

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

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| **Code assigned:** | **2020.103B** |  |
| **Short title:** Create one new genus (*Moabitevirus*) including two new species (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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**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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| 2020.103B.R.Moabitevirus.xlsx |

**Abstract**

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| The new genus, *Moabitevirus*, recognizes large *Serratia* myophages which have been identified in the USA and China. |

**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**

**Source of the name of this taxon:** This genus name is directly derived from that of *Serratia* phage Moabite.

**History:** These are both lytic phages. *Serratia marcescens* myophage Moabite was isolated in the USA. [Price L et al. 2019] Phage vB\_SmaM\_2050HW was isolated in China and “has an icosahedral capsid of 110 nm and a contractile tail of 190 nm × 20 nm. The latter consists of a complex system of tail spikes, displaying umbrella-like structures attached to the baseplate.” {Tian C et al. 2019]

**Specific Reference:** Price L, Rohren M, Newkirk H, Liu M, Ramsey J. Complete Genome Sequence of *Serratia marcescens* Myophage Moabite. Microbiol Resour Announc. 2019; 8(29). pii: e00741-19. doi: 10.1128/MRA.00741-19. PubMed PMID: 31320439.

Tian C, Zhao J, Zhang Z, Chen X, Wei X, Li H, Lin W, Ke Y, Hu L, Jiang A, Feng R, Yang W, Jing Y, Yuan J, Luo Y, Zhao X. Identification and molecular characterization of *Serratia marcescens* phages vB\_SmaA\_2050H1 and vB\_SmaM\_2050HW. Arch Virol. 2019;164(4):1085-1094. doi: 10.1007/s00705-019-04169-1. Epub 2019 Feb 20. PubMed PMID: 30788604.

**GenBank Summary:**

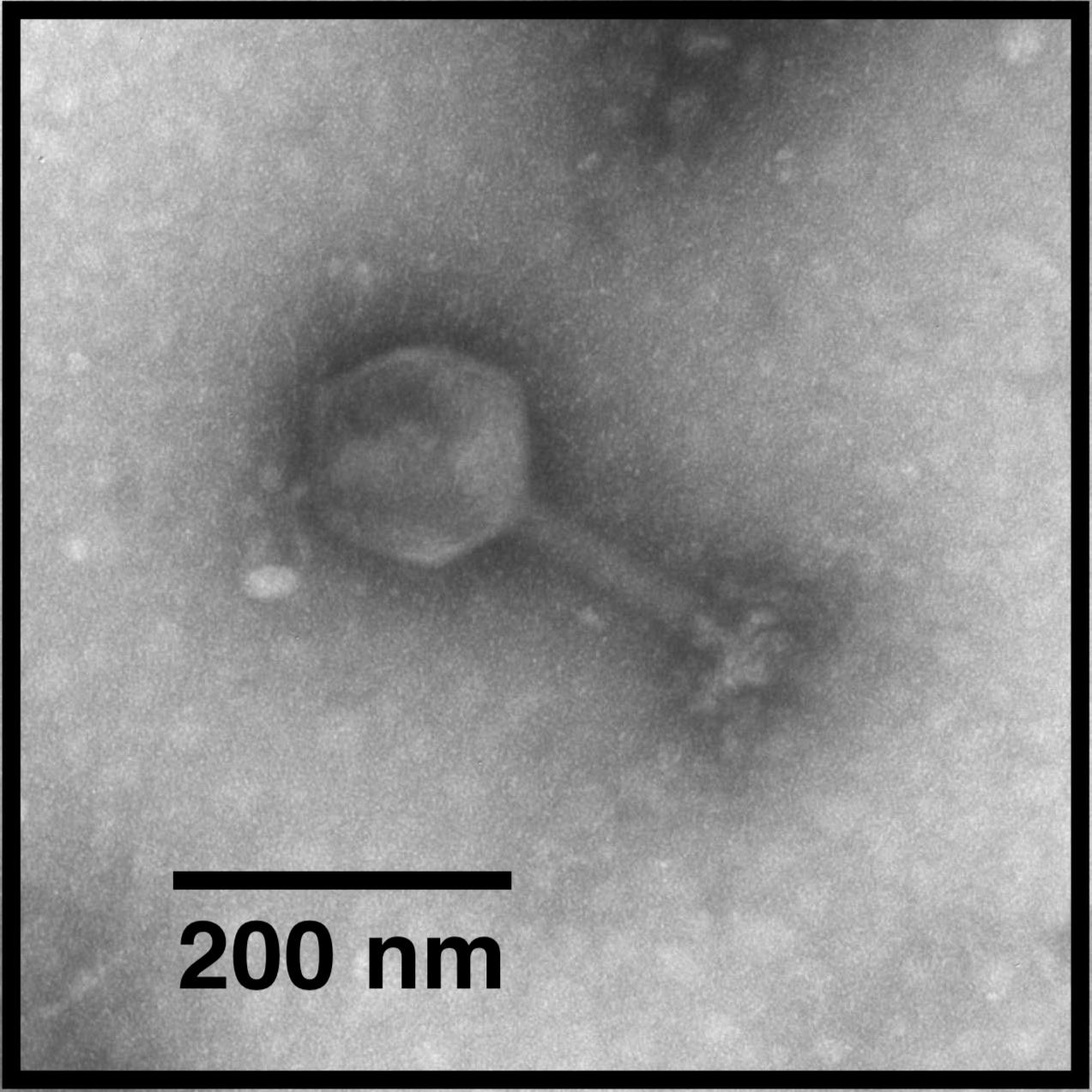
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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Moabite |  | [MK994515.1](about:blank) | 273.93 | 46.8 | [338](about:blank#!/proteins/81889/590113|Serratia phage Moabite/viral segment/) | 2 | 100 | 100 |
| vB\_SmaM\_ 2050HW |  | [MF285618.1](about:blank) | 276.03 | 46.8 | [363](about:blank#!/proteins/63791/466412|Serratia phage 2050HW/viral segment/) | 2(\*) | 94.1 | 92.0 |

**\* None indicated in Replicon Info; discovered using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](about:blank) **[5]**

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**BLASTN homologs:** Genomic orphans [1-3].

**Electron micrograph:**

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Imaged by: Lauren Lessor

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Moabite 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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10. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. [http://kronos.icbm.uni-oldenburg.de/viridic/](about:blank)