

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create one new species in the genus *Dianlovirus* (*Mononegavirales*: *Filoviridae*) | |
| **Code assigned:** | <to be assigned by ICTV officers> |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** |
| **Kuhn, JH** | **Integrated Research Facility at Fort Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Fort Detrick, Frederick, Maryland, USA** | **kuhnjens@mail.nih.gov** | **X** |
| **Liu, Y** | **National Genomics Data Center, Beijing Institute of Genomics, Chinese Academy of Sciences, China** | **liuyiyun@big.ac.cn** |  |
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**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 -Submit to Proposals Secretary |  |

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

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| **Submission date:** | 21/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting** <To be completed by the subcommittee chair after EC evaluation>

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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 |  |
| 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:** |
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**Part 1d: Revised Taxonomy Proposal Submission** <To be completed for the revised version>

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| **Response of proposer:** Please describe in detail how you have responded to the EC meeting feedback |
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| **Revision date:** | DD/MM/YYYY |

Enter date of the revised version.

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

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| **Name of accompanying Excel module:** |
| **2024.00xM.Filoviridae \_1nsp** |

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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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| **Is any taxon name used here derived from that of a living person:**  authorization. | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: Genus (*Dianlovirus*)  *Description of current taxonomy*: *Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Haploviricotina*: *Monjiviricetes*: *Mononegavirales*: *Filoviridae*: *Dianlovirus*: *Dianlovirus* *menglaense*  *Proposed* *taxonomic change(s):* add one species (*Dianlovirus* *dehongense*)  *Justification*: The complete genome sequence of Déhóng virus (DEHV) fulfills the pairwise-sequence-based demarcation criterion for the establishment of a novel species. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Genus (*Dianlovirus*)  *Description of current taxonomy*: *Riboviria*: *Orthornavirae*: *Negarnaviricota*: *Haploviricotina*: *Monjiviricetes*: *Mononegavirales*: *Filoviridae*: *Dianlovirus*: *Dianlovirus* *menglaense*  *Proposed* *taxonomic change(s)*: add one species (*Dianlovirus* *dehongense*)  *Demarcation criteria:* ≥23% pairwise coding-complete genome sequence divergence.  *Justification*: Déhóng virus (DEHV) was discovered by metagenomic sequencing in a Leschenault's rousette (*Rousettus leschenaultii* Desmarest, 1820) sampled in in 2016 in Déhóng Dǎi and Jǐngpǒ Autonomous Prefecture (德宏傣族景颇族自治州), Yúnnán Province (云南省 ), China. RNA-directed RNA polymerase phylogenetic analyses and genomic organization confidently placed DHEV into mononegaviral family *Filoviridae* as a close relative of dianloviruses and marburgviruses and the first filovirid from a bat of this species ([1](#_ENREF_1)).  The current filovirid species demarcation criterion is based on comparisons using at least coding-complete genomes with the NCBI PAirwise Sequence Comparison (PASC) tool ([2](#_ENREF_2)). Genomic sequences of filovirids of different species differ from each other by ≥23% ([3](#_ENREF_3)). Unfortunately, PASC is no longer supported by NCBI. The developers of PASC replaced the tool with an improved tool, VIrus Sequence-based Taxonomy Assignment (VISTA; <https://ngdc.cncb.ac.cn/vista>). VISTA employs a novel pairwise sequence comparison system that integrates alignment-free methods with machine learning techniques to automate virus taxonomy, focusing on the analysis of at least coding-complete genomes. This system includes a computational framework that automatically identifies demarcation thresholds, allowing for the objective selection of classification criteria across different viral ranks. Unlike PASC, which utilizes manually set, fixed thresholds, VISTA offers superior classification capabilities, faster computational speeds, and is better suited for handling large-scale data, enhancing both the efficiency and objectivity of virus classification. Re-analysis of filovirid genome sequences with VISTA (<https://ngdc.cncb.ac.cn/vista/family_results?family=Filoviridae>) confirmed the current *Filoviridae* Taxonomy originally established with PASC and confidently placed DEHV into a novel species within genus *Dianlovirus* (Figure 1). Together with establishment of this new species, we propose to change the PASC-based filovirid genus and species demarcation criteria to 0.492 and 0.137 in VISTA analysis, respectively. The demarcation value of 0.492 for genera indicates that sequences with genetic distances greater than this value belong to different genera, reflecting substantial evolutionary differences. Conversely, the 0.137 threshold for species implies that sequences with distances below this value are classified within the same species, while those with distances between 0.137 and 0.492 belong to the same genus but different species. |

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| **References:** |
| 1. He B, Hu T, Yan X, Pa Y, Liu Y, Liu Y, Li N, Yu J, Zhang H, Liu Y, Chai J, Sun Y, Mi S, Liu Y, Yi L, Tu Z, Wang Y, Sun S, Feng Y, Zhang W, Zhao H, Duan B, Gong W, Zhang F, Tu C.2024. Isolation, characterization, and circulation sphere of a filovirus in fruit bats. Proc Natl Acad Sci U S A 121:e2313789121.  2. Bào Y, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K, Dolnik O, Dye JM, Ebihara H, Formenty P, Hewson R, Kobinger GP, Leroy EM, Mühlberger E, Netesov SV, Patterson JL, Paweska JT, Smither SJ, Takada A, Towner JS, Volchkov VE, Wahl-Jensen V, Kuhn JH.2017. Implementation of objective PASC-derived taxon demarcation criteria for official classification of filoviruses. Viruses 9:106.  3. Biedenkopf N, Bukreyev A, Chandran K, Di Paola N, Formenty PBH, Griffiths A, Hume AJ, Mühlberger E, Netesov SV, Palacios G, Pawęska JT, Smither S, Takada A, Wahl V, Kuhn JH.2024. ICTV virus taxonomy profile: *Filoviridae* 2024. J Gen Virol 105:001955. |

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| **Tables, Figures** |

**Figure 1. Screenshot of VISTA analysis:**

