

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

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| **Code assigned:** | **2021.011B** |  |
| **Short title:** Create one new genus (*Bippervirus*) including one new species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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| Tolstoy I, Turner D, Kropinski AM | [tolstoy@ncbi.nlm.nih.gov](mailto:tolstoy@ncbi.nlm.nih.gov); [dann2.turner@uwe.ac.uk](mailto:dann2.turner@uwe.ac.uk);  [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com) |

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

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| University of the West of England, Bristol, UK [DT]  NCBI, USA [IT]  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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| Actinobacteriophage Study Group, Bacterial 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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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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

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

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

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

**Name of accompanying Excel module**

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| 2021.011B.R.Bippervirus |

**Abstract**

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| This genus was created for phages which belong to The Actinobacteriophages Database Cluster Y. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic distance calculator VIRIDIC [10].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [4] | |

**Supporting evidence**

**Source of the name of this taxon:** This genus is named directly after the first isolate of its type, Mycobacterium phage Bipper

**History:** TemperateMycobacterium phage Bipper was isolated from Pittsburgh, PA USA soil by Alexander Doyle (University of Pittsburgh) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2014. The host bacterium was Mycobacterium smegmatis mc²155. Its genome possess 12 nt 3'-cohesive termini (TGCCGCCCGGTA). The Actinobacteriophage Database places this phage in Cluster Y (<https://phagesdb.org/phages/Bipper/>). It and Cracklewink encode queosine biosynthesis proteins.

**ViPTree analysis:** NA

**VIRIDIC heat map:** NA

**Specific Reference:** None

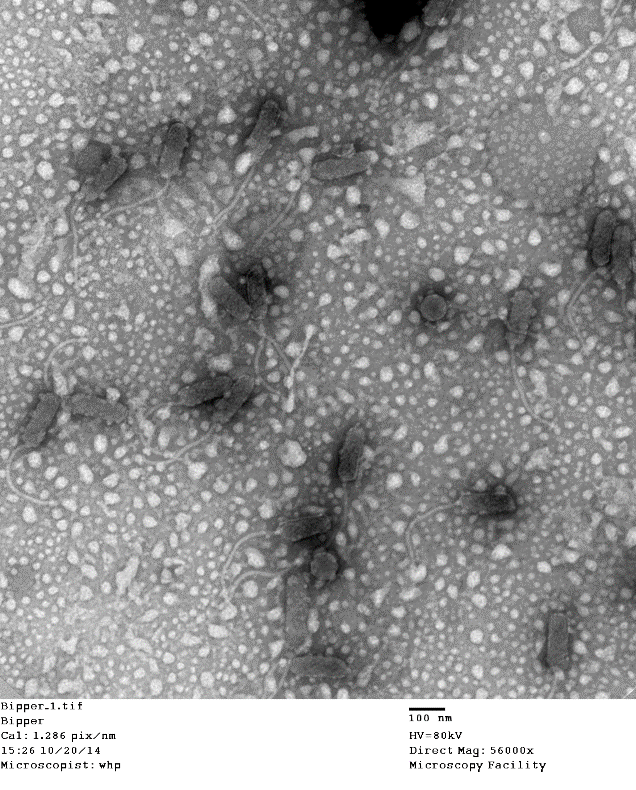
**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| Mycobacterium phage Bipper | [NC\_031253.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031253.1) | [KU728633.1](https://www.ncbi.nlm.nih.gov/nuccore/KU728633.1) | 77.83 | 67.3 | [135](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46482/462811%7CMycobacterium%20phage%20Bipper/viral%20segment/) | 1 |
|  |  |  |  |  |  |  |

**Strain:** Mycobacterium phage Cracklewink (MK977701), more than 95% similar.

**BLASTN homologs:** Genomic orphan [1-3]. The closest relative is Mycobacterium phage Typha with which it shares 51.7% DNA similarity. While this is sufficiently similar to propose a subfamily we don’t choose to do so at this time.

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Bipper (https://phagesdb.org/phages/Bipper/). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), 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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**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of Bipper 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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3: 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.

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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.

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10: Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805.