

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

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| **Code assigned:** | **2020.049B** |  |
| **Short title:** Create one new species in the genus *Ruthyvirus* (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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|  |  |
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**Corresponding author**

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| Andrew M. 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 | 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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| 2020.049B.R.Dumpstervirus.xlsx |

**Abstract**

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| This proposal recognizes two distinct viruses classified by The Actinobacteriophage Database to Cluster DW as being members of *Ruthyvirus*. |

**Text of proposal**

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**Supporting evidence**

**Proposal: To add one new species to the *Ruthyvirus***

**History:** Lytic Gordonia phage DumpsterDude was isolated in 2018 by Christian Hines (Durham Technical Community College) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science Program. It was isolated from soil using *Gordonia rubripertincta* NRRL B-16540 as the host bacterium. The Actinobacteriophage Database classifies this phage and its relatives to Cluster DW. The genome possesses 10 nt 3' Sticky Overhangs with the sequence – TGCCGAGGTA.

**Source of the name of this taxon:** NA

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Proteins | tRNAs | Overall % DNA sequence identity (\*) | % Common proteins (\*\*) |
| Ruthy | [MH536826.1](about:blank) | 51.27 | 66.7 | [73](about:blank#!/proteins/71937/399809|Gordonia phage Ruthy/viral segment/) | 0 | 100 | 100 |
| DumpsterDude | [MT024859.1](about:blank) | 52.02 | 66.6 | [71](about:blank#!/proteins/88397/838858|Gordonia phage DumpsterDude/viral segment/) | 0 | 66.8 | 80.3 |
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**(\*) determined using BLASTN at NCBI [1-3]**

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

**BLASTN homologs:** The next most related phage based upon BLASTN analysis at NCBI [1-3] is Gordonia phage DelRio which shares 32.1% DNA sequence identity with DumpsterDude.

**Electron micrograph:** Electron micrograph of negatively stained Gordonia phage DumpsterDude (left panel) and Ruthy (right panel) ([https://phagesdb.org/phages/DumpsterDude/](about:blank); [https://phagesdb.org/phages/Ruthy/](about:blank)) - Limited permission was granted by The

Actinobacteriophages Database, funded by the Howard Hughes Medical Institute, to use this

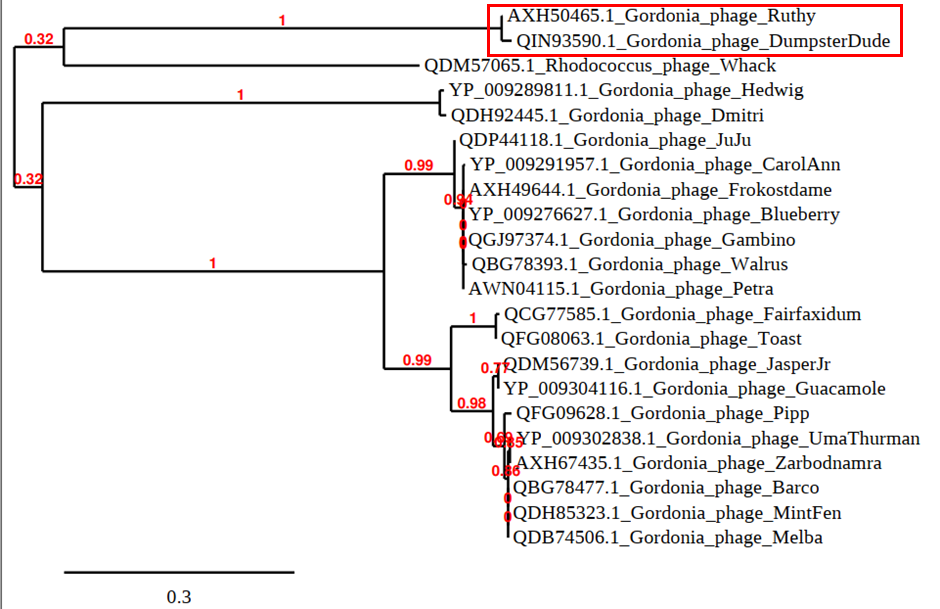
electron micrograph for this taxonomy proposal; it cannot be reused without permission of The

Actinobacteriophages Database

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**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of phage DumpsterDude 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."

**TerL protein**

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**References**

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