

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

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| **Code assigned:** | **2020.061B** |  |
| **Short title:** Create one new genus (*Fukuivirus*) including one new species and one existing species (*Microcystis virus Ma-LMM01*)(*Caudovirales*: *Myoviridae*) | | |
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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 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 |  |
| 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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| 2020.061B.R.Fukuivirus |

**Abstract**

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| According to ICTV Master Species List 2018b.v2 *Microcystis virus Ma-LMM01* is listed as unassigned species within the *Myoviridae*. This proposal corrects that problem. |

**Text of proposal**

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**Supporting evidence**

**Proposal: To create a new genus, *Fukuivirus*, to containing two species.**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Ma-LMM01 | [NC\_008562.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_008562.1) | [AB231700.1](https://www.ncbi.nlm.nih.gov/nuccore/AB231700.1) | 162.11 | 46.0 | [184](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/5857/456583|Microcystis virus Ma-LMM01/viral segment Unknown/) | 2 | 100 | 100 |
| MaMV-DC | [NC\_029002.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_029002.1) | [KF356199.1](https://www.ncbi.nlm.nih.gov/nuccore/KF356199.1) | 169.22 | 46.0 | [170](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/42542/462114|Microcystis phage MaMV-DC/viral segment Unknown/) | 3 (\*\*\*) | 93.6 | 81.0 |

**(\*) determined using BLASTN at NCBI [1-3]**

**(\*\*) determined using CoreGenes 3.5 [6]**

**(\*\*\*) while none are listed in the NCBI genomic record, three were discovered using tRNAscan-SE [5]**

**Origin of the name of this taxon:** This genus is named after Fukui which is the capital city of Fukui Prefecture in Japan where *Microcystis aeruginosa* phage Ma-LMM01 was isolated.

**Specific Reference: see** 2009.008a,bB

**BLASTN homologs:** related to two metagenomic fragments - LC425513 & LC425512 [1-3].

**Electron micrograph:** See2009.008a,bB

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Ma-LMM01 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**

1. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.
2. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.
3. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID:26553804.
4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6):e39107. doi: 10.1371/journal.pone.0039107. PMID: 22723939.
5. Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.
6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID:23566564.
7. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147. doi: 10.1371/journal.pone.0011147. PMID: 20593022.
8. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. PMID: 18424797.
9. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. doi: 10.1080/10635150600755453 PMID: 16785212.