

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

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| **Code assigned:** | ***2022.036B*** |  |
| **Short title:** Create a new genus (*Hiroshimavirus*) with a single species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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|  |  |
| Turner D, Moraru C, Kropinski AM | Dann2.Turner@uwe.ac.uk; liliana.cristina.moraru@uol.de; Phage.Canada@gmail.com |

**Author(s) institutional address(es) (optional)**

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| --- |
| University of the West of England, Bristol, UK [DT]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  University of Guelph, Canada [AMK] |

**Corresponding author**

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| Andrew M. Kropinski |

**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**

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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 | February 2022 |
| Date of this revision (if different to above) |  |

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

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**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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| 2022.036B.A.v2.Hiroshimavirus\_ng.xlsx |

**Abstract**

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| The genus *Hiroshimavirus* was created for the genomic singleton phage Pseudomonas phage PPpW-3. |

**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**

**Origin of the name of this taxon:** This taxon is named after the city in Japan where Pseudomonas phage PPpW-3 was isolated at Toshihiro Nakai Hiroshima University, Graduate School of Biosphere Science

**Historical aspects:** This potentially temperate phage was isolated in 2015 against Pseudomonas plecoglossicida [11]. PPpW-3 phages were observed to have an isometric capsid of 59.4 nm with a long rigid tail of 114.3 × 20.4 nm.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage PPpW-3 | [NC\_023006.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023006.1) | [AB775548.1](https://www.ncbi.nlm.nih.gov/nuccore/AB775548.1) | 43.56 | 61.1 | [66](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/23327/460360|Pseudomonas phage PPpW-3/viral segment Unknown/) | 100 | 100 |

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

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

**N.B. Its closest relative is Pseudomonas phage Persinger with which it shares 53.4% DNA sequence similarity. While this is sufficient to create a subfamily we choose not to do so at this time.**

**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.

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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 are indicated with **red stars**. N/A

**Phylogeny:** The phylogenetic tree was constructed using the MCP proteins from PPpW-3 and related phages with phylogeny.fr in “one click” mode [6]. "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 [7] for details." The members of the *Hiroshimavirus* are indicated with a **blue rectangle**.

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**References**

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