

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

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| **Code assigned:** | **2021.018B** |  |
| **Short title:** Create one new genus (*Clownvirus*)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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| Dann Turner |

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

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| Caudovirales 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 | 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 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2021.018B.R.Clownvirus |

**Abstract**

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| The Actinobacteriophage Database recognizes that there are two Subclusters in Cluster DC. Subcluster DC2 contains a single isolate, Gordonia phage Clown. This proposal creates a species and genus-level taxon for this phage. This phage is peripherally related to members of the genus *Wizardvirus*, but at this time we do not choose to propose a subfamily. |

**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 [3].  **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. [9] | |

**Supporting evidence**

**History:** Temperate Gordonia phage Clown was isolated from soil in 2019 by Pooja Tallapaneni (University of Pittsburgh) on Gordonia terrae 3612 as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. Its genome is circularly permuted. It is assigned to Cluster DC/Subcluster DC2 by The Actinobacteriophage Database (https://phagesdb.org/clusters/DC/).

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. (Attached)

**Specific Reference:** None

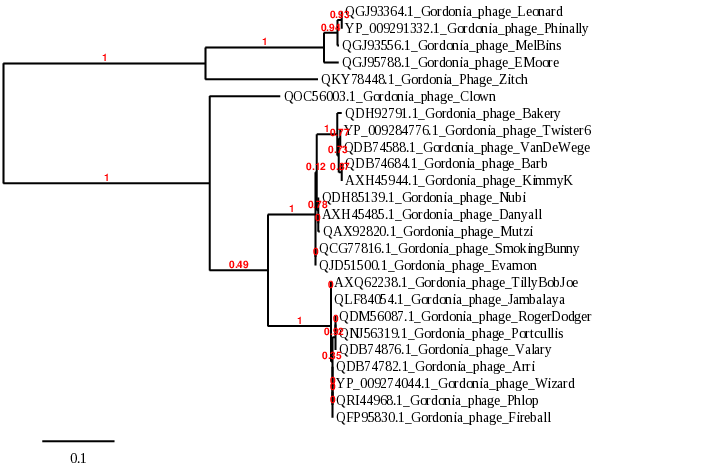
**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage Clown |  | [MT771343.1](https://www.ncbi.nlm.nih.gov/nuccore/MT771343.1) | 58.2 | 65.7 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/95581/1470070%7CGordonia%20phage%20Clown/viral%20segment/) | 100 | 100 |

**(\*) Determined using VIRIDIC [3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit these and related phages with phylogeny.fr in “one click” mode [5]. "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 [6] for details."

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**Electron micrographs:** Electron micrographs of negatively stained Gordonia phage Clown (https://phagesdb.org/phages/Clown/). 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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