

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

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| **Code assigned:** | **2021.073B** |  |
| **Short title:** Create one new subfamily (*Ruthgordonvirinae*) including six genera (*Caudoviricetes*) | | |
|  | | |

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

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**Corresponding author**

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| Andrew M. Kropinski |

**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 |

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

|  |
| --- |
| 2021.073B.R.Ruthgordonvirinae |

**Abstract**

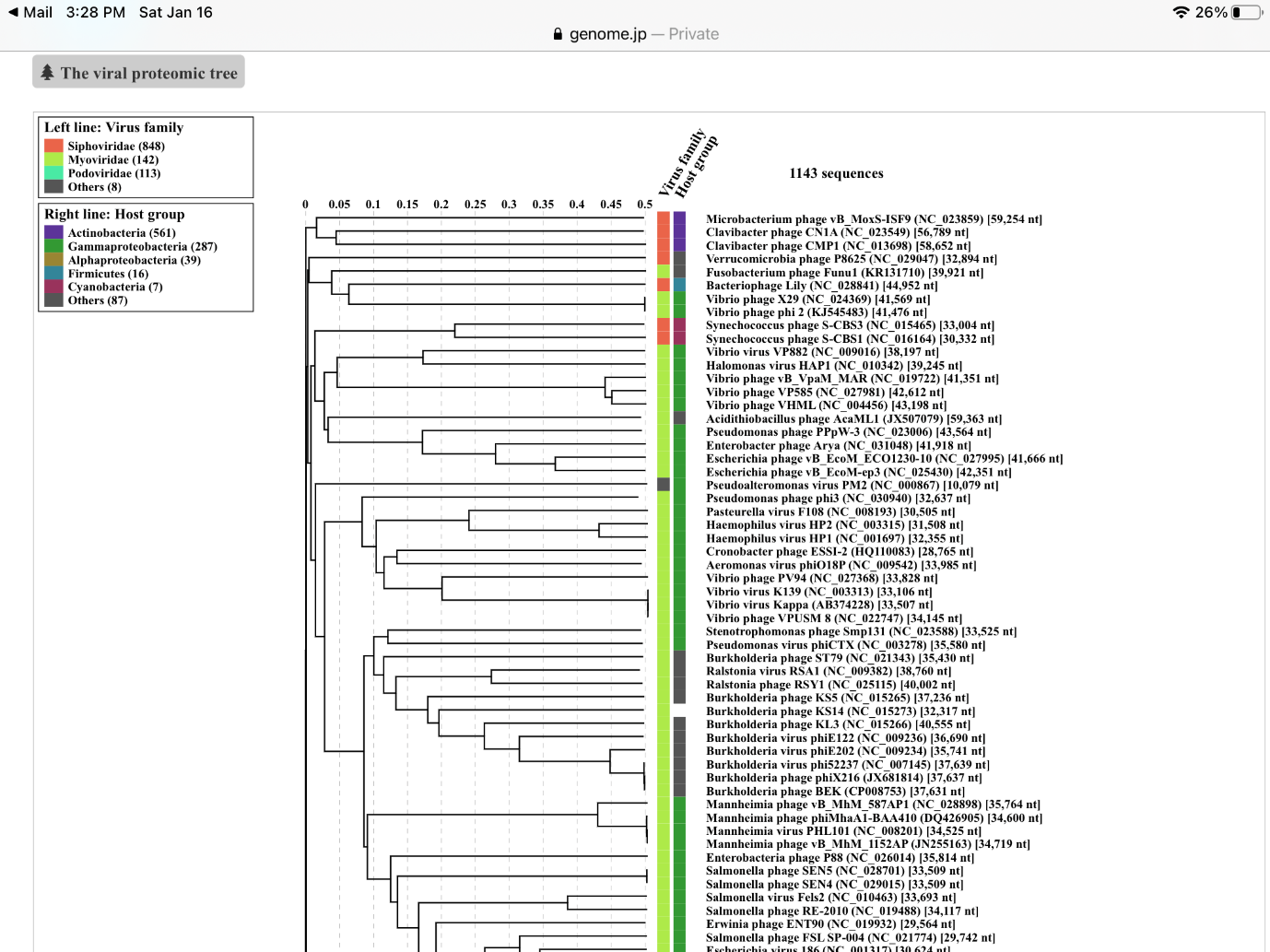
|  |
| --- |
| We have classified a number of new phages which The Actinobacteriophage Database groups into Cluster CU. The six genera all fit within a single subfamily, *Ruthgordonvirinae*, the members of which possess, on average, genomes of 44.0 kb (65,39 mol%G+C) and encode for 76 proteins and 0-1 tRNA. Using CoreGenes 5.0 (https://coregenes.ngrok.io/) revealed 33 homologs shared by this group of phages (43%). These homologs included: lysin B, lysin B, small and large terminase subunits, portal, capsid maturation protease, major capsid protein, head-to-tail adaptor, head-to-tail stopper, tail terminator, major tail protein, tail tape measure protein, three minor tail proteins, tail assembly chaperone, four ssDNA binding proteins, RecA-like DNA recombinase, and DNA helicase. |

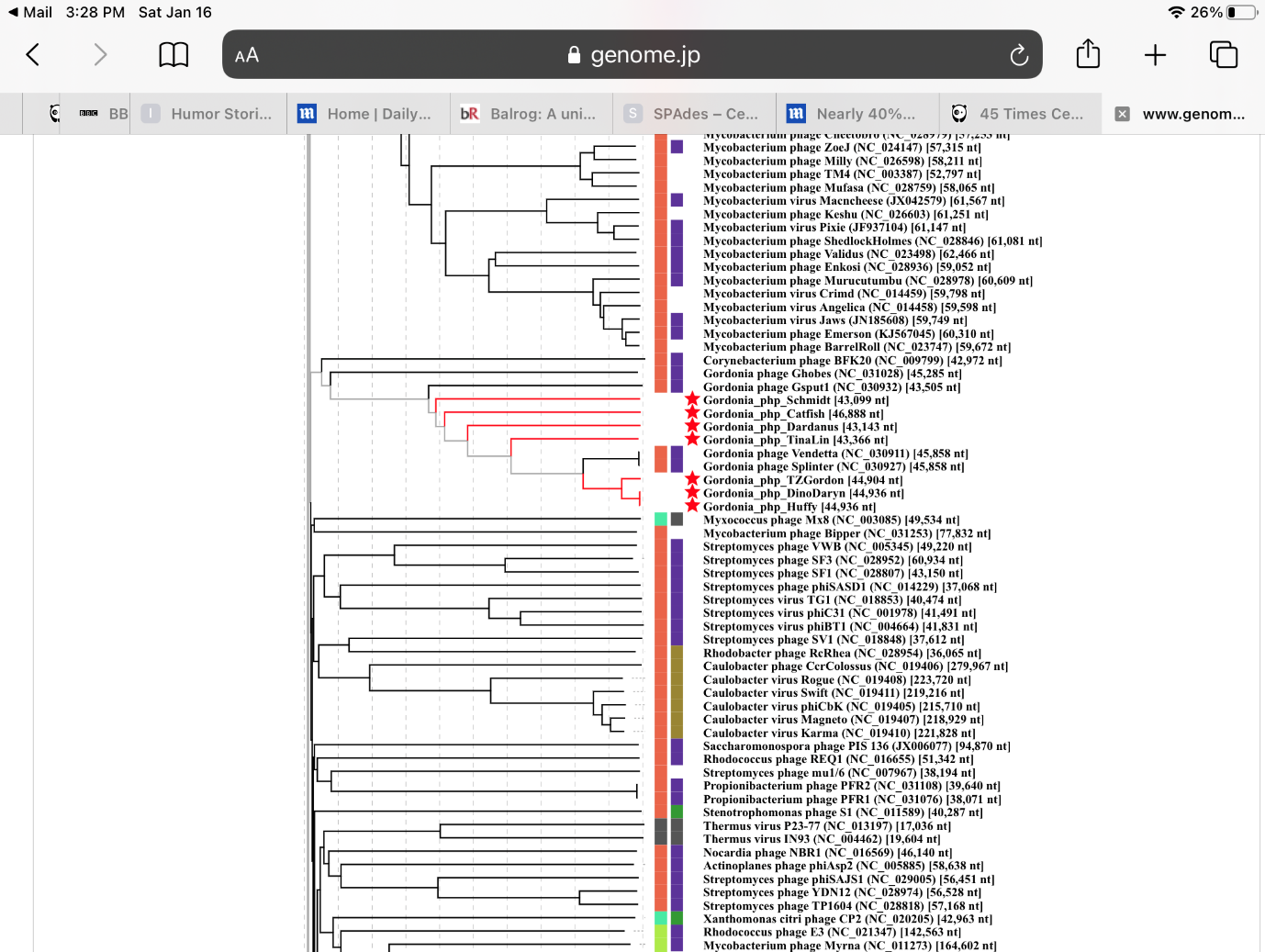
**Text of proposal**

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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.  **Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (here > 35%) and that the genera form a clade in a marker tree phylogeny. [9] | |

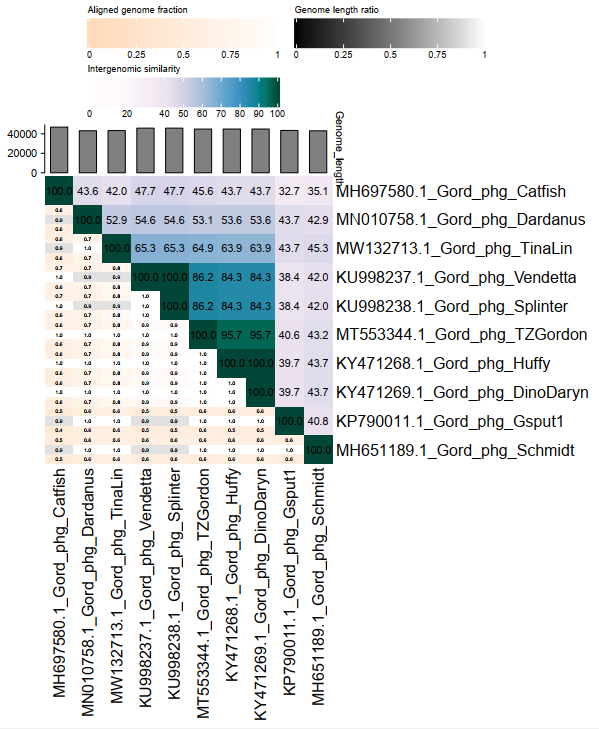
**Supporting evidence**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. The phages of interest are indicated with **red lines**.

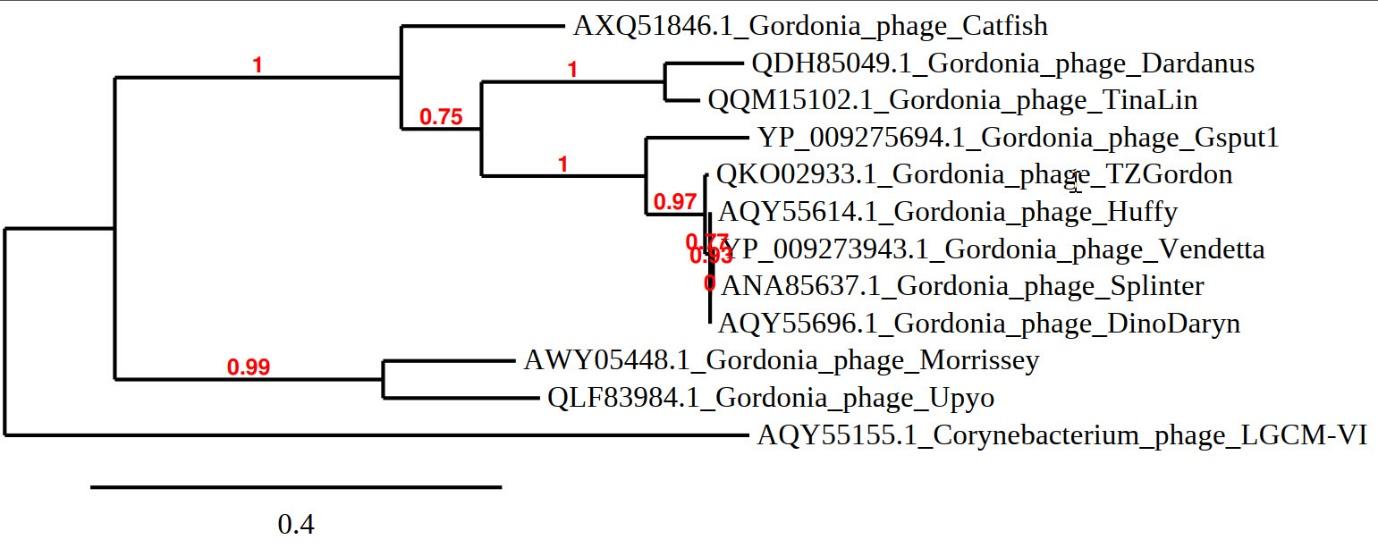


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**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.



**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins of *Ruthgordonvirinae* 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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**Proposals:**

1. **To create a new genus, *Catfishvirus* with a single species**
2. **To create a new genus, *Dardanusvirus* with a single species**
3. **To create a new genus, *Schmidtvirus* with a single species**
4. **To create a new genus, *Tinalinvirus* with a single species**
5. **To add one new species to the genus *Vendettavirus***
6. **To create a new subfamily *Ruthgordonvirinae***
7. **To move the genus *Gesputvirus* to this subfamily**

**To create a new genus, *Catfishvirus* with a single species**

**Source of the name of this taxon:** This taxon is named directly from the first virus of its type, Gordonia phage Catfish

**History:** Temperate Gordonia phage Catfish was isolated in 2018 by Lauren Nguyen (University of Louisiana at Monroe, TX, USA) from soil using Gordonia terrae 3612 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (AGTCCGCCGGT). The Actinobacteriophage Database places this phage in Cluster Cu, Subcluster CU5.

**Electron micrograph:** None available

**Specific Reference:** None available

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage Catfish | [MH697580.1](https://www.ncbi.nlm.nih.gov/nuccore/MH697580.1) | 46.89 | 65.0 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72103/400239%7CGordonia%20phage%20Catfish/viral%20segment/) | 1 | 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]**

**To create a new genus, *Dardanusvirus* with a single species**

**Source of the name of this taxon:** This taxon is named directly from the first virus of its type, Gordonia phage Dardanus

**History:** Temperate Gordonia phage Dardanus was isolated in 2016 by Samantha J. Wills (Florida Gulf Coast University, Gulf Myers, FL USA) from soil using Gordonia terrae 3612 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (CCCGGCAGGTA). The Actinobacteriophage Database places this phage in Cluster CU, Subcluster CU3.

**Electron micrograph:** Electron micrographs of negatively stained Gordonia phage Dardanus (https://phagesdb.org/phages/Dardanus/). 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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**Specific Reference:** NA

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage Dardanus | [MN010758.1](https://www.ncbi.nlm.nih.gov/nuccore/MN010758.1) | 43.14 | 66.6 | [72](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82564/609632%7CGordonia%20phage%20Dardanus/viral%20segment/) | 0 | 100 | 100 |

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

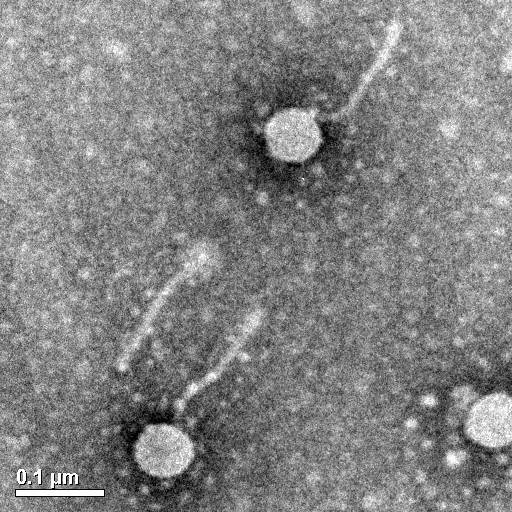
**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**To create a new genus, *Schmidtvirus* with a single species**

**Source of the name of this taxon:** This taxon is named directly from the first virus of its type, Gordonia phage Schmidt

**History:** Temperate Gordonia phage Schmidt was isolated in 2017 by Sydney Garcia and Stassi Henry (Truckee Meadows Community College, Reno, NV, USA) from soil using Gordonia terrae 3612 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 11 nt 3’-cohesive termini (TCCGGCCGGTT). The Actinobacteriophage Database places this phage in Cluster CU, Subcluster CU4.

**Electron micrograph:** Electron micrographs of negatively stained Gordonia phage Schmidt (https://phagesdb.org/phages/Schmidt/). 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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**Specific Reference:** NA

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage Schmidt | [MH651189.1](https://www.ncbi.nlm.nih.gov/nuccore/MH651189.1) | 43.1 | 65.7 | [76](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72157/400293%7CGordonia%20phage%20Schmidt/viral%20segment/) | 0 | 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]**

**To create a new genus, *Tinalinvirus* with a single species**

**Source of the name of this taxon:** This taxon is named directly from the first virus of its type, Gordonia phage TinaLin

**History:** Temperate Gordonia phage TinaLin was isolated in 2019 by Tina Hailer and Jarelin Huliganga (Truckee Meadows Community College, Reno, NV USA) from soil using Gordonia terrae NRRL B-16283 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 12 nt 3’-cohesive termini (TCCGGGCAGGTA). The Actinobacteriophage Database places this phage in Cluster CU, Subcluster CU1.

**Electron micrograph:** None available

**Specific Reference:** NA

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage TinaLin | [MW132713.1](https://www.ncbi.nlm.nih.gov/nuccore/MW132713.1) | 43.37 | 65.4 | [73](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97913/1542149%7CGordonia%20phage%20TinaLin/viral%20segment/) | 1 | 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]**

**To add one new species to the genus *Vendettavirus***

**Source of the name of this taxon:** Not applicable

**History:** The genus *Vendettavirus* was created through Taxonomy Proposal 2016.062a-dB.A.v1.Vendettavirus with a single species.

**Electron micrograph:** NA

**Specific Reference:** NA

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage Vendetta | [KU998237.1](https://www.ncbi.nlm.nih.gov/nuccore/KU998237.1) | 45.86 | 66.1 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46356/462712%7CGordonia%20phage%20Vendetta/viral%20segment/) | 1 | 100 | 100 |
| Gordonia phage TZGordon | [MT553344.1](https://www.ncbi.nlm.nih.gov/nuccore/MT553344.1) | 44.9 | 66.1 | [82](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92246/911697%7CGordonia%20phage%20TZGordon/viral%20segment/) | 1 | 84.3 |  |
|  |  |  |  |  |  |  |  |

**(\*) 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]**

**To create a new subfamily *Ruthgordonvirinae***

**Source of the name of this taxon:** This subfamily is named in honour of American microbial taxonomist Ruth Evelyn Gordon (1910–2003) after whom the genus *Gordonia* is named. 1934 Ph.D in Bacteriology from Cornell University (Ithaca, NY); 1954-1981 faculty member Department of Microbiology at Rutgers University working on antibiotics; 1946 onward she worked with the American Type Culture Collection first as a bacteriologist and then as a visiting investigator. (<https://en.wikipedia.org/wiki/Ruth_E._Gordon>)



(from: https://www.loc.gov/item/98504865/)

**Rationale:**

These five genera all fit within a single subfamily the members of which possess, on average, genomes of 44.0 kb (65,39 mol%G+C) and encode for 76 proteins and 0-1 tRNA. Using CoreGenes 5.0 (<https://coregenes.ngrok.io/>) revealed 33 homologs shared by this group of phages (43%). These homologs included: lysin B, lysin B, small and large terminase subunits, portal, capsid maturation protease, major capsid protein, head-to-tail adaptor, head-to-tail stopper, tail terminator, major tail protein, tail tape measure protein, three minor tail proteins, tail assembly chaperone, four ssDNA binding proteins, RecA-like DNA recombinase, and DNA helicase.

**To move the genus *Gesputvirus* to this subfamily**

**Source of the name of this taxon:** This taxon is named directly from the first virus of its type, Gordonia phage Gsput1

**History:** Temperate Gordonia phage Gsput1 was isolated in 2015 by Liu,M., Gill,J.J., Young,R. and Summer,E.J. (Texas A & M University-College Station USA) from wastewater using Gordonia sputi G11 as the host bacterium. The genome possesses 16 nt 5’-cohesive termini (GCTGACCCACGGACAC). The Actinobacteriophage Database places this phage in Cluster CU, Subcluster CU2. The Gsput1 head diameter and tail length are 62 ± 1 nm and 229 ± 5 nm, respectively (Liu M. et al. 2015]. The genus *Gesputvirus*, with a single species was established through Taxonomy Proposal 2018.021B.

**Electron micrograph:** NA

**Specific Reference:** Liu M, Gill JJ, Young R, Summer EJ. Bacteriophages of wastewater foaming-associated filamentous Gordonia reduce host levels in raw activated sludge. Sci Rep. 2015 Sep 9;5:13754. doi: 10.1038/srep13754. PMID: 26349678; PMCID: PMC4563357.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Gordonia phage Gsput1 | [NC\_030932.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_030932.1) | [KP790011.1](https://www.ncbi.nlm.nih.gov/nuccore/KP790011.1) | 43.51 | 62.8 | [71](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46366/462724%7CGordonia%20phage%20Gsput1/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]**

**References:**

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2: Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423

3: Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>

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