

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

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| **Code assigned:** | **2020.183B** |  |
| **Short title:** Create one new genus (*Wumptrevirus*) including two species (*Caudovirales*: *Podoviridae*) | | |
|  | | |

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

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| Dann Turner |

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

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| Bacterial and Archaeal Viruses Subcommittee; *Caudovirales* Study Group |

**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 | April 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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| 2020.183B.R.Wumptrevirus.xlsx |

**Abstract**

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| According to ICTV Master Species List 2019.v1 *Phormidium* virus WMP3 is listed as unassigned species within the *Caudovirales*. This is now corrected. |

**Text of proposal**

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**Supporting evidence**

**Proposal: To create a new genus, *Wumptrevirus*, to contain this species, and one new one.**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| Pf-WMP3 | [NC\_009551.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_009551.1) | [EF537008.1](https://www.ncbi.nlm.nih.gov/nuccore/EF537008.1) | 43.25 | 46.5 | 41 | 0 | 100 | 100 |
| PP(\*) | [NC\_022751.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_022751.1) | [KF598865.1](https://www.ncbi.nlm.nih.gov/nuccore/KF598865.1) | 42.48 | 46.4 | 41 | 0 | 89.5 | 87.8 |

\* host bacteria are *Phormidium foveolarum* and *Plectonema boryanum*

**\*\* Determined using BLASTn at NCBI [1-3]**

**\*\*\* Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[6]**

**Specific Reference:** Zhou Y, Lin J, Li N, Hu Z, Deng F. Characterization and genomic analysis of a plaque purified strain of cyanophage PP. Virol Sin. 2013 Oct;28(5):272-9.

**BLASTN homologs:** Genomic orphans [1-3].

**Electron micrograph:** see 2008.059B

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of WMP3 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

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**References**

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