

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.076B** |  |
| **Short title:** Create one new subfamily (*Humphriesvirinae*) including three existing genera (*Caudovirales*: *Schitoviridae*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Kropinski AM, Moraru C, Wittmann J | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  Phage.Canada@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]  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**

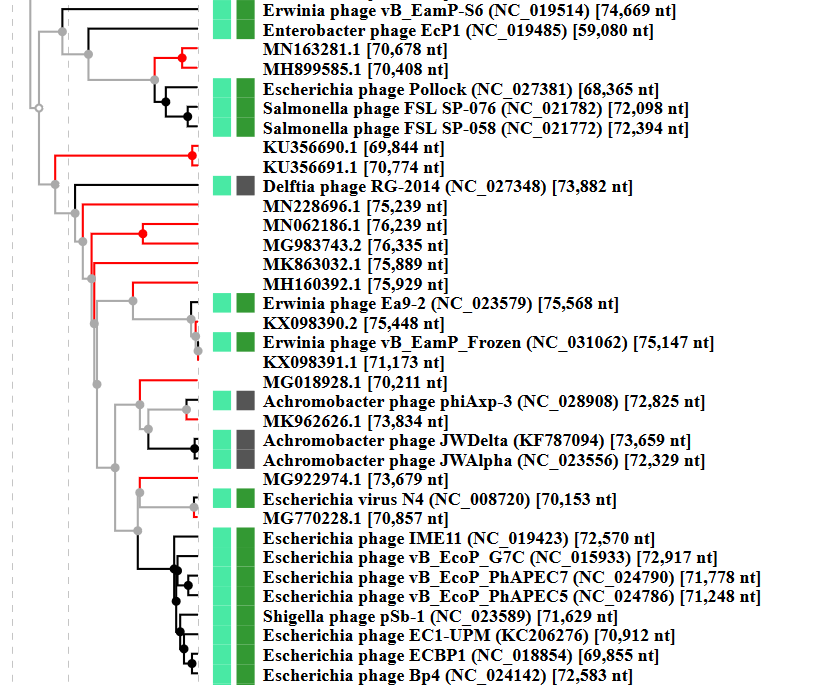
|  |
| --- |
| Here, we propose the creation of the subfamily “Humphriesvirinae” including three genera, Pollockvirus, Ithacavirus and Pylasvirus based on genome-based comparisons, proteomic analysis using ViPTree and phylogenetic analyses of terminase and vRNA polymerase protein sequences. |

**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 [1-3]. | |

**Supporting evidence**

**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. Arrowhead indicates 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. Colours in columns 3 and 4 indicate 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 [4]. 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 subfamily Humphriesvirinae**

**Source of the name of this taxon:** This subfamily is named after James C. Humphries (1914-1992) who was the first to isolate a Klebsiella phage. He was a professor in the Department of Bacteriology at the University of Kentucky, Lexington, Kentucky.

**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.