

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

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| **Code assigned:** | **2021.005M** |  |
| **Short title:** Create one new genus (*Tapjovirus*)including one new species (*Mononegavirales*: *Filoviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Horie M |

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

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| ICTV *Filoviridae* 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 | 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: add GenBank number.   Response: done.   * As written, it’s unclear how demarcation criteria for both genus and species are satisfied   Response: Now clarified in text: “The current filovirus sequence-based genus and species demarcation criteria are ≥55% and ≥23% sequence divergence over coding/near-complete genome sequences using PAirwise Sequence Comparison (PASC) (3,4). We found a pairwise divergence of 28.66% compared to the closest relative, Bombali virus (BOMV; *Filoviridae*: *Ebolavirus*), indicating that TAPV requires the establishment of a new species in a new genus.”   * 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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| 2021.005M.R.Filoviridae\_1ngen\_1nsp |

**Abstract**

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| We propose to establish one new filovirid genus, *Tapjovirus*, including one new species (*Tapjovirus bothropis*) to accommodate Tapajós virus (TAPV), which was discovered by high-throughput sequencing in a viperid snake from Tapajós National Forest, Brazil. |

**Text of proposal**

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| |  | | --- | | We discovered a new virus in in a common lancehead (*Bothrops atrox* (Linnaeus, 1758)) in Brazil by bioinformatic analysis using previously published RNA-sequencing data (1,2). We named this virus Tapajós virus (TAPV) after the Tapajós National Forest. The TAPV genome sequence is coding-completeand encodes the canonical proteins found in members of the mononegaviral family *Filoviridae*: nucleoprotein (NP), polymerase cofactor (VP35), matrix protein (VP40), glycoprotein (GP), transcriptional activator (VP30), ribonucleoprotein complex-associated protein (VP24) and large protein (L) containing an RNA‑directed RNA polymerase (RdRp) domain (Figure A).  Phylogenetic comparison of the TAPV *L* gene sequences with those of representative classified viruses of the family *Filoviridae* (Figure B) confirmed that TAPV forms a cluster with Xīlǎng virus (XILV; *Filoviridae*: *Striavirus*) but is still distantly related to XILV.  The current filovirus sequence-based genus and species demarcation criteria are ≥55% and ≥23% sequence divergence over coding/near-complete genome sequences using PAirwise Sequence Comparison (PASC) (3,4). We found a pairwise divergence of 28.66% compared to the closest relative, Bombali virus (BOMV; *Filoviridae*: *Ebolavirus*), indicating that TAPV requires the establishment of a new species in a new genus.  Based on these results we propose to establish one new filovirid genus, *Tapjovirus*, including one new species (*Tapjovirus* bothrops), to accommodate TAPV (see the Excel module for etymologies).  **Supporting information**  **Figure**  **A**    **B** | |

**Figure: A novel filovirid in a common lancehead. A)** Schematic representation of the genome organization of Tapajós virus (TAPV) compared to Bombali virus (BOMV, genus *Ebolavirus*), Marburg virus (MARV, genus *Marburgvirus*), and Xīlǎng virus (XILV, genus *Striavirus*): Open reading frames (ORFs) are indicated as colored arrows. ORFs encoding BOMV-like proteins are depicted by the same color. NP, nucleoprotein gene; VP35, polymerase cofactor gene; VP40 matrix protein gene; GP, glycoprotein gene; VP30, transcriptional activator gene; VP24, ribonucleoprotein complex-associated protein gene; L, large protein gene. **B)** A maximum likelihood phylogenetic tree of filovirus L gene sequences, including TAPV (bold blue). Numbers near nodes on the trees indicate bootstrap values. Branches are labeled by GenBank accession number, virus name, and virus name abbreviation in parenthesis. The scale (bottom left) indicates the number of substitutions per site, reflected by the branch lengths.

**Table**

Pairwise distances of complete or coding-complete genome nucleotide sequences between the newly identified Tapajós virus (TAPV), Bombali virus (BOMV, GenBank #MK340750), Xīlǎng virus (XILV, GenBank #MG599980), and Huángjiāo virus (HUJV; genus *Thamnovirus*, GenBank # MG599981).

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| **Virus** | **TAPV** |
| **BOMV** | **71%** |
| **XILV** | **74%** |
| **HUJV** | **78%** |

**References***:*

1. Horie M. Identification of a novel filovirus in a common lancehead (*Bothrops atrox* Linnaeus, 1758). Submitted.
2. Freitas-de-Sousa, L. A., Amazonas, D. R., Sousa, L. F., Sant'Anna, S. S., Nishiyama, M. Y., Jr., et al. Comparison of venoms from wild and long-term captive Bothrops atrox snakes and characterization of Batroxrhagin, the predominant class PIII metalloproteinase from the venom of this species. Biochimie. 2015. 118: 60-70. PMID: 26276061 DOI: 10.1016/j.biochi.2015.08.006
3. Kuhn JH, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K, et al. ICTV virus taxonomy profile: *Filoviridae*. J Gen Virol. 2019 Jun;100(6):911-2. PMID: 31021739 DOI: 10.1099/jgv.0.001252
4. Bào Y, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K, et al. Implementation of objective PASC-derived taxon demarcation criteria for official classification of filoviruses. Viruses. 2017 May 11;9(5):106. PMID: 28492506 DOI: 10.3390/v9050106