

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

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| **Code assigned:** | ***2022.090B*** |  |
| **Short title:** Create three new genera (*Kumottavirus, Sargevirus, Shoyavirus*) for Arthrobacter siphoviruses (*Caudoviricetes*) | | |
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**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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| 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 | April 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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| 2022.090B.N.v1.Caudoviricetes\_3ng\_arthrobacter.xlsx |

**Abstract**

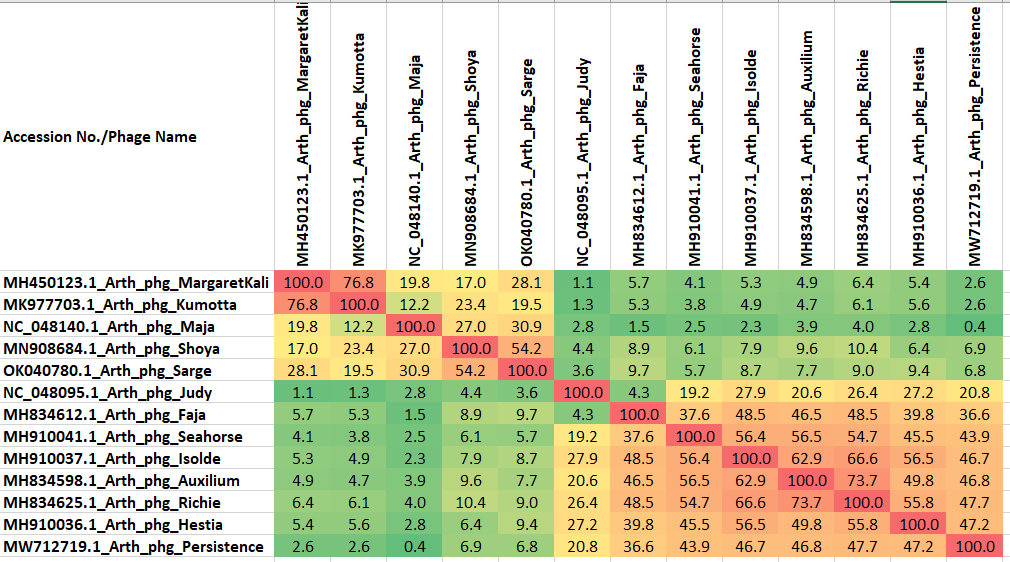
|  |
| --- |
| Based upon overall DNA sequence (VIRIDIC) and BLASTX (ViPTree) analyses we have split The Actinobacteriophage Database Cluster FB into four genera: *Majavirus* (existing genus)*, Kumottavirus, Sargevirus* and *Shoyavirus*. This proposal describes the latter three genera. |

**Text of proposal**

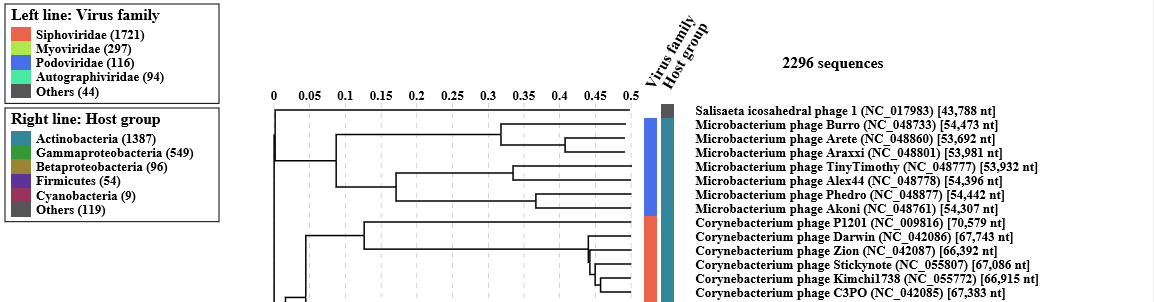
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1] – usually calculated using 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**

**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.

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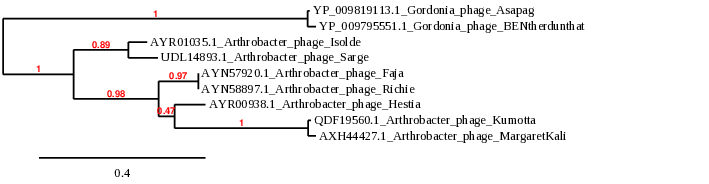
**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars**.



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**Phylogeny:** The phylogenetic tree was constructed using the MCPs from Kumotta 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." 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 [7] for details." A. Exonuclease – N.B. phage Shoya lacks this protein; B. Tail tape measure protein

A. Exonuclease



B. Tail tape measure protein



**Proposals:**

1. **Create a new genus, *Kumottavirus*, with two species**
2. **Create a new genus, *Sargevirus*, with one species**
3. **Create a new genus, *Shoyavirus*, with one species**

**Details:**

1. **Create a new genus, *Kumottavirus*, with two species**

**Origin of the name of this taxon:** This taxon is named after Arthrobacter phage Kumotta

**Historical aspects:** This temperate siphophage was isolated in 2018 by Ryan Flanagan and Fardowsa H (The Ohio State University, Columbus, USA) against Arthrobacter sp. ATCC 21022 from Clarksville, OH garden soil as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome is has 11 nt 3’-cohesive termini (TCCGCCAGGTA). The Actinobacteriophage Database classified Kumotta to Cluster FB which we are now subdividing*.*

**Electron micrograph:**. N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Kumotta | [MK977703.1](about:blank) | 40.32 | 60.8 | [75](about:blank#!/proteins/82340/596111|Arthrobacter phage Kumotta/viral segment/) | 0 | 100 | 100 |
| Arthrobacter phage MargaretKali | [MH450123.1](about:blank) | 39.45 | 61.1 | [72](about:blank#!/proteins/71874/399746|Arthrobacter phage MargaretKali/viral segment/) | 0 | 76.8 | 88.0 |

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

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

1. **Create a new genus, *Sargevirus*, with one species**

**Origin of the name of this taxon:** This taxon is named after Arthrobacter phage Sarge

**Historical aspects:** This temperate siphophage was isolated in 2017 by Audrey Jonas (University of Pittsburgh, PA, USA) against Arthrobacter globiformis B-2979 from soil as part of the Phage Hunters Integrating Research and Education program. The genome is has 11 nt 3’-cohesive termini (TCCGCCCGGTA). The Actinobacteriophage Database classified Richie to Cluster FB which we are now subdividing.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Sarge | [OK040780.1](about:blank) | 36.41 | 63.5 | [66](about:blank#!/proteins/107504/1731375|Arthrobacter phage Sarge/viral segment/) | 0 | 100 | 100 |

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

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

1. **Create a new genus, *Shoyavirus*, with one species**

**Origin of the name of this taxon:** This taxon is named after Arthrobacter phage Shoya

**Historical aspects:** This temperate siphophage was isolated in 2018 by Shawna Larson and Moya Murray (University of Wisconsin-River Falls, USA) against Arthrobacter globiformis B-2979 from moist soil as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome is has 11 nt 3’-cohesive termini (TCCGCCCGGTA). The Actinobacteriophage Database classified Shoya to Cluster FB which we are now subdividing.

**Electron micrograph:**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Shoya | [MN908684.1](about:blank) | 37.78 | 63.7 | [67](about:blank#!/proteins/87885/811645|Arthrobacter phage Shoya/viral segment/) | 0 | 100 | 100 |

**(\*) 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/](about:blank)
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/](about:blank)
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.