

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

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| **Code assigned:** | **2020.147B** |  |
| **Short title:** Create one new genus (*Sendosyvirus*) including two species (*Caudovirales*: *Podoviridae*) | | |
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**Author(s) and email address(es)**

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**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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**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 | April 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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| 2020.147B.R.Sendosyvirus.xlsx |

**Abstract**

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| Phage APSE1 is listed as an unclassified member of the *Podoviridae*. We are proposing to create a new taxon, *Sendosyvirus*, for this phage and it relative, APSE2. |

**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.

**Source of the name of this taxon:** This genus name is a sigla proposed by Dr. M. (Martin) Verbeek,

(Wageningen University & Research, The Netherlands) based upon **S**econdary **endosy**mbiont)

**History:** 2008.019B

**Reference:** 2008.019B

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*\*) | % common proteins (\*\*\*) |
| APSE-1 | [NC\_000935.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_000935.1) | [AF157835.1](https://www.ncbi.nlm.nih.gov/nuccore/AF157835.1) | 36.52 | 43.9 | 54 | 1(\*) | 100 | 100 |
| APSE-2 | [NC\_011551.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_011551.1) | [EU794049.1](https://www.ncbi.nlm.nih.gov/nuccore/EU794049.1) | 39.87 | 42.9 | 41 | 1 | 87.2 | 63.0 |

**\* None indicated in the NCBI Replicon Info data; found using tRNAscan-SE 2.0 at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[5]**

**\*\* Determined using BLASTn at NCBI [1-3]**

**\*\*\* Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[6]**

**BLASTn distance tree:** Distance tree of BLASTn results (Neighbor Joining, Max sequence difference 0.7) using phage APSE-1 as query shows only two confirmed complete phage genomes are currently available (in red, exemplar of type species highlighted in yellow). Scale bar shows number of substitutions per site. There are a lot of partial genomes and newly sequenced genomes that could be part of the genus after verification.

**A picture containing graphical user interface

Description automatically generated**

**References**

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