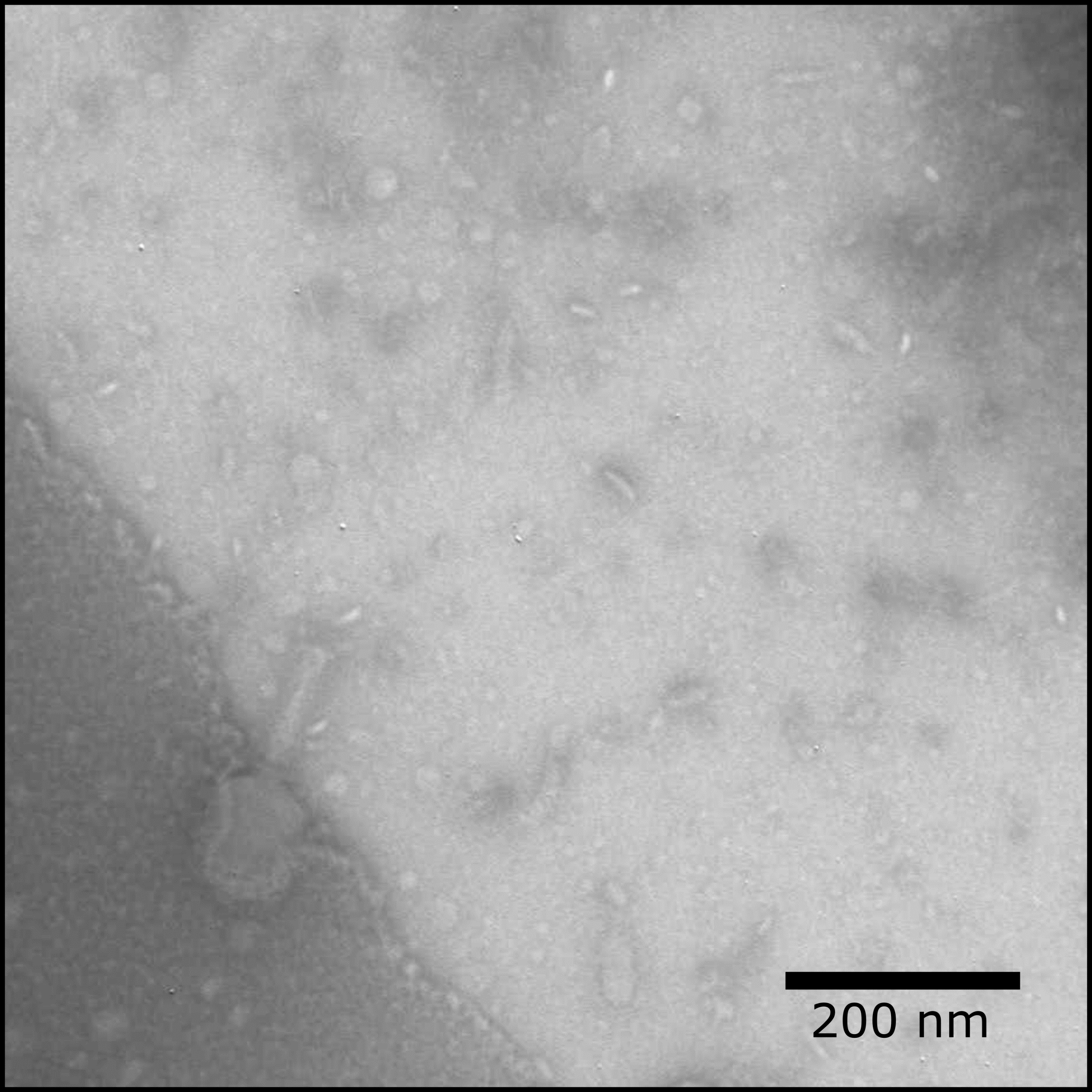
**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Muldoon |  | [MN095771.1](about:blank) | 167.55 | 41.8 | [256](about:blank#!/proteins/85157/723974|Serratia phage Muldoon/viral segment/) | 4 | 100 | 100 |
| PS2 | [NC\_024121.1](about:blank) | [KJ025957.1](about:blank) | 167.27 | 41.7 | [275](about:blank#!/proteins/33323/460666|Serratia phage PS2/viral segment Unknown/) | 4 | 78.4 | 97.7 |

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**BLASTN homologs:** The next most closely related phage is Citrobacter phage CF1 ERZ-2017 which shares 19.1% DNA sequence identity with Muldoon [1-3].

**Electron micrograph:**

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Micrograph by Heather Newkirk.

**Phylogeny:** The phylogenetic tree was constructed using the major capsid protein homologs of Muldoon and related phages with phylogeny.fr in “one click” mode [8]. "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 [9] for details."

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**References**

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