

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

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| **Code assigned:** | **2021.014B** |  |
| **Short title:** Create one new species in the genus *Bundooravirus* (*Salasmaviridae*) | | |
|  | | |

**Author(s) and email address(es)**

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| Malgorzata Łobocka |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Salasmaviridae*, *Rountreeviridae*, *Guelinviridae* 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**

|  |  |
| --- | --- |
| Date first submitted to SC Chair |  |
| 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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| 2021.014B.R.Bundooravirus |

**Abstract**

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| In a complete review of the *Bacillus* phages belonging to the *Salasmaviridae* family and their newly deposited relatives using VIRIDIC and ViPTree we have discovered one more species in the genus *Bundooravirus*.The phage of this species shares almost all properties with other phages of this genus, but differs significantly enough (less than 95% identity with phages of other *Bundooravirus* genus species) to classify it to a separate species of this genus. |

**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 and Viridic algorithm | |

**History:** This genus was established via Taxonomy Proposal 2020.143B.A,v1 Salasmaviridae

**Specific References:**  None concerning the new strain listed in this Taxonomy Proposal. General genus-relevant references are listed in Taxonomy Proposal 2020.143B.A,v1

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs\* | Overall % DNA sequence identity (\*\*) | Overall % homologous proteins (\*\*\*) |
| Bacillus phage WhyPhy |  | [MW419775.1](https://www.ncbi.nlm.nih.gov/nucleotide/MW419775.1?report=genbank&log$=nucltop&blast_rank=1&RID=AS5SUE60016) | 18,64 | 35.0 | 28 | 0 | 79.5 | 96.4 |

N.B.Type species strain exemplar of *Bundooravirus* genus is Bacillus phage vB\_Bpu\_PumA1 (MN524844.1).

(\*) determined using RNAscan-SE [1]

(\*\*) determined using Viridic [2] and Bacillus phage vB\_Bpu\_PumA1 as a type species strain exemplar

(\*\*\*) determined using CoreGenes 5.0 [3,4], and Bacillus phage vB\_Bpu\_PumA1 as a type species strain exemplar

**BLASTN homologs:**  VIRIDIC analysis reveals that the closest relative besides other phages of *Bundooravirus* genus is Bacillus phage vB\_BsuP\_Goe1 (MN857617.1) of *Beecentumtrevirus* genus (*Salasmaviridae* family). It shares 20.5% DNA sequence with Bacillus phage WhyPhy.

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [2]) computes pairwise intergenomic distances/similarities amongst phage genomes. The comparison below provides the results of DNA sequence comparison of strains of known and proposed new species of *Salasmaviridae* phages. The phage name indicated by the orange arrow represents the new species that will be added through this TaxoProp.

Chart

Description automatically generated

**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [5]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [6]. The **blue** arrowhead points to the *Salasmaviridae* family. The **orange arrow** points to the new species of the *Bundooravirus* genus.

Diagram

Description automatically generated with medium confidence

**Phylogeny:** The phylogenetic tree was constructed using the DNA polymerase, major capsid protein and portal protein homologs of Bacillus phage WhyPhy and related phages with phylogeny.fr in “one click” mode (7). "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 (8) for details."

Diagram

Description automatically generated

Diagram

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**References**

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3: Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.

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