

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:**  | Establish five new species in the genus *Mastrevirus* |
| **Code assigned:**  | 2024.009P.A.v1.Geminiviridae\_Mastrevirus\_5nsp |

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| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)** X |
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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* 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** |
| *Geminiviridae* and *Tolecusatellitidae* Study Group | 10 | 0 | 0 |
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| **Submission date:** |  10/06/2024 |

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

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| 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| W - Withdrawn |  |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:** |  DD/MM/YYYY |

Part 3: TAXONOMIC PROPOSAL

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| **Name of accompanying Excel module:**  |
| 2024.009P.A.v1.Geminiviridae\_Mastrevirus\_5nsp.xlsx |

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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:**  |  **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: Species*Description of current taxonomy*: Mastreviruses are currently classified according to the following hierarchy:*Monodnaviria*; *Shotokuvirae*; *Cressdnaviricota*; *Repensiviricetes*; *Geplafuvirales*; *Geminiviridae*; *Mastrevirus.*Within the genus *Mastrevirus*, viruses are classified into species based on a 78% genome-wide pairwise identity threshold [1].*Proposed* *taxonomic change(s):* We propose the establishment of five new species to classify a suite of new mastreviruses that have been identified over the last year or so. *Justification*:The members of the five new proposed species in the genus *Mastrevirus* share < 78% genome-wide pairwise identity with sequences of members of currently established mastrevirus species.  |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: Species *Description of current taxonomy*: There are currently 45 established species in the genus *Mastrevirus*. *Proposed* *taxonomic change(s)*: We propose to establish five new species in the genus *Mastrevirus*.*Demarcation criteria:*78% genome-wide pairwise identity threshold [1].*Justification*: The sequences of the viruses summarized in Table 1 can be classified into five new species that share <78% genome-wide pairwise identity with all classified mastreviruses (Figure 1). Furthermore, this is supported by maximum likelihood phylogenetic analysis (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. A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus Mastrevirus (family Geminiviridae). Arch Virol. 2013 Jun;158(6):1411-24. doi: 10.1007/s00705-012-1601-7. Epub 2013 Jan 23. PMID: 23340592.
2. Muhire BM, Varsani A, Martin DP. SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One. 2014 Sep 26;9(9):e108277. doi: 10.1371/journal.pone.0108277. PMID: 25259891; PMCID: PMC4178126.
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5. Darriba D, Taboada GL, Doallo R, Posada D. jModelTest 2: more models, new heuristics and parallel computing. Nat Methods. 2012 Jul 30;9(8):772. doi: 10.1038/nmeth.2109. PMID: 22847109; PMCID: PMC4594756.
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| **Tables, Figures:**  |

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**Figure 1:** A ‘two color’ genome-wide pairwise identity matrix of genomes from each mastrevirus species inferred using SDT v1.2 [2]. Representative sequences from the proposed new species (n=5) are shown in red font.

**Figure 2:** Maximum likelihood phylogenetic tree of representative genomes from each mastrevirus species (aligned with MAFFT v7 [3]) inferred using PHYML [4] with GTR+I+G4 chosen as the best fit model (using jModelTest [5]. The phylogenetic tree is rooted with genome sequences of capulaviruses. Proposed new species are in red font.

**Table 1:** Summary of the five new species in the genus *Mastrevirus* and their members.

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| **Species names** | **Accession** | **Virus name** | **Isolate** | **Country** | **Host / source** | **Reference** |
| *Mastrevirus urochloareunionense* | OQ451139 | Urochloa decumbens associated virus  | Reunion-Colimacons-Urochloa decumbens-21\_REU\_E0807\_D | France: Reunion | *Urochloa decumbens* |  *-*  |
| *Mastrevirus nomiae* | PP467585 | Nomiamastrel virus | NSB1\_13 | USA | *Nomia* sp. | [6] |
| *Mastrevirus brachypodiumprimi* | OR596402 | Brachypodium phoenicoides associated virus 1 | 3-N2-4 | France | *Brachypodium phoenicoides* | [7] |
| *Mastrevirus bothriochloae* | OR596403 | Bothriochloa barbinodis associated virus | 4-E1-7 | France | *Bothriochloa barbinodis* | [7] |
|  | OR596404 | Bothriochloa barbinodis associated virus | 3-E1-8 | France | *Bothriochloa barbinodis* | [7] |
| *Mastrevirus brachypodiumsecundi* | OR596405 | Brachypodium phoenicoides associated virus 2 | 2-N3-1 | France | *Brachypodium phoenicoides* | [7] |