

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

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| **Code assigned:** | **2020.098B** |  |
| **Short title:** Create one new genus (*Marfavirus*) including two new species (*Caudovirales*: *Myoviridae*) | | |
|  | | |

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

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| Andrew M. Kropinski |

**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 | 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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| 2020.098B.R.Marfavirus.xlsx |

**Abstract**

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| Classification of two new related *Klebsiella* phages into a new genus (*Marfavirus*) in the family *Myoviridae* |

**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 is named after the second isolate of its type Klebsiella phage Marfa.

**History:** Phage Marfa was isolated from mixed swine fecal samples from Texas and Michigan on Klebsiella pneumoniae 1776, while vB\_Kpn\_F48 was isolated from sewage wastewaters collected at the Florence Careggi University hospital using *Klebsiella pneumoniae* ST101 as the host (Ciacci et al. 2018). It possesses “a prolated head, approximately 120 nm × 80 nm, which is connected by an apparent collar to a helical, contractile tail (≈100 nm long) that ends with a baseplate provided with tail pins and several tail fibers.”

**Reference:** Ciacci N, D'Andrea MM, Marmo P, Demattè E, Amisano F, Di Pilato V, Fraziano M,

Lupetti P, Rossolini GM, Thaller MC. Characterization of vB\_Kpn\_F48, a Newly Discovered Lytic Bacteriophage for *Klebsiella pneumoniae* of Sequence Type 101. Viruses. 2018 Sep 9;10(9). pii: E482.

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| Marfa |  | [MN044033.1](https://www.ncbi.nlm.nih.gov/nuccore/MN044033.1) | 168.53 | 41.0 | 279 | 7 | 100 | 100 |
| vB\_Kpn\_F48 |  | [MG746602.1](https://www.ncbi.nlm.nih.gov/nuccore/MG746602.1) | 170.76 | 40.8 | 283 | 8(\*) | 88.1 | 91.4 |

**\* NCBI Replicon info indicate none; found using tRNAscan-SE 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]**

**BLASTN homologs:** The next most closely related sequence is that of *Edwardsiella* phage PEi26 which shares 43.1% DNA sequence identity with Marfa [1-3].

**Electron micrograph:** None available

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

A screenshot of a cell phone

Description automatically generated

**References**

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