

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

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| **Code assigned:** | **2021.070B** |  |
| **Short title:** Create three new species in the genus *Rerduovirus* (*Caudoviricetes*) | | |
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**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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| Actinobacteriophage 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 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.070B.R.Rerduovirus\_new\_species |

**Abstract**

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| Rhodococcus temperate siphovirus RER2 is currently classified in the Actinobacteriophage Database to Cluster CA, and to the *Rerduovirus* genus by ICTV. While phage RGL3 possibly belongs to this genus we have chosen not to add it at this time because it might fit better in a new subfamily. |

**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. [4] | |

**Supporting evidence**

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [11]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [12]. The phages of interest are indicated with **red lines and stars**.

A picture containing diagram

Description automatically generated  
Chart

Description automatically generated with low confidence  
**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [10]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) computes pairwise intergenomic distances/similarities amongst phage genomes.

Chart

Description automatically generated

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

A picture containing scatter chart

Description automatically generated

**Source of the name of this taxon:** This genus is named after Rhodococcus phage RER2.

**History:** The genus *Rerduovirus* was proposed in TaxoProp 2018.007B.A.v1.rename137gen6sp in which the genus *Rer2virus* was renamed. There are now over 38 phages in GenBank belonging to this genus, but only 1 species has been specified by ICTV. We have reanalysed all of these viruses.

**Specific Reference:** Petrovski S, Seviour RJ, Tillett D. Characterization and whole genome sequences of the Rhodococcus bacteriophages RGL3 and RER2. Arch Virol. 2013 Mar;158(3):601-9. doi: 10.1007/s00705-012-1530-5. Epub 2012 Nov 6. PMID: 23129131. **[RER2, RGL3]**

**GenBank Summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Rhodococcus phage RER2 | [NC\_016653.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_016653.1) | [JN116827.1](https://www.ncbi.nlm.nih.gov/nuccore/JN116827.1) | 46.59 | 58.6 | [66](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/12324/459616%7CRhodococcus%20phage%20RER2/viral%20segment%20Unknown/) | 3 | 100 | 100 |
| Rhodococcus phage PhailMary |  | [MW291027.1](https://www.ncbi.nlm.nih.gov/nuccore/MW291027.1) | 45.61 | 58.9 | [63](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/97237/1513237%7CRhodococcus%20phage%20PhailMary/viral%20segment/) | 2 | 92.7 | 93.9 |
| Rhodococcus phage Hiro | [NC\_048669.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048669.1) | [MF324898.1](https://www.ncbi.nlm.nih.gov/nuccore/MF324898.1) | 46.85 | 58.7 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63676/466297%7CRhodococcus%20phage%20Hiro/viral%20segment/) | 3 | 91.8 | 97.0 |
| Rhodococcus phage Takoda | [NC\_048708.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_048708.1) | [MH271315.1](https://www.ncbi.nlm.nih.gov/nuccore/MH271315.1) | 46.81 | 58.7 | [67](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/70901/388808%7CRhodococcus%20phage%20Takoda/viral%20segment/) | 3 | 90.7 | 92.4 |

**(\*) Determined using VIRIDIC [10]**

**(\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[6]**

**Electron micrograph:** Electron micrographs of negatively stained Rhodococcus phage Hiro(<https://phagesdb.org/phages/Hiro/>). 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.

**Graphical user interface

Description automatically generated**

**References**

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