

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

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| **Code assigned:** | **2020.057B** |  |
| **Short title:** Create 12 new species in the genus *Fernvirus* (formerly *Sitaravirus)* (*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 | July 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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| 2020.057B.R.Fernvirus\_12nsp.xlsx |

**Abstract**

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| We have identified 12 new species in the genus *Sitaravirus,* which we propose to rename *Fernvirus* in keeping with the taxonomy proposed by Dr. Tsourkas. |

**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**

**History:** The genus Sitaravirus was proposed/ratified through TaxoProp 2015.037a-dB with six species. DNA sequence analysis using VIRIDIC [1] reveals numerous new species and strains which have been deposited to GenBank since 2015. We propose to rename it *Fernvirus* in keeping with the wishes and publications of Dr. Tsourkas [2,3].

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; 10) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The phage names which have been highlighted in **red** correspond to existing species recognized by ICTV.

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**N.B. Paenibacillus phage Willow is a strain of *Paenibacillus virus Fern* in this genus**

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| **Phage name** | **Accession** | **Belongs to species** |
| Paenibacillus phage Gryphonian | MH431934 | *Paenibacillus virus Jacopo* |
| Paenibacillus phage Genki | MH454082 | *Paenibacillus virus Jacopo* |
| Paenibacillus phage Bloom | MH454077 | *Paenibacillus virus Jacopo* |
| Paenibacillus phage Arcticfreeze | MH431932 | *Paenibacillus virus Jacopo* |
| Paenibacillus phage DevRi | MH431933 | *Paenibacillus virus Jacopo* |
| Paenibacillus phage Likha | MG727702 | *Paenibacillus virus Shelly* |
| Paenibacillus phage Toothless | MH454084 | *Paenibacillus virus Pagassa* |
| Paenibacillus phage Honeybear | MH431935 | *Paenibacillus virus Pagassa* |
| Paenibacillus phage Willow | KT361650 | *Paenibacillus virus Fern* |
| Paenibacillus phage Saudage | MH454083 | *Paenibacillus virus Lucielle* |
| Paenibacillus phage Kiel007 | MG727696 | *Paenibacillus virus P123* |
| Paenibacillus phage Redbud | KP296794 | *Paenibacillus virus P123* |

**References**

1: Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>

2: Stamereilers C, Fajardo CP, Walker JK, Mendez KN, Castro-Nallar E, Grose JH, Hope S, Tsourkas PK. Genomic Analysis of 48 *Paenibacillus larvae* Bacteriophages. Viruses. 2018 Jul 19;10(7):377. doi: 10.3390/v10070377. PMID: 30029517; PMCID: PMC6070908.

3: Tsourkas PK. *Paenibacillus larvae* bacteriophages: obscure past, promising future. Microb Genom. 2020 Feb;6(2):e000329. doi: 10.1099/mgen.0.000329. PMID: 32111267; PMCID: PMC7067210.