

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

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| **Code assigned:** | **2020.174B** |  |
| **Short title:** Create one new genus (*Vibakivirus*) including one new species (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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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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| 2020.174B.R.Vibakivirus.xlsx |

**Abstract**

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| We propose to create a single species genus, *Vibakivirus,* for lytic Arthrobacter siphovirus Vibaki. |

**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:** Lytic Arthrobacter phage Vibaki was isolated in 2018 by Helena Humphreys (University of Wisconsin-River Falls) as part of Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science Program. It was isolated from soil (Kirksville, MO USA) using *Arthrobacter globiformis* B-2979 as the host. Its genome is circularly permuted. The Actinobacteriophage Database places it in Cluster FL.

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

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Arthrobacter phage Vibaki | [MN096362.1](https://www.ncbi.nlm.nih.gov/nuccore/MN096362.1) | 48.2 | 66.7 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82665/614441|Arthrobacter phage Vibaki/viral segment/) | 0 |

**VIRIDIC homologs:** The next most related phage, as shown using BLASTN, is Arthrobacter phage Abba which shares 28.0% DNA sequence identity with Vibaki. 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 Vibaki (<https://phagesdb.org/phages/Vibaki/>). 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
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