

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

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| **Code assigned:** | **2020.074B** |  |
| **Short title:** Create one new genus (*Hubeivirus*) including two new specieswithin (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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**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)** |
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**Submission dates**

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| Date first submitted to SC Chair | June 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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| 2020.074B.R.Hubeivirus.xlsx |

**Abstract**

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| The 2018 Master Species List describes only 21 siphoviruses which infect members of the order *Bacillales*. These fall into nine different genera. Here we propose a new genus *Hubeivirus* in the family *Siphoviridae.* |

**Text of proposal**

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**Supporting evidence**

**Proposal:** To create a new genus, *Hubeivirus*, containing two species.

**Origin of the name of this taxon:** The name of this genus is derived from Hubei, a province in Central China where at the Wuhan Institute of Virology, Chinese Academy of Sciences, University of Chinese Academy of Sciences, the type virus *Bacillus* phage PfEFR-4 was isolated.

**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.

**History:** *Bacillus cereus* phage PfEFR-4 was isolated in Wuhan, Hubei, China. *Bacillus cereus* phage vB\_BceS-MY19 was isolated from a *B. cereus* lysogen recovered from cooked rice. “Since no permuted, direct repeat, cos, or protein-primed ends were found in the genome sequence, the sequence is considered partial,” [Yang et al. 2016]. Both these phages are temperate.

**Publications:** Yang Y, Zhan L, Chen J, Zhang Y, Sun Y, Yang Z, Jiang L, Zhu H, Zhang Y, Lu Y, Mei L. Genome Sequence of *Bacillus cereus* Phage vB\_BceS-MY192. Genome Announc. 2016 Apr 21;4(2). pii: e01557-15. doi: 10.1128/genomeA.01557-15. PubMed PMID: 27103733 [vB\_BceS-MY192]

**BLASTN relationship:** The next closest relative is *Bacillus* phage BtiUFT6.51-F, which shares 21.2% DNA sequence identity with PfEFR-4 [1-3].

**GenBank Summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| PfEFR-4 |  | [KX227757.1](https://www.ncbi.nlm.nih.gov/nuccore/KX227757.1) | 43.22 | 35.4 | 67 | 100 | 100 |
| vB\_BceS-MY192 |  | [KT725776.1](https://www.ncbi.nlm.nih.gov/nuccore/KT725776.1) | 44.70 | 35.0 | 64 | 83.8 | 71.6 |

**\*\* 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]**

**N.B. Bacillus phage PfEFR-5 [KX227760.1] should be considered as a strain of *Bacillus virus PfEFR4* in this genus**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of PfEFR-4 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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