

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

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| **Code assigned:** | **2021.030M** |  |
| **Short title:** Create four new species in the genus *Orthophasmavirus* and create one new genus (*Cicadellivirus*) including one new species(*Bunyavirales: Phasmaviridae*) | | |
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**Author(s) and email address(es)**

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

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| **ICTV *Phasmaviridae* Study Group** |

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

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| N/A |

**Submission dates**

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| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) | September 13, 2021 |

**ICTV-EC comments and response of the proposer**

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| * Excel sheet: Correct errors (has a parent taxon that does not exist in the current MSL or created in this proposal: genus = 'Cicadellicvirus'; the taxon 'Cicadellivirus' is empty - it does not contain any lower taxons).   Response: fixed.   * Read the EC-distributed guidance on species naming document, confirm that proposed species names adhere to the guidance, and confirm that you would like to keep the proposed species names as originally proposed.   Response: Read, confirmed, and confirmed. |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.030M.R.Phasmaviridae\_1ngen\_5nsp |

**Abstract**

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| We propose the creation of 4 new species in the genus *Orthophasmavirus*, and the creation of 1 new genus termed *Cicadellivirus* including 1 new species. Species demarcation is based on coding-complete genome sequence analyses, phylogenetic analyses, and pairwise sequence comparison according to the established species demarcation criteria for the family *Phasmaviridae*. The new genus is proposed based on the phylogenetic distance of the proposed member to the members of other established phasmavirus genera. |

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| **Text of proposal**   |  | | --- | | Species demarcation criteria for the family *Phasmaviridae* are <95% identity in the amino acid sequence of the entire RNA-directed RNA polymerase (RdRp). Maximum pairwise identities among the new species described below and established phasmavirids range from 55 – 28% identity in the amino acid sequence of the entire RdRp.  We propose the creation of 4 new species in genus *Orthophasmavirus*. The respective viruses were all found in mosquitoes (*Mansonia titillans*: Coredo virus [CORV], *Aedes albopictus*: Barstukas virus [BARV], and *Culex erythrothorax*: Miglotas virus [MIGV], and *Ochlerotatus cantans*: Flen virus [FLNV]).  Genetic and phylogenetic distances of coding-complete genome (CCG) sequences support the creation of four novel orthophasmavirus species for these four viruses (Figure 1). The genus *Orthophasmavirus* is highly diversified and might be reorganized at a later stage when more phasmavirid genomes become available.  One virus representing a proposed new species was detected in a leafhopper (*Scaphoideus titanus*: Scaphoideus titanus bunya-like virus 1 [StHV]). The CCG shows the typical genome organization of phasmavirids but the virus did not group with any established phasmavirid genus and establishes a new sister taxon to genus *Orthophasmavirus* (Figure 1). We thus propose the creation of one new genus termed *Cicadellivirus* to accommodate the new species. | |

**Supporting evidence**

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**Figure 1:** Phylogenetic relationship of established and proposed phasmavirids. Complete L protein amino acid sequences were aligned using MAFFT. The approximately maximum likelihood tree was inferred with FastTree 2.1.11 using the WAG substitution model. Numbers on or beside branches represent approximate maximum likelihood support values. Proposed new phasmavirids are shown in bold and genus names are listed on the right side. The scale bar displays substitutions per site.

**References**

Batson J, Dudas G, Haas-Stapleton E, Kistler AL, Li LM, Logan P, Ratnasiri K, Retallack H. Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay. *Elife* 2021 **10**: e68353.

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Oehlund P, Hayer J, Lunden H, Hesson JC, Blomstroem A-L. Viromics Reveal a Number of Novel RNA Viruses in Swedish Mosquitoes. *Viruses* 2019 **11** (11): 1027.

PMID: 31694175, PMCID: [PMC6893623](http://www.ncbi.nlm.nih.gov/pmc/articles/pmc6893623/) , DOI: [10.3390/v11111027](https://doi.org/10.3390/v11111027)

Ottati S, Chiapello M, Galetto L, Bosco D, Marzachi C, Abba S. New Viral Sequences Identified in the Flavescence Doree Phytoplasma Vector Scaphoideus titanus. *Viruses* 2020 **12** (3): 287.

PMID: 32155753, PMCID: [PMC7150801](http://www.ncbi.nlm.nih.gov/pmc/articles/pmc7150801/) , DOI: [10.3390/v12030287](https://doi.org/10.3390/v12030287)