

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

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| **Code assigned:** | **2021.076B** |  |
| **Short title:** Create seven new genera (*Efbeekayvirus*, *Penintadodekavirus*, *Vicoquintavirus*, *Trioduovirus*, *Exceevirus*, *Electravirus*, *Glaucusvirus*) including nine new species (*Schitoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Schitoviridae Study Group, Bacterial and Archaeal Viruses Subcommittee |

**ICTV study group comments and response of proposer**

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**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 | May 2017 |
| Date of this revision (if different to above) |  |

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

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.076B.A.v1.Schitoviridae\_new\_genera.xlsx |

**Abstract**

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| Here, we propose the creation of the new genus “Efbeekayvirus” comprising two new species, the new genus “Penintadodekavirus” comprising one new species, the new genus “*Vicoquintavirus”* comprising one new species, the new genus “Trioduovirus” comprising one new species, the new genus “Exceevirus” comprising one new species, the new genus “Electravirus” comprising one new species and the new genus “Glaucusvirus” comprising two new species based on genome-based comparisons. |

**Text of proposal**

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| |  | | --- | | **Source of the name of the taxa and history of their members:**  *Efbeekayvirus*: The name is derived from the name of the first isolated phage of this type, Klebsiella phage vB\_KpP\_FBKp27. Klebsiella phage vB\_KpnP\_P184 was isolated in China, both species infect *Klebsiella pneumoniae*. The genome of vB\_KpP\_FBKp27 consists of 76,339 bp with 93 CDS and 6 tRNA genes while the genome of vB\_KpnP\_P184 consists of 76,617 bp with 101 CDS and 5 tRNA genes.  *Penintadodekavirus*: The name is derived from the name of the first isolated phage of this type, Vibrio phage phi50-12. It was isolated in Taiwan and infects *Vibrio owensii*. Its genome consists of 68,059 bp with 101 CDS.  *Vicoquintavirus*: The name is derived from the name of the first isolated phage of this type, Vibrio phage pVco-5. It was isolated from an oyster hatchery tank in South Korea and infects *Vibrio corallilyticus*. Its genome consists of 74,325 bp with 126 CDS.  *Trioduovirus*: The name is derived from the name of the first isolated phage of this type, Salmonella phage vB\_SalP\_TR2. It was isolated in China and infects *Salmonella enterica* subsp. *enterica* serovar Albany. Its genome consists of 70,823 bp with 95 CDS and 6 tRNA genes.  *Exceevirus*: The name is derived from the name of the first isolated phage of this type, Acinetobacter phage VB\_ApiP\_XC38. It was isolated from sewage in China and infects *Acinetobacter pittii*. Its genome consists of 79,328 bp with 97 CDS and 1 tRNA gene.  *Electravirus*: The name is derived from the name of the Greek water-nymph Electra. Vibrio virus vB\_VspP\_SBP1 was isolated in China. Its genome consists of 78,071 bp with 112 CDs and 4 tRNA genes.  *Glaucusvirus*: The name is derived from the name of the Greek fisherman´s sea god Glaucus. Vibrio phage 1.245.O.\_10N.261.54.C7 and Vibrio phage 1.238.A.\_10N.261.52.F10 were isolated from seawater in the USA and infect *Vibrio breoganii*. Their genomes consist of 71,702 bp with 94 CDS and 70,494 bp with 93 CDS, respectively. | |

**Supporting evidence**

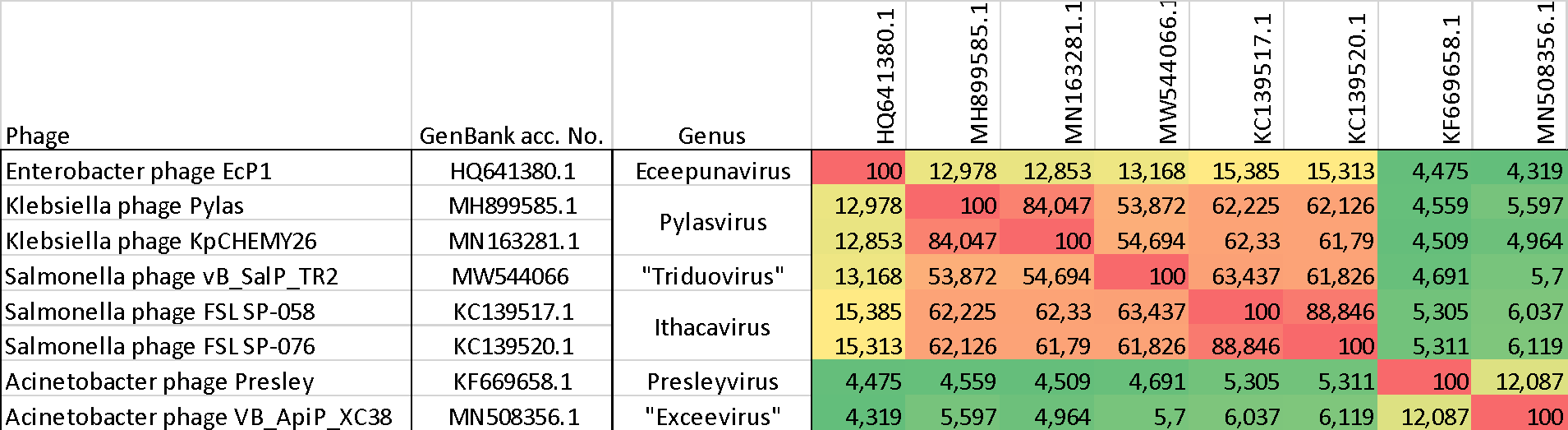
**Electron micrograph:** None available

**Species demarcation criteria** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with VIRIDIC [1, 2].

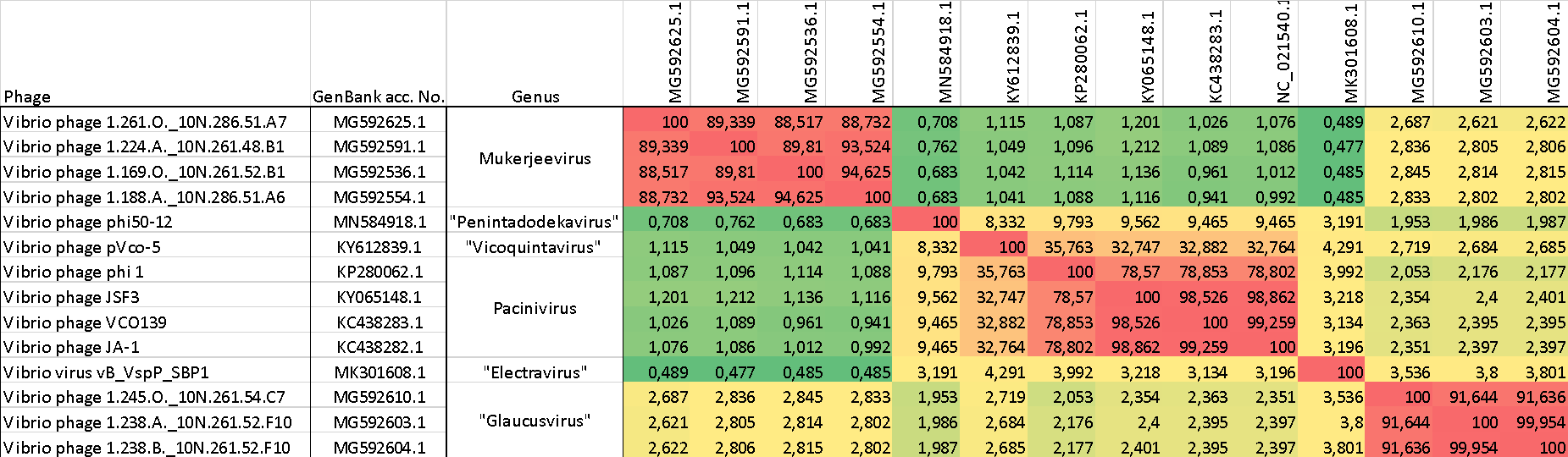
**Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [6]

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>) computes pairwise intergenomic distances/similarities amongst phage genomes.

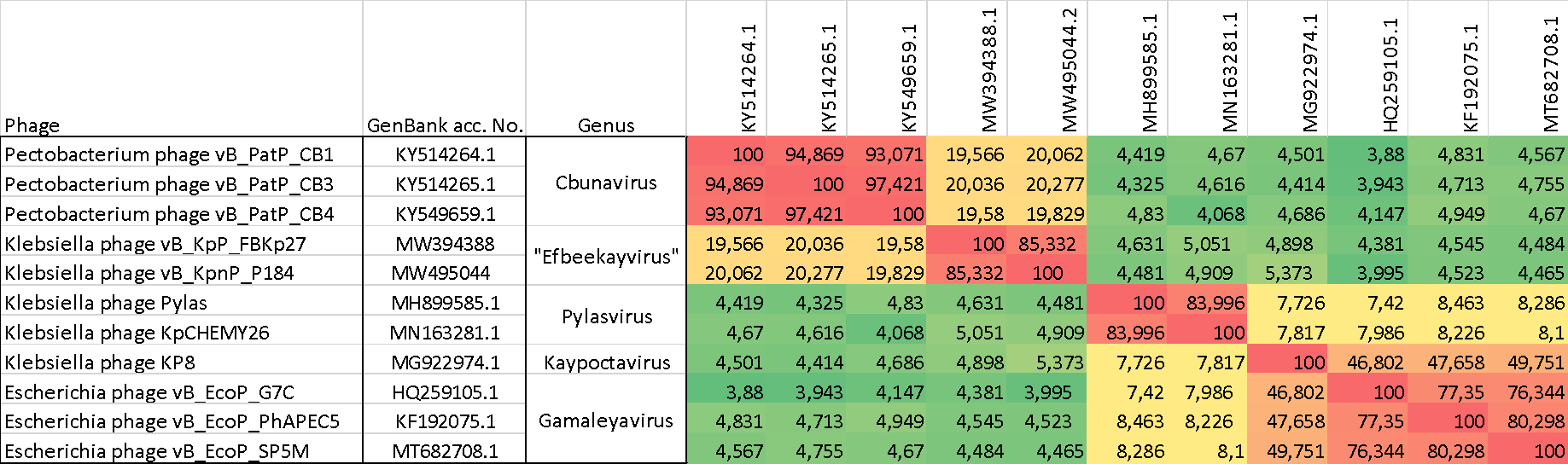
Triduovirus and Exceevirus



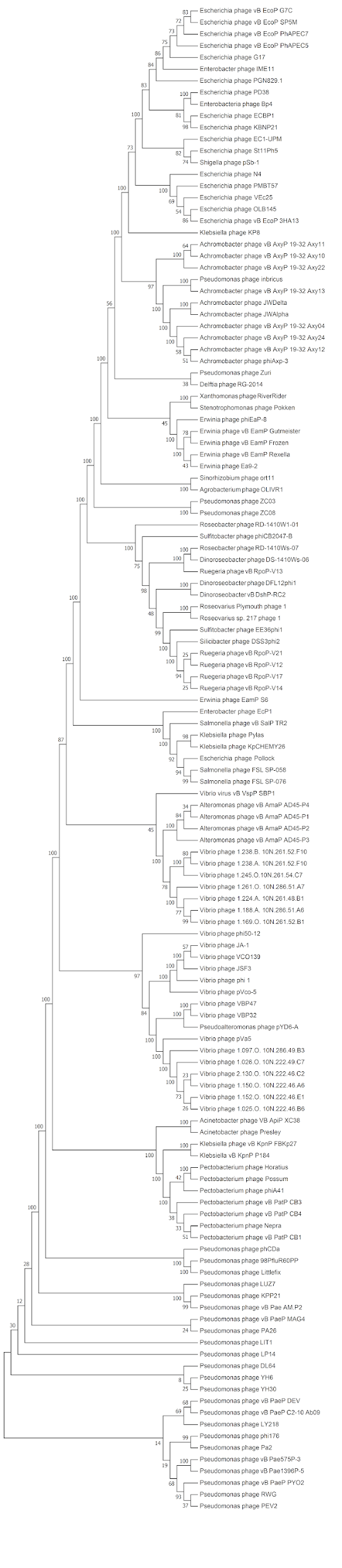
Penintadodekavirus, Vicoquintavirus, Electravirus and Glaucusvirus



Efbeekayvirus



**Phylogeny:** The phylogenetic tree was constructed, using the virion associated RNA polymerase subunits of members of the *Schitoviridae*, a signature gene for inclusion in the family [7]. The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model [3]. The bootstrap consensus tree inferred from 100 replicates [5] is taken to represent the evolutionary history of the taxa analyzed [5]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates) are shown next to the branches [5]. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The analysis involved 129 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 1753 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [4].



**References**

1. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>
2. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268
3. Jones DT, Taylor WR, Thornton JM. The rapid generation of mutation data matrices from protein sequences. Comput Appl Biosci. 1992 Jun;8(3):275-82. doi: 10.1093/bioinformatics/8.3.275.
4. Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol Biol Evol. 2016 Jul;33(7):1870-4. doi: 10.1093/molbev/msw054.
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6. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.
7. Wittmann J, Turner D, Millard A, et al. From Orphan Phage to a Proposed New Family–the Diversity of N4-Like Viruses. Antibiotics. 2020. 9:663. DOI: 10.3390/antibiotics9100663