

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

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| **Code assigned:** | **2020.027B** |  |
| **Short title:** Create one new genus (*Camtrevirus*) including three new species(*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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| 2020.027B.R.Camtrevirus.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 *Camtrevirus* with three species**.** |

**Text of proposal**

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**Supporting evidence**

**Proposal:** To create a new genus, *Camtrevirus*, containing three species

**Origin of the name of this taxon:** The names of this genus is directly derived from that of the type phage, Bacillus phage phiCM3.

**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* phage phiCM3 was isolated from a plate of *B. thuringiensis* subsp. *morrisoni* strain YM-03. Its genome is linear with 3′-cohesive ends. Yuan et al. (2014) considered it to be related to Bacillus phage Gamma. Phage BtCS33 was recovered from a *B. thuringiensis* subsp. *kurstaki* strain [Yuan et al. 2012]. “Transmission electron microscopy showed that BtCS33 had an icosahedral head (61 nm × 67 nm) and a long tail (204 nm × 5.7 nm).” All of these phages are temperate.

**Publications:** Yuan Y, Gao M, Peng Q, Wu D, Liu P, Wu Y. Genomic analysis of a phage and prophage from a *Bacillus thuringiensis* strain. J Gen Virol. 2014 Mar;95(Pt 3):751-61. doi: 10.1099/vir.0.058735-0. Epub 2013 Nov 27. PubMed PMID: 24285088. [phiCM3]

Moumen B, Nguen-The C, Sorokin A. Sequence Analysis of Inducible Prophage phIS3501 Integrated into the Haemolysin II Gene of *Bacillus thuringiensis* var *israelensis* ATCC35646. Genet Res Int. 2012;2012:543286. doi: 10.1155/2012/543286. Epub 2012 Mar 6. PubMed PMID: 22567391 [phIS3501]

Yuan Y, Gao M, Wu D, Liu P, Wu Y. Genome characteristics of a novel phage from *Bacillus thuringiensis* showing high similarity with phage from *Bacillus cereus*. PLoS One. 2012;7(5):e37557. doi: 10.1371/journal.pone.0037557. Epub 2012 May 23. PubMed PMID: 22649540 [BtCS33]

**Electron Microscopy:** morphology of phage BtCS33 particles negatively stained with 2% potassium phosphotungstate. Reproduced from Yuan Y, Gao M, Wu D, Liu P, Wu Y. Genome characteristics of a novel phage from *Bacillus thuringiensis* showing high similarity with phage from *Bacillus cereus*. PLoS One. 2012;7(5):e37557. doi: 10.1371/journal.pone.0037557. Epub 2012 May 23. PubMed PMID: 22649540 [BtCS33]

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**BLASTN relationship:** The next closest relative is Bacillus phage BceA1, which shares 39.3% DNA sequence identity with phiCM3 [1-3].

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| phiCM3 | [NC\_023599.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023599.1) | [KF296718.1](https://www.ncbi.nlm.nih.gov/nuccore/KF296718.1) | 38.77 | 35.5 | 56 | 0 | 100 | 100 |
| BtCS33 | [NC\_018085.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_018085.1) | [JN191664.1](https://www.ncbi.nlm.nih.gov/nuccore/JN191664.1) | 41.99 | 35.2 | 57 | 0 | 85.4 | 85.7 |
| phIS3501 | [NC\_019502.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_019502.1) | [JQ062992.1](https://www.ncbi.nlm.nih.gov/nuccore/JQ062992.1) | 44.40 | 34.9 | 51 | 1 | 75.3 | 67.9 |
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**\*\* 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]**

**Bacillus phages BtiUFT6.51-F [MG710484.1] and phi4I1 [KT967075.1] should be considered strains of BtCS33 in this genus**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of phiCM3 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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| **Phage name** | **Accession** | **Belongs to species** |
| Bacillus phage BtiUFT6.51-F | MG710484 | Bacillus virus BtCS33 |
| Bacillus phage phi4I1 | KT967075 | Bacillus virus BtCS33 |

**References**

1: Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.

2: Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.

3: O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.

4: Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6): doi: 10.1371/journal.pone.0039107. PMID: 22723939.

5: Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.

6: 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.

7: Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147. doi: 10.1371/journal.pone.0011147. PMID: 20593022.

8: Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.

9: Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.