

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

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| **Code assigned:** | **2020.148B** |  |
| **Short title:** Create ten new species in the subfamily *Sepvirinae* (*Caudovirales*: *Podoviridae*) | | |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| Lambda 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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| **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 | July 2020 |
| Date of this revision (if different to above) | November 2020 |

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

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

**Name of accompanying Excel module**

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| 2020.148B.R.Sepvirinae.xlsx |

**Abstract**

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| Proposal 2016.045a-oB created the *Sepvirinae* subfamily and 3 genera within it (currently named *Diegovirus*, *Oslovirus*, *Traversvirus*). This proposal creates a total of 8 new species within Oslovirus and Traversvirus. |

**Text of proposal**

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| |  | | --- | | 63 complete phage genomes were downloaded from GenBank, including 19 belonging to ICTV-recognized species and 44 that have been unofficially associated with *Sepvirinae* by GenBank submitters or NCBI algorithms. An all-against-all nucleotide sequence comparison was conducted in VIRIDIC (1). Genus assignments were based on a 70% similarity threshold and species assignments were based on a 95% similarity threshold. All prior species and genus assignments were confirmed. Changes within each genus are summarized below and shown in Figure 1. A phylogenetic tree constructed from the large terminase subunit (*terL*) genes supports the conclusion that this subfamily is monophyletic (Figure 2). Within the subfamily, genus assignments are based on the intergenomic similarity thresholds stated above and not on the similarity of *terL* genes. While terminase is a core phage gene, the prevalence of recombination among related phages means that single core gene phylogenies may not accurately represent species and genus relationships.  *Diegovirus*: No changes proposed  *Oslovirus*: 2 new species were created and named based on the single phage representing each one. Note that phage GER2 (MG710528) is included in *Oslovirus* despite a similarity score that is slightly below the 70% threshold. Visual inspection suggests that the low value is driven by extra (presumably bacterial) sequence present in the submitted genome. While phage GER2 appears to represent a new species within Oslovirus, such a species was not created because the MG710528 sequence likely does not represent only the phage genome and would therefore make a poor species exemplar.  *Traversvirus*: 8 new species were created and named based on the first identified or best-known phage isolate. | |

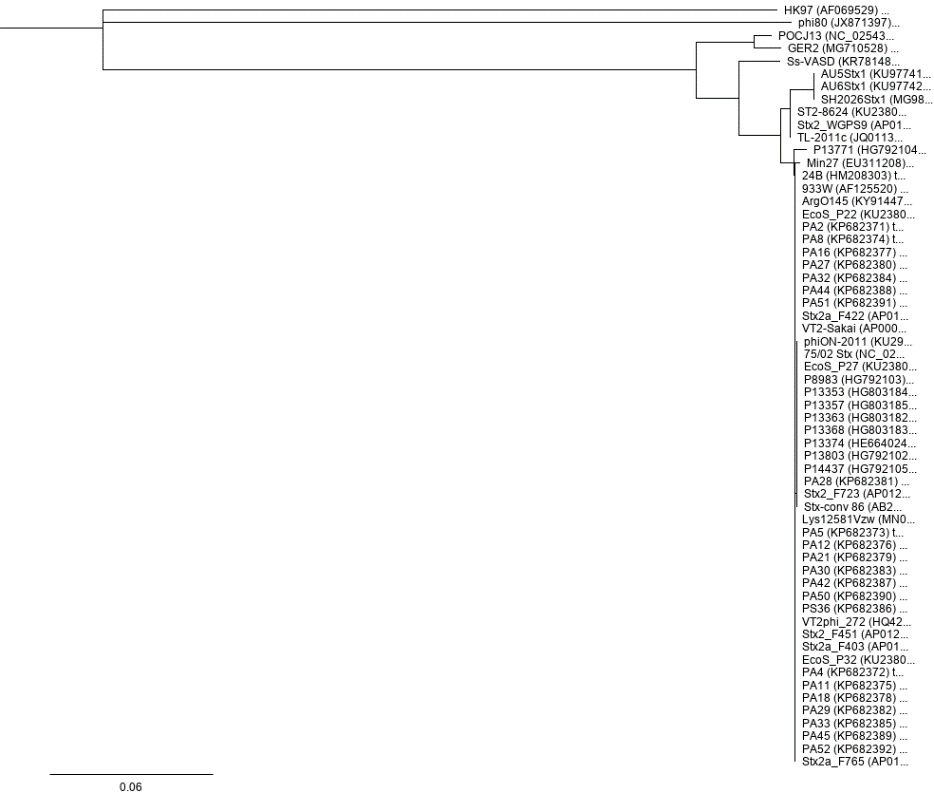
**Supporting evidence**

**Figure 1. VIRIDIC heatmap of *Sepvirinae* phages.** Phage names are provided with GenBank accession numbers and indicate any previously recognized ICTV genus and species assignments. Existing genera are marked in gold boxes and existing species in pink boxes. New species established in this proposal are marked in red boxes.

**A circuit board

Description automatically generated**

**Figure 2. *terL* gene phylogeny for *Sepvirinae*.** Fifty-eight of the 63 phages used for intergenomic similarity calculations were sufficiently annotated for inclusion in this analysis. In genomes where the large terminase subunit was not explicitly annotated, the encoding ORF was identified based on local gene synteny and primary nucleotide sequence. This is a neighbor-joining tree (2) constructed in Geneious (v. 2020.2.4, Biomatters Ltd) using a Tamura-Nei distance matrix (3), rooted using HK97 *terL* as the outgroup. The phi80 *terL* gene was included as an additional control.



**References**

1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv 2020.07.05.188268. <https://doi.org/10.1101/2020.07.05.188268>
2. Saitou, N.; Nei, M. (1 July 1987). "The neighbor-joining method: a new method for reconstructing phylogenetic trees". Molecular Biology and Evolution. 4 (4): 406–425. <https://doi.10.1093/oxfordjournals.molbev.a040454> PMID: 3447015
3. Tamura, Koichiro & Nei, Masatoshi. (1993). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Mol Biol Evol 10: 512-26. <https://10.1093/oxfordjournals.molbev.a040023> PMID: 8336541