

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

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| **Code assigned:** | **2021.037B** |  |
| **Short title:** Create one new genus (*Huangshavirus*) including one new species (*Salasmaviridae*) | | |
|  | | |

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

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**Corresponding author**

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**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**

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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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| 2021.037B.R.Huangshavirus |

**Abstract**

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| In a complete review of the *Bacillus* phages belonging to the *Salasmaviridae* family or their newly deposited relatives using VIRIDIC and ViPTree we have discovered one more species, whose level of DNA sequence similarity to other phages of this family justifies its classification to a new genus (*Huangshavirus*) of the family *Salasmaviridae*. The name of this genus was derived from the name of an aquatic product market in China (Huangsha), where from its first representative was isolated. |

**Text of proposal**

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| |  | | --- | | **Species & genus demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of new species in any genus, and 70% DNA sequence identity as the criterion for demarcation of new genera in any family. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN or Viridic algorithm. Each of the new genus differs from the others with more than 30% at the DNA level as confirmed with the BLASTN or Viridic algorithm. | |

**Supporting evidence**

**History:** The family *Salasmavirdae* was established via Taxonomy Proposal 2020.143B.A,v1 Salasmaviridae

**Specific References:**  None concerning the new strain listed in this Taxonomy Proposal. General references concerning *Salasmaviridae* family are listed in Taxonomic Proposal 2020.143B.A,v1

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs\* | Overall % DNA sequence identity (\*\*) | Overall % homologous proteins (\*\*\*) |
| Bacillus phage Dlc1 |  | [MW012634.1](https://www.ncbi.nlm.nih.gov/nucleotide/MW419775.1?report=genbank&log$=nucltop&blast_rank=1&RID=AS5SUE60016) | 28.95 | 31.1 | 50 | 0 | 100.0 | 100.0 |

N.B.Type species strain exemplar and a single representative of *Huangshavirus* genus is Bacillus phage Dlc1 (MW012634.1) listed in this TaxoProp.

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

**BLASTN homologs:**  Blastn analysis [2,3] reveals that the closest relative is Bacillus phage vB\_BthP-Goe4 (MH817022.1) of *Claudivirus* genus (*Northropvirinaesubfamily, Salasmaviridae family).* It shares 50.9% DNA sequence with Bacillus phage Dlc1, as calculated by Viridic (see below) [4].

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [4]) 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* family phages. Orange arrow indicates the new genus *Huangshavirus*, which 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** point to the new genus of *Salasmaviridae* family, which will be added through this Taxonomic Proposal.

A picture containing diagram

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**Phylogeny:** The phylogenetic tree was constructed using the DNA polymerase, major capsid protein, portal protein and a major tail protein homologs of Bacillus phage Dlc1 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."

**DNA polymerase**

Diagram, schematic

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**Capsid protein**

Diagram

Description automatically generated

**Portal protein**

Diagram, schematic

Description automatically generated

**Tail protein**

Diagram

Description automatically generated with medium confidence

**References**

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3: Sayers EW, Agarwala R, Bolton EE, et al. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res*. 2019;47(D1):D23-D28. doi:10.1093/nar/gky1069

2: Moraru C (2020) VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>

5: Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287.

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