

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

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| **Code assigned:** | **2021.071B** |  |
| **Short title:** Create one new genus (*Rosariovirus*) including one new species (*Caudoviricetes*) | | |
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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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| Caudovirales Study Group, Bacterial 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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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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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 2021 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.071B.R.Rosariovirus |

**Abstract**

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| Mycobacterium phage Weido19ES is a temperate siphovirus which is currently unclassified in GenBank and by the Actinobacteriophage Database. This proposal will create a new genus, *Rosariovirus*, for this and similar phages. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic distance calculator VIRIDIC [3].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [4] | |

**Supporting evidence**

**Source of the name of this taxon:** This genus is named after Universidad Nacional de Rosario (Argentina) where the first representative of this taxon, Mycobacterium phage Weirdo19ES, was isolated.

**History:** Temperate phage Weirdo19ES is a novel singleton mycobacteriophage that selects for glycolipid deficient phage-resistant *Mycobacterium smegmatis* mutants [Suarez CA et al. 2020]

**Specific Reference:** Suarez CA, Franceschelli JJ, Tasselli SE, Morbidoni HR. Weirdo19ES is a novel singleton mycobacteriophage that selects for glycolipid deficient phage-resistant M. smegmatis mutants. PLoS One. 2020 May 1;15(5):e0231881. doi: 10.1371/journal.pone.0231881. PMID: 32357186; PMCID: PMC7194413.

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Mycobacterium phage Weirdo19ES | [MN103533.1](https://www.ncbi.nlm.nih.gov/nuccore/MN103533.1) | 52.58 | 70.2 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/91526/898731%7CMycobacterium%20phage%20Weirdo19/viral%20segment/) | 0 | 100 | 100 |
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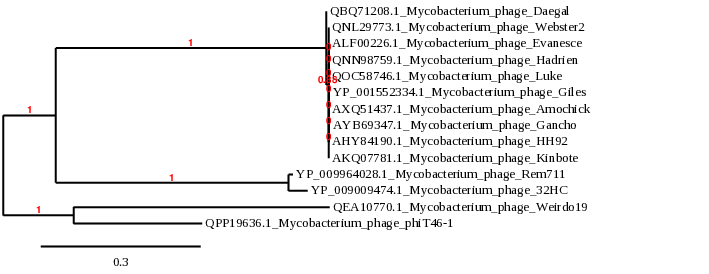
**(\*) Determined using BLASTN [1-3]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[4]**

**BLASTN homologs:** Genomic orphan [1-3]. The closest relative is Mycobacterium phage phiT46-1 with which it shares 17.2% DNA similarity.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of Weirdo19 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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