

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

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| **Code assigned:** | ***2022.019M*** |  |
| **Short title:** Create two new species in the genus *Orthophasmavirus* and one new species in the genus *Feravirus* (*Phasmaviridae*) |
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**Author(s) and email address(es)**

|  |  |
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**Corresponding author**

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| Junglen S |

**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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| Approved. |

**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Phasmaviridae* Study Group | 3 | 0 | 0 |

**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **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 | May 27, 2022 |
| 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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| 2022.019M.N.v1.Phasmaviridae\_3nsp.xlsx |

**Abstract**

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| We propose the creation of two new species in the genus *Orthophasmavirus* and one new species in the genus *Feravirus*. Species demarcation is based on coding-complete genome sequence analysis and pairwise sequence comparison according to the established species demarcation criteria for the family *Phasmaviridae*. |

**Text of proposal**

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| 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 two new species in genus *Orthophasmavirus*. The respective viruses were found in planthoppers (*Sogatella furcifera*: Fushun phasmavirus 1 [FsnPV-1], *Laodelphax striatellus*: Fushun phasmavirus 2 [FsnPV-2]). Genome organization and coding-complete genome (CCG) sequences support creation of two novel orthophasmavirus species for these two viruses (Figure 1).We propose the creation of one new species in the genus *Feravirus*. The respective virus was found in a mosquito (*Mansonia titillans*: Guagua virus [GUAV]). Genome organization and CCG sequence supports creation of one novel feravirus species for this virus (Figure 1). |

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**Supporting evidence**

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**Figure 1.** **Phylogenetic relationship of established and proposed phasmavirids.** Complete L protein amino acid sequences were aligned with MAFFT 7.45 using the E-INS-i algorithm. The approximate 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. The phylogeny is rooted using the complete L protein sequences of two members of family *Hantaviridae*.

**References**

No currently published articles report Fushun phasmavirus 1, Fushun phasmavirus 2, or Guagua virus.