

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

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| **Code assigned:** | **2020.167B** |  |
| **Short title:** Create one new genus (*Triplejayvirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Adriaenssens EM, Tolstoy I, Moraru C, Kropinski AM | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  liliana.cristina.moraru@uol.de;  Phage.Canada@gmail.com |

**Author(s) institutional address(es) (optional)**

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| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  University of Guelph, Canada [AMK] |

**Corresponding author**

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| Andrew M. 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 | June 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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| 2020.167B.R.Triplejayvirus.xlsx |

**Abstract**

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

**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 column 1 indicates ICTV recognized species.

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**History:** Temperate Arthrobacter phage TripleJ was isolated in 2017 by Audrey Jonas (University of Pittsburgh) as part of Phage Hunters Integrating Research and Education Program. It was isolated from soil (Pittsburgh, PA USA) using *Arthrobacter globiformis* B-2979 as the host. Its genome is characterized as being circularly permuted. The Actinobacteriophage Database classifies this phage as a singleton.

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

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Arthrobacter phage TripleJ | [MN234178.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234178.1) | 45.51 | 64.5 | [82](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84811/708368|Arthrobacter phage TripleJ/viral segment/) | 0 |

**BLASTN homologs:** genomic orphan.

**Electron micrograph:** Electron micrograph of negatively stained Arthrobacter phage TripleJ (<https://phagesdb.org/phages/TripleJ/>). 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, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv doi: 10.1101/2020.07.05.188268. <http://kronos.icbm.uni-oldenburg.de/viridic/>
2. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.
3. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432
4. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804