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

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| **Code assigned:** | **2020.079B** |  |
| **Short title:** Create one new genus (*Kamchatkavirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Jakub Barylski |

**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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| 2020.079B.R.Kamchatkavirus.xlsx |

**Abstract**

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| To create a genus for a unique thermophilic *Aeribacillus pallidus* phage. |

**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**

**Source of the name of this taxon:** This genus is named the location (Valley of Geysers, Kamchatka Peninsula, Russia) where the first virus of its type, Aeribacillus bacteriophage AP45, was isolated.

**History:** “Negative staining of phage AP45 revealed icosahedral

heads with a diameter of 60 nm connected with a tail approximately 160 nm in length. ORFs encoding phage integrases have not been identified, but it could not be excluded that bacteriophage AP45 uses

both lytic and lysogenic life cycles.” [Morozova V et al. 2019].

**Specific Reference:** Morozova V, Bokovaya O, Kozlova Y, Kurilshikov A, Babkin I, Tupikin A, Bondar A, Ryabchikova E, Brayanskaya A, Peltek S, Tikunova N. A novel thermophilic *Aeribacillus* bacteriophage AP45 isolated from the Valley of Geysers, Kamchatka: genome analysis suggests the existence of a new genus within the *Siphoviridae* family. Extremophiles. 2019;23(5):599-612. doi: 10.1007/s00792-019-01119-2. Epub 2019 Aug 2. PubMed PMID: 31376001.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| AP45 |  | [KX965989.1](https://www.ncbi.nlm.nih.gov/nuccore/KX965989.1) | 51.61 | 38.3 | [73](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63145/465768|Aeribacillus phage AP45/viral segment/) | 0 |

**BLASTN homologs:** Genomic orphan [1-3]. The next most closely related virus is Anoxybacillus phage A403 which shares 10.7% DNA sequence identity with AP45.

**Electron micrograph: **

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of AP45 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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