

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

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| **Code assigned:** | ***2023.052B*** |  |
| **Short title:** To create a new genus, *Porunavirus*, with one new species [*Caudoviricetes*] | | |
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**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Turner D, Moraru C, Tolstoy I, Kropinski AM | [Dann2.Turner@uwe.ac.uk](mailto:Dann2.Turner@uwe.ac.uk); [liliana.cristina.moraru@uol.de](mailto:liliana.cristina.moraru@uol.de); [tolstoy@ncbi.nlm.nih.gov](mailto:tolstoy@ncbi.nlm.nih.gov); [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com) |

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

|  |
| --- |
| University of the West of England, Bristol, UK [DT]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  National Center for Biotechnology Information, MD, USA [IT]  University of Guelph, Ontario, 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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| *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** |
|  |  |  |  |
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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)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 2023 |
| 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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| 2023.052B.N.v1.Porunavirus\_ng.xlsx |

**Abstract**

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| Pseudomonas phage POR1 is unique in several respects. Its genome and protein sequences are very deeply rooted, and this virus could be considered the first species in a new family. It is also the first phage isolated against P. oryzihabitans. |

**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 [1,2] – 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 [10]. | |

**Supporting evidence**

**Proposal:**

1. **Create a new single species genus, *Porunavirus***

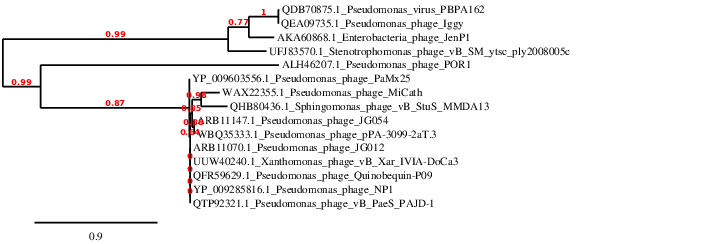
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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; Sten = Stenotrophomonas; Pseu = Pseudomonas; Sphi = Sphingomonas; Xant = Xanthomonas; Serr = Serratia; Burk = Burkholderia

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**Figure 2. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages of interest are indicated with **red lines and stars**.

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**Figure 3. Phylogeny:** The phylogenetic tree was constructed using the large subunit terminase proteins from these 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.”

**Taxonomic Proposals:**

1. **Create a new single species genus, *Porunavirus***

**Origin of the name of this taxon:** The name of this taxon is directed derived from the name of the member, Pseudomonas phage POR1.

**Historical aspects:** This lytic phage was isolated from activated sludge wastewater against Pseudomonas oryzihabitans J81P [Dyson et al. 2016]. This publication describes POR1 as a siphovirus, but it possesses a 452 aa protein (ALH46218.1) which is a tail sheath protein, as shown by HHpred analysis. This is a feature which POR1 only shares with Pseudomonas phage MiCath [OP88227].

**Electron micrograph:** N/A.

**Genome summary: (genomic orphan)**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage POR1 | [KT716399.1](https://www.ncbi.nlm.nih.gov/nuccore/KT716399.1) | 55.35 | 55.5 | [81](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62810/465435|Pseudomonas phage POR1/viral segment/) | 100 | 100 |

**Conclusion:** A genus comprising a single species is proposed on the basis of DNA (Fig. 1) and protein (Fig. 2) similarity; and phylogenetic analysis of the TerL proteins (Fig. 3).

**Reference:** Dyson ZA, Seviour RJ, Tucci J, Petrovski S. Genome Sequences of Pseudomonas oryzihabitans Phage POR1 and Pseudomonas aeruginosa Phage PAE1. Genome Announc. 2016 Jun 16;4(3):e01515-15. doi: 10.1128/genomeA.01515-15. PMID: 27313312; PMCID: PMC4911491.

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