

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

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| **Code assigned:** | **2020.164B** |  |
| **Short title:** Create one new genus (*Thetabobvirus*) including three 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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| 2020.164B.R.Thetabobvirus.xlsx |

**Abstract**

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| The Actinobacteriophage Database F cluster needs attention by ICTV. In this proposal we tackle subcluster F4 creating a new genus *Thetabobvirus*. |

**Text of proposal**

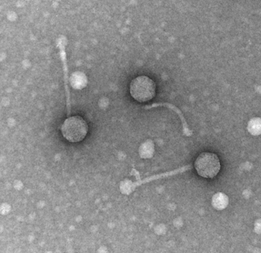
|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. | |

**Supporting evidence**

**Source of the name of this taxon:** The name of this genus is directly derived from the name of Mycobacterium phage ThetaBob.

**History:** (Subgroup F4) – Temperate phages Renaud18, TChen and ThetaBob are recognized by the Actinobacteriophage Database as being part of subcluster F4. Phage ThetaBob was the first fully characterized virus of this group. It was isolated in by Nathan Terry in 2014 from undisclosed material in Hot Springs, AR USA 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 10 nt 3’-cohesive termini (CGGATGGCTT).

**Electron micrograph:** None available for ThetaBob. Electron micrograph of negatively stained Mycobacterium phage TChen (<https://phagesdb.org/phages/TChen/>) - Limited permission was granted by The Actinobacteriophages Database, 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.



**No specific reference**

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | % common proteins (\*\*) |
| ThetaBob |  | [MK977709.1](https://www.ncbi.nlm.nih.gov/nuccore/MK977709.1) | 56.71 | 61.7 | [106](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82351/596122|Mycobacterium phage ThetaBob/viral segment/) | 100 | 100 |
| Renaud18 |  | [MH651187.1](https://www.ncbi.nlm.nih.gov/nuccore/MH651187.1) | 58.08 | 61.7 | [112](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72155/400291|Mycobacterium phage Renaud18/viral segment/) | 58.9 | 61.3 |
| TChen |  | [MH077585.1](https://www.ncbi.nlm.nih.gov/nuccore/MH077585.1) | 57.74 | 62.3 | [101](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/69676/379838|Mycobacterium phage TChen/viral segment/) | 64.4 | 63.2 |

**(\*) Determined using BLASTN at NCBI [1-3]**

**(\*\*) Determined using CoreGenes 3.5 [6]**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of these Mycobacterium 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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