

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

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| **Code assigned:** | **2021.092B** |  |
| **Short title:** Create 17 new species in the genus *Wizardvirus* (*Caudoviricetes*) | | |
|  | | |

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

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| Andrew 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 |

|  |  |  |
| --- | --- | --- |
| **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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| --- |
| 2021.092B.R.Wizardvirus\_new\_species |

**Abstract**

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| --- |
| The genus *Wizardvirus* was established through Taxonomy Proposal 2017.012B with two species – *Gordonia virus Wizard* and *Gordonia virus Twister6*. In the current proposal we are adding 17 new species. This genus of temperate siphoviruses are characterized by possessing circularly permuted genomes with an average size of 58.8 kb (67.8% GC) and encoding 94 proteins. |

**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:** The genus *Wizardvirus* with two species was established by Taxonomy Proposal 2017.012B. These are all temperate phages which are placed in the same Cluster (DC)/Subcluster DC1 by The Actinobacteriophage Database (<https://phagesdb.org/clusters/DC/>). Our VIRIDIC and phylogenetic analyses reveal there are 17 new species.

**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)

**Chart

Description automatically generated**

**Specific Reference:** None

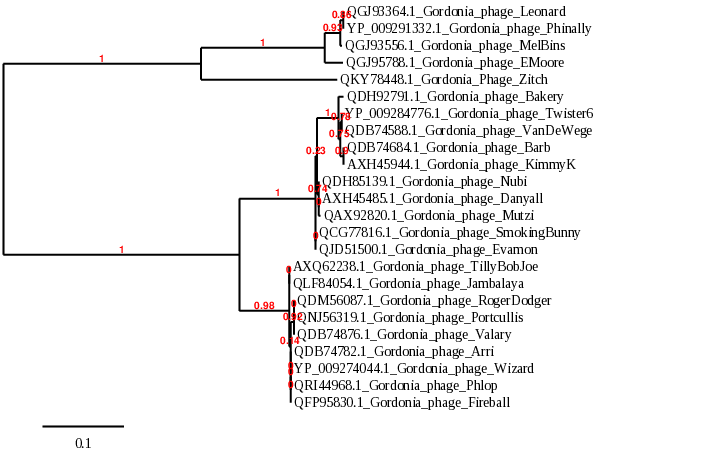
**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage Wizard |  | [KU998234.1](https://www.ncbi.nlm.nih.gov/nuccore/KU998234.1) | 58.31 | 67.9 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46367/462725%7CGordonia%20phage%20Wizard/viral%20segment/) | 100 | 100 |
| Gordonia phage Bakery |  | [MK937603.1](https://www.ncbi.nlm.nih.gov/nuccore/MK937603.1) | 60.47 | 67.6 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82584/609652%7CGordonia%20phage%20Bakery/viral%20segment/) | 64.5 | 82.0 |
| Gordonia phage Mutzi |  | [MK305889.1](https://www.ncbi.nlm.nih.gov/nuccore/MK305889.1) | 59.66 | 67.6 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76034/446692%7CGordonia%20phage%20Mutzi/viral%20segment/) | 72.3 | 86.5 |
| Gordonia phage TillyBobJoe |  | [MH669015.1](https://www.ncbi.nlm.nih.gov/nuccore/MH669015.1) | 58.68 | 67.8 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72130/400266%7CGordonia%20phage%20TillyBobJoe/viral%20segment/) | 82.6 | 88.8 |
| Gordonia phage Fireball |  | [MN284907.1](https://www.ncbi.nlm.nih.gov/nuccore/MN284907.1) | 58.92 | 67.8 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84991/717052%7CGordonia%20phage%20Fireball/viral%20segment/) | 81.9 | 88.8 |
| Gordonia phage Danyall |  | [MH479910.1](https://www.ncbi.nlm.nih.gov/nuccore/MH479910.1) | 58.7 | 67.8 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71886/399758%7CGordonia%20phage%20Danyall/viral%20segment/) | 80.2 | 87.6 |
| Gordonia phage Jambalaya |  | [MT521998.1](https://www.ncbi.nlm.nih.gov/nuccore/MT521998.1) | 57.76 | 67.8 | [91](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/93295/927340%7CGordonia%20phage%20Jambalaya/viral%20segment/) | 86.2 | 89.9 |
| Gordonia phage Portcullis |  | [MT639651.1](https://www.ncbi.nlm.nih.gov/nuccore/MT639651.1) | 58.36 | 67.8 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94302/980579%7CGordonia%20phage%20Portcullis/viral%20segment/) | 83.5 | 93.3 |
| Gordonia phage Nubi |  | [MN010760.1](https://www.ncbi.nlm.nih.gov/nuccore/MN010760.1) | 58.72 | 67.9 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82566/609634%7CGordonia%20phage%20Nubi/viral%20segment/) | 83.8 | 92.1 |
| Gordonia phage SmokingBunny |  | [MK814761.1](https://www.ncbi.nlm.nih.gov/nuccore/MK814761.1) | 59.45 | 67.9 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79551/511580%7CGordonia%20phage%20SmokingBunny/viral%20segment/) | 87.4 | 96.6 |
| Gordonia phage Evamon |  | [MT310872.1](https://www.ncbi.nlm.nih.gov/nuccore/MT310872.1) | 58.46 | 67.8 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89554/893416%7CGordonia%20phage%20Evamon/viral%20segment/) | 88.5 | 96.6 |
| Gordonia phage Phlop |  | [MW507125.1](https://www.ncbi.nlm.nih.gov/nuccore/MW507125.1) | 58.36 | 67.9 | [91](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98812/1557743%7CGordonia%20phage%20Phlop/viral%20segment/) | 92.9 | 98.9 |
| Gordonia phage KimmyK |  | [MH479917.1](https://www.ncbi.nlm.nih.gov/nuccore/MH479917.1) | 58.76 | 67.8 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71891/399763%7CGordonia%20phage%20KimmyK/viral%20segment/) | 93.0 | 97.7 |
| Gordonia phage Valary |  | [MK864267.1](https://www.ncbi.nlm.nih.gov/nuccore/MK864267.1) | 59.45 | 67.8 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/81881/590105%7CGordonia%20phage%20Valary/viral%20segment/) | 94.1 | 98.9 |
| Gordonia phage Barb |  | [MK864265.1](https://www.ncbi.nlm.nih.gov/nuccore/MK864265.1) | 59.51 | 67.8 | [98](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/81879/590103%7CGordonia%20phage%20Barb/viral%20segment/) | 80.7 | 89.9 |
| Gordonia phage RogerDodger |  | [MK967381.1](https://www.ncbi.nlm.nih.gov/nuccore/MK967381.1) | 59.12 | 67.9 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82911/624784%7CGordonia%20phage%20RogerDodger/viral%20segment/) | 85.0 | 95.5 |
| Gordonia phage VanDeWege |  | [MK864264.1](https://www.ncbi.nlm.nih.gov/nuccore/MK864264.1) | 58.97 | 67.8 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/81878/590102%7CGordonia%20phage%20VanDeWege/viral%20segment/) | 87.5 | 95.5 |
| Gordonia phage Arri |  | [MK864266.1](https://www.ncbi.nlm.nih.gov/nuccore/MK864266.1) | 58.65 | 67.8 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/81880/590104%7CGordonia%20phage%20Arri/viral%20segment/) | 86.9 | 94.4 |

**(\*) 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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