

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

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| **Code assigned:** | **2021.044B** |  |
| **Short title:** Create 13 new species in the genus *Korravirus* (*Caudoviricetes*) | | |
|  | | |

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

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**Corresponding author**

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| --- |
| Dann Turner |

**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**

|  |  |
| --- | --- |
| **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)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair |  |
| 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**

|  |
| --- |
| 2021.044B.R.Korravirus\_new\_species |

**Abstract**

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| --- |
| The genus *Korravirus* was created by Taxonomy Proposal 2016.006a-dB.A.v2.Korravirus and contained nine species. NCBI currently contains 71 Korra-like phages. This proposal officially recognizes 13 new species. These siphoviruses are all lytically infectious for Arthrobacter sp. ATCC 21022, and belong to Cluster AK in The Actinobacteriophage Database (<https://phagesdb.org/clusters/AK/>). |

**Text of proposal**

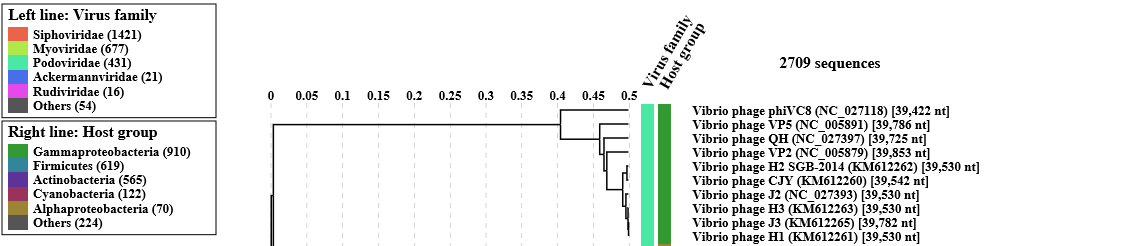
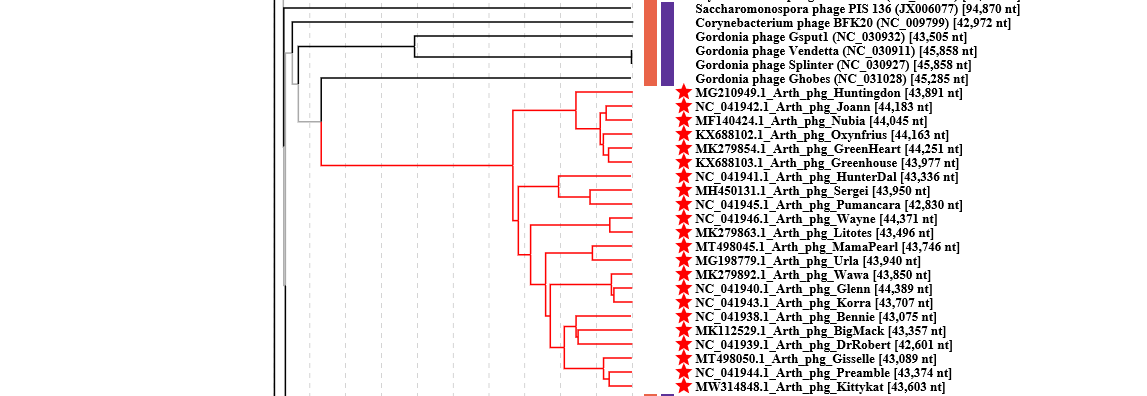
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic 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. [9] | |

**Supporting evidence**

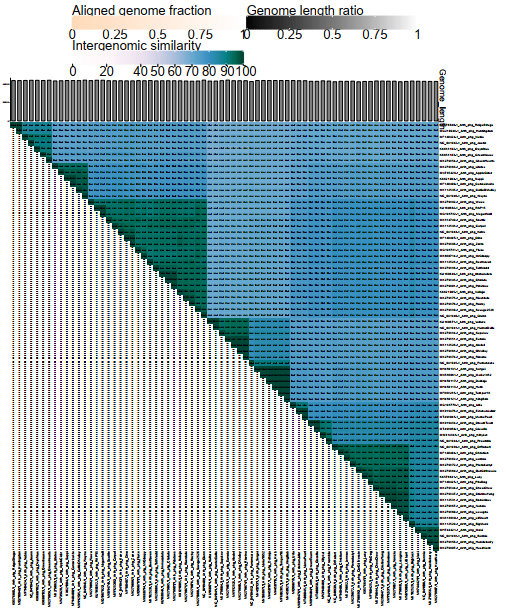
**Source of the name of this taxon:** NA

**History:** The genus *Korravirus* was created by Taxonomy Proposal 2016.006a-dB.A.v2.Korravirus and contained nine species. NCBI currently contains 71 Korra-like phages. This proposal officially recognizes 13 new species.

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

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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. (High resolution image attached)

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**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Arthrobacter phage Korra | [KU160653.2](https://www.ncbi.nlm.nih.gov/nuccore/KU160653.2) | 43.71 | 61.1 | [59](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63527/466147%7CArthrobacter%20phage%20Korra/viral%20segment/) | 100 | 100 |
| Arthrobacter phage BigMack | [MK112529.1](https://www.ncbi.nlm.nih.gov/nuccore/MK112529.1) | 43.36 | 61.3 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/74379/430057%7CArthrobacter%20phage%20BigMack/viral%20segment/) | 82.5 | 93.2 |
| Arthrobacter phage Gisselle | [MT498050.1](https://www.ncbi.nlm.nih.gov/nuccore/MT498050.1) | 43.09 | 60.7 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92648/916837%7CArthrobacter%20phage%20Gisselle/viral%20segment/) | 78.7 | 93.2 |
| Arthrobacter phage GreenHearts | [MK279854.1](https://www.ncbi.nlm.nih.gov/nuccore/MK279854.1) | 44.25 | 60.8 | [62](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75052/435029%7CArthrobacter%20phage%20GreenHearts/viral%20segment/) | 73.8 | 96.6 |
| Arthrobacter phage Greenhouse | [KX688103.1](https://www.ncbi.nlm.nih.gov/nuccore/KX688103.1) | 43.98 | 60.8 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63002/465625%7CArthrobacter%20phage%20Greenhouse/viral%20segment/) | 76.4 | 94.9 |
| Arthrobacter phage Huntingdon | [MG210949.1](https://www.ncbi.nlm.nih.gov/nuccore/MG210949.1) | 43.89 | 60.7 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68170/369317%7CArthrobacter%20phage%20Huntingdon/viral%20segment/) | 74.1 | 94.9 |
| Arthrobacter phage Kittykat | [MW314848.1](https://www.ncbi.nlm.nih.gov/nuccore/MW314848.1) | 43.6 | 60.7 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97488/1520672%7CArthrobacter%20phage%20Kittykat/viral%20segment/) | 77.4 | 91.5 |
| Arthrobacter phage Litotes | [MK279863.1](https://www.ncbi.nlm.nih.gov/nuccore/MK279863.1) | 43.5 | 61.1 | [62](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75058/435035%7CArthrobacter%20phage%20Litotes/viral%20segment/) | 78.2 | 98.3 |
| Arthrobacter phage MamaPearl | [MT498045.1](https://www.ncbi.nlm.nih.gov/nuccore/MT498045.1) | 43.75 | 61.3 | [60](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92649/916838%7CArthrobacter%20phage%20MamaPearl/viral%20segment/) | 76.8 | 91.5 |
| Arthrobacter phage Nubia | [MF140424.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140424.1) | 44.05 | 60.7 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63711/466332%7CArthrobacter%20phage%20Nubia/viral%20segment/) | 74.1 | 96.6 |
| Arthrobacter phage Oxynfrius | [KX688102.1](https://www.ncbi.nlm.nih.gov/nuccore/KX688102.1) | 44.16 | 60.8 | [62](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63003/465626%7CArthrobacter%20phage%20Oxynfrius/viral%20segment/) | 74.8 | 98.3 |
| Arthrobacter phage Sergei | [MH450131.1](https://www.ncbi.nlm.nih.gov/nuccore/MH450131.1) | 43.95 | 61.9 | [60](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71882/399754%7CArthrobacter%20phage%20Sergei/viral%20segment/) | 71.5 | 93.2 |
| Arthrobacter phage Urla | [MG198779.1](https://www.ncbi.nlm.nih.gov/nuccore/MG198779.1) | 43.94 | 61.2 | [62](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68199/369346%7CArthrobacter%20phage%20Urla/viral%20segment/) | 76.6 | 93.2 |
| Arthrobacter phage Wawa | [MK279892.1](https://www.ncbi.nlm.nih.gov/nuccore/MK279892.1) | 43.85 | 60.9 | [62](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75083/435060%7CArthrobacter%20phage%20Wawa/viral%20segment/) | 94.4 | 98.3 |

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

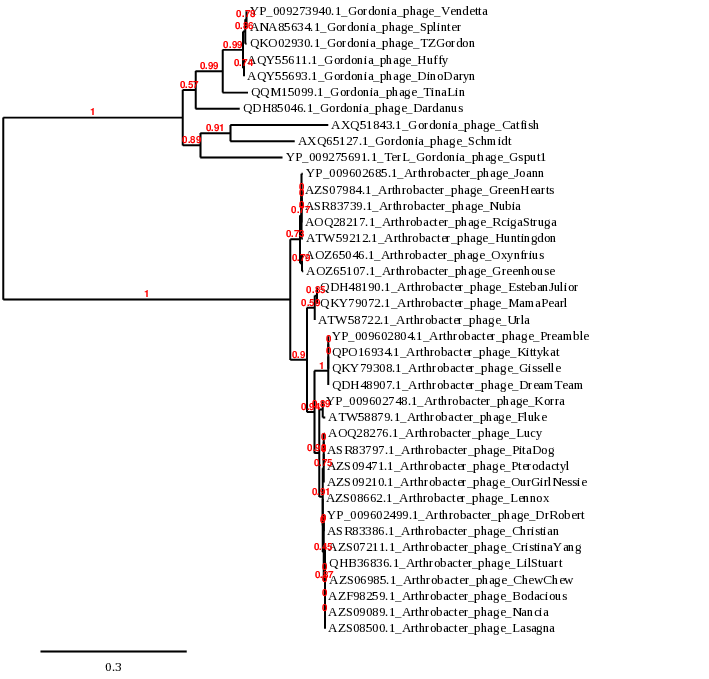
**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Strains:**

|  |  |  |
| --- | --- | --- |
| **Phage name** | **Accession No.** | **Strains of:** |
| Arthrobacter phage RcigaStruga | KX576640.1 | *Korravirus Huntington* |
| Arthrobacter phage AppleCider | MN735429.1 | *Korravirus Litotes* |
| Arthrobacter phage Suppi | KX621004.1 | *Korravirus Litotes* |
| Arthrobacter phage Canowicakte | MF140400.1 | *Korravirus Litotes* |
| Arthrobacter phage CallieOMalley | MK112535.1 | *Korravirus Litotes* |
| Arthrobacter phage RAP15 | KU160662.1 | *Korravirus Korra* |
| Arthrobacter phage MeganNoll | MG198782.1 | *Korravirus Korra* |
| Arthrobacter phage Scuttle | MK814749.1 | *Korravirus Korra* |
| Arthrobacter phage Carpal | MK112538.1 | *Korravirus Korra* |
| Arthrobacter phage Dino | MF140407.1 | *Korravirus Korra* |
| Arthrobacter phage Zorro | MK279896.1 | *Korravirus Korra* |
| Arthrobacter phage Fluke | MG198781.1 | *Korravirus Korra* |
| Arthrobacter phage MrGloopy | MK660714.1 | *Korravirus Korra* |
| Arthrobacter phage Beethoven | MK112528.1 | *Korravirus Korra* |
| Arthrobacter phage TattModd | MK279886.1 | *Korravirus Korra* |
| Arthrobacter phage Immaculata | KU160649.1 | *Korravirus Korra* |
| Arthrobacter phage Cholula | MK279845.1 | *Korravirus Korra* |
| Arthrobacter phage Potatoes | MK279901.1 | *Korravirus Korra* |
| Arthrobacter phage Vallejo | KX621005.1 | *Korravirus Korra* |
| Arthrobacter phage Riverdale | MK279875.1 | *Korravirus Korra* |
| Arthrobacter phage Rozby | MK279876.1 | *Korravirus Korra* |
| Arthrobacter phage Savage2526 | MK279880.1 | *Korravirus Korra* |
| Arthrobacter phage Vulture | KU160671.1 | *Korravirus HunterDalle* |
| Arthrobacter phage Supakev | MK279884.1 | *Korravirus HunterDalle* |
| Arthrobacter phage Eunoia | MK279851.1 | *Korravirus HunterDalle* |
| Arthrobacter phage Aledel | MK112526.1 | *Korravirus HunterDalle* |
| Arthrobacter phage OMalley | MK279868.1 | *Korravirus HunterDalle* |
| Arthrobacter phage Riovina | MK279874.1 | *Korravirus HunterDalle* |
| Arthrobacter phage Maria1952 | MN586061.1 | *Korravirus Sergei* |
| Arthrobacter phage Daiboju | MH450117.1 | *Korravirus Sergei* |
| Arthrobacter phage Herb | MH450118.1 | *Korravirus Sergei* |
| Arthrobacter phage Temper16 | MF668285.1 | *Korravirus Sergei* |
| Arthrobacter phage KingBob | MH450121.1 | *Korravirus Sergei* |
| Arthrobacter phage EstebanJulior | MK919476.1 | *Korravirus MamaPearl* |
| Arthrobacter phage DreamTeam | MK919484.1 | *Korravirus Gisselle* |
| Arthrobacter phage Christian | MF140404.1 | *Korravirus DrRobert* |
| Arthrobacter phage Lennox | MK279862.1 | *Korravirus DrRobert* |
| Arthrobacter phage Pterodactyl | MK279872.1 | *Korravirus DrRobert* |
| Arthrobacter phage OurGirlNessie | MK279869.1 | *Korravirus DrRobert* |
| Arthrobacter phage Lucy | KX576641.1 | *Korravirus DrRobert* |
| Arthrobacter phage PitaDog | MF140425.1 | *Korravirus DrRobert* |
| Arthrobacter phage ChewChew | MK279844.1 | *Korravirus DrRobert* |
| Arthrobacter phage CristinaYang | MK279847.1 | *Korravirus DrRobert* |
| Arthrobacter phage Bodacious | MK112531.1 | *Korravirus DrRobert* |
| Arthrobacter phage Nancia | MK279867.1 | *Korravirus DrRobert* |
| Arthrobacter phage Lasagna | MK279860.1 | *Korravirus DrRobert* |
| Arthrobacter phage LilStuart | MN813680.1 | *Korravirus DrRobert* |
| Arthrobacter phage Moki | MH744421.1 | *Korravirus Bennie* |
| Arthrobacter phage Huckleberry | MK279856.1 | *Korravirus Bennie* |
| Arthrobacter phage HeadNerd | MK279907.1 | *Korravirus Bennie* |

**Electron micrograph:** NA

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of some of these 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."



**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.

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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.

6: 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.

7: Lowe, T.M. and Chan, P.P. (2016) tRNAscan-SE On-line: Search and Contextual Analysis of Transfer RNA Genes. Nucl. Acids Res. 44: W54-57.

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