

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

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| **Code assigned:** | **2020.060B** |  |
| **Short title:** Create one new subfamily, (*Fuhrmanvirinae*) including two new genera (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

|  |  |
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| 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 [HJ, MBS]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  DSMZ, Germany [JW] |

**Corresponding author**

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| --- |
| Johannes Wittmann |

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

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| *Caudovirales* 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)** |
| *Fuhrmanvirinae* | J.A. Fuhrman | Y |
|  |  |  |
|  |  |  |

**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 ”Fuhrmanvirinae” and two new genera “Stoningtonvirus” and “Matsuvirus”, 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 | |

**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 marked with **red arrowhead**; other arrowheads indicate subfamilies 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.



**Phylogenetic analysis** using the (A) terminase and (B) virion-associated RNA 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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B

A

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

**Source of the name of this taxon:** This genus is named after Stonington, a town in Hancock County, Maine, United States where the first virus of its type Vibrio phage VBP47 was isolated.

**History:** Lytic phages VBP47 and VPB32 were isolated from Lobster Hatchery Stonington, ME (USA) on Vibrio parahaemolyticus RIMD2210633 as the host bacterium.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Vibrio phage VBP47 | [NC\_020848.1](about:blank) | [HQ634194.1](about:blank) | 76.71 | 42.5 | [115](about:blank#!/proteins/3934/455875|Vibrio phage VBP47/viral segment Unknown/) | 2 |

**N.B. Vibrio phage VBP32 should be considered a strain in this genus**

**Electron micrograph:** None available

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

**Source of the name of this taxon:** This genus is named after Matsu the Chinese goddess of the sea and protector of seafarers.

**History:** Lytic Pseudoalteromonas phage pYD6-A was isolated in 2008 from the South China Sea.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Pseudoalteromonas phage pYD6-A | [NC\_020849.1](about:blank) | [JF974296.1](about:blank) | 76.8 | 38.7 | [99](about:blank#!/proteins/3882/455853|Pseudoalteromonas phage pYD6-A/viral segment Unknown/) | 2 |

**Electron micrograph:** None available

**Proposal 3: To create a new subfamily, *Fuhrmanvirinae***

**Source of the name of this taxon:** This genus is named in honour of eminent American oceanographer and marine biologist Jed Alan Fuhrman (b. 1956; Ph.D., Oceanography, Scripps Institution of Oceanography (1981), McCulloch-Crosby Chair of Marine Biology, University of Southern California (1995 – present), winner of the Hutchinson Medal, American Society of Limnology and Oceanography (2006), and Sustaining Fellow (Inaugural class), Assoc for the Sciences of Limnology and Oceanography (2015- ). Dr. Fuhrman was one of the first scientists to study marine viruses.

**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] which places these phages into cluster VC\_266\_0.

**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. 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: Bin Jang H, 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