

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

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| **Code assigned:** | **2021.021B** |  |
| **Short title:** Create two new species in the genus *Corndogvirus* (*Caudoviricetes*) | | |
|  | | |

**Author(s) and email address(es)**

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

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| Bacterial Viruses Subcommittee, Actinobacteriophages Study Group |

**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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| 2021.021B.R.Corndogvirus |

**Abstract**

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| In our annual analysis of phages in the Actinobacteriophage Database we noted a number of new lytic phages belonging to Cluster O – ICTV’s *Corndogvirus*. Using genomic (VIRIDIC), proteomic (ViPTree, CoreGenes 3.5 [7]) and phylogenetic analyses these fell into two new species and a number of strains. |

**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 [6].  **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. [10] | |

**Supporting evidence**

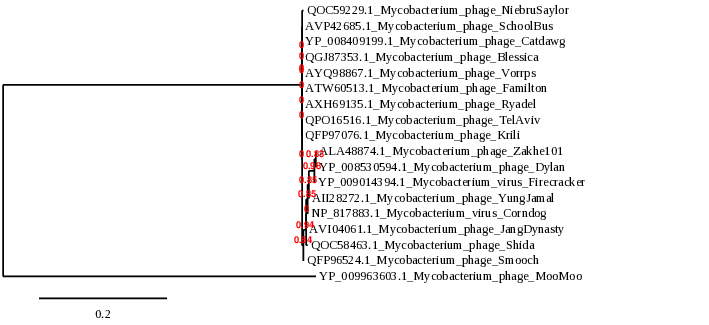
**Molecular analysis:**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. Phages under consideration are marked with a **blue bar**.

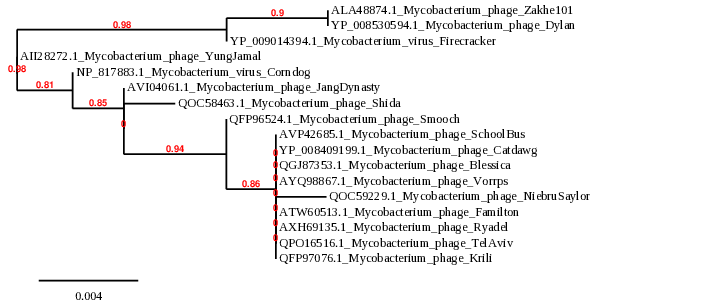
  
  


**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [6]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. (Attached)

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of some 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." **A. Rooted**

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**B. Unrooted**

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**Proposal: To create two new species in the genus *Corndogvirus***

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

**History:** The genus Corndogvirus was established by Taxonomy Proposal 2012.002a-dB and originally contained two species Mycobacterium virus Corndog and Mycobacterium virus Firecracker.

**Specific Reference:** Pedulla ML, Ford ME, Houtz JM, Karthikeyan T, Wadsworth C, Lewis JA, Jacobs-Sera D, Falbo J, Gross J, Pannunzio NR, Brucker W, Kumar V, Kandasamy J, Keenan L, Bardarov S, Kriakov J, Lawrence JG, Jacobs WR Jr, Hendrix RW, Hatfull GF. Origins of highly mosaic mycobacteriophage genomes. Cell. 2003 Apr 18;113(2):171-82. doi: 10.1016/s0092-8674(03)00233-2. PMID: 12705866.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Corndog | NC\_004685.1 | [AY129335.1](https://www.ncbi.nlm.nih.gov/nuccore/AY129335.1) | 69.78 | 65.4 | [122](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4484/892537%7CMycobacterium%20virus%20Corndog/viral%20segment%20Unknown/) | 100 | 100 |
| Mycobacterium phage Ryadel |  | [MH590592.1](https://www.ncbi.nlm.nih.gov/nuccore/MH590592.1) | 72.66 | 65.2 | [132](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71977/399849%7CMycobacterium%20phage%20Ryadel/viral%20segment/) | 90.7 | 92.6 |
| Mycobacterium phage Catdawg | [NC\_022057.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_022057.1) | [KF017002.1](https://www.ncbi.nlm.nih.gov/nuccore/KF017002.1) | 72.11 | 65.4 | [128](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/22409/460206%7CMycobacterium%20phage%20Catdawg/viral%20segment%20Unknown/) | 93.4 | 94.3 |
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**(\*) Determined using VIRIDIC [6]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Strains:**

|  |  |  |
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| **Accession No.** | **Phage Name** | **Strain of:** |
| MN428052.1 | Mycobacterium phage Smooch | *Mycobacterium virus Corndog* |
| KJ829260.1 | Mycobacterium phage YungJamal | *Mycobacterium virus Corndog* |
| KT281796.1 | Mycobacterium phage Zakhe101 | *Mycobacterium virus Corndog* |
| KF024730.1 | Mycobacterium phage Dylan | *Mycobacterium virus Corndog* |
|  |  |  |
| MT818418.1 | Mycobacterium phage Shida | *Mycobacterium virus Catdawg* |
| MH926062.1 | Mycobacterium phage Vorrps | *Mycobacterium virus Catdawg* |
| MN428058.1 | Mycobacterium phage Krili | *Mycobacterium virus Catdawg* |
| MT818425.1 | Mycobacterium phage NiebruSaylor | *Mycobacterium virus Catdawg* |
| MG872838.1 | Mycobacterium phage JangDynasty | *Mycobacterium virus Catdawg* |
| MN585964.1 | Mycobacterium phage Blessica | *Mycobacterium virus Catdawg* |
| MW314845.1 | Mycobacterium phage TelAviv | *Mycobacterium virus Catdawg* |
| MG099943.1 | Mycobacterium phage Familton | *Mycobacterium virus Catdawg* |
| MH020246.1 | Mycobacterium phage SchoolBus | *Mycobacterium virus Catdawg* |

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Corndog (https://phagesdb.org/phages/Corndog/). 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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**References**

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