

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

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| **Code assigned:** | **2020.149B** |  |
| **Short title:** Create one new genus (*Shandongvirus*) including one new species in (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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| Kropinski AM, Turner D, Adriaenssens EM | [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com);  [dann2.turner@uwe.ac.uk](mailto:dann2.turner@uwe.ac.uk);  Evelien.Adriaenssens@quadram.ac.uk |

**Author(s) institutional address(es) (optional)**

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| University of Guelph, Canada [AMK]  University of the West of England, UK [DT]  Quadram Institute Bioscience, UK [EMA] |

**Corresponding author**

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| Andrew M. Kropinski |

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

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| Bacterial and Archaeal Viruses Subcommittee  *Caudovirales* Study Group |

**ICTV study group comments and response of proposer**

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| Proposal originally submitted and provisionally accepted in 2019, EC 51, but mistakenly left out of ratification vote. |

**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 2019 |
| 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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| 2020.149B.R.Shandongvirus.xlsx |

**Abstract**

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| To create a new genus *Shandongvirus* containing a single species *Pseudoalteromonas virus H101*. |

**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.  **Source of the name of this taxon:** The name of this genus is derived from Shandong Province, The People's Republic of China where at the College of Marine Life Science, Ocean University of China *Pseudoalteromonas* phage H101 was isolated.  **History:** Phage H101 was isolated in 2014 from coastal water using *Pseudoalteromonas marina* as the host bacterium.  **GenBank Summary:**   |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | | *Pseudoalteromonas* phage H101 | NC\_029094 | KR534323.1 | 131.90 | 37.4 | 228 | 0 |   **BLASTN homologs:** Genomic orphan. The most closely related phage is *Pseudoalteromonas* phage SL20 which shares on 10% sequence identity with H101. [1-4]  **Electron micrograph:** None available | |

**Supporting evidence**

**Phylogeny:** The phylogenetic tree was constructed using the major capsid protein homologs of H101 and related phages with phylogeny.fr in “one click” mode [9]. "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 (Syst Biol. 2006;55(4):539-52., 10) for details."

![A screenshot of a cell phone

Description automatically generated]()

**References**

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