

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

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| --- | --- | --- |
| **Code assigned:** | **2021.061B** |  |
| **Short title:** Create 13 new species in the genus *Pbunavirus* (*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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| 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**

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

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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**

|  |
| --- |
| 2021.061B.A.v1.Pbunavirus\_new\_species.xlsx |

**Abstract**

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| The genus *PB1likevirus* was created by Taxonomy Proposal 2009,001a-gB, and subsequently renamed *Pbunalikevirus* and *Pbunavirus*. It contains myoviruses infectious for Pseudomonas aeruginosa. We have added thirteen more species to the Pseudomonas myovirus genus *Pbunavirus,* based upon overall DNA sequence similarity. |

**Text of proposal**

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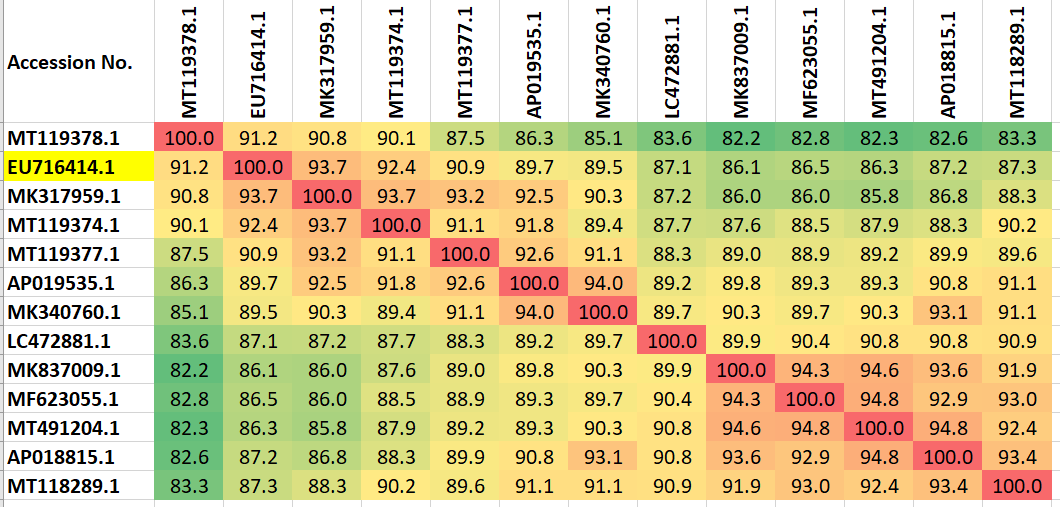
**Supporting evidence**

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

**History:** The genus *PB1likevirus* was created by Taxonomy Proposal 2009,001a-gB, and sequentially renamed *Pbunalikevirus* and *Pbunavirus*. It is one of the most rapidly growing Pseudomonas myovirus genera.

**ViPTree analysis:** NA

**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, see attachment. The heatmap for the new phages is shown below. Phage PBI is highlighted in yellow

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**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Pseudomonas phage PB1 | [NC\_011810.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_011810.1) | [EU716414.1](https://www.ncbi.nlm.nih.gov/nuccore/EU716414.1) | 65.76 | 54.9 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/6401/891405%7CPseudomonas%20phage%20PB1/viral%20segment%20Unknown/) | 100 | 100 |
| Pseudomonas phage datas | [NC\_050143.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050143.1) | MT119378.1 | 60.75 | 54.8 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89066/889181%7CPseudomonas%20phage%20datas/viral%20segment/) | 91.2 | 93.5 |
| Pseudomonas phage EPa61 | [NC\_048744.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048744.1) | [MK317959.1](https://www.ncbi.nlm.nih.gov/nuccore/MK317959.1) | 65.91 | 55.1 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75207/437908%7CPseudomonas%20phage%20EPa61/viral%20segment/) | 93.7 | 94.6 |
| Pseudomonas phage R12 | [NC\_048662.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048662.1) | [LC472881.1](https://www.ncbi.nlm.nih.gov/nuccore/LC472881.1) | 65.42 | 55.4 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/80045/559690%7CPseudomonas%20phage%20R12/viral%20segment/) | 87.2 | 87.1 |
| Pseudomonas phage Epa7 | [NC\_050146.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050146.1) | [MT118289.1](https://www.ncbi.nlm.nih.gov/nuccore/MT118289.1) | 65.63 | 55.5 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89038/889153%7CPseudomonas%20phage%20Epa7/viral%20segment/) | 87.3 | 93.5 |
| Pseudomonas phage PaGU11 | [NC\_050145.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050145.1) | [AP018815.1](https://www.ncbi.nlm.nih.gov/nuccore/AP018815.1) | 65.55 | 55.6 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/91810/902172%7CPseudomonas%20phage%20PaGU11/viral%20segment/) | 87.2 | 92.5 |
| Pseudomonas virus Pa193 | [NC\_050148.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050148.1) | [MK837009.1](https://www.ncbi.nlm.nih.gov/nuccore/MK837009.1) | 66.66 | 55.7 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85220/728535%7CPseudomonas%20virus%20Pa193/viral%20segment/) | 86.1 | 92.5 |
| Pseudomonas phage BrSP1 | [NC\_048675.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048675.1) | [MF623055.1](https://www.ncbi.nlm.nih.gov/nuccore/MF623055.1) | 66.19 | 55.7 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72367/405469%7CPseudomonas%20phage%20BrSP1/viral%20segment/) | 86.5 | 92.5 |
| Pseudomonas phage vB\_PaeM\_USP\_1 | [NC\_050149.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050149.1) | [MT491204.1](https://www.ncbi.nlm.nih.gov/nuccore/MT491204.1) | 65.92 | 55.6 | [87](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/93329/927374%7CPseudomonas%20phage%20vB_PaeM_USP_1/viral%20segment/) | 86.3 | 89.2 |
| Pseudomonas phage antinowhere | [NC\_050150.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050150.1) | [MT119374.1](https://www.ncbi.nlm.nih.gov/nuccore/MT119374.1) | 65.85 | 55.2 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89060/889175%7CPseudomonas%20phage%20antinowhere/viral%20segment/) | 92.4 | 95.7 |
| Pseudomonas phage crassa | [NC\_050151.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050151.1) | [MT119377.1](https://www.ncbi.nlm.nih.gov/nuccore/MT119377.1) | 66.3 | 55.2 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89065/889180%7CPseudomonas%20phage%20crassa/viral%20segment/) | 90.9 | 93.5 |
| Pseudomonas phage PA01 | [NC\_048626.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048626.1) | [AP019535.1](https://www.ncbi.nlm.nih.gov/nuccore/AP019535.1) | 66.22 | 55.4 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79992/559637%7CPseudomonas%20phage%20PA01/viral%20segment/) | 89.7 | 93.5 |
| Pseudomonas phage vB\_PaeM\_SCUT-S1 | [NC\_048745.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048745.1) | [MK340760.1](https://www.ncbi.nlm.nih.gov/nuccore/MK340760.1) | 66.09 | 55.4 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75770/445147%7CPseudomonas%20phage%20vB_PaeM_SCUT-S1/viral%20segment/) | 89.5 | 95.7 |
| Pseudomonas phage Epa14 | [NC\_050144.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_050144.1) | [MT118293.1](https://www.ncbi.nlm.nih.gov/nuccore/MT118293.1) | 65.8 | 55.3 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/89024/889139%7CPseudomonas%20phage%20Epa14/viral%20segment/) | 93.1 | 93.5 |

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

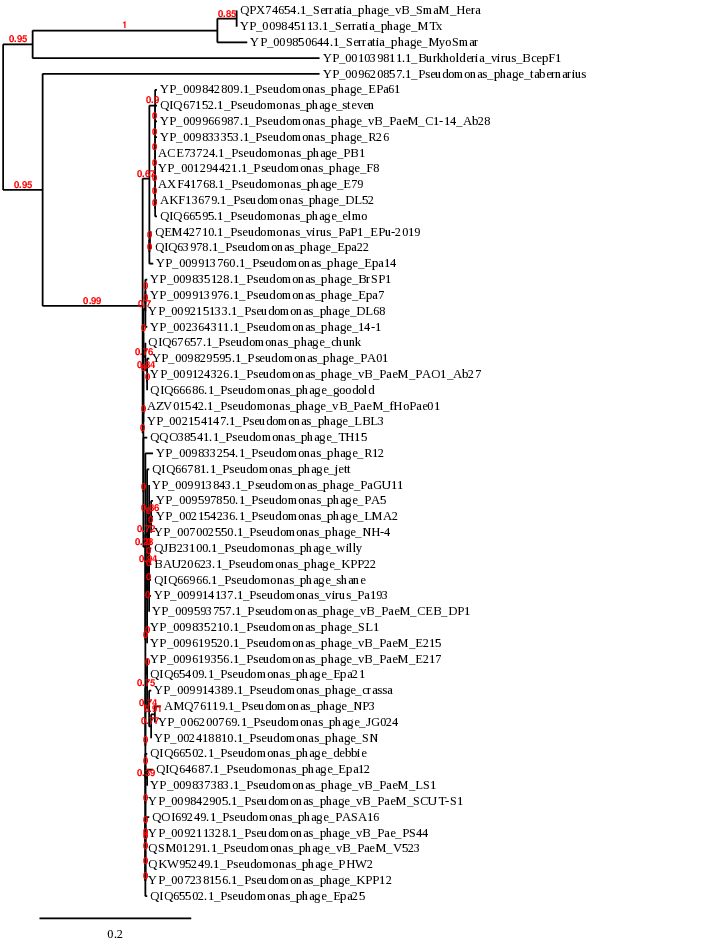
**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**Strains:**

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| --- | --- | --- |
| **Phage name** | **Accession No.** | **Strains of:** |
| Pseudomonas phage DRL-P1 | MN564818.1 | *Pbunavirus PB1* |
| Pseudomonas phage Epa13 | MT118292.1 | *Pbunavirus Pa193* |
| Pseudomonas phage PASA16 | MT933737.1 | *Pbunavirus Pa193* |
| Pseudomonas phage vB\_PaeM\_USP\_2 | MT491205.1 | *Pbunavirus Pa193* |
| Pseudomonas phage chumba | MT119375.1 | *Pbunavirus EPa61* |

**Electron micrograph:** None available

**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:**

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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.

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.

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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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