

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

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| **Code assigned:** | **2021.042B** |  |
| **Short title:** Create one new genus (*Kimonavirus*) including one new species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew M. Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

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| 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 | May 2021 |
| 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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| 2021.042B.R.Kimonavirus |

**Abstract**

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| A detailed molecular and phylogenetic reexamination of the temperate Mycobacterium phages which the Actinobacteriophage Database placed in Cluster A, and ICTV classified as members of the genus *Fromanvirus* has revealed great diversity. This proposal will create a new genus, *Kimonavirus*, for this and similar phages which belong to Subcluster A19. |

**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**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [11]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [12]. The phage of interest is indicated with **red arrow**.

A picture containing diagram

Description automatically generated  
**A picture containing schematic

Description automatically generated**Diagram, schematic

Description automatically generated  
**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [10]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.

Chart

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**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins of these 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." The new genera are indicated with arrows or boxes.

A screenshot of a computer

Description automatically generated with low confidence

**Origin of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Kimona

**Historical aspects:** Temperate phage Kimona was isolated in 2016 by Kimona Rampersadh (University of Kwazulu-Natal, Durban, South Africa) from residential soil using Mycobacterium smegmatis mc²155 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. Its genome contains 10 nt 3’-cohesive termini (CGGGCGGTAA). The Actinobacteriophage Database classifies this phage to Cluster A/Subcluster A19.

**Specific References:** None

**Genome summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Mycobacterium phage Kimona |  | [MF472895.1](https://www.ncbi.nlm.nih.gov/nuccore/MF472895.1) | 50.28 | 64.4 | [87](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63820/466441%7CMycobacterium%20phage%20Kimona/viral%20segment/) | 2 | 100 | 100 |

**(\*) Determined using VIRIDIC [10]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[6]**

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Kimona (<https://phagesdb.org/phages/Kimona/>). 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.

**Graphical user interface

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**References**

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