

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

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| **Code assigned:** | **2021.013B** |  |
| **Short title:** Create two new species in the genus *Brujitavirus* (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial Viruses Subcommittee, Actinobacteriophages 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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| --- | --- |
| **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 |  |
| 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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| 2021.013B.R.Brujitavirus\_new\_species |

**Abstract**

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| The genus *Brujitavirus* was established by Taxonomy Proposal 2017.004B and contains two species. Our reanalysis using genomic (VIRIDIC), proteomic (ViPTree, CoreGenes 3.5) and phylogenetic analyses reveals two additional members – *Brujitavirus xula* and *Brujitavirusvirus HC*. All of these phages belong to Actinobacteriophage Database Cluster I/Subcluster I1. |

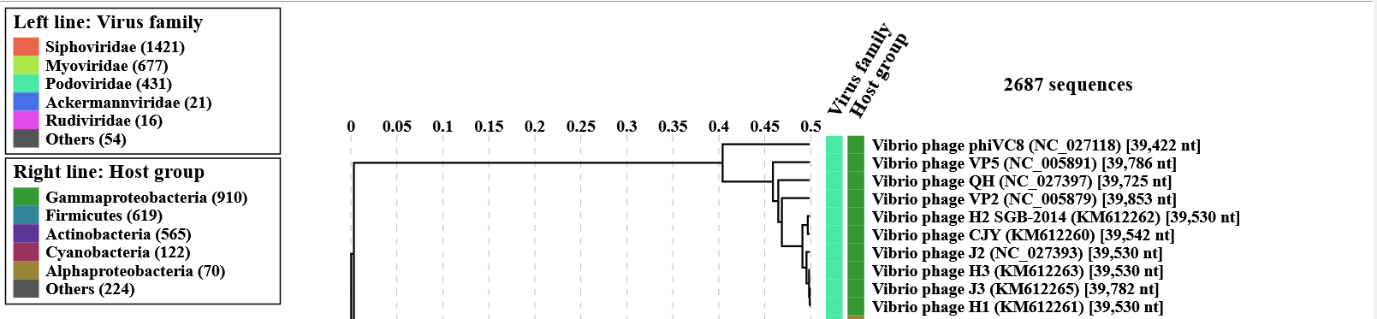
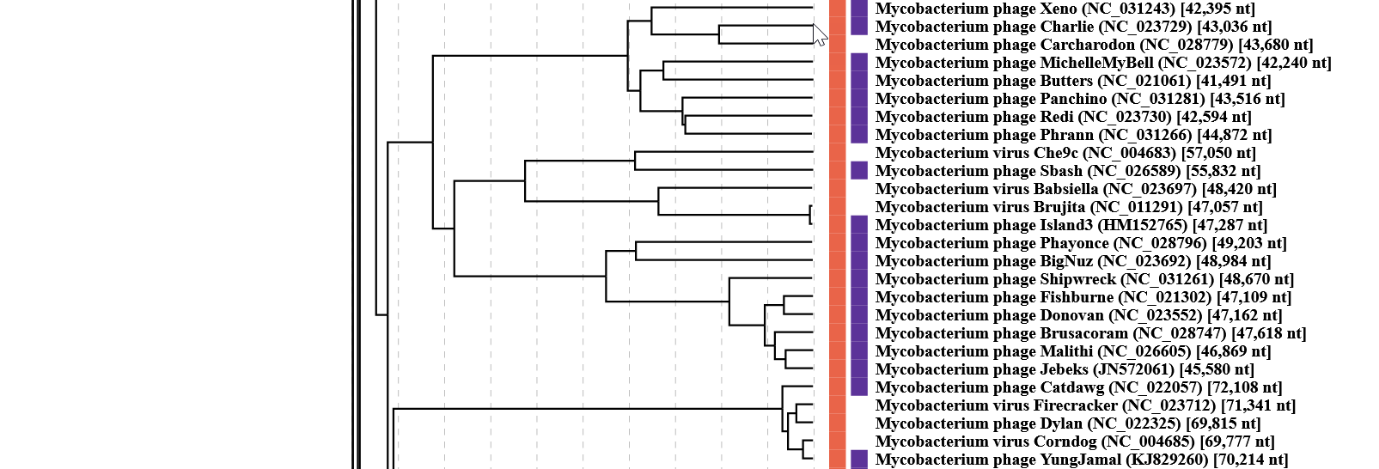
**Text of proposal**

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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 [17]. | |

**Supporting evidence**

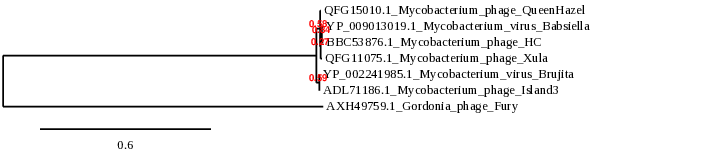
**Molecular analysis:**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. Brujita is marked with a **red star**


**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. (attached)

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit of some of these 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 [16] for details."

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**Proposal: To create two new species in the genus *Brujitavirus***

**Source of the name of this taxon:** This genus is named after the first virus of its type, Mycobacterium phage Brujita.

**History:** The genus Brujitavirus was established by Taxonomy Proposal 2017.004B and contains two species Mycobacterium virus Brujita and Mycobacterium virus Babsiella.

**Specific Reference:** None

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Brujita | NC\_011291.1 | FJ168659.1 | 47.17 | 66.8 | 75 | 100 | 100 |
| Mycobacterium phage Xula |  | [MN234195.1](https://www.ncbi.nlm.nih.gov/nuccore/MN234195.1) | 48.54 | 66.7 | [74](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84827/708384%7CMycobacterium%20phage%20Xula/viral%20segment/) | 64.9 | 70.3 |
| Mycobacterium phage HC |  | [AP018487.1](https://www.ncbi.nlm.nih.gov/nuccore/AP018487.1) | 46.31 | 67.2 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68387/369534%7CMycobacterium%20phage%20HC/viral%20segment/) | 66.9 | 70.3 |

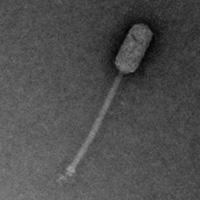
**(\*) Determined using VIRIDIC [6]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[7]**

**Strains:**

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| **Phage Name** | **Accession No.** | **Strain of:** |
| Mycobacterium phage Island3 | HM152765.1 | *Brujitavirus brujita* |
| Mycobacterium phage QueenHazel | MN234236.1 | *Brujitavirus xula* |

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Brujita (https://phagesdb.org/phages/Brujita/). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.

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