

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

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| **Code assigned:** | ***2023.067B*** |  |
| **Short title:** To create 35 new species in the genus *Tequintavirus* [*Caudoviricetes*; Family *Demerecviridae*] | | |
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**Author(s) and email address(es)**

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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** |
|  |  |  |  |
|  |  |  |  |

**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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| 2023.067B.A.v1.Tequintavirus\_35ns.xlsx |

**Abstract**

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| We have added thirty-five new species of to the genus *Tequintavirus,* resulting in the genus containing 70 species. |

**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**

**Proposals:**

1. **To add thirty-five (35) new species to the genus, *Tequintavirus***

**Data:**

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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. Yellow, existing species; green, exemplar viruses of new species. Abbreviations: phg = phage; vir = virus; Esch = Escherichia; Shig = Shigella; Ente = Enterobacteria; Salm = Salmonella. The Excel spreadsheet for this figure it attached to this proposal – 2023.067B.A.v1.Tequintavirus\_35ns\_Suppl.xlsx

1. **To add thirty-five (35) new species to the genus, *Tequintavirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** The genus *Tequintavirus virus* was created through Taxonomy Proposal 2019.099B. It currently consists of 35 species and we are now adding a further 35 new species.

**Genome summary: .**

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| **Accession No.** | **Phage name** | **% DNA sequence similarity(\*)** |
| **NC\_005859.1** | **Enterobacteria phage T5** | **100.0** |
| MZ501103.1 | Escherichia phage SelmaRatti | 70.5 |
| OQ680478.1 | Salmonella phage phA11 | 72.7 |
| MN445182.1 | Salmonella phage vB\_SalS\_SA001 | 69.8 |
| OK272477.1 | Escherichia phage JLBYU43 | 72.4 |
| MZ501075.1 | Escherichia phage IrisVonRoten | 79.3 |
| LR597655.1 | Escherichia phage T5\_ev219 | 79.5 |
| MZ501058.1 | Escherichia phage DaisyDussoix | 74.9 |
| OQ383622.1 | Salmonella phage MET\_P1\_179\_112 | 74.6 |
| MT080103.1 | Escherichia phage ECOP18 | 75.9 |
| OQ031075.1 | Klebsiella phage KPP2018 | 75.6 |
| MW149275.1 | Salmonella phage vB\_SalS\_ABTNLsp9 | 74.3 |
| OP394141.1 | Salmonella phage GSP044 | 73.8 |
| MT311645.1 | Salmonella phage vB\_Sen-E22 | 74.9 |
| OK108607.1 | Salmonella phage vB\_SenS\_S124 | 74.4 |
| MW149273.1 | Salmonella phage vB\_SalS\_ABTNLsp4 | 75.1 |
| OK254197.1 | Escherichia phage PNJ1902 | 76.3 |
| OK665835.1 | Escherichia phage EC100 | 80.8 |
| ON185585.1 | Escherichia phage EC148 | 76.1 |
| OK272480.1 | Escherichia phage JLBYU40 | 77.0 |
| MZ398246.1 | Escherichia phage IME178 | 72.7 |
| OK143207.1 | Escherichia phage Lindwurm | 75.1 |
| OQ680479.1 | Salmonella phage phB7 | 74.5 |
| OQ680481.1 | Salmonella phage phC17 | 73.9 |
| OM386660.1 | Escherichia phage vB\_EcoS\_ESCO40 | 76.1 |
| MZ501074.1 | Escherichia phage HildyBeyeler | 74.6 |
| MK373792.1 | Escherichia phage vB\_EcoS\_VAH1 | 78.2 |
| OM386657.1 | Escherichia phage vB\_EcoS\_ESCO30 | 77.7 |
| MT233524.1 | Salmonella phage vB\_Sen\_I1 | 79.5 |
| MW006479.1 | Salmonella phage GEC\_vB\_N5 | 82.7 |
| MT653143.1 | Salmonella phage 3sent1 | 81.6 |
| MT653146.1 | Salmonella phage 8sent1748 | 78.1 |
| MT577844.1 | Salmonella phage vB\_StyS-LmqsSP1 | 78.6 |
| OQ383620.1 | Salmonella phage MET\_P1\_100\_107 | 79.5 |
| MK373797.1 | Escherichia phage vB\_EcoS\_HASG4 | 79.6 |
| MT843274.1 | Escherichia phage BB1 | 77.1 |

**(\*) determined using VIRIDIC [3]**

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