

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

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| **Code assigned:** | ***2022.073B*** |  |
| **Short title:** Create one new subfamily, nine new genera and 30 new species in the family *Schitoviridae* (*Caudoviricetes*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Schitoviridae Study Group, Bacterial Viruses Subcommittee |

**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** |
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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 2022 |
| 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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| 2022.073B.A.v2.Schitoviridae\_1nsf\_9ng\_30nsp.xlsx |

**Abstract**

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| Here, we propose the creation of the new subfamily *Demetervirinae*, comprising two new genera *Cyamitesvirus*, containing two new species, and *Acanvirus*, comprising four new species; seven new genera, *Philippevirus*, containing one new species; *Varunavirus*, containing one new species; *Petruschkyvirus*, containing one new species; *Xoxocotlavirus*, containing one new species; *Moovirus*, containing one new species; *Cavevirus*, containing one new species; *Gonggongvirus*, containing one new species; two new species in *Cbunavirus*; six new species in *Litunavirus*; one new species in *Littlefixvirus*; two new species in *Pokkenvirus*; six new species in *Gamaleyavirus* in the *Enquatrovirinae* subfamily in the family *Schitoviridae* based on genome-based comparisons. |

**Text of proposal**

***Demetervirinae***: The name is derived from the Olympian goddess of harvest and agriculture and contains two genera, Acanvirus and Cyamitesvirus, both consisting of two member species each. Their names are derived from the Maya god of agriculture, Acan, and the Greek god of beans, Cyamites, respectively.

***Acanvirus***: Rhizobium phage RHph\_Y38, Rhizobium phage RHEph16, Rhizobium phage RHEph22 and Rhizobium phage RHph\_Y2\_6 were all isolated from agricultural lands in Mexico. The genome of Rhizobium phage RHph\_Y38 consists of 77,869 bp with 102 CDS and 2 tRNA genes, the genome of Rhizobium phage RHph\_Y2\_6 consists of 78,314 bp with 101 CDS and 2 tRNA genes the genome of Rhizobium page RHEph16 consists of 77,178 bp with 94 CDS and 2 tRNA genes and the genome of Rhizobium page RHEph22 consists of 77,655 bp with 99 CDS and 2 tRNA genes.

***Cyamitesvirus***: Rhizobium phage RHph\_N38 and Rhizobium phage RHph\_I1\_6 were both isolated from agricultural lands in Argentina. The genome of Rhizobium phage RHph\_N38 consists of 78,126 bp with 101 CDS and 2 tRNA genes, the genome of Rhizobium phage RHph\_I1\_6 consists of 77,174 bp with 99 CDS and 3 tRNA genes.

***Xoxocotlavirus***: Th name is derived from the city where the first phage of this type was isolated. Rhizobium phage RHph\_X2\_28B has a genome size of 76,359 bp with102 CDS and 4 tRNA genes.

***Philippevirus***: The name is derived from the name of the first isolated phage of this type, Stenotrophomonas phage Philippe. Stenotrophomonas phage Philippe was isolated from a salt water sample in the US. Its genome consists of 74,717 bp with 95 CDS and 6 tRNA genes.

***Varunavirus***: The name is derived from the Hindu god of ocean. Dinoroseobacter phage vB\_DshP-R7L was isolated in China and infects *Vibrio alginolyticus*. Its genome consists of 73,099 bp with 106 CDS and 2 tRNA genes.

***Gonggongvirus***: The name is derived from Gonggong, a Chinese water god. Vibrio phage BUCT194 was isolated from sewage in China and infects *Dinoroseobacter shibae DFL12*. Its genome consists of 73,099 bp with 83 CDS and 2 tRNA genes.

# *Petruschkyvirus*: The name is derived from J. Petruschky who first isolated described *Alcaligenes faecalis*. *Alcaligenes faecalis* phage vB\_AfaP\_QDWS595 was isolated from sewage at a wastewater treatment plant in Tuandao, Qingdao, China [1]. Its genome consists of 75,871 bp with 74 CDS and 11 tRNA genes.

***Moovirus***: The name is derived from the name of the first isolated phage of this type, Shigella virus Moo19. It was isolated from standing water in cow pasture in US and infects *Shigella flexneri*. Its genome consists of 72,458 bp with 86 CDS and 5 tRNA genes.

***Cavevirus***: The name is derived from the origin of the first isolated phage of this type, Stenotrophomonas phage C121. It was isolated from cave sediment in China and infects *Stenotrophomonas maltophilia*. Its genome consists of 73,045 bp with 98.

**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 [2, 3].

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

*Acanvirus,Cyamitesvirus, Xoxocotlavirus* and *Petruschkyvirus*



*Gonggongvirus*



*Moovirus* and new species in *Gamaleyavirus*



*Varunavirus*



*Cavevirus* and new species in *Pokkenvirus*



New species in *Cbunavirus, Litunavirus* and *Littlefixvirus*



**Phylogeny:** The phylogenetic tree was constructed, using a hallmark gene for this family, the virion associated RNA polymerase subunit of members of the *Schitoviridae*. The evolutionary history was inferred by using the Maximum Likelihood method using Jones-Taylor-Thornton (JTT) model for amino acid substitution with FastTree 2 [4]. The bootstrap consensus tree inferred from 1000 replicates [6] is taken to represent the evolutionary history of the taxa analyzed.



Kaypoctavirus

Enquatrovirus

Moovirus

Gamaleyavirus

Luzseptimavirus

Litunavirus

Efbeekayvirus

Cbunavirus

Pacinivirus

Mukerjeevirus

Varunavirus

Rhodovirinae

Humphriesvirinae

Acanvirus

Cyamitesvirus

„Demetervirinae“

Gonggongvirus

Xoxocotlavirus

Petruschkyvirus

Philippevirus

Cavevirus

Rothmandenesvirinae

Enquatrovirinae

Migulavirinae

**References**

# Jing Y, Lin H, Ning H, Wang J. Complete genome analysis of the novel Alcaligenes faecalis phage vB\_AfaP\_QDWS595. Arch Virol. 2022 Mar;167(3):931-934. doi: 10.1007/s00705-022-05373-2

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. Price MN, Dehal PS, Arkin AP. FastTree 2--approximately maximum-likelihood trees for large alignments. PLoS One. 20210 Mar10;56(3):e9490. doi: 10.1371/journal.pone.0009490.