

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:**  | Create four new species in the family *Phasmaviridae* |
| **Code assigned:**  | 2025.006M.Ac.v4.Phasmaviridae\_4nsp |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
| Matthew J  | Ballinger | Biological Sciences, Mississippi State University, Mississippi State, USA | ballinger@biology.msstate.edu | X |
| Sandra | Junglen | Institute of Virology, Charité – Berlin University Medicine, Berlin, Germany | sandra.junglen@charite.de |  |
| Lander | De Coninck | Division of Clinical and Epidemiological Virology, KU Leuven, Leuven, Belgium | lander.deconinck@kuleuven.be |  |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses | **X** | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| *Phasmaviridae* Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
| *Phasmaviridae* | 3 |  |  |
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| **Submission date:** |  13/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **X** |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
| Ac for minor typographical edits and consistent Abstract format across all Subcommittees |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
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| **Revision date:** | 18/09/2025 |

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

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| **Taxonomic changes proposed:**  |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:**  |
| **Taxon name**  | **Etymology of the term** |
| *Wuhivirus inferensa* | Named for the host, *Sesamia inferens* |
| *Orthophasmavirus vrasenense* | Named for the *Culex pipiens* collection location (Vrasene, Belgium) |
| *Orthophasmavirus vitinea* | Named for host common name, the grapevine worm (*vitis* + *tinea*) |
| *Orthophasmavirus lycotinea* | Named for the host common name, the tomato worm (*lyco-* + *tinea*) |

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| **Abstract of Taxonomy Proposal:**  |
| ***Taxonomic rank(s) affected*:** Species in the family *Phasmaviridae*.***Description of current taxonomy*:** The family *Phasmaviridae* includes 32 species organized across seven genera.***Proposed* *taxonomic change(s):*** Create four new species in the family *Phasmaviridae*. ***Justification*:**Coding-complete virus genome sequences are available to justify creation of four new species. Each exhibits < 95% L protein amino acid sequence identity to other exemplar viruses in the family *Phasmaviridae*.  |

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| ***Taxonomic rank(s) affected*:** Species.***Description of current taxonomy*:** The family *Phasmaviridae* includes 32 species organized across seven genera. These include *Jonvirus, Wuhivirus, Hymovirus, Sawastrivirus, Feravirus, Cicadellivirus,* and *Orthophasmavirus*.***Proposed* *taxonomic change(s)*:** We propose the creation of one new species in the genus *Wuhivirus* and three new species in the genus *Orthophasmavirus*:***Demarcation criteria:***The species demarcation criterion across all genera in the family *Phasmaviridae* is < 95% identity in the amino acid (aa) sequence of the complete L protein (the RNA-dependent RNA polymerase [RdRp])1. The maximum aa identities shared between proposed new exemplar viruses and established phasmavirids ranges from 39.36 to 94.36%.***Justification*:** The presence of coding-complete sequences for each of the three genome segments is sufficient for phasmavirid classification in the absence of a cultured isolate. *Wuhivirus inferensa* is represented by exemplar virusSanya sesamia inferens phasmavirus 1 (SSiPV). The virus was discovered in metagenomic sequences of *Sesamia inferens* and *Scirpophaga incertulas* collected in Sanya, China.*Orthophasmavirus vrasenense* is represented byCulex orthophasmavirus 2 (CPV2), discovered in metagenomes of *Culex pipiens* biotype molestus collected in Vrasene, Belgium2. *Orthophasmavirus vitinea* is represented byLobesia botrana phasmavirus (LbPV), discovered in metagenomes of *Lobesia botrana* collected in Germany3.*Orthophasmavirus lycotinea* is represented byTuta absoluta phasmavirus 1 (TaPhV1), discovered in metagenomes of *Tuta absoluta* collected in Piracicaba, Brazil4.  |

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| **References:**  |
| 1. Kuhn, J. H. & Hughes, H. R. ICTV Virus Taxonomy Profile: Phasmaviridae 2024. *J. Gen. Virol.* **105**, 1–2 (2024).2. De Coninck, L. *et al.* Lack of abundant core virome in Culex mosquitoes from a temperate climate region despite a mosquito species-specific virome. *mSystems* **9**, (2024).3. Debat, H., Gomez-Talquenca, S. & Bejerman, N. RNA Virus Discovery Sheds Light on the Virome of a Major Vineyard Pest, the European Grapevine Moth (Lobesia botrana). *Viruses* **17**, 1–20 (2025).4. Becerra-García, R. E., Hernández-Pelegrín, L., Crava, C. M. & Herrero, S. Characterization of the Tuta absoluta virome reveals higher viral diversity in field populations. *J. Invertebr. Pathol.* **211**, (2025). |

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| **Tables, Figures:**  |



**Figure 1. Phylogenetic relationships of proposed and established virus taxa in the family *Phasmaviridae*.** A phylogram of L protein amino acid sequences of exemplar phasmavirids. Two members of the family *Hantaviridae* are included as an outgroup. Branches with SH-like FastTree support values >0.95 are labeled with a black circle. Tips are labeled with names of exemplar viruses. Clade labels on the right are genus names. Exemplar names of four proposed species are shown in bold typeface.