

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

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| **Code assigned:** | **2020.067B** |  |
| **Short title:** Create one new subfamily (*Gutmannvirinae*) including two new genera and 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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| 2020.067B.R.Gutmannvirinae.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 subfamily, *Gutmannvirinae*, and two genera *Carmenvirus* and *Pebcunavirus*. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **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 | |

**Supporting evidence**

**Proposal:** To create a new subfamily, *Gutmannvirinae* containing two new genera, *Carmenvirus* and *Pebcunavirus*.

**Origin of the name of this taxon:** The names of the genera are directly derived from that of the type phages, *Bacillus* phage Carmen and *Bacillus* phage PCB1. The subfamily is named in honour of Antoinette Gutmann (d) who assisted Andre Lwoff with his experiments on the lysogeny of *Bacillus* species in the late 1940s and early 1950s.

**History:** *Bacillus* phage Carmen17 was isolated from soil using *Bacillus thuringiensis* as the host bacterium, while *Bacillus* phage Wes44 was isolated by the same group but no host is indicated. *Bacillus* phage PBC1 was isolated against *Bacillus cereus* in Korea [Kong et al, 2012]. “PBC1 has terminally redundant and partially permuted genomes, suggesting that PBC1 uses a headful packaging mechanism.” All of these phages are lytic.

**Publications:** Kong M, Kim M, Ryu S. Complete genome sequence of *Bacillus cereus*

bacteriophage PBC1. J Virol. 2012 Jun;86(11):6379-80. doi: 10.1128/JVI.00706-12.

PubMed PMID: 22570248

**BLASTN relationship:** The next closest relative is *Brevibacillus* phage Emory, which shares <10% DNA sequence identity with Carmen17 [1-3]. The level of sequence identity between Carmen17 and PBC1 indicated that they belong to separate genera.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| Bacillus phage Carmen17 |  | [MG784342.1](https://www.ncbi.nlm.nih.gov/nuccore/MG784342.1) | 41.82 | 42.0 | 51 | 100 | 100 |
| Bacillus phage Wes44 |  | [MH598512.1](https://www.ncbi.nlm.nih.gov/nuccore/MH598512.1) | 42.25 | 42.0 | 54 | 88.8 | 94.1 |
|  |  |  |  |  |  |  |  |
| Bacillus phage PBC1 | [NC\_017976.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_017976.1) | [JQ619704.1](https://www.ncbi.nlm.nih.gov/nuccore/JQ619704.1) | 41.16 | 41.7 | 50 | 57.0 | 82.3 |

**\*\* 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]**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Carmen17 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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