

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

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| **Code assigned:** | **2020.160B** |  |
| **Short title:** Create one new genus (*Takahashivirus*) including one existing species (*Bacillus virus PBS1*)(*Caudovirales*: *Myoviridae*) | | |
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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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| 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) | 6/12/2020 |

**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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| 2020.160B.R.Takahashivirus.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 *Takahashivirus* containing a single species*.* |

**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 named in honour of Iwao (François) Takahashi (1926-2009, former Professor of Biology, McMaster University, Hamilton, Ontario) who isolated *Bacillus* phage PBS1.

A person posing for the camera

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According to ICTV Master Species List 2018b.v2 *Bacillus virus PBS1* is listed as unassigned species within the *Caudovirales*.

**History:** 2009.011a,bB

**Reference:** 2009.011a,bB & Lavysh D, Sokolova M, Minakhin L, Yakunina M, Artamonova T, Kozyavkin S, Makarova KS, Koonin EV, Severinov K. The genome of AR9, a giant transducing *Bacillus* phage encoding two multisubunit RNA polymerases. Virology. 2016 Aug;495:185-96. [AR9]. This phage was isolated by David Dubnau.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| PBS1 | [NC\_043027.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_043027.1) | [MF360957.1](https://www.ncbi.nlm.nih.gov/nuccore/MF360957.1) | 252.2 | 27.7 | 311 | 1 | 100 | 100 |
| AR9 | [NC\_031039.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031039.1) | [KU878088.1](https://www.ncbi.nlm.nih.gov/nuccore/KU878088.1) | 251.04 | 27.8 | 291 | 1(\*) | 98.3 | 91.3 |

**\* None indicated in the NCBI Replicon Info data; found using tRNAscan-SE 2.0 at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[5]**

**\*\* 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 AR9 should be considered a strain of PBS1.**

**VIRIDIC:** The most closely related phages with members of this new genus are Bacillus phage vB\_BpuM-BpSp and Bacillus phage BSP7 with respectively 31.1% and 0.1% intergenomic similarity [10].

**Table

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**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein of PBS1 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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