This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
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| **Code assigned:** | ***2017.008P*** | | | | (to be completed by ICTV officers) |
| **Short title:** Five new species in the genus *Mastrevirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Arvind Varsani and Darren P. Martin | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Arvind.varsani@asu.edu | | | | | |
| **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* SG** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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| 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:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.008P.N.v1.Mastrevirus\_5sp |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 3:** **NON-STANDARD**

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

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| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
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**Part 4:** **APPENDIX**: supporting material

There are currently 33 species in the genus *Mastrevirus* in the family *Geminiviridae*. Of these 33 species, members of six infect dicots and the rest (n=27) infect monocots. Most of the viruses in this latter group have been identified infecting various grasses in Africa and Australia (Muhire et al., 2013).

Muhire et al. (2013) proposed a framework for the classification of mastreviruses where a 78% genome-wide pairwise identity (PI) threshold coupled with phylogenetic support is used for species demarcation. Based on this framework, now officially accepted and applied for this taxon, five new species need to be established to allow the classification of new mastrevirus isolates that have been recently characterized.

**New species to be created and isolates that should be assigned to these species**

1. **Chickpea yellow dwarf virus**

Two isolates of chickpea yellow dwarf virus were identified infecting chickpea (*Cicer arietinum*) in Pakistan (Kraberger et al., 2015). The two isolates (Table 1) share >99% pairwise identity (PI) and <75% PI with all other mastreviruses (Figure 1).

1. **Sweet potato symptomless virus 1**

The seven isolates of sweet potato symptomless virus 1 (Table 1) from China (n=1), Kenya (n=1), Taiwan (n=3), Uruguay (n=1) and USA (n=1) share >97% PI between themselves and <63% PI with other mastreviruses (Figure 1). All seven isolates have been found infecting sweet potatoes (*Ipomoea batatas*) (Cao et al., 2017).

1. **Sugarcane chlorotic streak virus**

The 17 isolates of sugarcane chlorotic streak virus share >98% PI and <76% PI with other mastreviruses. All 17 isolates have been identified infecting sugarcane (*Saccharum officinarum*) in Nigeria (Yahaya et al., 2017).

1. **Sugarcane striate virus**

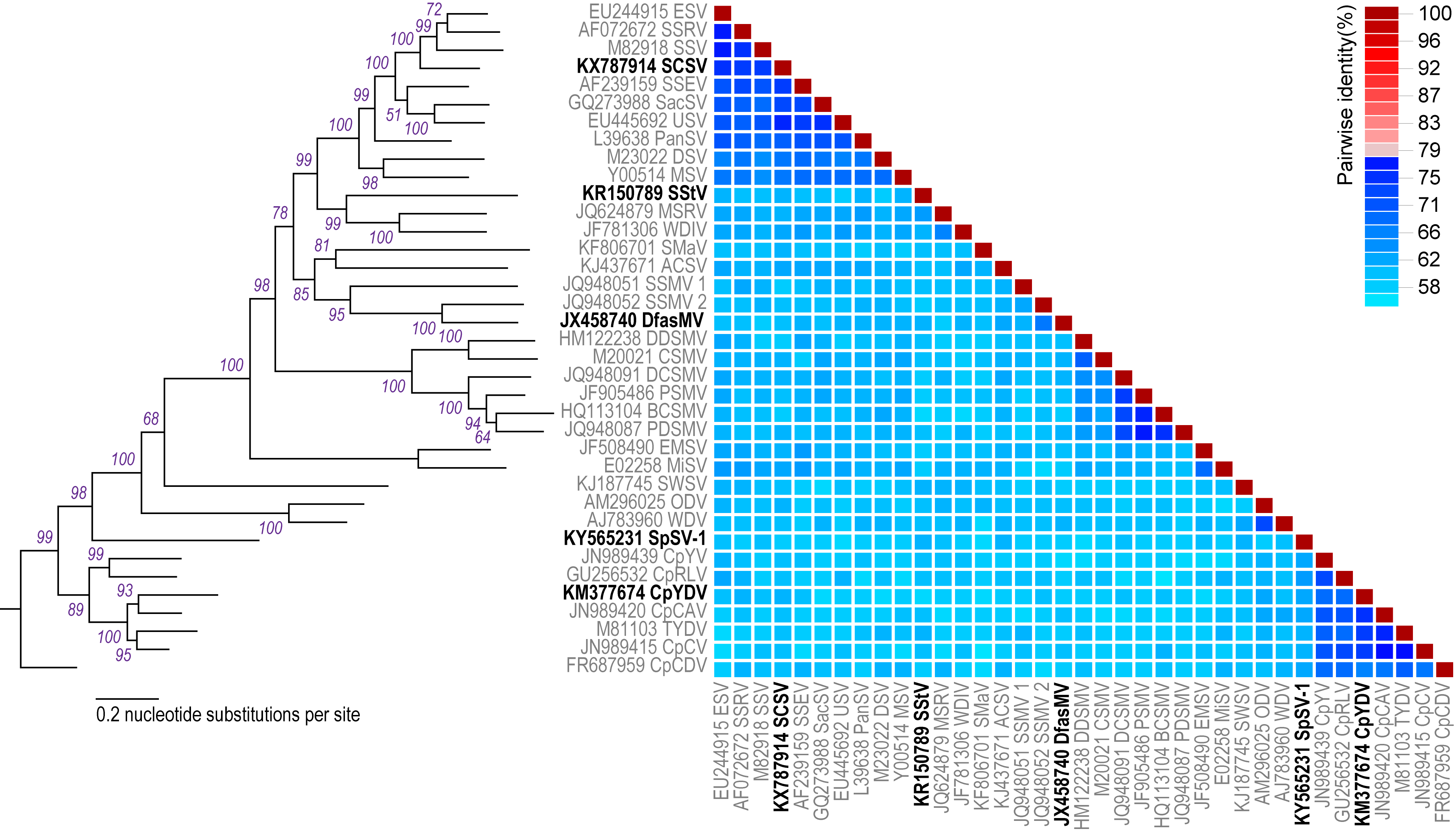
The single isolate of sugarcane striate virus has been identified infecting sugarcane (*Saccharum* sp*.*) in China. This isolate shares <64% PI with all recognized mastreviruses.

1. **Dragonfly-associated mastrevirus**

The two mastrevirus genomes were recovered from *Erythrodiplax fusca* sampled in Puerto Rico (Rosario et al., 2013), share 99% PI with each other and <68%PI with known mastreviruses.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species name** | **GenBank**  **accession #** | **Virus acronym** | **Isolate name** | **Country**  **of isolate** | **Host** |
| *Chickpea yellow dwarf virus* | KM377674 | CpYDV | CpYDV-PK\_PK103\_2012 | Pakistan | *Cicer arietinum* |
|  | KM377675 |  | CpYDV-PK\_PK37\_2012 | Pakistan | *Cicer arietinum* |
| *Sweet potato symptomless virus 1* | KY565231 | SpSV-1 | Q44429 | Kenya | *Ipomoea batatas* |
|  | KY565232 |  | GWB | USA | *Ipomoea batatas* |
|  | KY565233 |  | Z01046 | Taiwan | *Ipomoea batatas* |
|  | KY565234 |  | Z01117 | Uruguay | *Ipomoea batatas* |
|  | KY565235 |  | Z01019 | China | *Ipomoea batatas* |
|  | KY565236 |  | Z01057a | Taiwan | *Ipomoea batatas* |
|  | KY565237 |  | Z01057b | Taiwan | *Ipomoea batatas* |
| *Sugarcane chlorotic streak virus* | KX787914 | SCSV | Sc10-SR-1 | Nigeria | *Saccharum officinarum* |
|  | KX787915 |  | Sc10-SR-6 | Nigeria | *Saccharum officinarum* |
|  | KX787916 |  | Sc10-SC-7 | Nigeria | *Saccharum officinarum* |
|  | KX787917 |  | Sc11-SR-4 | Nigeria | *Saccharum officinarum* |
|  | KX787918 |  | Sc11-SC-4 | Nigeria | *Saccharum officinarum* |
|  | KX787919 |  | Sc11-SC-5 | Nigeria | *Saccharum officinarum* |
|  | KX787920 |  | Sc29-SR-8 | Nigeria | *Saccharum officinarum* |
|  | KX787921 |  | Sc29-SC-6 | Nigeria | *Saccharum officinarum* |
|  | KX787922 |  | Sc29-SC-7 | Nigeria | *Saccharum officinarum* |
|  | KX787923 |  | Sc30-SR-1 | Nigeria | *Saccharum officinarum* |
|  | KX787924 |  | Sc30-SR-8 | Nigeria | *Saccharum officinarum* |
|  | KX787925 |  | Sc30-SC-8 | Nigeria | *Saccharum officinarum* |
| *Sugarcane striate virus* | KR150789 | SStV | WZG | China | *Saccharum* sp. |
| *Dragonfly-associated mastrevirus* | JX458740 | DfasMV | PR\_NZ50\_2009 | Puerto Rico | *Erythrodiplax fusca* |
|  | JX458741 |  | PR\_NZ70\_2009 | Puerto Rico | *Erythrodiplax fusca* |



**Figure 1.** Maximum likelihood phylogenetic tree (rooted with becurtovirus sequences) of representative genomes from each mastrevirus species inferred using IQ-TREE (Nguyen et al., 2015) with GTR+I+G4 chosen as the best fit model and a ‘two colour’ pairwise identity matrix inferred using SDT v1.2 (Muhire et al., 2014). Sequences of representative isolates for each new species are in bold font.

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| **References:** |
| Cao, M., Lan, P., Li, F., Abad, J., Zhou, C., Li, R., 2017. Genome characterization of sweet potato symptomless virus 1: a mastrevirus with an unusual nonanucleotide sequence. Arch Virol.  Kraberger, S., Mumtaz, H., Claverie, S., Martin, D.P., Briddon, R.W., Varsani, A., 2015. Identification of an Australian-like dicot-infecting mastrevirus in Pakistan. Arch Virol 160(3), 825-830.  Muhire, B., Martin, D.P., Brown, J.K., Navas-Castillo, J., Moriones, E., Zerbini, F.M., Rivera-Bustamante, R., Malathi, V.G., Briddon, R.W., Varsani, A., 2013. A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus Mastrevirus (family Geminiviridae). Arch Virol 158(6), 1411-1424.  Muhire, B.M., Varsani, A., Martin, D.P., 2014. SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9(9), e108277.  Nguyen, L.T., Schmidt, H.A., von Haeseler, A., Minh, B.Q., 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol 32(1), 268-274.  Rosario, K., Padilla-Rodriguez, M., Kraberger, S., Stainton, D., Martin, D.P., Breitbart, M., Varsani, A., 2013. Discovery of a novel mastrevirus and alphasatellite-like circular DNA in dragonflies (Epiprocta) from Puerto Rico. Virus Res 171(1), 231-237.  Yahaya, A., Dangora, D.B., Alegbejo, M.D., Kumar, P.L., Alabi, O.J., 2017. Identification and molecular characterization of a novel sugarcane streak mastrevirus and an isolate of the A-strain of maize streak virus from sugarcane in Nigeria. Arch Virol 162(2), 597-602. |

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| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |