

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

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| **Code assigned:** | ***2022.032B*** |  |
| **Short title:** Create a five new genera of Gordonia siphophages (*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, Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **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**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2022 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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| ICTV-EC: Please make following corrections: In Proposal B Historical aspects GRU3 is mistakenly provided in place of Coeur, In proposal C Historical aspects name Coeur is mistakenly provided in place of Emperor.  Proposer: Corrections made. |

**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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| --- |
| 2022.032B.A.v1.Caudoviricetes\_5ng.xlsx |

**Abstract**

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| We have classified phages belonging to the Actinobacteriophage Database Clusters CW and DM to five new genera. |

**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 [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **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. [8] | |

**Supporting evidence – common molecular data**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. In each of the following diagrams the genera are represented thus:

*Grutrevirus* 

*Coeurvirus *

*Emperorvirus*

*Ericdabvirus*

*Mcgonagallvirus*

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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated as follows: *Grutrevirus* 

*Coeurvirus *

*Emperorvirus*

*Ericdabvirus*

*Mcgonagallvirus*



**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from these and related phages with phylogeny.fr in “one click” mode [6]. "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." "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 [7] for details."

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**Proposal A. Create a new genus,** ***Grutrevirus*, with two species**

**Origin of the name of this taxon:** The name of this taxon is derived from Gordonia phage GRU3.

**Historical aspects:** Temperate siphophage GRU3 was isolated in 2015 by Zoe A. Dyson, J. Tucci, R.J. Seviour, and S. Petrovski (La Trobe University, Bendigo, Victoria, Australia) against Gordonia rubripertincta Grub38 from wastewater (Inverell, Queensland, Australia). Its capsid is 43 nm in diameter and its tail is 95 nm long [10]. The Actinobacteriophage Database classified GRU3 to Cluster CW/Subcluster CW2. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage GRU3 | KR053197.1 | 17.73 | 66.5 | 26 | 0 | 100 | 100 |
| Gordonia phage GMA5 | KR053198.1 | 17.56 | 66.3 | 28 | 0 | 64.1 | 88.5 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal B. Create a new genus, *Coeurvirus,* with a single species**

**Origin of the name of this taxon:** This taxon is named after the first virus of its type, Gordonia phage Coeur.

**Historical aspects:** Temperate siphophage Coeur was isolated in 2016 by Lalit Molleti (University of Pittsburgh, PA, USA) against Gordonia terrae 3612 from a flower bed as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 6 nt 3’-cohesive termini (ACCCCT). The Actinobacteriophage Database classified GRU3 to Cluster CW/Subcluster CW2, but we think that it is sufficiently different to deserve classification to a new genus. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage Coeur | [MK801723.1](about:blank) | 16.22 | 67.9 | [26](about:blank#!/proteins/82322/596093|Gordonia phage Coeur/viral segment/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal C. Create a new genus, *Emperorvirus,* with two species**

**Origin of the name of this taxon:** This taxon is named after Gordonia phage Emperor.

**Historical aspects:** Temperate siphophage Emperor was found as a prophage of Gordonia westfalica NRRL-B-24152. Liquid Gordonia westfalica was spotted on Gordonia terrae 3612, and the resulting phage release was picked and amplified, and called Emperor. Isolated by Matthew Montgomery (University of Pittsburgh, PA, USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 10 nt 3’-cohesive termini (CCTGCGCCCT). The Actinobacteriophage Database classified Coeur to Cluster DM. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage Emperor | [MH271296.1](about:blank) | 16.6 | 70.1 | [24](about:blank#!/proteins/70882/388789|Gordonia phage Emperor/viral segment/) | 0 | 100 | 100 |
| Gordonia phage SallySpecial | [MG812496.1](about:blank) | 15.9 | 70.1 | [21](about:blank#!/proteins/68543/369692|Gordonia phage SallySpecial/viral segment/) | 0 |  |  |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal D. Create a new genus, *Ericdabvirus,* with a single species**

**Origin of the name of this taxon:** This taxon is named after Gordonia phage EricDab.

**Historical aspects:** Temperate siphophage EricDab was isolated in 2018 by Grace Klein (University of South Florida, Tampa, FL, USA) from compost using Gordonia rubripertincta NRRL B-16540 as the host bacterium as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 8 nt 3’-cohesive termini (CCCGCGCC). The Actinobacteriophage Database classified EricDab to Cluster DM, which we have subdivided. Indicated in phylogenetic tree by

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage EricDab | [MK660712.1](about:blank) | 16.66 | 69.1 | [24](about:blank#!/proteins/84287/690336|Gordonia phage EpicDab/viral segment/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**Proposal E. Create a new genus, *Mcgonagallvirus,* with a single species**

**Origin of the name of this taxon:** This taxon is named after Gordonia phage McGonagall.

**Historical aspects:** Temperate siphophage McGonagall was isolated in 2015 by Ann-Catherine Stanton (University of Pittsburgh, PA, USA) from soil using Gordonia neofelifaecis NRRL 59395 as the host bacterium as part of the Phage Hunters Integrating Research and Education program. The genome has 10 nt 3’-cohesive termini (AGCCCCCGGT). The Actinobacteriophage Database classified McGonagall to Cluster CW/Subcluster CW1. Indicated in phylogenetic tree by

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



**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage McGonagall | [KU998255.1](about:blank) | 17.12 | 68.6 | [27](about:blank#!/proteins/46370/462728|Gordonia phage McGonagall/viral segment/) | 0 | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

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