

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

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| **Code assigned:** | **2021.094B** |  |
| **Short title:** Create one new family (*Zierdtviridae*) including two new subfamilies (*Emilbogenvirinae* and *Toshachvirinae*) and eight genera (*Caudoviricetes*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Actinobacteriophages 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**

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

|  |  |
| --- | --- |
| 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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| --- |
| 2021.094B.R.Zierdtviridae |

**Abstract**

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| --- |
| We have created a new family *Zierdtviridae* containing two subfamilies *Petrovskivirinae* (Gordonia phages from Actinobacteriophage Database Cluster CR) and *Toshachvirinae* (Corynebacterium phages - Actinobacteriophage Database Cluster EN). These viruses are all lytic and their ca. 65 kb genomes are terminated with 10 nt 3’-cohesive termini. On average the genomes of the *Petrovskivirinae* are 66.51 kb (65.69 mol%G+C) and encode 93 proteins and no tRNAs. CoreGenes 5.0 analysis at <https://coregenes.ngrok.io/> revealed 53 homologs shared by members of this taxon (57.0% homologs) which included: RecA-like DNA recombinase, thioredoxin, DnaE-like DNA polymerase III, RuvC-like resolvase, DNA primase/helicase, lysin A & B proteins, four minor tail proteins, tail tape measure protein, tail assembly chaperone, major tail protein, two head-to-tail adaptor, major capsid protein, LamD-like capsid decoration protein, scaffolding protein, MuF-like minor capsid protein, portal protein, and large subunit terminase protein.  The *Toshachvirinae* members possess 68.2 kb (51.8 mol%G+C) genomes encoding 94 proteins and 4 tRNA. CoreGenes 5.0 analysis at <https://coregenes.ngrok.io/> revealed 39 homologs shared by this taxon (41.4% homologs). These include: ribonucleotide reductase, DNA helicase, AAA-ATPase, thioredoxin, DnaE-like DNA polymerase III subunit alpha, Lysin A, holin, two minor tail protein, tail tape measure protein, major tail protein, tail assembly chaperone, major capsid protein, capsid decoration protein, capsid maturation protease, portal, terminase large and small subunit proteins and thymidylate synthase.  Collectively, the members of the *Zierdtviridae* share 18 homologs (19.4%) which is in-keeping with what defines a family. [9] |

**Text of proposal**

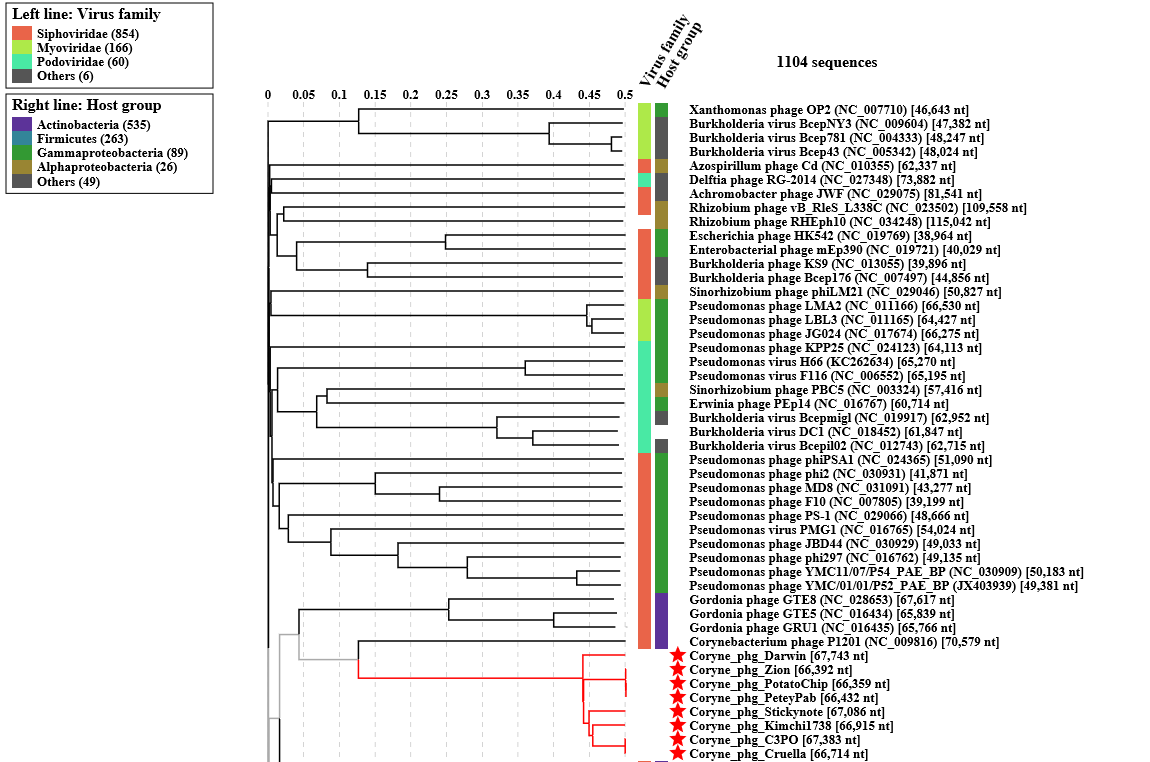
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic 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 and that the genera form a clade in a marker tree phylogeny.  **Family demarcation criteria: -** The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (VipTree, GRAViTy, vConTACT2). Members of the family share a significant number of orthologous genes (more than 10% of the genome). [9] | |

**Supporting evidence**

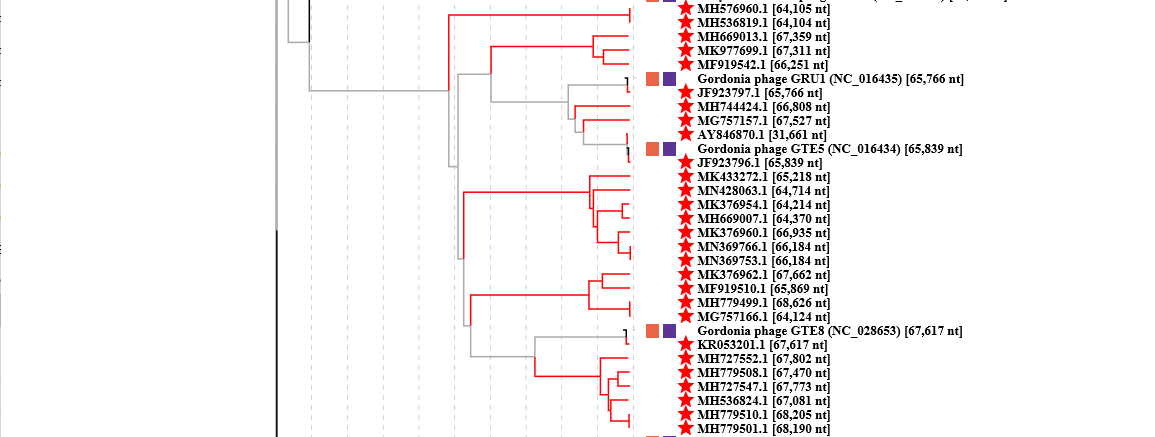
**Molecular overview:**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. Phage GTE8 is marked with a **blue star**.

1. Corynebacterium phages - expanded

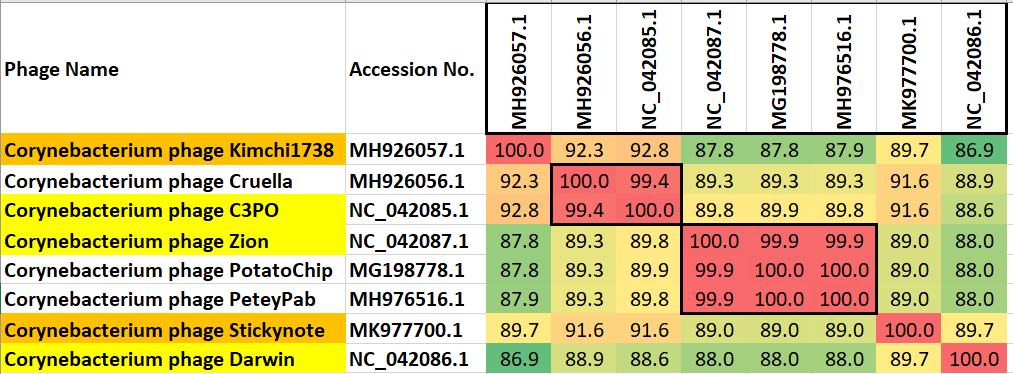


1. Gordonia phages – expanded



**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. The black box delineates strains. The yellow coloured boxes indicate existing species, while the gold-coloured boxes indicate new species.

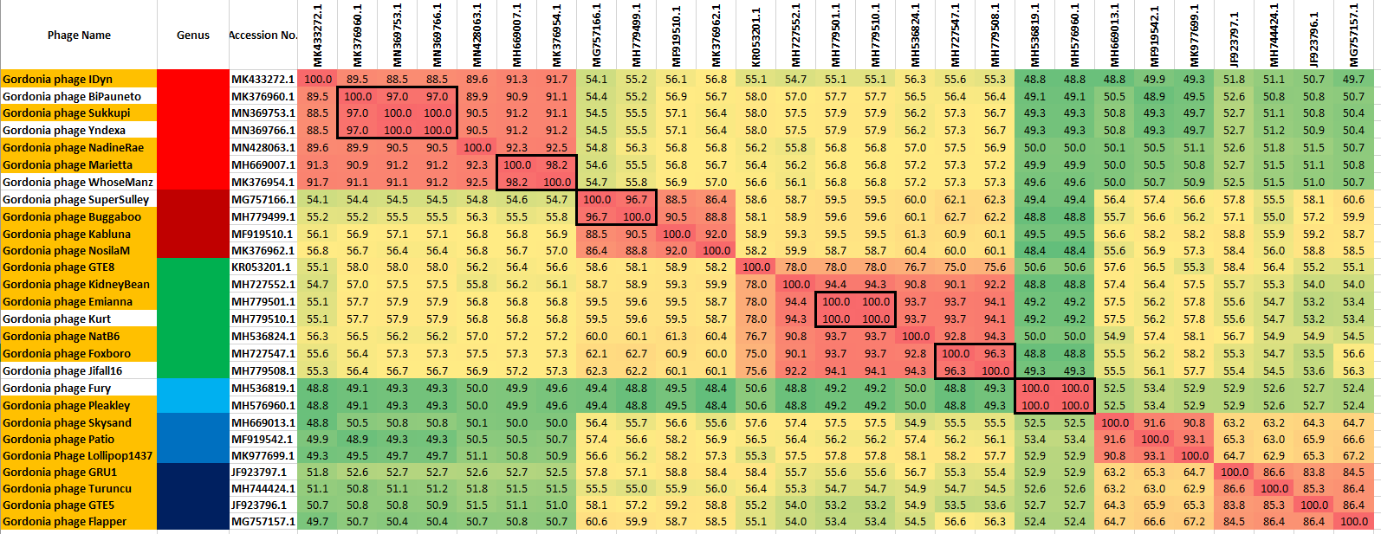
1. Corynebacterium phages

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**Chart

Description automatically generated**

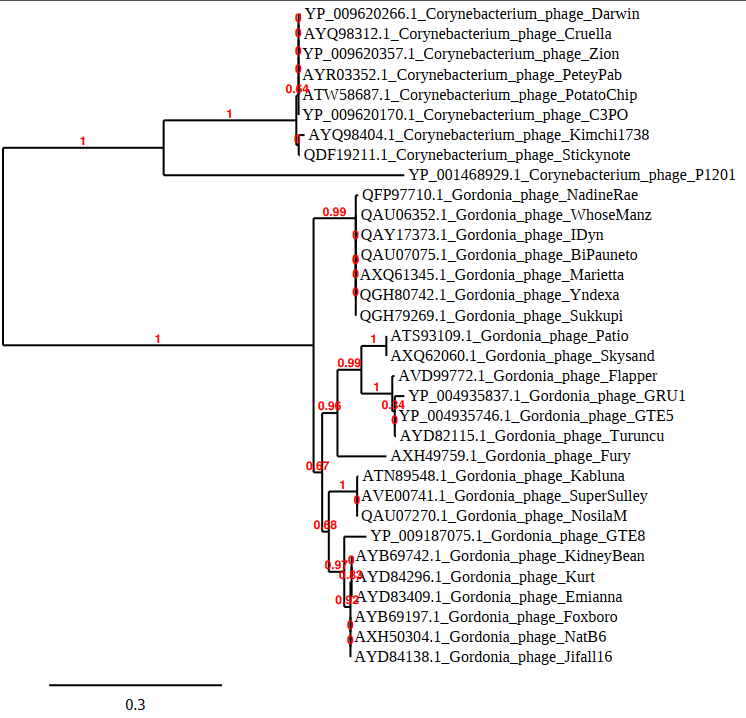
1. Gordonia phages



Chart

Description automatically generated

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of the phages described in this proposal 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."



**Proposals:** **A. To create a new subfamily, *Emilbogenvirinae,* with six genera of Gordonia siphoviruses.**

**A1. To create a new genus *Sukkupivirus* with four species**

**A2. To create a new genus *Kablunavirus* with three species**

**A3. To create a new genus *Foxborovirus* with five species**

**A4. To create a new genus *Pleakleyvirus* with one species**

**A5. To create a new genus *Skysandvirus* with three species**

**A6. To create a new genus *Gruunavirus* with four species**

**Source of the names of these taxa:** The names of the genera are directly derived from the names of the Gordonia phages, while the subfamily is named in honour of Dr Emil Bogen (M.D. 1896–1962) who was one of the first people to study mycobacteriophages. (https://academic.oup.com/ajcp/article-abstract/40/6/640/1763438?redirectedFrom=PDF)



(https://collections.nlm.nih.gov/catalog/nlm:nlmuid-101434840-img#)

**History:** Gordonia phage Sukkupi was isolated from Gurabo, PR USA soil by Agnes M. Cotto-Pereira (University of Puerto Rico at Cayey) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2017. The host bacterium was Gordonia terrae 3612. Its genome possess 10 nt 3'-cohesive termini (CGCCGCGTAC). The Actinobacteriophage Database places this phage in Cluster/Subcluster CR/CR4 (<https://phagesdb.org/phages/Sukkupi/>).

Gordonia phage Kabluna was isolated from Pittsburgh, PA USA soil by Solomon Klombers (University of Pittsburgh) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2016. The host bacterium was Gordonia terrae 3612. Its genome possess 10 nt 3'-cohesive termini (CGCCGCGTAC). The Actinobacteriophage Database places this phage in Cluster/Subcluster CR/CR2 (<https://phagesdb.org/phages/Kabluna/>).

Gordonia phage Foxboro was isolated from Foxboro, WI, USA soil by Alex Larson (College of St. Scholastica) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2017. The host bacterium was Gordonia terrae 3612. Its genome possess 10 nt 3'-cohesive termini (CGCCGCGTAC). The Actinobacteriophage Database places this phage in Cluster/Subcluster CR/CR4 (<https://phagesdb.org/phages/Foxboro/>).

Gordonia phage Pleakley was isolated from Pensacola, FL USA soil by Rebecca Saults and Gina Rodriguez (University of West Florida) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2017. The host bacterium was Gordonia terrae NRRL B-16283. Its genome possess 10 nt 3'-cohesive termini (CGCCGCGTAC). The Actinobacteriophage Database places this phage in Cluster/Subcluster CR/CR5 (<https://phagesdb.org/phages/Pleakley/>).

Gordonia phage Skysand was isolated from Williamsburg, VA USA soil by Divinity Summers (College of William & Mary) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2016. The host bacterium was Gordonia terrae 3612. Its genome possess 10 nt 3'-cohesive termini (CGCCGCGTAC). The Actinobacteriophage Database places this phage in Cluster/Subcluster CR/CR3 (<https://phagesdb.org/phages/Skysand/>).

Gordonia phage GRU1 was isolated from Loganholme, Australia soil by Steve Petrovski, Daniel Tillet, and Robert Seviour (La Trobe University) in 2011. The host bacterium was Gordonia rubripertincta Grub38. Its genome ends were not characterized. The Actinobacteriophage Database places this phage in Cluster/Subcluster CR/CR1 (<https://phagesdb.org/phages/GRU1/>).

**Specific Reference:** 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. [GTE8]

Petrovski S, Tillett D, Seviour RJ. Genome sequences and characterization of the related Gordonia phages GTE5 and GRU1 and their use as potential biocontrol agents. Appl Environ Microbiol. 2012 Jan;78(1):42-7. doi: 10.1128/AEM.05584-11. Epub 2011 Oct 28. PMID: 22038604; PMCID: PMC3255624. [GTE5 and GRU1]

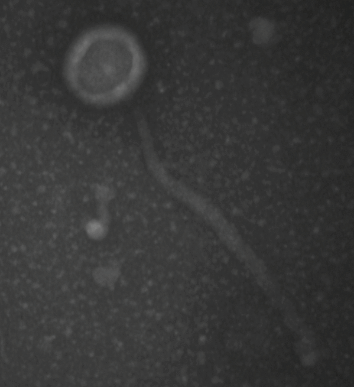
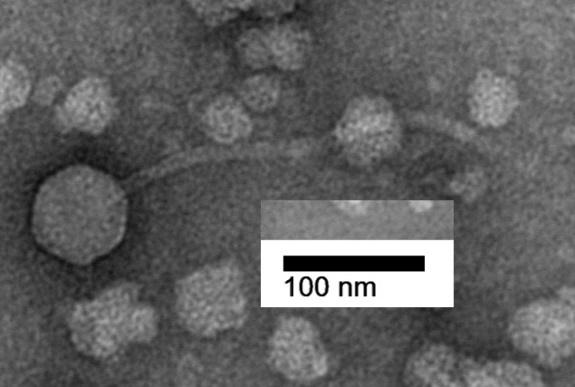
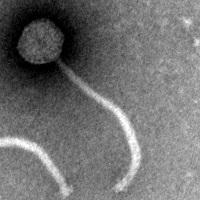
**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| 1. ***Sukkupivirus*** |  |  |  |  |  |  |  |
| Gordonia phage Sukkupi |  | MN369753.1 | 66.18 | 66.2 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85559/743718%7CGordonia%20phage%20Sukkupi/viral%20segment/) | 100 | 100 |
| Gordonia phage IDyn |  | MK433272.1 | 65.22 | 66.2 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76047/446705%7CGordonia%20phage%20IDyn/viral%20segment/) | 88.5 | 89.2 |
| Gordonia phage NadineRae |  | MN428063.1 | 64.71 | 66.1 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84983/717044%7CGordonia%20phage%20NadineRae/viral%20segment/) | 90.5 | 92.5 |
| Gordonia phage Marietta |  | MH669007.1 | 64.37 | 66.1 | [91](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72122/400258%7CGordonia%20phage%20Marietta/viral%20segment/) | 91.2 | 93.5 |
|  |  |  |  |  |  |  |  |
| 1. ***Kablunavirus*** |  |  |  |  |  |  |  |
| Gordonia phage Kabluna |  | MF919510.1 | 65.87 | 65.6 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64188/466595%7CGordonia%20phage%20Kabluna/viral%20segment/) | 100 | 100 |
| Gordonia phage Buggaboo |  | MH779499.1 | 68.63 | 65.6 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72802/409423%7CGordonia%20phage%20Buggaboo/viral%20segment/) | 90.5 | 95.8 |
| Gordonia phage NosilaM |  | MK376962.1 | 67.66 | 65.6 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75782/445159%7CGordonia%20phage%20NosilaM/viral%20segment/) | 92.0 | 93.7 |
|  |  |  |  |  |  |  |  |
| 1. ***Foxborovirus*** |  |  |  |  |  |  |  |
| Gordonia phage Foxboro |  | MH727547.1 | 67.77 | 65.8 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72667/408795%7CGordonia%20phage%20Foxboro/viral%20segment/) | 100 | 100 |
| Gordonia phage GTE8 |  | KR053201.1 | 67.62 | 66.0 | 94 | 75.0 | 89.1 |
| Gordonia phage KidneyBean |  | MH727552.1 | 67.80 | 65.8 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72671/408799%7CGordonia%20phage%20KidneyBean/viral%20segment/) | 90.1 | 98.9 |
| Gordonia phage Emianna |  | MH779501.1 | 68.19 | 65.8 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72804/409425%7CGordonia%20phage%20Emianna/viral%20segment/) | 93.7 | 98.9 |
| Gordonia phage NatB6 |  | MH536824.1 | 67.08 | 65.7 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71935/399807%7CGordonia%20phage%20NatB6/viral%20segment/) | 92.8 | 97.8 |
|  |  |  |  |  |  |  |  |
| 1. ***Pleaskleyvirus*** |  |  |  |  |  |  |  |
| Gordonia phage Pleakley |  | MH576960.1 | 64.10 | 65.2 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71954/399826%7CGordonia%20phage%20Pleakley/viral%20segment/) | 100 | 100 |
|  |  |  |  |  |  |  |  |
| 1. ***Skysandvirus*** |  |  |  |  |  |  |  |
| Gordonia phage Skysand |  | MH669013.1 | 67.36 | 65.5 | [95](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72128/400264%7CGordonia%20phage%20Skysand/viral%20segment/) | 100 | 100 |
| Gordonia phage Patio |  | MF919542.1 | 66.25 | 65.6 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68163/369310%7CGordonia%20phage%20Patio/viral%20segment/) | 91.6 | 93.7 |
| Gordonia Phage Lollipop1437 |  | MK977699.1 | 67.31 | 65.7 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82354/596125%7CGordonia%20Phage%20Lollipop1437/viral%20segment/) | 90.8 | 92.6 |
|  |  |  |  |  |  |  |  |
| 1. ***Gruunavirus*** |  |  |  |  |  |  |  |
| Gordonia phage GRU1 | [NC\_016435.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_016435.1) | JF923797.1 | 65.77 | 65.5 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/12103/459603%7CGordonia%20phage%20GRU1/viral%20segment%20Unknown/) | 100 | 100 |
| Gordonia phage Turuncu |  | MH744424.1 | 66.81 | 65.4 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72797/409418%7CGordonia%20phage%20Turuncu/viral%20segment/) | 86.6 | 88.3 |
| Gordonia phage GTE5 | [NC\_016434.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_016434.1) | JF923796.1 | 65.84 | 65.1 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/12104/459604%7CGordonia%20phage%20GTE5/viral%20segment%20Unknown/) | 83.8 | 86.2 |
| Gordonia phage Flapper |  | MG757157.1 | 67.53 | 65.3 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68425/369572%7CGordonia%20phage%20Flapper/viral%20segment/) | 84.5 | 90.4 |
|  |  |  |  |  |  |  |  |

**(\*) 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]**

**Electron micrograph:** Electron micrographs of negatively stained Gordonia phages Foxboro, Kabluna and Skysand - 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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**B. To create a new subfamily, *Toshachvirinae,* with two existing genera of Corynebacteriophage siphoviruses.**

**B1. To add two new species to the genus *Ceetrepovirus***

For details on this genus see: 2018.047B

**B2. To move the genus *Chunghsingvirus***

For details on this genus see: 2018.048B

**Source of the name of this taxon:** This taxon is named in honour of the pioneering Canadian Corynebacterium phage worker - Sheila Toshach (1921 – 1998). A graduate of the University of Toronto’s School of Hygiene where she isolated her first Corynebacterium phage in 1950; her career was spent at the University of Alberta’s Public Health Laboratory (ProvLab).

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(Sheila Toshach in 1945; <https://www.pressreader.com/canada/edmonton-journal/20080107/282273841037318>)

**History:** Corynebacterium phage Kimchi1738 was isolated from Birmingham, AL USA soil by Sameen Ali and Sam Castillo (University of Alabama at Birmingham) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2016. The host bacterium was Corynebacterium vitaeruminis NCIB 9291. Its genome possess 10 nt 3'-cohesive termini (CCTACGGTGC). The Actinobacteriophage Database places this phage in Cluster EN (https://phagesdb.org/phages/Kimchi1738/).

Corynebacterium phage Stickynote was isolated from Birmingham, AL USA soil by Cameron McPhail (University of Alabama at Birmingham) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program in 2016. The host bacterium was Corynebacterium vitaeruminis NCIB 9291. Its genome possess 10 nt 3'-cohesive termini (CCTACGGTGC). The Actinobacteriophage Database places this phage in Cluster EN (https://phagesdb.org/phages/StickyNote/).

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Corynebacterium phage C3PO | [NC\_042085.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_042085.1) | [MG198776.1](https://www.ncbi.nlm.nih.gov/nuccore/MG198776.1) | 67.38 | 52.3 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68200/369347%7CCorynebacterium%20phage%20C3PO/viral%20segment/) | 4 | 100 | 100 |
| Corynebacterium phage Kimchi1738 |  | [MH926057.1](https://www.ncbi.nlm.nih.gov/nuccore/MH926057.1) | 66.92 | 52.3 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73838/418536%7CCorynebacterium%20phage%20Kimchi1738/viral%20segment/) | 5 | 92.8 | 98.9 |
| Corynebacterium phage Stickynote |  | [MK977700.1](https://www.ncbi.nlm.nih.gov/nuccore/MK977700.1) | 67.09 | 52.2 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82337/596108%7CCorynebacterium%20phage%20Stickynote/viral%20segment/) | 4 | 91.6 | 91.4 |
|  |  |  |  |  |  |  |  |  |

**(\*) 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]**

**C. To create a new family, *Zierdtviridae*, containing two subfamilies *Toshachvirinae* and *Emilbogenvirinae*; and an orphan genus.**

**Source of the name of this taxon:** Charles Henry Zierdt (1922 - 2015) was an American microbiologist and National Institutes of Health, Clinical Pathology Department scientist. He was a Fellow of the American Academy Microbiology; member American Society Microbiology (chapter president 1976), United States Federation Culture Collections (membership chairman 1985) <https://prabook.com/web/charles_henry.zierdt/646983> . He isolated and studied some of the first Corynebacterium (Propionibacterium) acnes phages (mid 1970s).

**References:**

1: 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.

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.

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5: 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.

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