

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

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| **Code assigned:** | **2021.016B** |  |
| **Short title:** Create one new subfamily (*Ceeclamvirinae)* including two genera (*Caudoviricetes*) | | |
|  | | |

**Author(s) and email address(es)**

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| Andrew M. Kropinski |

**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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| 2021.016B.R.Ceeclamvirinae |

**Abstract**

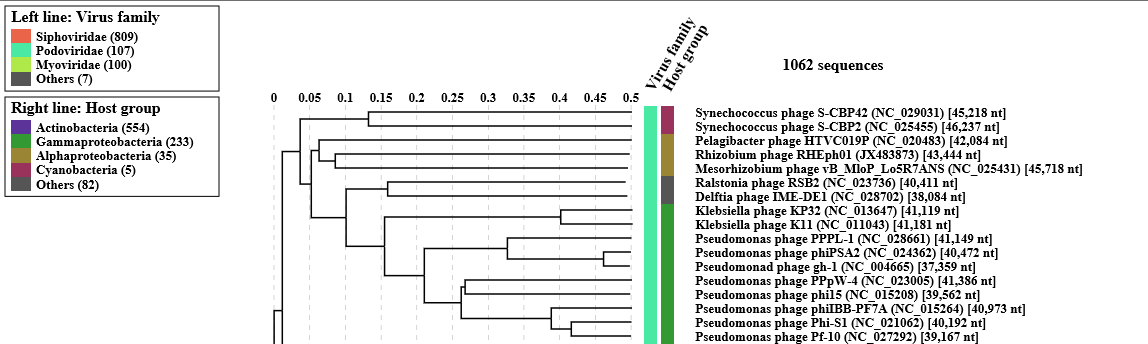
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| The genus I3-like viruses (later renamed *Bixzunavirus*) was originally established through Taxonomy Proposal 2005.139-42B. It currently contains eight species. According to the Actinobacteriophage Database these and related phages belong to Cluster C/Subcluster C1. Due to the rapid growth of this cluster we have reanalyzed the related phages in GenBank. The *Bixzunavirus* and *Myrnavirus* genera fit within a single subfamily the members of which possess, on average, genomes of 160.0 kb (65.0 mol%G+C) and encode for 232 proteins and 34 tRNA. At the DNA level these phages share at least 25.5% DNA similarity.  CoreGenes 3.5 analysis (<http://binf.gmu.edu:8080/CoreGenes3.5/>) revealed 89 homologs (38.4%) including portal protein, thymidylate synthase, RNA ligase, major capsid protein, tail sheath protein, two tail assembly chaperones, baseplate wedge protein, DNA helicase, peptidyl tRNA hydrolase, aminotransferase, DNA primase, DnaJ-like chaperonin, ssDNA binding protein, RecA-like DNA recombinase, glycosyltransferase, and polynucleotide kinase |

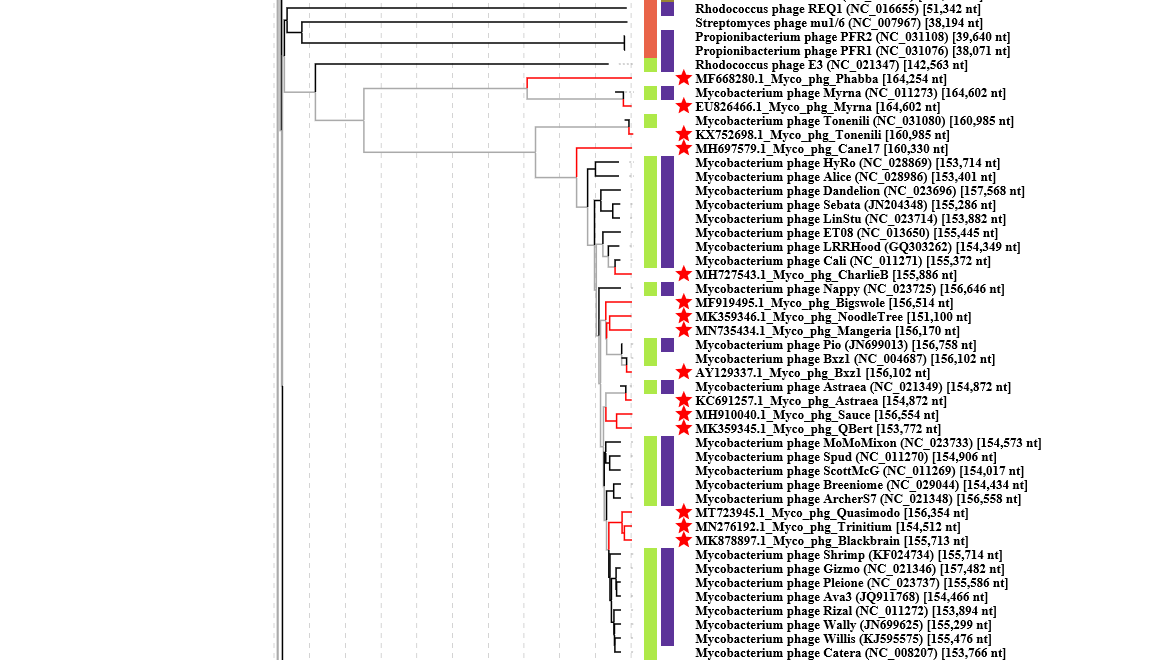
**Text of proposal**

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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:** 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] | |

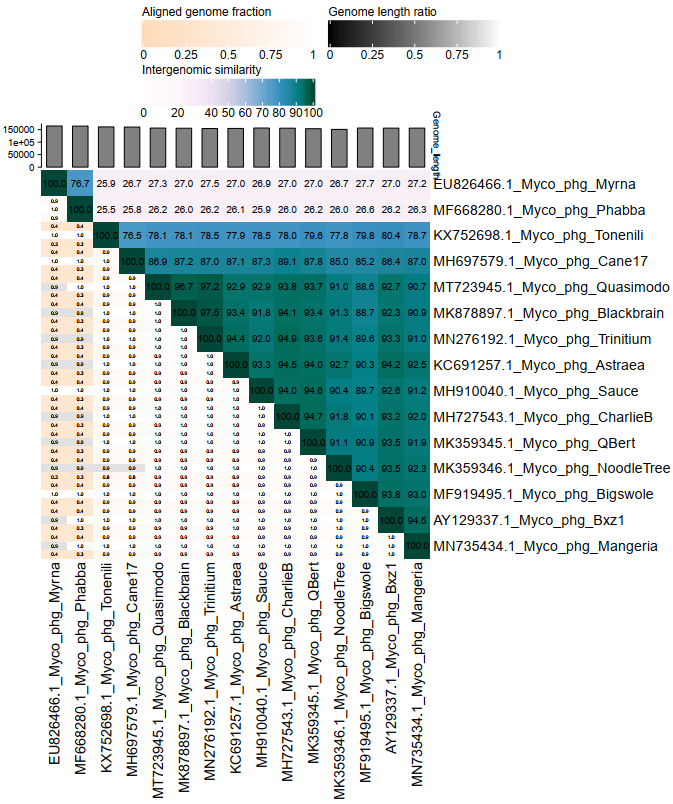
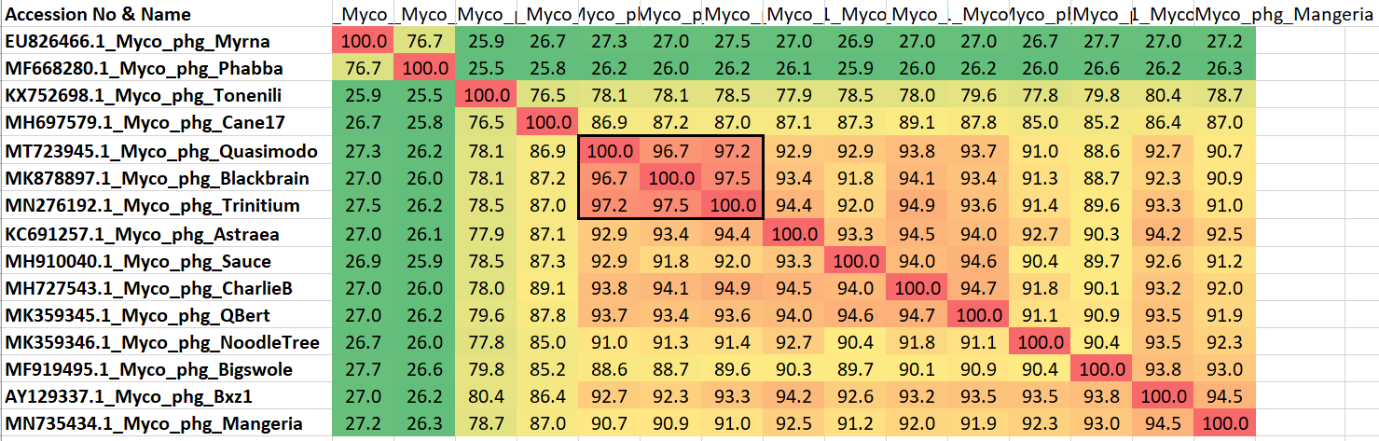
**Supporting evidence**

**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**.

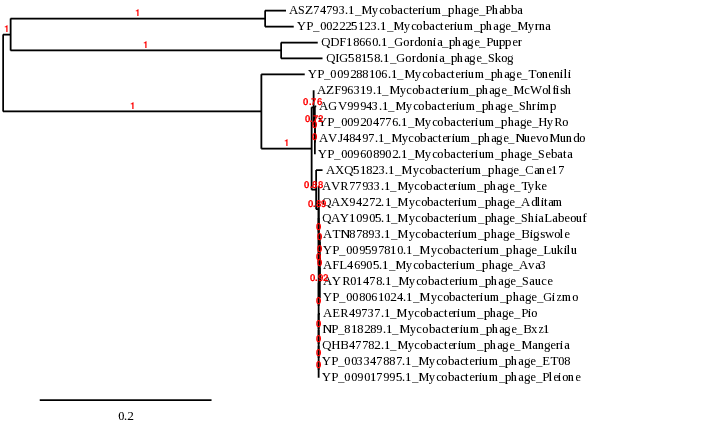




**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes. Strains are indicated in black boxes.



**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit proteins of these 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." The new genera are indicated with arrows or boxes.

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**Proposals:**

1. **To create a new genus, *Myrnavirus* with two single species**
2. **To add ten (10) new species to the genus *Bixzunavirus***
3. **To create a new subfamily, *Ceeclamvirinae***

**To create a new genus, *Myrnavirus* with two species**

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Mycobacterium phage Myrna.

**History:** Lytic Mycobacterium myovirus Myrna was isolated in 2005 by M. Klinex (Upper St. Clair High School, Upper St. Clair, PA, USA) from soil using Mycobacterium smegmatis mc²155 as the host bacterium. This was part of the Phage Hunters Integrating Research and Education program. The genome is circularly permuted. The Actinobacteriophage Database places this phage in Cluster C, Subcluster C2.

**Electron micrograph:** Electron micrographs of negatively stained Mycobacterium phage Myrna (https://phagesdb.org/phages/Myrna/). 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.

**Specific Reference:** None

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Myrna | [EU826466.1](https://www.ncbi.nlm.nih.gov/nuccore/EU826466.1) | 164.6 | 65.4 | [229](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/6296/456711%7CMycobacterium%20phage%20Myrna/viral%20segment%20Unknown/) | 41 | 100 | 100 |
| Mycobacterium phage Phabba | [MF668280.1](https://www.ncbi.nlm.nih.gov/nuccore/MF668280.1) | 164.25 | 65.2 | [244](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63861/466481%7CMycobacterium%20phage%20Phabba/viral%20segment/) | 37 | 76.7 | 90.0 |

**(\*) 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]**

**To add ten (10) new species to the genus *Bixzunavirus***

**Source of the name of this taxon:** This taxon is named after the first representative of its type, Mycobacterium phage Bxz1.

**History:** This genus (originally I3-like viruses, later renamed *Bixzunavirus*) was establish through Taxonomy Proposal 2005.139-42B. The Actinobacteriophage Database places this phage in Cluster C, Subcluster C1. There are currently >100 strains in this genus.

**Electron micrograph:** NA

**Specific Reference:** Pedulla ML, Ford ME, Houtz JM, Karthikeyan T, Wadsworth C, Lewis JA, Jacobs-Sera D, Falbo J, Gross J, Pannunzio NR, Brucker W, Kumar V, Kandasamy J, Keenan L, Bardarov S, Kriakov J, Lawrence JG, Jacobs WR Jr, Hendrix RW, Hatfull GF. Origins of highly mosaic mycobacteriophage genomes. Cell. 2003 Apr 18;113(2):171-82. doi: 10.1016/s0092-8674(03)00233-2. PMID: 12705866.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Mycobacterium phage Bxz1 | [AY129337.1](https://www.ncbi.nlm.nih.gov/nuccore/AY129337.1) | 156.10 | 64.8 | [225](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/4518/892560%7CMycobacterium%20phage%20Bxz1/viral%20segment%20Unknown/) | 28 | 100 | 100 |
| Mycobacterium phage Astraea | [KC691257.1](https://www.ncbi.nlm.nih.gov/nuccore/KC691257.1) | 154.87 | 64.7 | [232](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/17871/460072%7CMycobacterium%20phage%20Astraea/viral%20segment%20Unknown/) | 31 | 94.2 | 92.4 |
| Mycobacterium phage Bigswole | [MF919495.1](https://www.ncbi.nlm.nih.gov/nuccore/MF919495.1) | 156.51 | 64.8 | [237](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/64197/466604%7CMycobacterium%20phage%20Bigswole/viral%20segment/) | 33 | 93.8 | 95.1 |
| Mycobacterium phage Cane17 | [MH697579.1](https://www.ncbi.nlm.nih.gov/nuccore/MH697579.1) | 160.33 | 64.6 | [223](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71994/399866%7CMycobacterium%20phage%20Cane17/viral%20segment/) | 32 | 86.4 | 84.0 |
| Mycobacterium phage CharlieB | [MH727543.1](https://www.ncbi.nlm.nih.gov/nuccore/MH727543.1) | 155.89 | 64.7 | [232](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73756/418194%7CMycobacterium%20phage%20CharlieB/viral%20segment/) | 30 | 93.2 | 90.7 |
| Mycobacterium phage Mangeria | [MN735434.1](https://www.ncbi.nlm.nih.gov/nuccore/MN735434.1) | 156.17 | 64.8 | [234](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86781/756046%7CMycobacterium%20phage%20Mangeria/viral%20segment/) | 31 | 94.5 | 95.6 |
| Mycobacterium phage NoodleTree | [MK359346.1](https://www.ncbi.nlm.nih.gov/nuccore/MK359346.1) | 151.10 | 64.7 | [225](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75982/446640%7CMycobacterium%20phage%20NoodleTree/viral%20segment/) | 32 | 93.5 | 91.6 |
| Mycobacterium phage QBert | [MK359345.1](https://www.ncbi.nlm.nih.gov/nuccore/MK359345.1) | 153.77 | 64.8 | [225](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/75981/446639%7CMycobacterium%20phage%20QBert/viral%20segment/) | 32 | 93.5 | 92.0 |
| Mycobacterium phage Quasimodo | [MT723945.1](https://www.ncbi.nlm.nih.gov/nuccore/MT723945.1) | 156.35 | 64.6 | [235](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94297/980574%7CMycobacterium%20phage%20Quasimodo/viral%20segment/) | 33 | 92.7 | 93.8 |
| Mycobacterium phage Sauce | [MH910040.1](https://www.ncbi.nlm.nih.gov/nuccore/MH910040.1) | 156.55 | 64.7 | [230](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73826/418524%7CMycobacterium%20phage%20Sauce/viral%20segment/) | 31 | 92.6 | 93.3 |
| Mycobacterium phage Tonenili | [KX752698.1](https://www.ncbi.nlm.nih.gov/nuccore/KX752698.1) | 160.98 | 64.1 | [258](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46282/462678%7CMycobacterium%20phage%20Tonenili/viral%20segment/) | 32 | 80.4 | 92.0 |

**(\*) 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]**

**To create a new subfamily, *Ceeclamvirinae***

**Source of the name of this taxon:** All these phages are classified into Cluster C by the Actinobacteriophage Database. As with other similar subfamilies we have named them Cee Cluster Actinophage Myovirus.

**Rationale:**

The *Bixzunavirus* and *Myrnavirus* genera fit within a single subfamily the members of which possess, on average, genomes of 160.0 kb (65.0 mol%G+C) and encode for 232 proteins and 34 tRNA. At the DNA level these phages share at least 25.5% DNA similarity.

CoreGenes 3.5 analysis (<http://binf.gmu.edu:8080/CoreGenes3.5/>) revealed 89 homologs (38.4%) including portal protein, thymidylate synthase, RNA ligase, major capsid protein, tail sheath protein, two tail assembly chaperones, baseplate wedge protein, DNA helicase, peptidyl tRNA hydrolase, aminotransferase, DNA primase, DnaJ-like chaperonin, ssDNA binding protein, RecA-like DNA recombinase, glycosyltransferase, and polynucleotide kinase

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