

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

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| **Code assigned:** | ***2023.066B*** |  |
| **Short title:** Create new phage species in the genus *Tequatrovirus* | | |
|  | | |

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

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| --- | --- |
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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, Tevenviruses 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**

|  |
| --- |
| 2023.066B.N.v1.Tequatrovirus\_1ns.xlsx |

**Abstract**

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| Building on the species demarcation criteria of 95%, we proposed a creation of a new phage species from genus *Tequatrovirus*. The three isolates namely Escherichia phage vB\_VIPECOOM01, Escherichia phage vB\_VIPECOOM02, and Escherichia phage vB\_VIPECOOM03, are the same species with genomic similarity of 100%. Genome comparison showed that the three Escherichia phages are only 94.1% similar to the existing phage genome *Tequatrovirus ecnp1 (*Accession no. MK886800.1) suggesting that the isolates are new phage species from the genus *Tequatrovirus*. |

**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 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]. | |

**Supporting evidence**

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

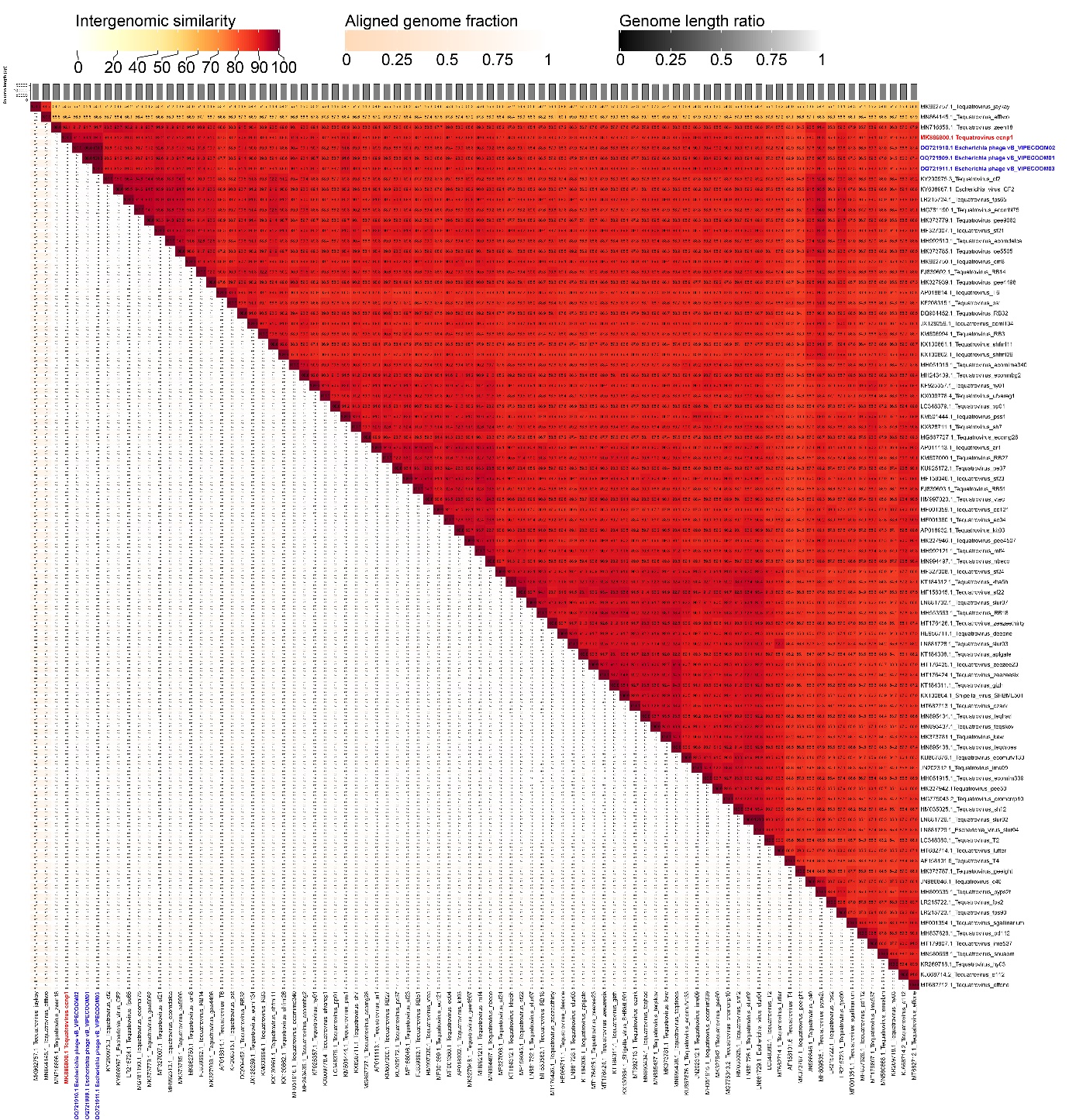
Create new phage species in the genus *Tequatrovirus*. The proposed binomial name of *Tequatrovirus vipecoom* was after the name of the three Escherichia phage isolates vB\_VIPECOOM01, vB\_VIPECOOM02, and vB\_VIPECOOM03.

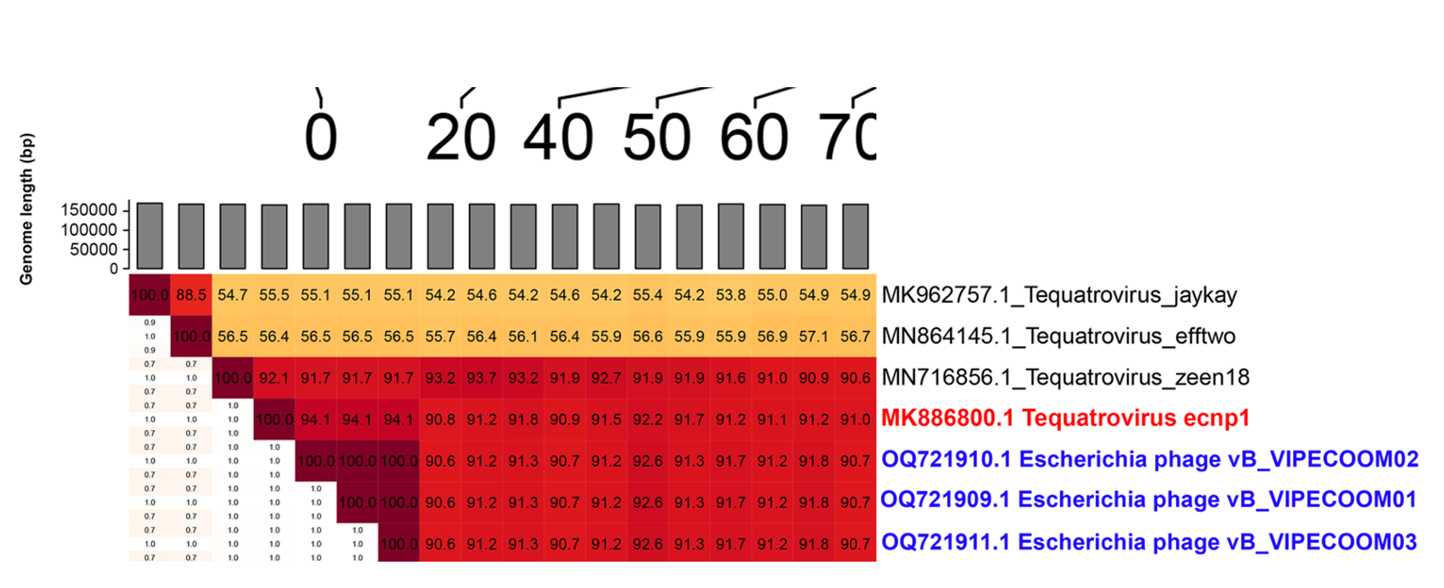
**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Phage name** | **NCBI accession no** | **Genome length**  **(bp)** | **GC content** | **CDS** | **tRNA** |
| Escherichia phage vB\_VIPECOOM03 | OQ721911 | 168,519 | 35.49 | 269 | 10 |

**VIRIDIC heat map:** Taxonomic classification of phage genomes 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 *Tequatrovirus* phage species were downloaded from NCBI database and intergenomic similarities were calculated using VIRIDIC (Virus Intergenomic Distance Calculator). A zoom-in image of the three isolates (blue font), the closest relative (red font), and the percent similarity values (94.1%) were shown below suggesting that the isolates are new species.



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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** |
| Escherichia phage vB\_VIPECOOM03 | 0.0220623 | 459/1000 | Escherichia phage EcNP1 (NC\_054910) |

**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