

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.122B** |  |
| **Short title:** Create one new subfamily (*Pontosvirinae*) including three new genera (C*audovirales*: *Schitoviridae*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Kropinski AM, Jang HB, Sullivan MB, Moraru C, Wittmann J | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  Phage.Canada@gmail.com; jang.377@osu.edu; mbsulli@gmail.com; liliana.cristina.moraru@uol.de; jow12@dsmz.de |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of Guelph, Canada [AMK]  Ohio State University, USA [HBJ, MBS]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  DSMZ, Germany [JW] |

**Corresponding author**

|  |
| --- |
| Johannes Wittmann |

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

|  |
| --- |
| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

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

|  |
| --- |
|  |

**Authority to use the name of a living person**

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | July 2020 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

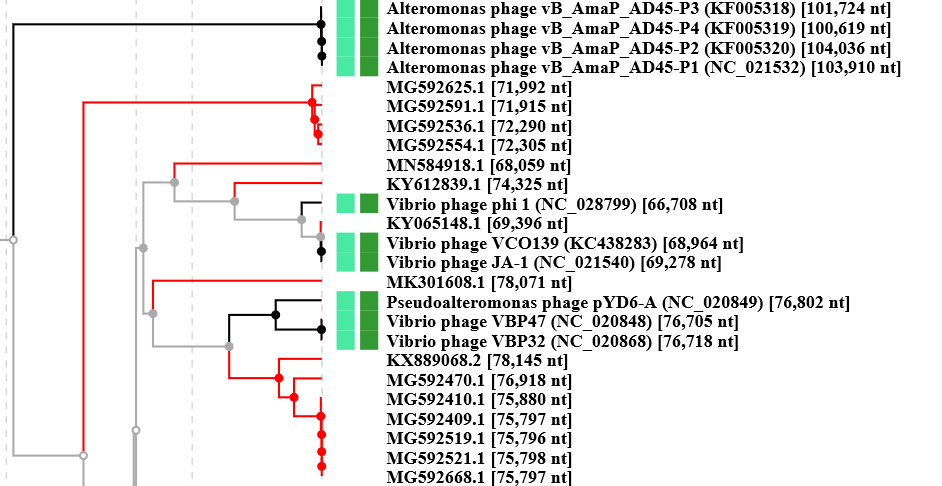
|  |
| --- |
|  |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | **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 | |

**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 large **blue 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 colour codes in columns 3 and 4 indicate the boundaries of the proposed subfamilies and genera. 

**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 [6]. The tree was constructed using the maximum likelihood algorithm. The percentages of replicate trees were assessed with the bootstrap test (100).

****

B

A

**Proposal 1: To create a new genus *Nahantvirus***

**Source of the name of this taxon:** This taxon was named after the geographic origin (Nahant, Massachusetts) of the type phage Vibrio phage 1.026.O.\_10N.222.49.C7.

**History:** Vibrio phage 1.026.O.\_10N.222.49.C7 was isolated from filtered seawater.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Vibrio phage 1.026.O.\_10N.222.49.C7 |  | MG592410.1 | 75.88 | 43.1 | 107 | 1 |

N.B. Vibrio phage 1.025.O.\_10N.222.46.B6, Vibrio phage 1.150.O.\_10N.222.46.A6, Vibrio phage 1.152.O.\_10N.222.46.E1 and Vibrio phage 2.130.O.\_10N.222.46.C2 should be considered strains in this genus.

**Electron micrograph:** None available

**Proposal 2: To create a new genus *Dorisvirus***

**Source of the name of this taxon:** This taxon was named after the Greek sea goddess Doris.

**History:** Vibrio phage 1.097.O.\_10N.286.49.B3 was isolated from filtered seawater.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Vibrio phage 1.097.O.\_10N.286.49.B3 | - | MG592470.1 | 76.92 | 42.6 | 98 | - |

**Electron micrograph:** None available

**Proposal 3: To create a new genus *Galateavirus***

**Source of the name of this taxon:** This taxon was named after Galatea, the Greek goddess of calm sea.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Vibrio phage vB\_VspP\_pVa5 | - | KX889068.2 | 78.15 | 43.2 | 106 | 1 |

**Electron micrograph:** None available

**Proposal 4: To create a new subfamily *Pontosvirinae***

**Source of the name of this taxon:** This subfamily was named after Pontos, a primordial god of the sea

**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. PubMed 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. PubMed PMID: 12142423
3. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv doi: 10.1101/2020.07.05.188268. <http://kronos.icbm.uni-oldenburg.de/viridic/>
4. 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.
5. 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 PMID: 31061483