

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

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| **Code assigned:** | **2020.036B** |  |
| **Short title:** Create one new genus of *Mycobacterium* siphoviruses (*Cornievirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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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 | June 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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| 2020.036B.R.Cornievirus.xlsx |

**Abstract**

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| The Actinobacteriophage Database classifies Mycobacterium phage Cornie to the F cluster, specifically subcluster F5. In this proposal we propose a new genus, *Cornievirus* for this subcluster. |

**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 the first virus of its type Mycobacterium phage Cornie.

**History:** (Subgroup F5) – The pseudo-temperate (N.B. it has a non-functional integrase) phage Cornie (<https://phagesdb.org/phages/Cornie/>) was isolated in by Justin Lugo in 2016 from Fayetteville (NC USA) soil using *Mycobacterium* *smegmatis* mc²155 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science Program. The genome of this phage has 9 nt 3’-cohesive termini (CCCGGCCCA).

**Electron micrograph:** None available

**Reference:** None

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein |
| Cornie |  | [MN908688.1](https://www.ncbi.nlm.nih.gov/nuccore/MN908688.1) | 56.39 | 61.4 | [101](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/87893/811653|Mycobacterium phage Cornie/viral segment/) |

**BLASTN homologs:** BLASTN analysis reveals that the closest relative is Mycobacterium phage Kingsley [1-3]. It shares 48 % DNA sequence identity with Cornie.

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of phages related to Mycobacterium Cornie 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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