

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

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| **Code assigned:** | **2020.102B** |  |
| **Short title:** Create one new subfamily (*Migulavirinae*) including two existing genera (*Caudovirales*: *Schitoviridae*) | | |
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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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| N4-like viruses 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) |  |

**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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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| Here, we propose the creation of the new subfamily *Migulavirinae* including two genera, *Litunavirus* and *Luzseptimavirus*, based on genome-based comparisons, proteomic analysis using ViPTree and phylogenetic analyses of terminase and vRNA polymerase protein sequences. |

**Text of proposal**

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| |  | | --- | | **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 the BLASTN algorithm  **To create a new subfamily, *Migulavirinae***  **Source of the name of this taxon:**  This genus is named in honour of Emil F.A.W. Migula (1863-1938) who described the proteobacterial genus Pseudomonas.  **History:** The two genera described above share sufficient DNA sequence relatedness to be considered part of a subfamily. This is supported by vConTACT v.2.0 analysis [6]. | |

**Supporting evidence**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. The *Herelleviridae* root used as a reference is marked with **red arrowhead**; other arrowhead indicates subfamily to be created.



**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. Column 2 - (P) partial genome. The colour codes in columns 3 and 4 indicate the boundaries of the proposed subfamilies and genera. The subfamily *Migulavirinae* is indicated in light blue (col4), with the genus *Luzseptimavirus* in light green and the genus *Litunavirus* in dark green (col3).



**Phylogenetic analysis** using the (A) terminase and (B) vRNA polymerase protein sequences of N4-like phages. The amino acid sequences were compared using MUSCLE with MEGA7 [4]. The tree was constructed using the maximum likelihood algorithm. The percentages of replicate trees were assessed with the bootstrap test (100).

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**References**

1. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PMID: 28379287.
2. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PMID: 12142423
3. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)
4. Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol. Biol. Evol. 2016,33, 1870–4, doi:10.1093/molbev/msw054.
5. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID 23566564.
6. Jang HB, Bolduc B, Zablocki O, et al. Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. *Nat Biotechnol*. 2019;37(6):632-639. doi:10.1038/s41587-019-0100-8