

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

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| **Code assigned:** | **2021.023B** |  |
| **Short title:** Create two new genera in the family *Demerecviridae* (*Caudoviricetes*) | | |
|  | | |

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

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| Andrew Kropinski |

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

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| Caudoviricetes 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)** |
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**Submission dates**

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

|  |
| --- |
| 2021.023B.R.Demerecviridae\_new\_genera |

**Abstract**

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| --- |
| We were informed by our NCBI collaborator, Dr. Igor Tolstoy that the *Demerecviridae* lacked two groups of T5-like phages. We have therefore moved the *Priunavirus* from the *Siphoviridae* to the *Demerecviridae*. With the realization that the *Cetovirus* was not monophyletic we have created a new genus, *Thalassavirus* with the homologous isolates. |

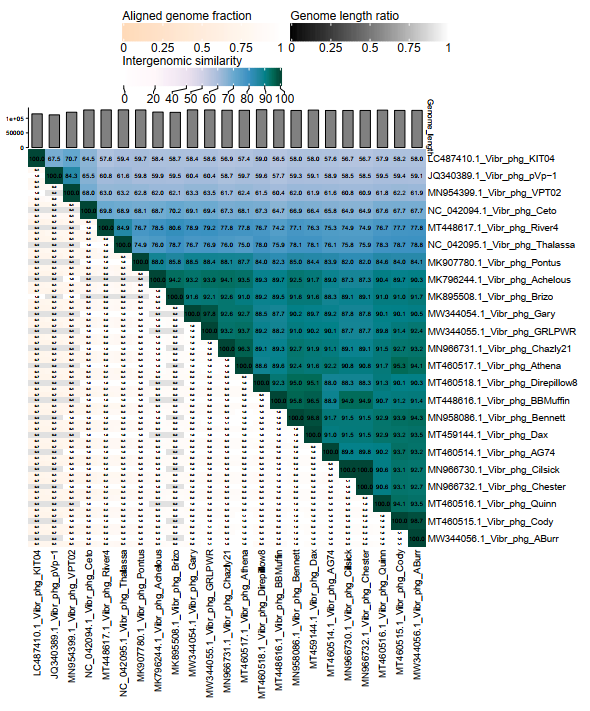
**Text of proposal**

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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 – 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).  (Taken from: Turner D et al. [9] ) | |

**Genera Supporting evidence**

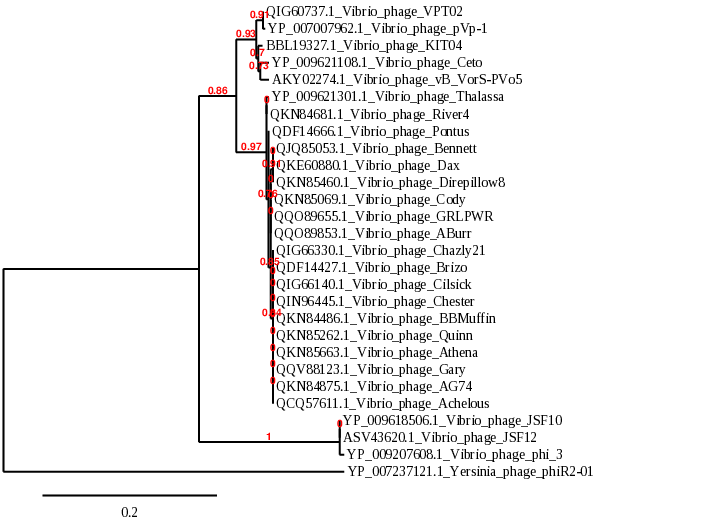
**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. **Not included.**

**VIRIDIC heat maps:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.

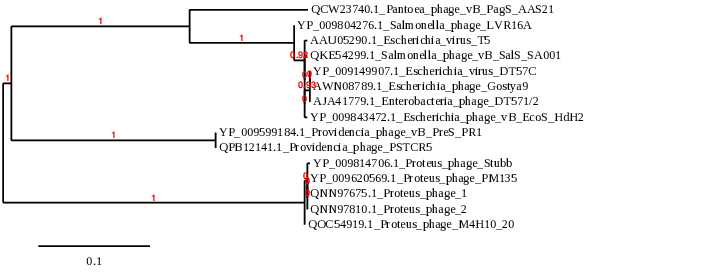
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**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of these phages with phylogeny.fr in “one click” mode [5]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By 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." ***A. Thalassavirus, B. Priunavirus***

**A. TerL *Thalassavirus* and relatives**



**B. TerL *Priunavirus* and its relatives**



**Proposals:**

1. **To create a new genus *Thalassavirus* with twelve (12) species**
2. **To move the genus *Priunavirus* from *Siphoviridae* to *Demerecviridae***

**Proposal 1: To create a new genus *Thalassavirus* with twelve (12) species**

**Preamble:** The genus *Cetovirus* was created by Taxonomy Proposal 2018.134B and moved to the family *Demerecviridae* through proposal 2019.099B. It contained two species corresponding to phage Ceto and Thalassa but a reanalysis reveals that these are sufficiently different (see VIRIDIC and phylogenetic analyses above) to warrant the creation of a new genus *Thalassavirus*.

**Source of the name of this taxon:** This taxon is named in directly after Vibrio phage Thalassa.

**History:** Vibrio phage Thalassa was isolated from a Chesapeake Bay oyster on Vibrio harveyi BAA-1116

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) |
| Vibrio phage Thalassa | [MG649967.1](https://www.ncbi.nlm.nih.gov/nuccore/MG649967.1) | 128.6 | 40.2 | [203](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68319/369466%7CVibrio%20phage%20Thalassa/viral%20segment/) | 23 | 100 |
| Vibrio phage River4 | [MT448617.1](https://www.ncbi.nlm.nih.gov/nuccore/MT448617.1) | 128.43 | 40.2 | [197](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92186/911086%7CVibrio%20phage%20River4/viral%20segment/) | 23 | 84.9 |
| Vibrio phage Pontus | [MK907780.1](https://www.ncbi.nlm.nih.gov/nuccore/MK907780.1) | 128.29 | 40.2 | [188](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82302/596073%7CVibrio%20phage%20Pontus/viral%20segment/) | 24 | 74.9 |
| Vibrio phage Achelous | [MK796244.1](https://www.ncbi.nlm.nih.gov/nuccore/MK796244.1) | 121.09 | 40.0 | [183](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79801/549706%7CVibrio%20phage%20Achelous/viral%20segment/) | 22 | 76.0 |
| Vibrio phage Brizo | [MK895508.1](https://www.ncbi.nlm.nih.gov/nuccore/MK895508.1) | 120.11 | 40.1 | [181](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82301/596072%7CVibrio%20phage%20Brizo/viral%20segment/) | 22 | 78.7 |
| Vibrio phage Gary | [MW344054.1](https://www.ncbi.nlm.nih.gov/nuccore/MW344054.1) | 128.6 | 40.2 | [199](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/98276/1553513%7CVibrio%20phage%20Gary/viral%20segment/) | 23 | 76.7 |
| Vibrio phage Athena | [MT460517.1](https://www.ncbi.nlm.nih.gov/nuccore/MT460517.1) | 127.02 | 40.1 | [192](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92172/911072%7CVibrio%20phage%20Athena/viral%20segment/) | 25 | 75.0 |
| Vibrio phage Bennett | [MN958086.1](https://www.ncbi.nlm.nih.gov/nuccore/MN958086.1) | 126.55 | 40.1 | [193](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/91534/898942%7CVibrio%20phage%20Bennett/viral%20segment/) | 23 | 78.1 |
| Vibrio phage AG74 | [MT460514.1](https://www.ncbi.nlm.nih.gov/nuccore/MT460514.1) | 126.5 | 40.2 | [191](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92171/911071%7CVibrio%20phage%20AG74/viral%20segment/) | 23 | 76.1 |
| Vibrio phage Chester | [MN966732.1](https://www.ncbi.nlm.nih.gov/nuccore/MN966732.1) | 126.55 | 40.2 | [191](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/88378/838839%7CVibrio%20phage%20Chester/viral%20segment/) | 24 | 75.9 |
| Vibrio phage Quinn | [MT460516.1](https://www.ncbi.nlm.nih.gov/nuccore/MT460516.1) | 127.68 | 40.1 | [197](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92175/911075%7CVibrio%20phage%20Quinn/viral%20segment/) | 22 | 78.3 |
| Vibrio phage Cody | [MT460515.1](https://www.ncbi.nlm.nih.gov/nuccore/MT460515.1) | 126.68 | 40.2 | [192](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92173/911073%7CVibrio%20phage%20Cody/viral%20segment/) | 24 | 78.7 |

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

**Proposal 2.To move the genus *Priunavirus* from *Siphoviridae* to *Demerecviridae***

**Source of the name of this taxon:** This taxon is named after Providencia virus PR1.

**History:** This phage became the type virus in Taxonomy Proposal 2018.128B. Obligatory lytic phage, vB\_PreS\_PR1 (PR1), was isolated from wastewater using Providencia rettgeri as the host bacterium. “Based on transmission electron microscopy (TEM)

analysis, PR1 has a 75-nm head with an icosahedral symmetry and a long noncontractile

tail (160 nm by 10 nm), indicating that it belongs to the family *Siphoviridae*.” [Oliveiro H et al. 2017]. Its genome possesses terminal repeats (10,461 bp). The presence of nicks in the 3'-to-5' strand are similar to those of phage T5. There are five minor and four major nick sites, which start from the same sequence (5’GCGC). The authors point out that this phage “Is a Deep-Branching Member of the T5virus Genus.” [Oliveiro H et al. 2017].

**Specific Reference:** Oliveira H, Pinto G, Hendrix H, Noben JP, Gawor J, Kropinski AM, Łobocka M, Lavigne R, Azeredo J. A Lytic Providencia rettgeri Virus of Potential Therapeutic

Value Is a Deep-Branching Member of the T5virus Genus. Appl Environ Microbiol.

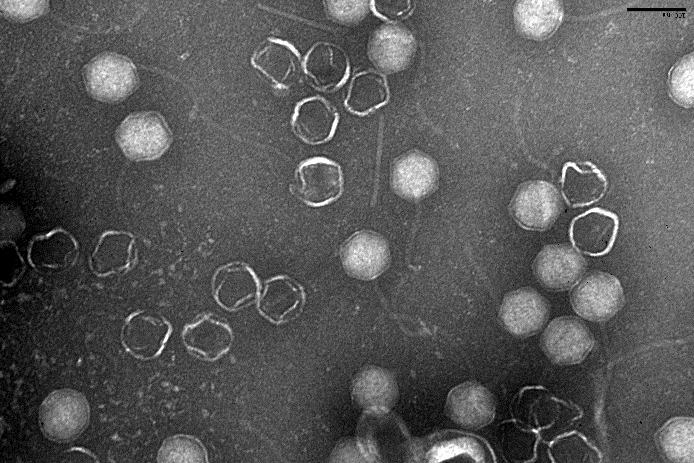
2017 Nov 16;83(23). pii: e01567-17.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) |
| Providencia phage vB\_PreS\_PR1 | [KY363465.1](https://www.ncbi.nlm.nih.gov/nuccore/KY363465.1) | 118.54 | 39.5 | [157](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63277/465900%7CProvidencia%20phage%20vB_PreS_PR1/viral%20segment/) | 22 | 100 |
| Providencia phage PSTCR5 | [MW057857.1](https://www.ncbi.nlm.nih.gov/nuccore/MW057857.1) | 109.43 | 40.0 | [152](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/96754/1493979%7CProvidencia%20phage%20PSTCR5/viral%20segment/) | 19 | 86.3 |
|  |  |  |  |  |  |  |

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

**Electron microscopy:** electron micrography of negatively stained phage PR1 (Kindly provided by Hugo Oliveira, Centre of Biological Engineering, University of Minho, Braga, Portugal).

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**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. <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>

4: 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.

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.

8: Zimmermann L, Stephens A, Nam SZ, et al. A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. J Mol Biol. 2018;430(15):2237-2243. doi:10.1016/j.jmb.2017.12.007

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

10. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol. 1990 Oct 5;215(3):403-10. doi: 10.1016/S0022-2836(05)80360-2. PMID: 2231712.