

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

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| **Code assigned:** | **2020.182B** |  |
| **Short title:** Create one new genus (*Wumpquatrovirus*) including one new species (*Caudovirales*: *Podoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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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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| 2020.182B.R.Wumpquatrovirus.xlsx |

**Abstract**

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| According to the 2019 Master Species List *Phormidium virus WMP4* is listed as an unclassified member of the *Podoviridae*. This proposal corrects that problem. |

**Text of proposal**

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**Supporting evidence**

According to ICTV Master Species List 2019.v1 *Phormidium virus WMP4* is listed as unassigned species within the family *Podoviridae*, order *Caudovirales*.

**Proposal: To create a new genus, *Wumpquatrovirus*, to contain this species.**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| WMP4 | [NC\_008367.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_008367.1) | [DQ875742.1](https://www.ncbi.nlm.nih.gov/nuccore/DQ875742.1) | 40.94 | 51.8 | 45 | 0 |

**Specific Reference:** Liu X, Shi M, Kong S, Gao Y, An C. Cyanophage Pf-WMP4, a T7-like phage infecting the freshwater cyanobacterium *Phormidium foveolarum*: complete genome

sequence and DNA translocation. Virology. 2007 Sep 15;366(1):28-39.

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

**Electron micrograph:** See2008.060B

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of WMP4 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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Description automatically generated

| **References** |
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