This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Code assigned:** | ***2019.002P*** | | |  |
| **Short title:** Create one new species in the genus *Mastrevirus* (*Geminiviridae*) | | | | |
|  | | | | |
| **Author(s) and email address(es):** | | | | |
| Lett J-M, Martin DP, Roumagnac P, Varsani A | | lett@cirad.fr; darrenpatrickmartin@gmail.com;  philippe.roumagnac@cirad.fr;  arvind.varsani@asu.edu | | |
| **Corresponding author** | | | | |
| Jean-Michel Lett ([lett@cirad.fr](mailto:lett@cirad.fr)) | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | *Geminiviridae and Tolecusatellitidae SG* | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | |
|  | | | | |
|  | | | | |
| Date first submitted to ICTV: | | | |  |
| Date of this revision (if different to above): | | | |  |

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

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.002P.A.v1.Mastrevirus\_1sp.xlsx |

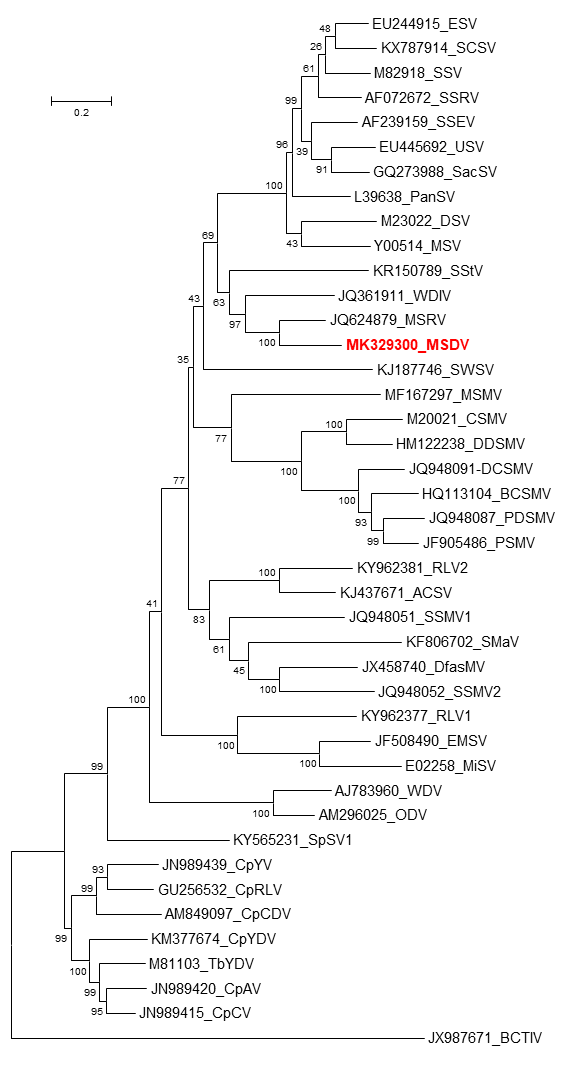
**Supporting material:**

**One new species in the genus *Mastrevirus* (family *Geminiviridae*)**

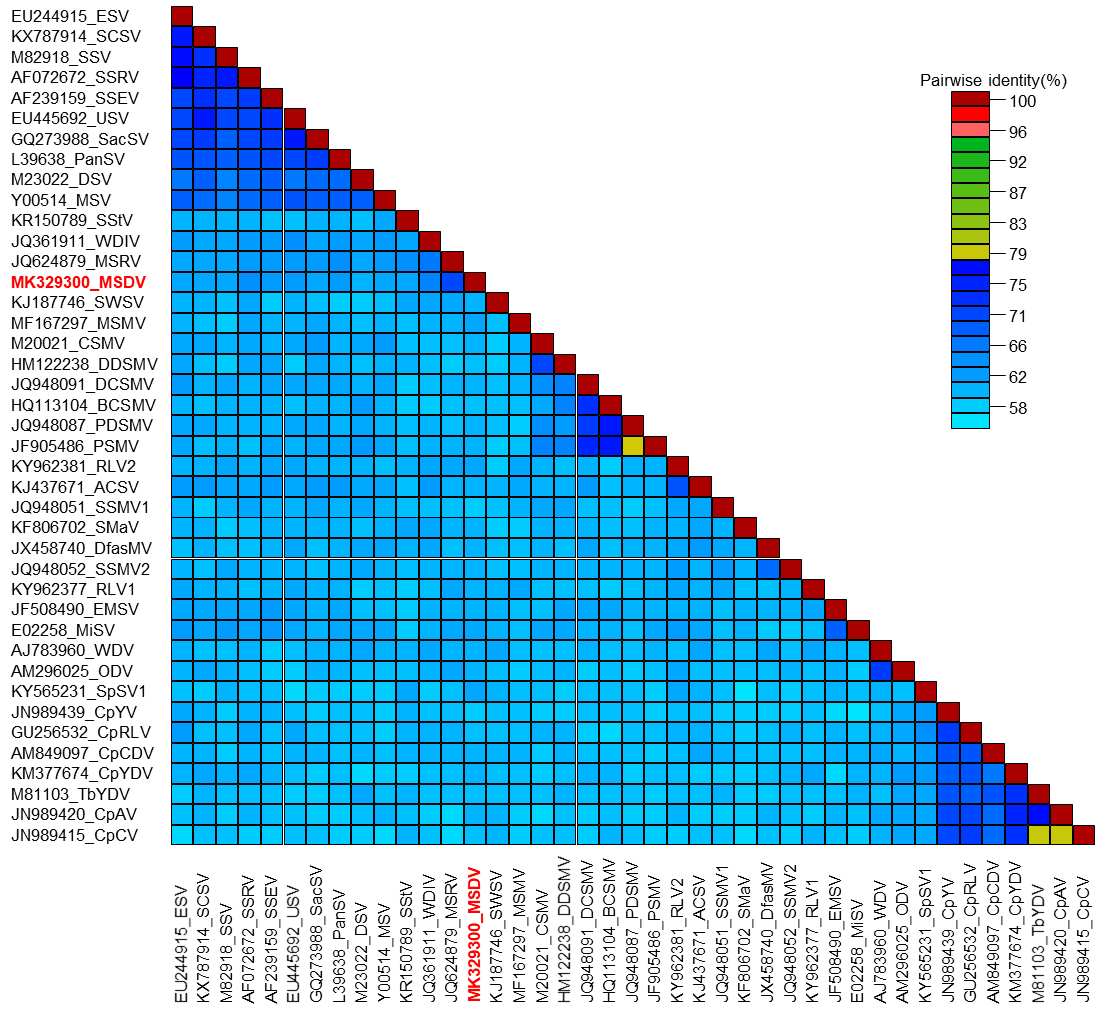
There are currently 40 species in the genus *Mastrevirus* (family *Geminiviridae*). Of these, members of eight species infect dicotyledonous plants and the remaining 32 members infect monocotyledonous plants. Based on the framework for classification of mastreviruses outlined in Muhire *et al*. (2013), where a **78% genome-wide pairwise identity (PI) threshold** coupled with phylogenetic support are used as species demarcation criteria, four new viruses have recently been identified that represent **a new species** from Africa infecting maize (Guadie et al., 2019).

**Maize streak dwarfing virus**

Four isolates of maize streak dwarfing virus (Table 1) have been identified in *Zea mays* (Guadie *et al*., 2019). The four sequences (MK329300 - MK329303) share 99-100% genome-wide pairwise identity with each other and **less than 70.4% with all other known mastreviruses** within currently established species (Figures 1 and 2).



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



**Figure 2.** Two-color pairwise identity matrix inferred using SDT v1.2 (Muhire *et al*., 2014). The sequence of the isolate representative of the new species *Maize streak dwarfing virus* is shown in red font.

**Table 1.** Details of isolates of *Maize streak dwarfing virus,* a proposed new species in the genus *Mastrevirus*.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species name** | **Virus name / acronym** | **Isolates** | **GenBank accession** | **Country** | **Host** |
| *Maize streak dwarfing virus* | maize streak dwarfing virus (MSDV) | ET-Adama Zuria-MV1-16 | MK329300 | Ethiopia | *Zea mays* |
|  | maize streak dwarfing virus (MSDV) | ET-Shevaba-MV56-16 | MK329301 | Ethiopia | *Zea mays* |
|  | maize streak dwarfing virus (MSDV) | ET-Boset-MV66-16 | MK329302 | Ethiopia | *Zea mays* |
|  | maize streak dwarfing virus (MSDV) | ET-Analume-MV74-16 | MK329303 | Ethiopia | *Zea mays* |

| **References:** |
| --- |
| Guadie D, Tesfaye K, Knierim D, Winter S, Abraham A, 2019. Molecular analysis of maize (*Zea mays* L.)-infecting mastreviruses in Ethiopia reveals marked diversity of virus genomes and a novel species. *Virus Genes* 55:339-345.  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*). *Arch Virol* 158:1411-1424.  Muhire BM, Varsani A, Martin DP, 2014. SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. *PLoS One* 9:e108277.  Tamura K, Stecher G, Peterson D, Filipski A, Kumar S, 2013. MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. *Mol Biol Evol* 30:2725-2729. |