

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

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| **Code assigned:** | **2021.074B** |  |
| **Short title:** Create one new genus (*Sagamiharavirus*) including one new species (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew M Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial 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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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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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 2021 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.074B.R.Sagamiharavirus |

**Abstract**

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| A detailed molecular and phylogenetic reexamination of the temperate Mycobacterium phages which the Actinobacteriophage Database placed in Cluster A, and ICTV classified as members of the genus *Fromanvirus* has revealed great diversity. This proposal will create a new genus, *Sagamiharavirus*, for this and similar phages which are currently not classified by the Actinobacteriophage Database. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic distance calculator VIRIDIC [10].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [4] | |

**Supporting evidence**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [11]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [12]. The phages of interest are indicated with **red arrow**.

A picture containing diagram

Description automatically generated  
**A picture containing schematic

Description automatically generated**Diagram, schematic

Description automatically generated  
**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [10]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.

Chart

Description automatically generated

**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins of these 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." The new genera are indicated with arrows or boxes.

A screenshot of a computer

Description automatically generated with low confidence

**Origin of the name of this taxon:** This taxon is named after Sagamihara city, Kanagawa ken (prefecture), Honshu, Japan where in Azabu University, School of Veterinary Medicine Dr. Jumpei Uchiyama isolated the type virus, Mycobacterium phage PP

**Historical aspects:** Data on this phage has not been added to the Actinobacteriophage Database. The closest related phages is Mycobacterium phage Sheen with which it shares 46.8% DNA sequenced relatedness.

**Specific References:** 1. Uchiyama J\*, Mizukami K, Yahara K, Kato S, Murakami H, Nasukawa T, Ohara N, Ogawa M, Yamazaki T, Matsuzaki S, Sakaguchi M. Genome sequences of 12 mycobacteriophages recovered from archival stocks in Japan. Genome Announcements, 6(25), pii: e00472-18, 2018.

2. Ujihara T, Uchiyama J, Nasukawa T, Ando H, Murakami H, Ohara N, Ogawa M, Yamazaki T, Daibata M, Sakaguchi M, Matsuzaki S\*. Recovery of mycobacteriophages from archival stocks stored for approximately 50 years in Japan. Archives of Virology, 163(7), 1915-1919, 2018.

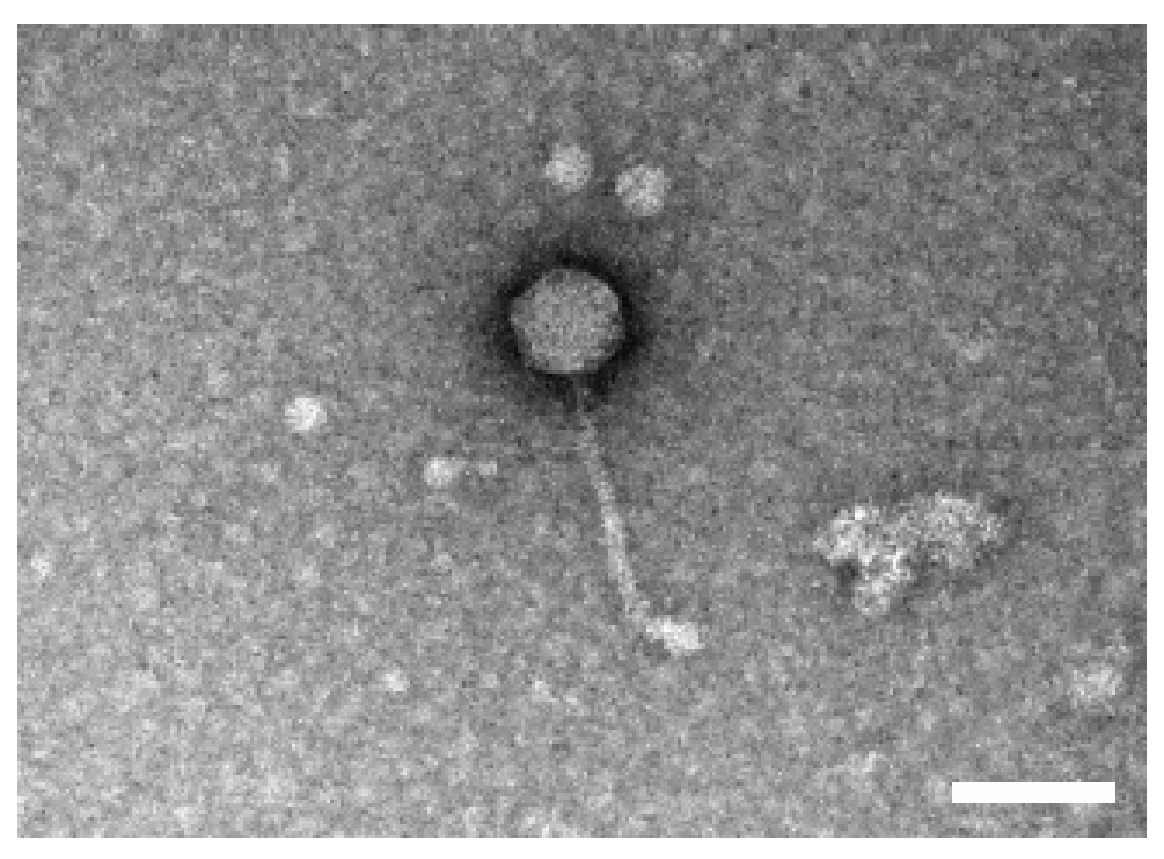
**Genome summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Mycobacterium phage PP |  | [AP018486.1](https://www.ncbi.nlm.nih.gov/nuccore/AP018486.1) | 51.51 | 64.5 | [80](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68386/369533%7CMycobacterium%20phage%20PP/viral%20segment/) | 2 | 100 | 100 |

**(\*) Determined using VIRIDIC [10]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[6]**

**Electron micrograph:** The electron micrograph is derived from Figure S2 in the supplementary materials [2].

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**References**

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