

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

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| **Code assigned:** | **2021.040B** |  |
| **Short title:** Create one new genus (*Jamesmcgillvirus*) including two species (*Caudoviricetes*) | | |
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**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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| Caudovirales 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**

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| **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**

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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**

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| 2021.040B.R.Jamesmcgillvirus |

**Abstract**

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| Pseudomonas phage/virus 119X has been an unclassified species in the family *Podoviridae* since 2009. This Taxonomy Proposal addresses this problem through creation of a new genus, *Jamesmcgillvirus*. |

**Text of proposal**

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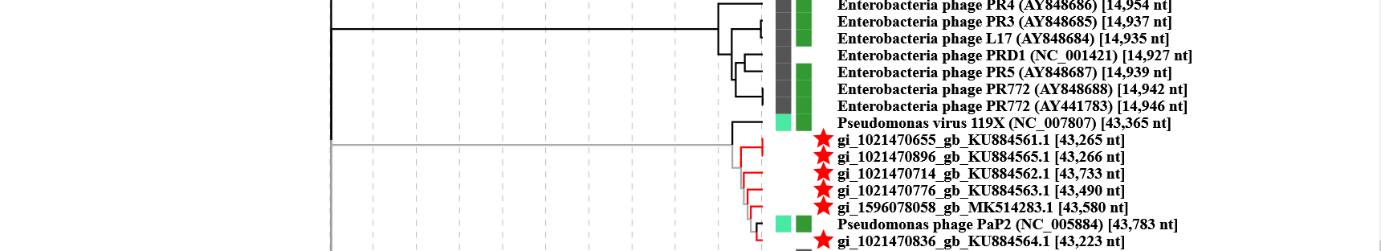
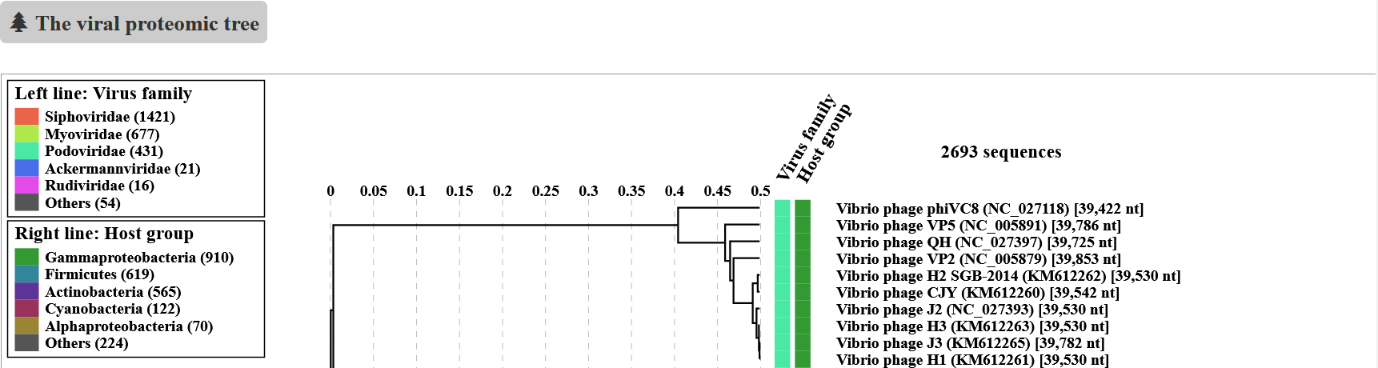
**Supporting evidence**

**Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm through VIRIDIC [3].

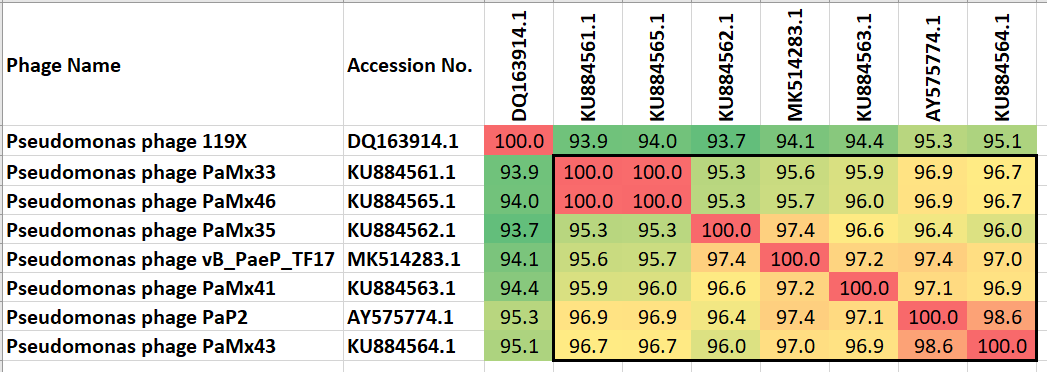
**Source of the name of this taxon:** This taxon is named in honour of James McGill (1744 – 1813), a Scottish merchant whose bequest in 1813 formed the McGill University's precursor, University of McGill College (or simply, McGill College); the name was officially changed to McGill University in 1885. (<https://en.wikipedia.org/wiki/McGill_University>). Phage 119X was sequenced at McGill University.

**History:** see 2008.015B. Phage 119X was isolated in Australia while the PaMx series of viruses were isolated from environmental and sewage water samples collected from four states in Central Mexico (Sepúlveda-Robles et al. 2012). Their sequence revealed long terminal direct repeats (Cruz-Plancarte et al, 2016).

**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 119X is marked with a **blue star**.



**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 assigned to the same species.

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**Phylogeny:** The phylogenetic tree was constructed using the RNA polymerases 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 picture containing graphical user interface

Description automatically generated**

**Specific Reference:** A. Sepúlveda-Robles O, Kameyama L, Guarneros G. High diversity and novel species of Pseudomonas aeruginosa bacteriophages. Appl Environ Microbiol. 2012 Jun;78(12):4510-5. doi: 10.1128/AEM.00065-12. Epub 2012 Apr 13. PMID: 22504803; PMCID: PMC3370533.

B. Cruz-Plancarte I, Cazares A, Guarneros G. Genomic and Transcriptional Mapping of PaMx41, Archetype of a New Lineage of Bacteriophages Infecting Pseudomonas aeruginosa. Appl Environ Microbiol. 2016 Oct 27;82(22):6541-6547. doi: 10.1128/AEM.01415-16. PMID: 27590812; PMCID: PMC5086548.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| 119X | NC\_007807.1 | DQ163914.1 | 43.36 | 44.9 | 53 | 100 | 100 |
| PaMx41 |  | [KU884563.1](https://www.ncbi.nlm.nih.gov/nuccore/KU884563.1) | 43.49 | 45.2 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79700/530743%7CPseudomonas%20phage%20PaMx41/viral%20segment/) | 94.4 | 96.4 |

**(\*) 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]**

**Strains:**

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| **Strains of *Jamesmcgillvirus PaMx41*** | **Accession No.** |
| Pseudomonas phage PaMx33 | KU884561.1 |
| Pseudomonas phage PaMx46 | KU884565.1 |
| Pseudomonas phage PaMx35 | KU884562.1 |
| Pseudomonas phage vB\_PaeP\_TF17 | MK514283.1 |
| Pseudomonas phage PaP2 | AY575774.1 |
| Pseudomonas phage PaMx43 | KU884564.1 |

**Electron micrograph:** NA

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of xxx and related 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."

See: 2008.015B

**General 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. [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank); and <https://www.biorxiv.org/content/10.1101/2020.07.05.188268v1>

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