

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2021.051B** |  |
| **Short title:** Create one new family (*Mesyanzhinovviridae*) including seven genera (*Caudoviricetes*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Moraru C Kropinski AM | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  liliana.cristina.moraru@uol.de;  Phage.Canada@gmail.com |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT] Institute for Chemistry and Biology of the Marine Environment, Germany [CM]  University of Guelph, Canada [AMK] |

**Corresponding author**

|  |
| --- |
| Andrew M. Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

|  |
| --- |
| Caudoviricetes Study Group, Bacterial Viruses Subcommittee |

**ICTV study group comments and response of proposer**

|  |
| --- |
|  |

**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 | May 2021 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
| 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**

|  |
| --- |
|  |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2021.051B.R.Mesyanzhinovviridae |

**Abstract**

|  |
| --- |
| We have analyzed a number of classified and unclassified temperate Pseudomonas siphoviruses using a variety of molecular tools (VIRIDIC, ViPTree, CoreGenes, phylogeny.fr) and conclude the data warrants the creation of a new family. The viruses within the *Mesyanzhinovviridae.* Taking one representative from each genus, the average characteristics of the genomes for this family are: 60.6 kb, 64.2 mol%G+C, encode 80 proteins and no tRNAs. CoreGenes 5.0 (<https://coregenes.ngrok.io>) analysis reveals eight homologs (10%) which include: DNA helicase, thymidylate synthase, deoxycytidylate deaminase, integrase, large subunit terminase, portal protein and two structural proteins, one defined as a "Mu protein F like protein." The overall % homologous proteins is within the bounds of what we use to define families (Turner et al. 2021; [11]). |

**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:** Not applicable to this proposal. 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).  (Taken from: Turner D et al. [11]) | |

**Supporting evidence**

1. **To create a new subfamily, *Rabinowitzvirinae* composed of two genera, *Yuavirus* and *Vojvodinavirus***
2. **To create a new genus, *Epaquintavirus***
3. **To create a new genus, *Xooduovirus***
4. **To create a new genus, *Bosavirus*.**
5. **To create a new subfamily *Bradleyvirinae*, composed of four genera *Epaquintavirus*, *Abidjanvirus, Xooduovirus* and *Bosavirus*.**
6. **To move *Alphaproteobacteria virus PhiJL001* to its own genus, *Keylargovirus*.**
7. **To create a new family, *Mesyanzhinovviridae* for these taxa.**

**Preliminary analysis:** VIRIDIC, ViPTree and phylogeny

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [5]) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains, while the [P] associated with the accession number indicates a partial genome.

Chart, table, treemap chart

Description automatically generated

**Phylogeny – Proteomic tree (ViPTree):** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [7]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [8]. The unstarred names are RefSeq members in the ViPTree database, while the red starred values are phage genomes uploaded during this study. The red asterisks point to the classified or reclassified phages.

**A picture containing diagram

Description automatically generated**

**A picture containing diagram

Description automatically generated**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of phage Yua and related phages with phylogeny.fr in “one click” mode [9]. "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 [10] for details."

**Diagram

Description automatically generated**

**To create a new subfamily, *Rabinowitzvirinae* composed of two genera, *Yuavirus* and *Vojvodinavirus***

**Source of the name of this taxon:** This subfamily is named in honour of Genia Rabinowitz M.S.(1883 - 1977) was a bacteriologist Department of Pathology and Bacteriology, Beth-El Hospital, Brooklyn, New York who was one of the first scientists (1934) to study bacteriophages of Bacillus pyocyaneus (Pseudomonas aeruginosa)

**History:** These two genera were proposed by Taxonomy Proposals 2012.008a-dB (*Yualikevirus*) and 2019.094B (*Vojvodinavirus*). Genomic (VIRIDIC), Proteomic (ViPTree) and phylogenetic data all confirm that these genera are related. This was also described in 2019.094B (*Vojvodinavirus*).

**To create a new genus, *Epaquintavirus***

**Source of the name of this taxon:** This genus name is directly derived from that of the first isolate of its type, Pseudomonas phage Epa5.

**History:** These lytic phages were isolated from sewage collected in Washington, DC [Farlow J et al. 2020]. The authors tentatively assigned them to the genus *Abidjanvirus.*

**Specific Reference:** Farlow J, Freyberger HR, He Y, et al. Complete Genome Sequences of 10 Phages Lytic against Multidrug-Resistant Pseudomonas aeruginosa. Microbiol Resour Announc. 2020;9(29):e00503-20. Published 2020 Jul 16. doi:10.1128/MRA.00503-20

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Pseudomonas phage Epa5 |  | [MT108725.1](https://www.ncbi.nlm.nih.gov/nuccore/MT108725.1) | 64.1 | 62.2 | [6](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89056/889171%7CPseudomonas%20phage%20Epa5/viral%20segment/) | 0 |
|  |  |  |  |  |  |  |

**N.B. These phages are severely underannotated. Pseudomonas phage Epa43 should be considered a strain of Epa5. The genome of Pseudomonas phage Epa19 is only 50% complete.**

**VIRIDIC homologs:** This reveals that the closest homolog is Pseudomonas phage ZC01 which shares 52.4% sequence identity with Epa5.

**Electron micrograph:** None available

**To create one new species in the genus, *Abidjanvirus***

**History: “**Using Pseudomonas aeruginosa as host, we isolated three new phages from a composting operation at the Sao Paulo Zoo Park (Brazil). One of the isolated phages is similar to Pseudomonas phage Ab18 and belongs to the Siphoviridae YuA-like viral genus. Phage ZC01 has the typical morphology for phages of the *Siphoviridae* family and more specifically for phages of the *YuA-like* group. We identified a prolate and more elongated head of ~80 nm by ~58 nm (morphotype B2). Tail is ~150 nm long, cross-banded, flexible and non-contractile, with a terminal structure resembling short fibers.” [Amgarten D et al. 2017].

**Specific Reference:** Amgarten D, Martins LF, Lombardi KC, et al. Three novel Pseudomonas phages isolated from composting provide insights into the evolution and diversity of tailed phages. BMC Genomics. 2017;18(1):346. Published 2017 May 4. doi:10.1186/s12864-017-3729-z

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Pseudomonas phage ZC01 |  | [KU356689.1](https://www.ncbi.nlm.nih.gov/nuccore/KU356689.1) | 57.06 | 63.4 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62720/465345%7CPseudomonas%20phage%20ZC01/viral%20segment/) | 0 |
|  |  |  |  |  |  |  |

**Electron micrograph:** None available

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

**Source of the name of this taxon:** This genus is named after the first virus of its type Xanthomonas phage Xoo-sp2

**History:** This lytic phage was isolated from soil in China against Xanthomonas oryzae pv. oryzae. GenBank considered it to be a “unclassified *Pamexvirus*”

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Xanthomonas phage Xoo-sp2 |  | [KX241618.1](https://www.ncbi.nlm.nih.gov/nuccore/KX241618.1) | 60.5 | 66.5 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62911/465534%7CXanthomonas%20phage%20Xoo-sp2/viral%20segment/) | 0 |
|  |  |  |  |  |  |  |

**VIRIDIC homologs:** Its closest relative is Xanthomonas phage Bosa with which it shares 64.8% DNA sequence identity.

**Electron micrograph:** None available

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

**Source of the name of this taxon:** This genus is named after the first virus of its type, Xanthomonas phage Bosa

**History:** Lytic Xanthomonas phage Bosa was obtained from French sewage water extract on Xanthomonas. Albilineans. GenBank has classified it as “unclassified Pamexvirus.” Interestingly the GenBank record for DLP4 states “Lysogenic conversion of Stenotrophomonas maltophilia by temperate phage DLP4.” Bosa protein CAA2409933.1 is defined as “integrase” but this is an error.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Xanthomonas phage Bosa |  | LR743532.1 | 63.83 | 64.8 | 80 | 0 |
|  |  |  |  |  |  |  |

**N.B. Stenotrophomonas phage DLP4 should be considered a strain in this genus.**

**VIRIDIC homologs:** Its closest relative is Xanthomonas phage Xoo-sp2 with which it shares 64.8% DNA sequence identity.

**Electron micrograph:** None available

**To create a new subfamily *Bradleyvirinae*, composed of four genera *Epaquintavirus*, *Abidjanvirus*, *Bosavirus***  **and *Xooduovirus***

**Source of the name of this taxon:** This genus is named in honour of David Edward Bradley (b. 1930 Bournemouth England; d. 2018, Kingston, Canada). He received a PhD in Microbiology at the University of Edinburgh (1966) then took up a position in that University's Department of Zoology. In 1974, Dr. Bradley immigrated to Canada where he worked in the faculty of Medicine at Memorial University of Newfoundland, until retiring in 1995. He is best known in the for developing the morphology and nucleic acid typing system which evolved into the classification system we use today for bacteriophages; and for his studies of drug resistance and its conjugal transfer.

A person in a suit and tie

Description automatically generated with medium confidence

**(derived from:** [**http://www.authorsden.com/davidebradley**](http://www.authorsden.com/davidebradley)**)**

**History:** These two genera were proposed by the current Taxonomy Proposal and Proposals 2016.001aB, 2018.007B (*Abidjanvirus*). Genomic (VIRIDIC), Proteomic (ViPTree) and phylogenetic data all confirm that these genera are related.

**To move *Alphaproteobacteria virus PhiJL001* into its own genus, *Keylargovirus*.**

**Source of the name of this taxon:** The name is derived from the location at which the sponge harbouring this bacterium was isolated.

**History:** “The sponge ***Ircinia*** strobilina was collected at Tennessee Reef just off Key Largo during a research cruise of the Harbor Branch Oceanographic Institution on 24 August 1999. The phage was recovered from this material. It was originally classified as a member of the genus *Yuavirus*, but the new analyses reveal that it is significantly different from other members of this genus.

**Specific Reference:** Lohr JE, Chen F, Hill RT. Genomic analysis of bacteriophage PhiJL001: insights into its interaction with a sponge-associated alpha-proteobacterium. Appl Environ Microbiol. 2005;71(3):1598-1609. doi:10.1128/AEM.71.3.1598-1609.2005

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Alphaproteobacteria phage phiJl001 | [NC\_006938.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_006938.1) | [AY576273.1](https://www.ncbi.nlm.nih.gov/nuccore/AY576273.1) | 63.65 | 62.1 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/5658/891125%7CAlphaproteobacteria%20phage%20PhiJL001/viral%20segment%20Unknown/) | 0 |
|  |  |  |  |  |  |  |

**VIRIDIC homologs:** Its closest relative is Pseudomonas phage YuA with which is shares 10.3% DNA sequence identity.

**Electron micrograph:** None available

**To create a new family, *Mesyanzhinovviridae* for these taxa.**

**Source of the name of this taxon:** This family is named in honour of Professor Vadim V. Mesyanzhinov (b. 1940 Andreapol, Tver region, Russia; d. 2019 Moscow, Russia). PhD (1970), D.Sci (1980), Moscow State University. Chaired laboratories in the Belozersky Institute of Lomonosov Moscow State University (1980-1984), Ivanovsky Institute of Virology (1985-1994), Bach Institute of Biochemistry (1994-1997), and Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry (1997-2014). Known for establishing international relations between Russian and Western phage biologists (E. Kellenberger, L. Gold, M. Rossmann). His research was devoted to the mechanisms of protein folding and assembly, and structural genomics.

A person wearing a white shirt

Description automatically generated with medium confidence

**History:** Genomic (VIRIDIC), Proteomic (ViPTree) and phylogenetic data all confirm that these genera are related, and for this we have create a new family.

**References**

1: Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.

2: Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.

3: 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.

4: Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.

5: 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/](about:blank)

6: 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.

7: 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.

8: 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

9: 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.

10: 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.

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