

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

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| --- | --- | --- |
| **Code assigned:** | ***2023.050B*** |  |
| **Short title:** Create a new phage species in the genus *Pakpunavirus* |
|  |

**Author(s) and email address(es)**

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

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**Corresponding author**

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| Michael Angelou L. Nada |

**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)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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

|  |
| --- |
| 2023.050B.N.v1.Pakpunavirus\_1ns.xlsx |

**Abstract**

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| Building on the species demarcation criteria of 95%, we proposed a creation of a new phage species within the genus *Pakpunavirus*. The Pseudomonas phage isolate vB\_VIPPAEUMC01 shared 93.5% genomic similarity to the existing phage species, *Pakpunavirus CAb02*, (Pseudomonas phage vB\_PaeM\_C2-10\_Ab02; Accession no LN610572.1) indicating that it is new phage species belonging to genus *Pakpunavirus*.  |

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| **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 using VIRIDIC [1, 2].**Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the ICTV 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 [1, 2]. |

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**Supporting evidence**

**Origin of the name of this taxon:**

Create new phage species in the genus *Pakpunavirus*. The proposed binomial name of *Pakpunavirus vippaeumc* was after the phage name, Pseudomonas phage vB\_VIPPAEUMC01.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Phage name** | **NCBI accession no** | **Genome length (bp)** | **GC content** | **CDS** | **tRNA** |
| Pseudomonas phage vB\_VIPPAEUMC01 | OQ721915 | 92158 | 49.35 | 173 | 14 |

**VIRIDIC heat map:** Taxonomic classification of Pseudomonas phage vB\_VIPPAEUMC01 was first identified via blastn search in NCBI database and by using MASH distances in pharokka [3] utilizing the INPHARED database [4]. After which, all *Pakpunavirus* phage species were downloaded from NCBI database and intergenomic similarities were calculated using VIRIDIC (Virus Intergenomic Distance Calculator).

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**Table 2. Closest relative identified by Pharokka using the INPHARED database.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Phage name** | **Mash distance** | **Mash matching****hashes** | **Closest relative and accession number** |
| Pseudomonas phage vB\_VIPPAEUMC01 | 0.0209501 | 475/1000 | Pseudomonas phage YS35 (MF974178) |

**References**

1. Turner D., Kropinski AM, Adriaenssens EM (2021) A roadmap for genome-based phage taxonomy *Viruses*, *13*(3), 506. https://doi.org/10.3390/v13030506

2. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC — A Novel Tool to Calculate the Intergenomic Similarities of prokaryote-infecting viruses. Viruses 12(11):1268. https://doi.org/10.3390/v12111268

3. Bouras G, Nepal R, Houtak G, Psaltis AJ, Wormald PJ, Vreugde S (2023) Pharokka: a fast scalable bacteriophage annotation tool. Bioinformatics 39(1):btac776. https://doi.org/10.1093/bioinformatics/btac776

4. Cook R, Brown N, Redgwell T, Rihtman B, Barnes M, Clokie M, Stekel DJ, Hobman J, Jones MA, Millard A (2021) INfrastructure for a PHAge REference Database: Identification of Large-Scale Biases in the Current Collection of Cultured Phage Genomes. Phage, 2(4), 214-223. https://doi.org/10.1089/phage.2021.0007