

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create five new species in the genus *Mastrevirus* (family *Geminiviridae*) |
| **Code assigned:** | 2025.012P.Geminiviridae\_Mastrevirus\_5nsp | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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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 |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General |  |

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

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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** |
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| **Submission date:** | 06/06/2025 |

**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 |  |
| 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| W - Withdrawn |  |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**

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| **Response of proposer:** |
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| **Revision date:** |  |

**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** |
| *Mastrevirus cenchri* | Genus + plant host (Genitive form -us -> -i) **- *Cenchr****us echinatus* |
| *Mastrevirus croci* | Genus + plant host (Genitive form -us -> -i) - ***Croc****us sativus* |
| *Mastrevirus mexicoense* | Genus + latinized country of sampling - **Mexico** |
| *Mastrevirus purpurei* | Genus + plant host (Genitive form -us -> -i) - *Cenchrus* ***purpure****us* |
| *Mastrevirus tripterygii* | Genus + plant host (Genitive form -ium -> -ii) - ***Tripterygi****um wilfordii* |

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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  *Monodnaviria; Shotokuvirae; Cressdnaviricota; Repensiviricetes; Geplafuvirales; Geminiviridae; Mastrevirus*  New species in the genus *Mastrevirus* are determined based on a 78% pairwise identity threshold coupled with phylogenetic support.  *Proposed* *taxonomic change(s):*  Create five new species in the genus *Mastrevirus*  *Justification*:  In the last year, eight genomes of mastreviruses have been identified that cannot be classified at the species level ~~within the current taxonomy framework~~. These can be classified into five new species sharing <78% pairwise identity with all classified mastreviruses. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  *Monodnaviria; Shotokuvirae; Cressdnaviricota; Repensiviricetes; Geplafuvirales; Geminiviridae; Mastrevirus*  There are currently 50 established species in the genus *Mastrevirus*.  *Proposed* *taxonomic change(s)*:  We propose to create five new species in the genus *Mastrevirus* to classify eight new genomes of mastreviruses that have been identified in the last year.  *Demarcation criteria:*  78% genome-wide pairwise identity threshold coupled with phylogenetic support [1].  *Justification*:  The genome sequences of the mastreviruses summarized in Table 1 can be classified into five new species that share <78% genome-wide pairwise identity as determined using Sequence Demarcation Tool (SDT) v1.2 [2] with all classified mastreviruses (Figure 1). The classification of these into five new species is supported by maximum likelihood phylogenetic inferred using PHYML [3] from the aligned genomes using MAFFT [4] with GTR+I+G4 chosen as the best fit determined using jModelTest [5] (Figure 2). |

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| **References:** |
| 1. Muhire B, Martin DP, Brown JK, Navas-Castillo J, Moriones E, Zerbini FM, Rivera-Bustamante R, Malathi VG, Briddon RW, Varsani A. 2013. A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus Mastrevirus (family Geminiviridae). Archives of Virology. 158(6):1411-24. doi: 10.1007/s00705-012-1601-7. Epub 2013 Jan 23. PMID: 23340592. 2. Muhire BM, Varsani A, Martin DP. 2014. SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One. 26;9(9):e108277. doi: 10.1371/journal.pone.0108277. PMID: 25259891; PMCID: PMC4178126. 3. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systems Biology 59(3):307-21. doi: 10.1093/sysbio/syq010. Epub 2010 Mar 29. PMID: 20525638. 4. Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinformatics. 19;20(4):1160-1166. doi: 10.1093/bib/bbx108. PMID: 28968734; PMCID: PMC6781576. 5. Darriba D, Taboada GL, Doallo R, Posada D. 2010. jModelTest 2: more models, new heuristics and parallel computing. Nature Methods. 30;9(8):772. doi: 10.1038/nmeth.2109. PMID: 22847109; PMCID: PMC4594756. 6. Ben Chéhida S, Devi Bunwaree H, Hoareau M, Moubset O, Julian C, Blondin L, Filloux D, Lavergne C, Roumagnac P, Varsani A, Martin DP, Lett JM, Lefeuvre P. 2024. Increase of niche filling with increase of host richness for plant-infecting mastreviruses. Virus Evolution. 13;10(1):veae107. doi: 10.1093/ve/veae107. PMID: 39717705; PMCID: PMC11665825. 7. Hosseini SA, Julian C, Galzi S, Filloux D, Roumagnac P. 2024. First report of saffron-associated mastrevirus 1 from saffron in Iran. Plant Diseases. doi: 10.1094/PDIS-11-24-2462-PDN. Epub ahead of print. PMID: 39673340. 8. Tavoosi M, Moradi Z, Mehrvar M, Zakiaghl M. 2025. First identification and complete genomic characterization of saffron dwarf virus from Iran, a novel mastrevirus infecting Crocus sativus. European Journal of Plant Pathology. https://doi.org/10.1007/s10658-025-03051-y 9. Valouzi H, Dizadji A, Golnaraghi A, Salami SA, Selmi I, Fontdevila Pareta N, Önder S, Massart S. 2025. First detection of saffron dwarf virus, wheat dwarf virus, wheat dwarf virus-associated alphasatellite and a new putative potyvirus species in saffron in Iran. New Disease Reports 51:e70022. https://doi.org/10.1002/ndr2.70022 10. Alcalá-Briseño RI, Casarrubias-Castillo K, López-Ley D, Garrett KA, Silva-Rosales L. 2020. Network Analysis of the Papaya Orchard Virome from Two Agroecological Regions of Chiapas, Mexico. mSystems. 14;5(1):e00423-19. doi: 10.1128/mSystems.00423-19. PMID: 31937673; PMCID: PMC6967384. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.012P.N.v2.Geminiviridae\_Mastrevirus\_5nsp | spreadsheet |
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| **Tables, Figures:** |

Table 1: Summary of the members of the five new species.

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| **Species name** | **Accession no.** | **Virus name** | **Isolate name** | **Country** | **Host/source** | **Ref** | |
| *“Mastrevirus cenchri”* | PQ434710 | Cenchrus echinatus associated virus | 21\_REU\_E0117\_CEAV | Reunion | *Cenchrus echinatus* | | [6] |
|  | PQ434734 | Cenchrus echinatus associated virus | 22\_REU\_E0101\_CEAV | Reunion | *Cenchrus echinatus* | | [6] |
| *“Mastrevirus croci”* | PQ392009 | Mastrevirus sp. croci | CSAV\_A9PstI | Iran | *Crocus sativus* | | [7] |
|  | PP848143 | Saffron dwarf virus | IR | Iran | *Crocus sativus* | | [8] |
|  | PQ740909 | Saffron dwarf virus | IR:Teh:Saf6:22 | Iran | *Crocus sativus* | | [9] |
| *“Mastrevirus mexicoense”* | MN203180 | Mastrevirus sp. UHMV-1.PC-W | UHMV-1.PC-W | Mexico | Unknown (weeds) | | [10] |
| *“Mastrevirus purpurei”* | PQ434729 | Cenchrus purpureus mild streak virus | 21\_REU\_E0816\_CPMSV | Reunion | *Cenchrus purpureus* | | [6] |
| *“Mastrevirus tripterygii"* | MT159331 | Tripterygium mastrevirus A | Won | China | *Tripterygium wilfordii* | | - |

**Immagine che contiene schermata, linea, Policromia, modello

Il contenuto generato dall'IA potrebbe non essere corretto.Figure 1:** Genome-wide pairwise identity matrix of genomes from each mastrevirus species together with those that are members of the five new species inferred using SDT v1.2 [2]. Representative sequences from the proposed new species (n=5) are marked with “\*”.

Immagine che contiene testo, schermata, design

Il contenuto generato dall'IA potrebbe non essere corretto.**Figure 2:** Maximum likelihood phylogenetic tree of representative genomes from each mastrevirus species together with those that are members of the five new species. The phylogenetic tree is rooted genome sequences of capulaviruses. Representative sequences from the proposed new species (n=5) are marked with “\*”.