

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

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| **Code assigned:** | **2020.118B** |  |
| **Short title:** Create one new genus (*Pemunavirus*) including one new species (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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| Jakub Barylski |

**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 | May 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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| 2020.118B.R.Pemunavirus.xlsx |

**Abstract**

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| According to the 2018 Master Species List the majority of myoviruses which infect members of the order *Bacillales* belong to the family *Herelleviridae*. There are nine phages, in five genera within the family *Myoviridae*. Here we propose a new genus *Pemunavirus*. |

**Text of proposal**

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**Supporting evidence**

**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.

**Source of the name of this taxon:** This genus name is derived from that of the type virus, *Bacillus* phage PM1.

**History:** *Bacillus subtilis* subsp. natto phage PM1 was isolated in Japan as a result of viral interrupted natto production in a factory. “PM1 was shown to have a long non-contractile tail in a morphological study, it was believed to belong to the family *Siphoviridae*. The genome of PM1 was shown to be a linear double-stranded DNA of approximately 50 kb. Based on the results of studies using restriction endonucleases, PM1 DNA was found to be circularly permuted” (Umene et al. 2009). While an integrase has not been identified the phage encodes an anti-repressor protein (Umene et al. 2013).

**Reference:** K. Umene, S. Oohashi, F. Yamanaka, A. Shiraishi, Molecular characterization of the genome of *Bacillus subtilis* (natto) bacteriophage PM1. a phage associated with disruption of food production. World J. Microbiol. Biotechnol. 25, 1877–1881(2009)

Umene K, Shiraishi A. Complete nucleotide sequence of *Bacillus subtilis* (natto) bacteriophage PM1, a phage associated with disruption of food production. Virus Genes. 2013 Jun;46(3):524-34.

**GenBank Summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| PM1 | [NC\_020883.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_020883.1) | [AB711120.1](https://www.ncbi.nlm.nih.gov/nuccore/AB711120.1) | 50.86 | 41.3 | 86 | 0 |

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

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of PM1 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."

![A screenshot of a cell phone

Description automatically generated]()

**References**

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