

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

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| **Code assigned:** | **2020.084B** |  |
| **Short title:** Create one new genus (*Kuleanavirus*) 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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| 2020.084B.R.Kuleanavirus.xlsx |

**Abstract**

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

**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 Kuleana was isolated in 2018 by Kamalani Oshiro (University of Hawaii at Manoa) as part of Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science Program. It was isolated from soil ( Honolulu, HI USA ) using Arthrobacter globiformis B-2979 as the host. Its genome possesses 12bp 3’-cohesive termini (GAGCTGCCGGCA). The Actinobacteriophage Database places it in Cluster AS/Subcluster AS2.

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

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Arthrobacter phage Kuleana | [MN484600.1](https://www.ncbi.nlm.nih.gov/nuccore/MN484600.1) | 38.85 | 65.8 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85543/743702|Arthrobacter phage Kuleana/viral segment/) | 0 |

**VIRIDIC homologs:** The next most related phage is Arthrobacter phage Galaxy which shares 50.9% DNA sequence identity with Kuleana. This suggests a subfamily relationship which we do not intend to formally recognize at this time.

**Electron micrograph:** Electron micrograph of negatively stained Arthrobacter phage Kuleana (<https://phagesdb.org/phages/Kuleana/>). 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/>
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.

5: Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.