This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

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| --- | --- | --- |
| **Code assigned:** | ***2019.028M*** |  |
| **Short title:** Create one new species, abolish one genus and abolish three species in the genus *Orthophasmavirus*, family *Phasmaviridae*, order *Bunyavirales* |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Matthew J. Ballinger, Roy A. Hall, Stanley A. Langevin, Alex Pauvolid-Corrêa, Sandra Junglen | ballinger@biology.msstate.edu;roy.hall@uq.edu.au;slangevi@uw.edu;pauvolid@gmail.com;Sandra.junglen@charite.de |
| **Corresponding author** |
| Sandra Junglen; Sandra.junglen@charite.de  |
| **List the ICTV study group(s) that have seen this proposal:** |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | **ICTV *Phasmaviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
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| Date first submitted to ICTV: | June 19, 2019 |
| Date of this revision (if different to above): |       |

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

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2019.028M.A.v1.Phasmaviridae\_1newsp\_abol1gen3sp.xlsx |

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**Supporting material:**

| **One new orthophasmavirus, Anopheles triannulatus orthophasmavirus,** has been found in *Anopheles triannulatus* mosquitoes (Scarpassa et al., 2019). The coding complete genome sequence shows the same genome organization as those of classified phasmavirids. Genetic and phylogenetic distances support the creation of a novel orthophasmavirus species (Figure 1). |
| --- |
| Sequence based **species demarcation criteria** within the order *Bunyavirales* have been established for the genus *Orthobunyavirus* (<96% identity in the amino acid sequence of the entire RdRp) and are currently proposed for the entire family *Phenuiviridae* (<95% identity in the amino acid sequence of the entire RNA-directed RNA polymerase [RdRp]). To unify the species demarcation criteria within the order *Bunyavirales*, we propose similar species demarcation criteria for the family *Phasmaviridae* (<95% identity in the amino acid sequence of the entire RdRp). The genomes of Shuāngào insect virus 2 (species *Insect inshuvirus*), Seattle orthophasmavirus (species *Seattle orthophasmavirus*) and Nome phantom virus (species *Nome phantom orthophasmavirus*) are not coding-complete. In addition, the sequence of Shuāngào insect virus 2 contains four segments due to the presence of two segments encoding a nucleocapsid gene. This is in contrast to all other bunyaviruses which contain only one nucleocapsid. The sequences were derived from a pool of mixed insects by Next Generation Sequencing and it is likely that one of the genome segments belongs to another virus. We thus propose to **abolish these three phasmavirus species**, including the genus *Inshuvirus* itself, as it contained only one virus with an incomplete genome sequence that is being abolished.  |



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-NG and the LG substitution model. Numbers on branch nodes represent bootstrap values (1,000 replicates). Sequence names contain the following designation: species\_\_virus\_accession number.

| **References:** |
| --- |
| Vera Margarete Scarpassa, Humbeto Julio Debat, Ronildo Baiatone Alencar, José Ferreira Saraiva, Eric Calvo, Bruno Arcà and José M. C. Ribeiro. An insight into the sialotranscriptome and virome of Amazonian anophelines. BMC Genomics 2019 **20**:166. |