

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

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| **Code assigned:** | **2020.154B** |  |
| **Short title:** Create one new genus (*Sleepyheadvirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew Kropinski |

**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 | May 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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| 2020.154B.R.Sleepyheadvirus.xlsx |

**Abstract**

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| This creates a taxon for *Rhodococcus* phage Sleepyhead, a singleton in The Actinobacteriophage Database. |

**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:** The name of this genus is derived directly from that of the type virus Rhodococcus phage Sleepyhead.

**History:** Phage Sleepyhead was isolated in 2018 by Trevor Dugal and Dylan Taplin (University of Maine, Orono ME, USA) using *Rhodococcus erythropolis* NRRL B-1574 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses 9 bp 3' Sticky Overhang ends (ACACGGCGA). The Actinobacteriophage Database classifying this phage as a Singleton.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Sleepyhead |  | [MK967380.1](https://www.ncbi.nlm.nih.gov/nuccore/MK967380.1) | 43.94 | 61.0 | [67](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82910/624783|Rhodococcus phage Sleepyhead/viral segment/) | 0 |

**BLASTN homologs:** Genomic orphan [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Sleepyhead and related 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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