

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

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| **Code assigned:** | **2020.005P** |  |
| **Short title:** Create four new species in the genus *Mastrevirus* (*Geplafuvirales*: *Geminiviridae*) | | |
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**Author(s) and email address(es)**

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

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| *Geminiviridae* and *Tolecusatellitidae* SG |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | July 30, 2020 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2020.005P.R.Mastrevirus\_4nsp.xlsx |

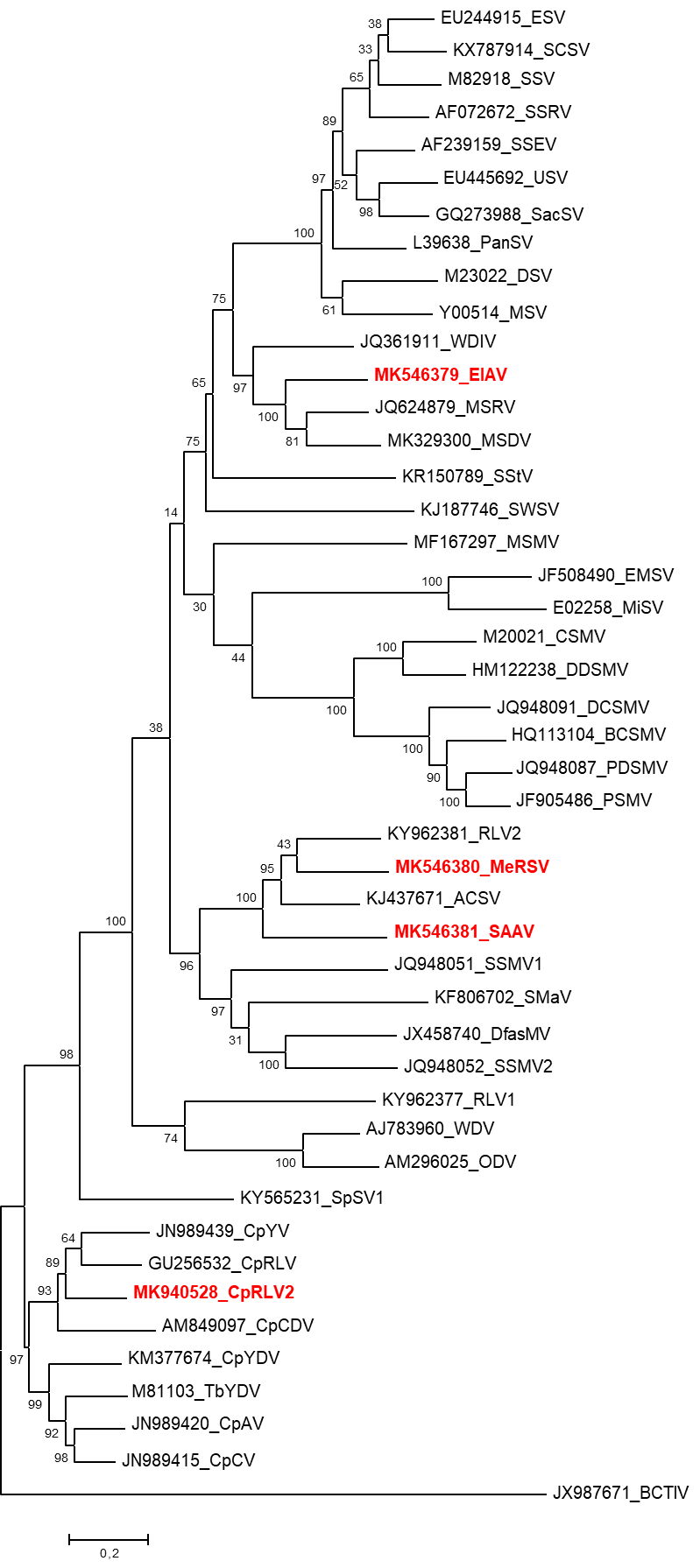
**Abstract**

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| Here we propose to classify mastreviruses that cannot be assigned to currently established species into four new species based on the species demarcation guidelines already established for the *Mastrevirus* genus (familly *Geminiviridae*). |

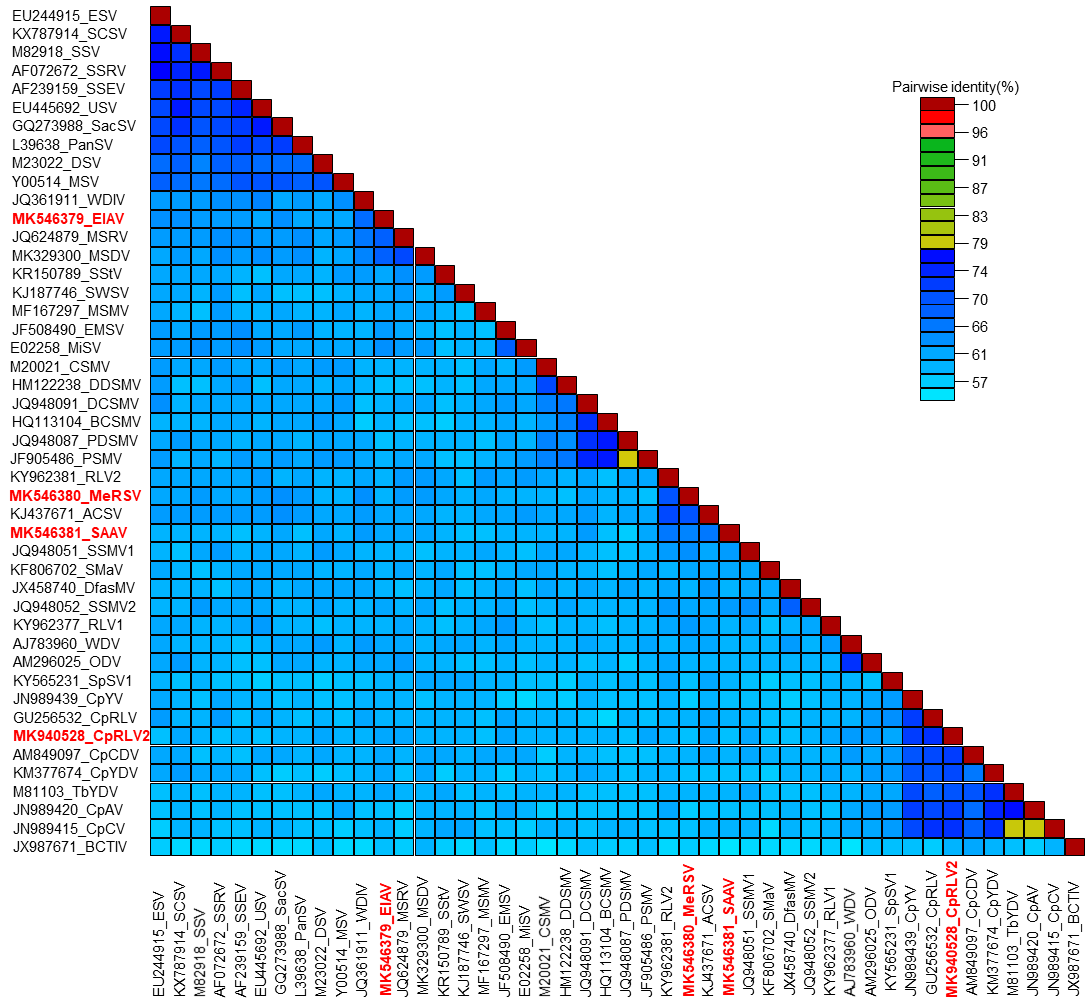
**Text of proposal**

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| |  | | --- | | **Four new species in the genus *Mastrevirus* (family *Geminiviridae*)**  There are currently 41 species in the genus *Mastrevirus* in the family *Geminiviridae*. Of these, members of eight infect dicotyledonous plants and the remaining 32 members infect monocotyledonous plants.  Based on the framework for classification of mastreviruses established by Muhire *et al*. (2013), where a **78% genome-wide pairwise identity (PI) threshold** coupled with phylogenetic support were proposed and accepted as species demarcation criteria, **four new species** have been recently characterized from Reunion Island (Claverie et al., 2019) and Australia (Filardo and Sharman, 2019).  **Chickpea redleaf virus 2**  One isolate of chickpea redleaf virus 2 (CpRLV2, table 1) has been characterized from chickpea (*Cicer arietinum;* Filardo and Sharman, 2019). The complete sequence (MK940528) shares less than 70% genome-wide pairwise identity with all other known mastreviruses within currently established species (Figures 1 and 2).  **Eleusine indica associated virus**  One isolate of Eleusine indica associated virus (EIAV, table 1) has been characterized in *Eleusine indica* (Claverie *et al*., 2019). The complete sequence (MK546379) shares less than 66% genome-wide pairwise identity with all other known mastreviruses within currently established species (Figures 1 and 2).  **Melinis repens associated virus**  One isolate of Melinis repens associated virus (MeRAV, table 1) has been characterized from *Melinis repens* (Claverie *et al*., 2019). The genome sequence (MK546380) shares less than 66% nucleotide identity with all other known mastreviruses within currently established species (Figures 1 and 2).  **Sorghum arundinaceum associated virus**  Two isolates of Sorghum arundinaceum associated virus (SAAV, table 1) have been characterized from *Sorghum arundinaceum* (Claverie *et al*., 2019). The two sequences (MK546381, MK546382) share 99.2% genome-wide pairwise identity with each other and a less than 62% with all other known mastreviruses within currently established species (Figures 1 and 2). | |

**Supporting evidence**

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**Figure 1.** Maximum likelihood phylogenetic tree of representative genomes from each Mastrevirus species inferred using MEGA6 (Tamura *et al*., 2013) and rooted with a becurtovirus sequence of *Beet curly top Iran virus* (JX987671).

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**Figure 2.** Three-color pairwise identity matrix inferred using SDT v1.2 (Muhire *et al*., 2014). Sequences of representative isolates for each new species are in red font.

**Table 1.** Details of isolates of new species being proposed in the genus *Mastrevirus*

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| **Species name** | **Virus acronym** | **Isolates** | **GenBank accession** | **Origin** | **Host** |
| *Chickpea redleaf virus 2* | CpRV2 | Australia-5495-2017 | MK940528 | Australia | *Cicer arietinum* |
| *Eleusine indica associated virus* | EIAV | Reunion-Bassin Plat-RE004-2014 | MK546379 | Réunion | *Eleusina indica* |
| *Melenis repens associated virus* | MeRAV | Reunion-Bassin Plat-RE027-2014 | MK546380 | Réunion | *Melenis repens* |
| *Sorghum arundinaceum associated virus* | SAAV | Reunion-Bassin Plat-RE034-2014 | MK546381 | Réunion | *Sorghum arundinaceum* |
|  |  | Reunion-Bassin Plat-RE084-2014 | MK546382 | Réunion | *Sorghum arundinaceum* |

**References**

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4. Muhire BM, Varsani A, Martin DP (2014) SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9: e108277. https://doi.org/10.1371/journal.pone.0108277. PMID: 25259891 DOI: 10.1371/journal.pone.0108277
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