

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

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| **Code assigned:** | **2021.039B** |  |
| **Short title:** Create two new species in the genera *Trigintaduovirus* and *Bernalvirus* (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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| Turner D, Tolstoy I, Kropinski AM, Adriaenssens EM | tolstoy@ncbi.nlm.nih.gov;  Phage.Canada@gmail.com; evelien.adriaenssens@quadram.ac.uk |

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

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| --- |
| University of the West of England at Bristol, UK [DT]  NCBI, USA [IT]  University of Guelph, Canada [AMK]  Quadram Institute Bioscience, UK [EMA] |

**Corresponding author**

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| Andrew M. Kropinski |

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

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| Caudoviricetes SG, Bacterial Viruses SC |

**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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| 2021.039B.R.Infilling |

**Abstract**

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| Add two new species to existing genera in the class *Caudoviricetes*. |

**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 [1].  **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. [2] | |

**Supporting evidence**

**GenBank Summary:**

1. ***Trigintaduovirus***

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Mycobacterium phage 32HC | [NC\_023602.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023602.1) | [KJ028219.1](https://www.ncbi.nlm.nih.gov/nuccore/KJ028219.1) | 50.78 | 65.7 | [86](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/24345/460449%7CMycobacterium%20phage%2032HC/viral%20segment%20Unknown/) | 0 | 100 | 100 |
| Mycobacterium phage Rem711 |  | [MG770216.1](https://www.ncbi.nlm.nih.gov/nuccore/MG770216.1) | 50.83 | 66.2 | [85](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68398/369545%7CMycobacterium%20phage%20Rem711/viral%20segment/) | 0 | 90.5 | 95.5 |

1. ***Bernalvirus***

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Mycobacterium phage Bernal11 | [NC\_024135.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_024135.1) | [KJ510413.1](https://www.ncbi.nlm.nih.gov/nuccore/KJ510413.1) | 42.39 | 66.2 | [60](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/33337/460680%7CMycobacterium%20phage%20Bernal13/viral%20segment%20Unknown/) | 0 | 100 | 100 |
| Mycobacterium phage Mendokysei |  | [MG925349.1](https://www.ncbi.nlm.nih.gov/nuccore/MG925349.1) | 43.51 | 66.4 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68562/369711%7CMycobacterium%20phage%20Mendokysei/viral%20segment/) | 0 | 80.5 | 91.7 |

**Strains:** Mycobacterium phage Nairb, Mycobacteriophage Whitty, Mycobacterium phage Ibrahim, Mycobacterium phage RonRayGun, & Mycobacterium phage ZenTime222

\*\* Determined using BLASTn at NCBI [3–5]

\*\*\* Determined using CoreGenes 3.5 [6]

**References**

1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses 12:1268. https://doi.org/10.3390/v12111268

2. Turner D, Kropinski AM, Adriaenssens EM (2021) A Roadmap for Genome-Based Phage Taxonomy. Viruses 13:506. https://doi.org/10.3390/v13030506

3. Brister JR, Ako-Adjei D, Bao Y, Blinkova O (2015) NCBI viral genomes resource. Nucleic Acids Res 43:D571-7. https://doi.org/10.1093/nar/gku1207

4. Tolstoy I, Kropinski AM, Brister JR Bacteriophage taxonomy: an evolving discipline. In: Azeredo J, Sillankorva S (eds) Methods in Molecular Biology: Bacteriophage Therapy. Springer Nature

5. O’Leary NA, Wright MW, Brister JR, et al (2016) Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res 44:D733–D745. https://doi.org/10.1093/nar/gkv1189

6. Turner D, Reynolds D, Seto D, Mahadevan P (2013) CoreGenes3.5: A webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes 6:16–19. https://doi.org/10.1186/1756-0500-6-140