

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

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| **Code assigned:** | **2020.050B** |  |
| **Short title:** Create one new genus (*Eceepunavirus*) including one new species (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| J Wittmann |

**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 (not applicable)**

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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 | 6 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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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| Here, we propose the creation of a new genus “Eceepunavirus” comprising one new species, based on genome-based comparisons and phylogenetics of the major capsid protein. |

**Text of proposal**

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**Supporting evidence**

**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 [1-3].

**Source of the name of this taxon:** The name is derived from the name of the isolated phage of this type, Enterobacter phage EcP1.

**History:** Phage EcP1 is a member of the *Podoviridae* family that infects *Enterobacter cloacae*. It is a member of the N4-super family of viruses.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| EcP1 | NC\_019485.1 | HQ641380.1 | 59.08 | 36.9 | 77 | 3 |

**BLASTN homologs:** None, genomic orphan/singleton

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed, using MEGA5 [4], using the major coat protein of phage EcP1 and related N4-like phages.



**References**

1: Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.  
  
2: Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.  
  
3: O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID:26553804.

4: Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. [MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods.](http://www.ncbi.nlm.nih.gov/pubmed/21546353) Mol Biol Evol. 2011; 28(10):2731-9. PMID: 21546353 PMCID: PMC3203626 DOI: 10.1093/molbev/msr121