

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

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| **Code assigned:** | **2021.057B** |  |
| **Short title:** In the subfamily *Nclasvirinae,* abolish two genera (*Redivirus*, *Buttersvirus*), move and rename six species, rename three species and create nine new species in the single genus *Charlievirus* (*Caudoviricetes*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Actinobacteriophages 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 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2021.057B.R.Nclasvirinae |

**Abstract**

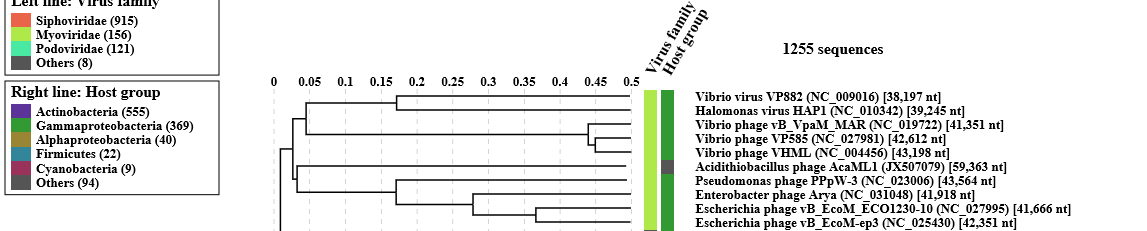
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| The subfamily *Nclasvirinae* currently consists of three genera – *Redivirus, Charlievirus* and *Buttersvirus*. These and their related viruses are grouped in The Actinobacteriophage Database group into Cluster N, with no subclusters. We have reanalyzed this group of phages and are of the opinion that the separation cannot be justified and so propose to amalgamate the three genera into a single genus *Charlievirus*. |

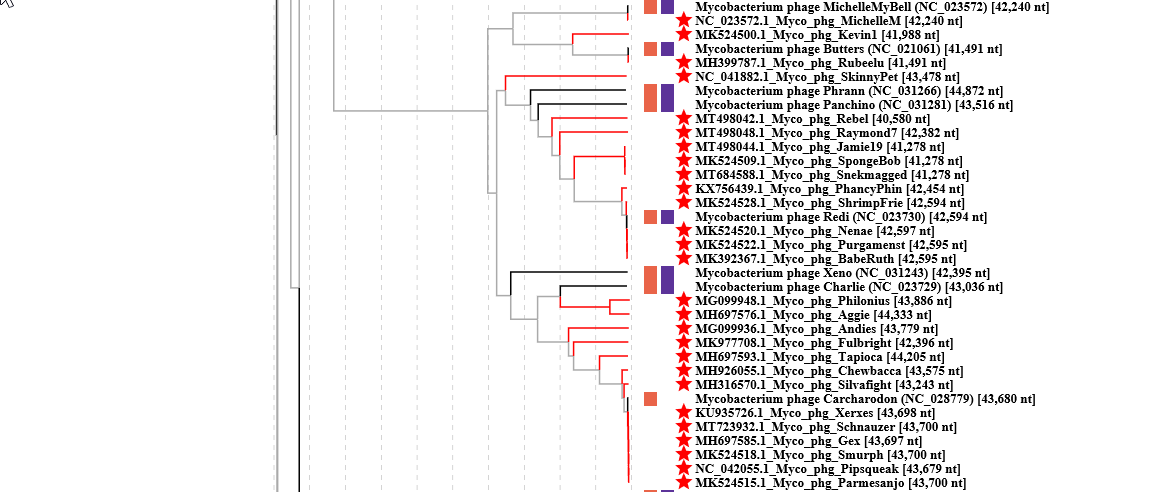
**Text of proposal**

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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.  **Subfamily demarcation criteria:** Not applicable to this proposal. Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity and that the genera form a clade in a marker tree phylogeny. [9] | |

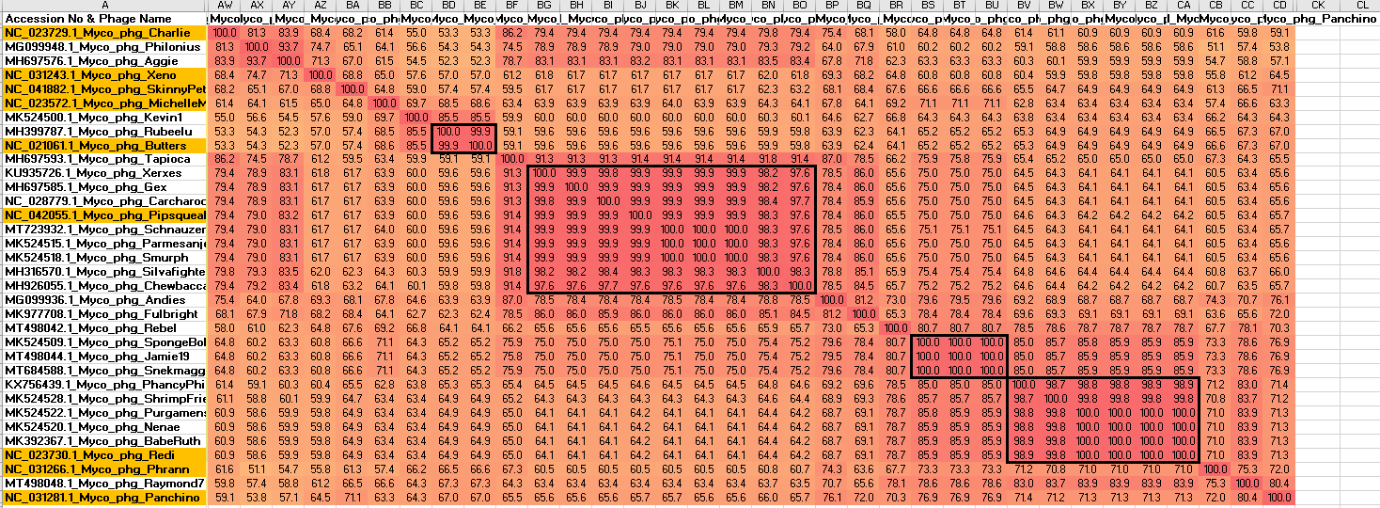
**Supporting evidence**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. The phages of interest are indicated with **red lines**.

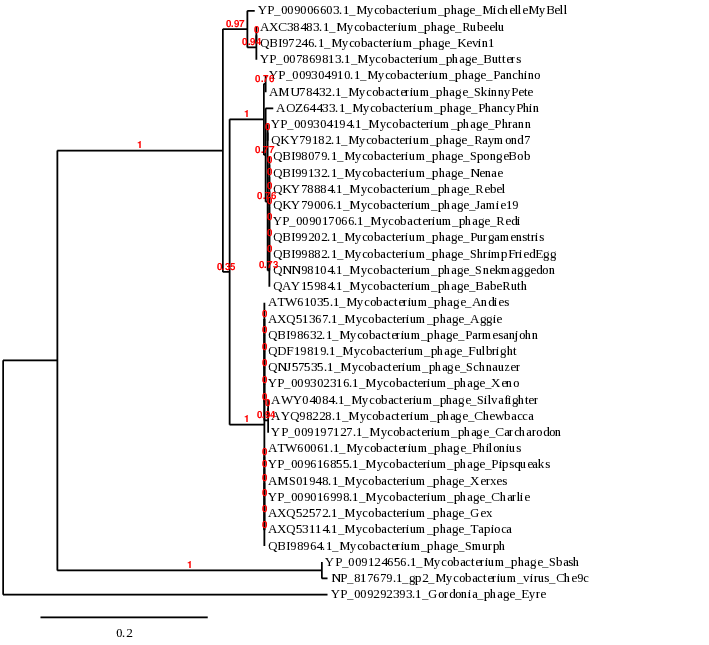




**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. The gold-coloured names represent current taxa, while the black boxed sequences are strains.



**Phylogeny:** The phylogenetic tree was constructed using the major capsid proteins of *Nclasvirinae* phages with phylogeny.fr in “one click” mode [5]. "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 [6] for details."

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**In each of these cases and with BLASTN analysis at NCBI there is some evidence for the creation of separate genera. Unfortunately, collectively these analyses create a confusing picture probably as a results of horizontal genome transfer. Therefore we propose to amalgamate those phages which are currently classified in the three genera into a single genus, *Charlievirus*.**

**Proposals:**

**To transfer the membership of the Redivirus and Buttersvirus to Charlievirus and add nine (9) new species**

**Source of the name of this taxon:** This taxon was named directly from the first virus of its type, Mycobacterium phage Charlie

**History:** The *Charlievirus* genus was created through Taxonomy Proposal 2017.010B. The Actinobacteriophage Database places this phage in Cluster N.

**Electron micrograph:** NA

**Specific Reference:** Hatfull GF; Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science Program; KwaZulu-Natal Research Institute for Tuberculosis and HIV Mycobacterial Genetics Course Students; Phage Hunters Integrating Research and Education Program. Complete genome sequences of 138 mycobacteriophages. J Virol. 2012 Feb;86(4):2382-4. doi: 10.1128/JVI.06870-11. PMID: 22282335; PMCID: PMC3302410.

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Charlie | [JN256079.1](https://www.ncbi.nlm.nih.gov/nuccore/JN256079.1) | 43.04 | 66.3 | [68](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/24533/460532%7CMycobacterium%20phage%20Charlie/viral%20segment%20Unknown/) | 0 | 100 | 100 |
| Mycobacterium phage Raymond7 | [MT498048.1](https://www.ncbi.nlm.nih.gov/nuccore/MT498048.1) | 42.38 | 66.0 | [63](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92672/916861%7CMycobacterium%20phage%20Raymond7/viral%20segment/) | 0 | 59.8 | 72.1 |
| Mycobacterium phage Philonius | [MG099948.1](https://www.ncbi.nlm.nih.gov/nuccore/MG099948.1) | 43.89 | 66.5 | [72](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68192/369339%7CMycobacterium%20phage%20Philonius/viral%20segment/) | 0 | 81.3 | 82.3 |
| Mycobacterium phage Aggie | [MH697576.1](https://www.ncbi.nlm.nih.gov/nuccore/MH697576.1) | 44.33 | 66.5 | [67](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72100/400236%7CMycobacterium%20phage%20Aggie/viral%20segment/) | 0 | 83.9 | 80.9 |
| Mycobacterium phage Kevin1 | [MK524500.1](https://www.ncbi.nlm.nih.gov/nuccore/MK524500.1) | 41.99 | 66.2 | [69](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76392/468447%7CMycobacterium%20phage%20Kevin1/viral%20segment/) | 0 | 55.0 | 69.1 |
| Mycobacterium phage Andies | [MG099936.1](https://www.ncbi.nlm.nih.gov/nuccore/MG099936.1) | 43.78 | 66.2 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/68183/369330%7CMycobacterium%20phage%20Andies/viral%20segment/) | 0 | 75.4 | 77.9 |
| Mycobacterium phage Fulbright | [MK977708.1](https://www.ncbi.nlm.nih.gov/nuccore/MK977708.1) | 42.40 | 66.3 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82344/596115%7CMycobacterium%20phage%20Fulbright/viral%20segment/) | 0 | 68.1 | 72.1 |
| Mycobacterium phage Rebel | [MT498042.1](https://www.ncbi.nlm.nih.gov/nuccore/MT498042.1) | 40.58 | 66.5 | [66](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92673/916862%7CMycobacterium%20phage%20Rebel/viral%20segment/) | 0 | 58.0 | 64.7 |
| Mycobacterium phage Tapioca | [MH697593.1](https://www.ncbi.nlm.nih.gov/nuccore/MH697593.1) | 44.21 | 66.1 | [70](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72114/400250%7CMycobacterium%20phage%20Tapioca/viral%20segment/) | 0 | 86.2 | 86.8 |
| Mycobacterium phage Jamie19 | [MT498044.1](https://www.ncbi.nlm.nih.gov/nuccore/MT498044.1) | 41.28 | 66.2 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/92670/916859%7CMycobacterium%20phage%20Jamie19/viral%20segment/) | 0 | 64.9 | 73.5 |

**(\*) Determined using VIRIDIC [3]**

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

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**References:**

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