

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

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| **Code assigned:** | ***2022.092B*** |  |
| **Short title:** Create three new genera of lytic Gordonia phages (*Caudoviricetes*) | | |
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**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**

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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 2022 |
| Date of this revision (if different to above) |  |

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

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**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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| --- |
| 2022.092B.N.v1.Caudoviricetes\_3ng\_gordonia.xlsx |

**Abstract**

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| We have classified phages belonging to the Actinobacteriophage Database Clusters DO and DS to five new genera (*Skogvirus, Puppervirus, Gimaduovirus, Sixamavirus* and *Forzavirus*) and add one new species to an existing genus (*Godonkavirus*). |

**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.

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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 with **red stars**.







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**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from these and related phages with phylogeny.fr in “one click” mode [6]. 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, *Gimaduovirus,* with a single species**

**Origin of the name of this taxon:** The name of this taxon is derived from Gordonia phage GMA2.

**Historical aspects:** Lytic siphophage GMA2 was isolated by Zoe A. Dyson, J. Tucci, R.J. Seviour, and S. Petrovski (La Trobe University, Australia) from Kyneton, Victoria, Australia activated sludge using Gordonia malaquae A448 as the host bacterium [10]. The capsid is 61 nm in diameter, and the noncontractile tail is 386 nm long. The Actinobacteriophage Database classified GMA2 to Cluster DS. 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 GMA2 | [KR063281.1](https://www.ncbi.nlm.nih.gov/nuccore/KR063281.1) | 103.42 | 53.4 | [126](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62734/465359|Gordonia phage GMA2/viral segment/) | 16 | 100 | 100 |

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

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

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

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

**Historical aspects:** Lytic siphophage Sixama was isolated in 2018 by Konstantinos Koustas (Durham Technical Community College, NC, USA) using Gordonia terrae NRRL B-16283 as the host bacterium as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 1702 bp direct terminal repeats. The Actinobacteriophage Database classified Sixama to Cluster DS, which we have subdivided. Indicated in phylogenetic tree by

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

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage Sixama | [MN484601.1](https://www.ncbi.nlm.nih.gov/nuccore/MN484601.1) | 115.45 | 52.7 | [171](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85371/740772|Gordonia phage Sixama/viral segment/) | 28 | 100 | 100 |

**(\*) determined using BLASTn [1]**

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

**Proposal C. Create a new genus, *Forzavirus,* with a single species**

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

**Historical aspects:** Lytic siphophage Forza was isolated in 2016 by Gabrielle Giglietti (University of Pittsburgh, PA, USA) from soil using Gordonia terrae 3612 as the host bacterium as part of the Phage Hunters Integrating Research and Education program. The genome has 1605 bp direct terminal repeats. The Actinobacteriophage Database classified Forza to Cluster DS, which we have chosen to subdivide. 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 Forza | [MK814760.1](https://www.ncbi.nlm.nih.gov/nuccore/MK814760.1) | 114.17 | 53.2 | [164](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86235/748625|Gordonia phage Forza/viral segment/) | 28 | 100 | 100 |

**(\*) determined using BLASTn [1]**

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

**Proposal D. Add one new species to the genus *Godonkavirus***

**Origin of the name of this taxon:** N/A.

**Historical aspects:** This taxon was created through Taxonomy Proposal 2019.009B

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage GodonK | [MK620899.1](https://www.ncbi.nlm.nih.gov/nuccore/MK620899.1) | 122.56 | 54.4 | [214](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79349/494235|Gordonia phage GodonK/viral segment/) | 31 | 100 | 100 |
| Gordonia phage Phendrix | [MN096369.1](https://www.ncbi.nlm.nih.gov/nuccore/MN096369.1) | 121.35 | 54.6 | [205](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82671/614447|Gordonia phage Phendrix/viral segment/) | 30 | 91.0 | 82.2 |

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

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

**References**

1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870
2. 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://kronos.icbm.uni-oldenburg.de/viridic/>
3. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. <https://www.genome.jp/viptree/>
4. 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
5. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.
6. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.
7. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.
8. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.
9. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.
10. Dyson ZA, Tucci J, Seviour RJ, Petrovski S. Lysis to Kill: Evaluation of the Lytic Abilities, and Genomics of Nine Bacteriophages Infective for Gordonia spp. and Their Potential Use in Activated Sludge Foam Biocontrol. PLoS One. 2015 Aug 4;10(8):e0134512. doi: 10.1371/journal.pone.0134512. PMID: 26241321; PMCID: PMC4524720.