

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

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| **Code assigned:** | **2020.071B** |  |
| **Short title:** Create one new genus (*Henunavirus*) including two new species in the subfamily *Vequintavirinae* (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew 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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| 2020.071B.R.Henunavirus.xlsx |

**Abstract**

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| This proposal creates a genus for some currently unclassified myoviruses infecting *Erwinia* strains within the subfamily *Vequintavirinae* in the family *Myoviridae*. |

**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 | |

**Supporting evidence**

**Source of the name of this taxon:** The name of this genus is derived from that of *Erwinia* phage Hena1

**History:** Lytic phage Hena1 was isolated from garden soil in Belarus using *Erwinia amylovora* 1/79Sm as the host bacterium. Phage pEp\_SNUABM\_01 was isolated in South Korea against *Erwinia pyrifoliae*.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Hena1 | [MN732867.1](https://www.ncbi.nlm.nih.gov/nuccore/MN732867.1) | 148.84 | 48.4 | [240](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86433/751409|Erwinia phage Hena1/viral segment/) | 26 | 100 | 100 |
| pEp\_SNUABM\_01 | [MN184887.1](https://www.ncbi.nlm.nih.gov/nuccore/MN184887.1) | 147.32 | 48.7 | [249](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84626/697036|Erwinia phage pEp_SNUABM_01/viral segment/) | 26 | 69.1 | 90.4 |

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**BLASTN homologs:** The next most closely related phage is *Escherichia* phage 4MG which shares 28.6% DNA sequence identity with Hena1 [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the large subunit terminase homologs of Hena1 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."

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**References**

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