

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

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| **Code assigned:** | **2020.109B** |  |
| **Short title:** Create one new genus (*Myosmarvirus*) including two new specieswithin (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew Kropinski |

**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 | May 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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| 2020.109B.R.Myosmarvirus.xlsx |

**Abstract**

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| The genus *Myosmarvirus*, contains of two species, *Serratia virus MyoSmar* and *Serratia virus MTx*. These species possess 68 kb genomes with 3.5 kb direct terminal repeats. They are lytic phages. |

**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**

**Origin of the name of this taxon:** The name is directly derived from that of the first isolate: *Serratia* phage MyoSmar.

**History:** *Serratia* phage MyoSmar and MTx was isolated from Texas (USA) wastewater treatment plant sample and pond water, respectively, using *Serratia marcescens* as the host. *Erwinia* phage vB\_EamM\_TropicalSun was isolated in Indonesia using *Erwinia amylovora* as the host bacterium. MyoSmar has a 3559 bp direct terminal repeat predicted by PhageTerm, while the genome of MTx has a 3566 TR.

**Publications:** None

**BLASTN relationship:** The next closest relative is *Escherichia* phage vB\_EcoM\_WFC, which shares 15.7% DNA sequence identity with MyoSmar [1-3].

**GenBank Summary:**

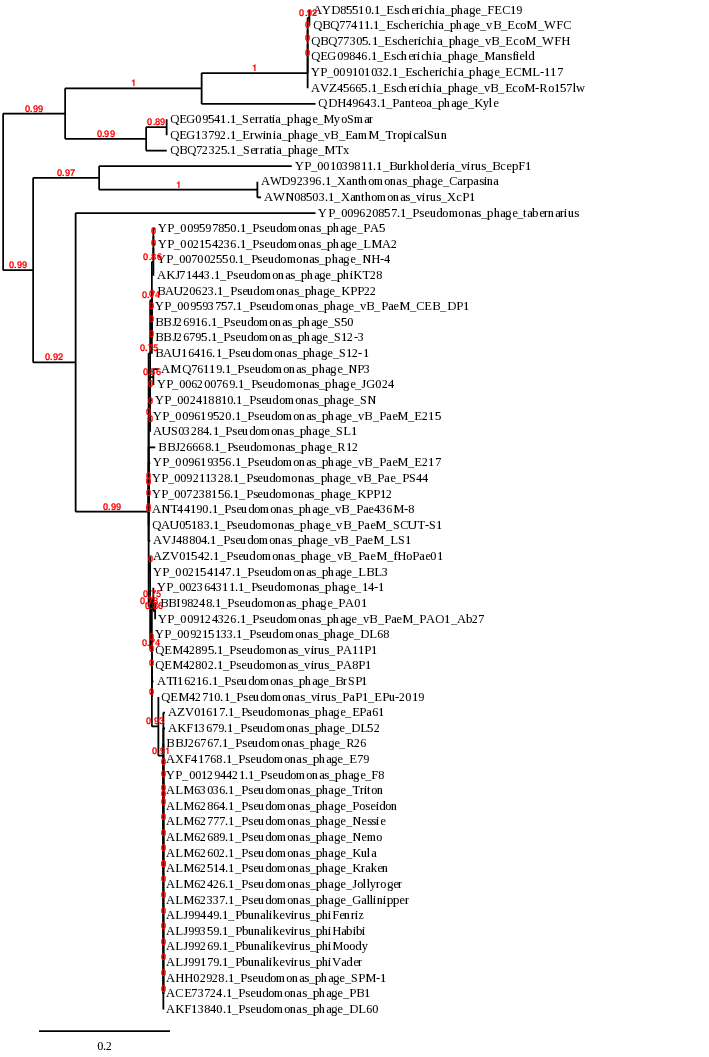
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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| Serratia phage MyoSmar |  | [MN062189.1](https://www.ncbi.nlm.nih.gov/nuccore/MN062189.1) | 68.75 | 49.2 | 105 | 100 | 100 |
| Erwinia phage vB\_EamM\_TropicalSun (\*) |  | [MN013090.1](https://www.ncbi.nlm.nih.gov/nuccore/MN013090.1) | 68.44 | 49.1 | 105 | 97.7 | 95.2 |
| Serratia phage MTx |  | [MK618717.1](https://www.ncbi.nlm.nih.gov/nuccore/MK618717.1) | 68.62 | 49.9 | 103 | 69.7 | 90.5 |

**\* Erwinia phage vB\_EamM\_TropicalSun should be considered a strain of *Serratia virus MyoSmar* in this genus**

**\*\* 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]**

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

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