

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

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| **Code assigned:** | ***2023.059B*** |  |
| **Short title:** Create a new genus, *Samaravirus* encompassing one species in the class *Caudoviricetes*  |
|  |

**Author(s) and email address(es)**

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| --- | --- |
| Kazantseva OA, Piligrimova EG, Shadrin AM | olesyakazantseva@bk.ru; e.piligrimova@ibpm.ru; andrey2010s@gmail.com |

**Author(s) institutional address(es) (optional)**

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**Corresponding author**

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| Kazantseva OA |

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

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| *Caudoviricetes* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

|  |  |
| --- | --- |
| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**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 2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2023.059B.N.v1.Samaravirus\_ng.xlsx |

**Abstract**

Please provide a concise summary of your taxonomic proposal (maximum 150 words).

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| We propose creating a new genus, *Samaravirus,* containing one species, *Samaravirus* *Sam46* |

**Text of proposal**

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| Sam46 is a virulent *Bacillus*-infecting myovirus. The genome is 45,419 bp long, with 77 predicted CDSs and GC-content of 41.6%. The whole-genome arrangement is typical of virulent phages with middle-size genomes, with all the predicted genes located on the same DNA strand.It was shown experimentally that Sam46 uses headful DNA packaging with site-specific initiation, and the *pac*-site was located [1].We have chosen 95% DNA sequence identity as the criterion for species demarcation. We have chosen the previously established cut-off of 70% nucleotide identity of the full genome length as the genus demarcation threshold [2]. As of August 2022, the closest relative, Bacillus phage Wes44, is only 5% identical to Sam46 at the nucleotide level (total BLASTN identity, calculated as % coverage multiplied by % identity), meaning that Sam46 cannot be assigned to any of the existing phage genera.We therefore propose the creation of a new phage genus, *Samaravirus*, containing one phage species, *Samaravirus* s*am46*. The name of the proposed genus is derived from the name of the city (Samara) in Russia, where soil samples containing the phage were collected. |

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**Supporting evidence**

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Figure 1 - The phylogenetic tree constructed in Phylogeny.fr (“one click” mode) using the terminase large subunit sequences of phages Sam46, Sam112 and the closest relatives.

**References**

1) Kazantseva OA, Piligrimova EG, Shadrin AM (2021) vB\_BcM\_Sam46 and vB\_BcM\_Sam112, members of a new bacteriophage genus with unusual small terminase structure. Scientific reports. PMC8190038 [10.1038/s41598-021-91289-x](https://dx.doi.org/10.1038/s41598-021-91289-x)

2) Turner D, Kropinski AM, Adriaenssens EM (2021) A roadmap for genome-based phage taxonomy. Viruses <https://doi.org/10.3390/v13030506>