

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

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| **Code assigned:** | **2021.036B** |  |
| **Short title:** Create one new genus (*Harrisonburgvirus*) including one new species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew M. Kropinski |

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

**Name of accompanying Excel module**

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| 2021.036B.R.Harrisonburgvirus |

**Abstract**

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| NCBI has identified several orphan phages which belong to the Class *Caudoviricetes*. Our multidimensional analyses place Pseudomonas phage Persinger in a new genus, *Harrisonburgvirus*. |

**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. [4] | |

**Supporting evidence**

**Source of the name of this taxon:** This genus is named after the city in Virginia, where at James Madison University first representative of this taxon, Pseudomonas phage Persinger was isolated.

**History:** Temperate phage Persinger was isolated from compost against Pseudomonas aeruginosa UVA4 by Rachel Persinger in 2019. It possesses 5' 13bp overhang – GGGGCAGACACTC - cohesive termini.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Pseudomonas phage Persinger |  | [MT613935.1](https://www.ncbi.nlm.nih.gov/nuccore/MT613935.1) | 44.03 | 62.9 | [63](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/93714/965897%7CPseudomonas%20phage%20Persinger/viral%20segment/) | 1 | 100 | 100 |
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**(\*) Determined using BLASTN [1-3]**

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

**BLASTN homologs:** Genomic orphan [1-3]. The closest relative is Pseudomonas phage PPpW-3 with which it shares 52.6% DNA similarity. While this is sufficiently similar to propose a subfamily we don’t choose to do so at this time.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of Persinger and related phages with phylogeny.fr in “one click” mode [8]. "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 [9] for details."

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**References**

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