

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

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| **Code assigned:** | ***2022.066B*** |  |
| **Short title:** Create five new genera of Pseudomonas jumbo phages (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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**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)** | Y |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| Serwervirus | Philip Serwer | Y |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | April 2022 |
| Date of this revision (if different to above) | November 2022 |

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

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| ICTV-EC: Change one genus name that already existed. |

**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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| --- |
| 2022.066B.A.v2.Caudoviricetes\_6ng.xlsx |

**Abstract**

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| Until recently NCBI classifies the phages described in this proposal to the *Phikzvirus* genus. Our molecular (VIRIDIC, VIPTREE) and phylogenetic analyses all agree that these phages are sufficiently different from PhiKZ and each other to warrant the creation of five new genera. |

**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 [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. The black box delineates strains. The grey-highlighted names indicate partial 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 areindicated with a **blue rectangle**.





**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins from these phages and related phages with phylogeny.fr in “one click” mode [6]. 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." The members of the *Phikzvirus* and *Noxifervirus* are indicated with **blue rectangles**.

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**Proposals:**

1. **Create a new genus, *Tepukevirus* with a single species**
2. **Create a new genus, *Phabiovirus* with a single species**
3. **Create a new genus, *Serwervirus* with a single species**
4. **Create a new genus, *Miltoncavirus* with a single species**
5. **Create a new genus, *Pawinskivirus* with a single species**
6. **Create a new genus, *Tepukevirus* with a single species**

**Origin of the name of this taxon:** This taxon is named after Te Puke /tɛˈpʊkɛ/ (pronunciation: "teh-pook-ee") a town located 28 kilometres southeast of Tauranga in the Western Bay of Plenty of New Zealand (Wikipedia), where the first phage of its type was located.

**Historical aspects:** This lytic phage was isolated against Pseudomonas syringae actinidae from leaf litter.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage Psa21 | [MK552327.1](https://www.ncbi.nlm.nih.gov/nuccore/MK552327.1) | 305.26 | 43.1 | [420](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76426/468481|Pseudomonas phage Psa21/viral segment/) | 8 | 100 | 100 |

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

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

1. **Create a new genus, *Phabiovirus* with a single species**

**Origin of the name of this taxon:** The name of this taxon is directly derived from the name of this phage Phabio

**Historical aspects:** This lytic phage was isolated against Pseudomonas fluorescens SBW25 from New Zealand compost.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage Phabio | [MF042360.1](https://www.ncbi.nlm.nih.gov/nuccore/MF042360.1) | 309.16 | 43.0 | [468](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63633/466254|Pseudomonas phage Phabio/viral segment/) | 3 | 100 | 100 |

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

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

1. **Create a new genus, *Serwervirus* with a single species**

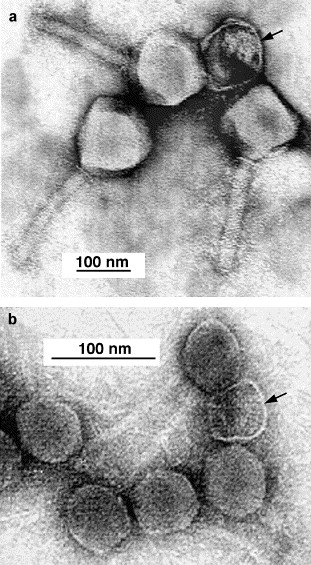
**Origin of the name of this taxon:** This taxon is named in honour of Philip Serwer (b. 1942). Doctor of Philosophy in Biophysics, Harvard University, 1973. He has been a faculty member at University Texas Health Science Center, San Antonio, since 1976. Full professor of biochemistry and structural biology since 1985. A polymath, he has: (a) studied the dynamics of the DNA packaging of bacterial viruses; (b) developed improved procedures for isolating environmental phages, with direct application to the phage therapy of infectious disease; (c) isolated and characterized capsids that have the characteristics needed for bypassing all limitations of current drug delivery vehicles; (d) investigated translational concepts that lead to a proposed cause and therapy for neurodegenerative diseases and (e) researched translational concepts that suggest an improved strategy for generating anti-viral compounds with broad application. (<https://directory.uthscsa.edu/academics/profile/serwer>). He was involved in the isolation and characterization of phage 201Φ2-1.



(copied from: https://directory.uthscsa.edu/academics/profile/serwer)

**Historical aspects:** This lytic phage was isolated against Pseudomonas chlororaphis in the USA. The outer shell is 63 nm in radius [10,11]. The authors note that it contains 69 protein homologs to phiKZ. At this time we have not chosen to create a higher taxon with the latter virus.

**Electron micrograph:** (modified from reference 11)

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**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage 201phi2-1 | [EU197055.1](https://www.ncbi.nlm.nih.gov/nuccore/EU197055.1) | 316.67 | 45.3 | [461](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/6221/456681|Pseudomonas phage 201phi2-1/viral segment Unknown/) | 1 | 100 | 100 |

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

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

1. **Create a new genus, *Miltoncavirus* with a single species**

**Origin of the name of this taxon:** This taxon is named after the location (Milton, Cambridge, UK) where the first phage of its type was discovered.

**Historical aspects:** This lytic generalized transducing phage was isolated against Pseudomonas aeruginosa from treated sewage effluent (Milton, Cambridge, UK). ΦPA3 has an icosahedral head 100 nm in diameter, a 185 nm tail, a 45 nm baseplate and tail fibres 80 nm in length.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage PhiPA3 | [HQ630627.1](https://www.ncbi.nlm.nih.gov/nuccore/HQ630627.1) | 309.21 | 47.7 | [375](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42374/461957|Pseudomonas phage PhiPA3/viral segment Unknown/) | 5 | 100 | 100 |

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

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

1. **Create a new genus, *Pawinskivirus* with a single species**

**Origin of the name of this taxon:** This taxon is named after the street address (Pawinskiego 5A) in Warsaw of the Department of Microbial Biochemistry, Institute of Biochemistry and Biophysics of the Polish Academy of Sciences where Pseudomonas phage vB\_PaeM\_PS119XW was sequenced.

**Historical aspects:** This lytic phage was assumed to be 119X until it was and it was realized that it was distinct. The genome of P. aeruginosa strain PAER4\_119 used for its propagation was deposited in GenBank under the accession number CP013113.1.

**Electron micrograph:**

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(negatively stained Pseudomonas phage vB\_PaeM\_PS119XW; electron micrograph from Monika Hejnowicz, IBB, Polish Academy of Sciences, Warsaw)

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage vB\_PaeM\_PS119XW | [MN103543.1](https://www.ncbi.nlm.nih.gov/nuccore/MN103543.1) | 301.54 | 43.6 | [389](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84253/679222|Pseudomonas phage vB_PaeM_PS119XW/viral segment/) | 7 | 100 | 100 |

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

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

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