

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

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| **Code assigned:** | **2020.020M** |  |
| **Short title:** Create four new species in the genus *Orthophasmavirus*, create two new species in the genus *Feravirus*, and create one new genus (*Hymovirus*) including two new species (*Bunyavirales*: *Phasmaviridae*) | | |
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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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**Submission dates**

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| Date first submitted to SC Chair | July 31, 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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| 2020.020M.R.Phasmaviridae.xlsx |

**Abstract**

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| We propose the creation of 4 new species in the genus *Orthophasmavirus*, the creation of 2 new species in the genus *Feravirus*, and the creation of 1 new genus termed *Hymovirus* including 2 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 two proposed members 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 RdRp. Maximum pairwise identities among the new species described below and established phasmaviruses range between 77 – 37% identity in the amino acid sequence of the entire RdRp.  We propose the creation of 4 new species in the genus *Orthophasmavirus*. The respective species were found in phantom midges (*Chaoborus americanus*: Niukluk phantom orthophasmavirus [NUKV]), in cuckoo wasps (*Chrysis fasciata*: hymenopteran phasma-related virus OKIAV227 [HyOV-2; *Philoctetes bogdanovii*: hymenopteran phasma-related virus OKIAV228 [HyOV-1]), and in a harlequin ladybeetle (*Harmonia axyridis*: coleopteran phasma-related virus OKIAV235 [CPRV]). Genetic and phylogenetic distances of coding-complete genome (CCG) sequences support the creation of four novel orthophasmavirus species (Figure 1). The genus *Orthophasmavirus* is highly diversified and might be reorganized at a later stage when more phasmavirus genomes are available.  Two new species are proposed in the genus *Feravirus* for viruses found in a hawthorn shield bug (*Acanthosoma haemorrhoidale;* hemipteran phasma-related virus OKIAV247 [HeFV]) and in a green lacewing (*Peyerimhoffina gracilis*; neuropteran phasma-related virus OKIAV248 [NeFV]). CCG were derived from both viruses and their phylogenetic grouping confirm the creation of two new species in the genus *Feravirus* (Figure 1).  Viruses representing two proposed new species were detected in cuckoo wasps (*Chrysis gracillima*: hymenopteran phasma-related virus OKIAV250 [HyHV-2]; *Chrysura cupres*: hymenopteran phasma-related virus OKIAV252 [HyHV-1]). The CCG show the typical genome organization of phasmaviruses but the viruses did not group with any established phasmavirus genus and established a new sister clade to the genus *Feravirus* (Figure 1). We thus propose the creation of one new genus termed *Hymovirus* to accommodate the two new species. | |

**Supporting evidence**

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**Figure 1:** Phylogenetic relationship of established and proposed phasmaviruses. The phylogenetic tree is based on a MAFFT-alignment of the RdRp amino acid sequences using the E-INS algorithm and was inferred using the PhyML and the LG substitution model. Numbers on branch nodes represent bootstrap values (1,000 replicates). Proposed new phasmavirus species are shown in bold.

**References**

Käfer S, Paraskevopoulou S, Zirkel F, Wieseke N, Donath A, Petersen M, Jones TC, Liu S, Zhou X, Middendorf M, Junglen S, Misof B, Drosten C. [Re-assessing the diversity of negative strand RNA viruses in insects.](https://www.ncbi.nlm.nih.gov/pubmed/31830128) *PLoS Pathogens* 2019 **15** (12): e1008224.

PMID: 31830128, PMCID: [PMC6932829](http://www.ncbi.nlm.nih.gov/pmc/articles/pmc6932829/) , doi: https://doi.org/10.1371/journal.ppat.1008224

Ballinger MJ and Taylor DJ. Evolutionary persistence of insect bunyavirus infection despite host acquisition and expression of the viral nucleoprotein gene. Virus Evolution 2019 **5** (2): vez017.

PMID: 31308960, PMCID: [PMC6620529,](http://www.ncbi.nlm.nih.gov/pmc/articles/pmc6620529/) doi: 10.1093/ve/vez017