



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: TITLE, AUTHORS, etc

Code assigned:	2015.016aP	(to be completed by ICTV officers)				
Short title: Three new species in the genus <i>Mastrevirus</i> of the family <i>Geminiviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)						
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>	
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>	

Author(s):

Darren P. Martin and Arvind Varsani, on behalf of the *Geminiviridae* Study Group

Corresponding author with e-mail address:

Darren Martin, darrenpatrickmartin@gmail.com

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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	<i>Geminiviridae</i>
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ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:

15 June 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

EC Comments: Please provide a brief explanation as to how the sequences were assembled. Please also define abbreviations in the figure.

Response: An explanation on how sequencing and sequence assembly were conducted is now provided.
 Abbreviations were defined in the legend of Figure A1.

MODULE 2: NEW SPECIES

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2015.016aP	(assigned by ICTV officers)
To create 3 new species within:		
Genus:	<i>Mastrevirus</i>	Fill in all that apply. <ul style="list-style-type: none"> If the higher taxon has yet to be created (in a later module, below) write “(new)” after its proposed name. If no genus is specified, enter “unassigned” in the genus box.
Subfamily:		
Family:	<i>Geminiviridae</i>	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Sugarcane white streak virus</i>	SWSA-A [SD-VARX-2013]	KJ187746
<i>Axonopus compressus streak virus</i>	ACSV [NG-g84-oba-2007]	KJ437671
<i>Switchgrass mosaic-associated virus</i>	SgMaV-1 [US-DB-2012]	KF806702

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
 - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria.**
 - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Three new Mastrevirus species have been proposed: *Sugarcane white streak virus* (SWSV; Candresse et al., 2014), *Axonopus compressus streak virus* (ACSV; Oluwafemi et al., 2014), and *Switchgrass mosaic associated virus* (SgMaV; Agindotan et al., 2015). The full-length genomes of axonopus compressus streak virus (ACSV) and switchgrass mosaic associated virus (SgMaV) were amplified by rolling-circle amplification (RCA), cloned and sequenced by conventional (Sanger) sequencing. The complete sequences were determined by primer-walking and assembled using DNA Baser. Sugarcane white streak virus was initially detected and sequenced by NGS, but eventually a full-length clone was obtained by RCA and cloning, and sequenced by primer-walking. Using the pairwise alignment and sequence identity-calculation approaches recommended by the geminivirus study group (Muhire et al., 2013) it is evident that all three of these isolates share less than 78% genome-wide pairwise identity to any currently classified mastrevirus isolates (i.e. they meet the current mastrevirus pairwise similarity-based species demarcation criterion of <78% nucleotide sequence identity for the whole genome with any official mastrevirus species; Figure 1A). All three of the isolates also fall on branches of the mastrevirus phylogenetic tree that are basal to clades containing multiple different mastrevirus species.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

References

Agindotan BO, Domier LL, Bradley CA. 2015. Detection and characterization of the first North American mastrevirus in switchgrass. Arch Virol. 160:1313-1317.

Candresse T, Filloux D, Muhire B, Julian C, Galzi S, Fort G, Bernardo P, Daugrois JH, Fernandez E, Martin DP, Varsani A, Roumagnac P. 2014. Appearances can be deceptive: revealing a hidden viral infection with deep sequencing in a plant quarantine context. PLoS One. 9:e102945.

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.

Oluwafemi S, Kraberger S, Shepherd DN, Martin DP, Varsani A. 2014. A high degree of African streak virus diversity within Nigerian maize fields includes a new mastrevirus from *Axonopus compressus*. Arch Virol. 159:2765-2770.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

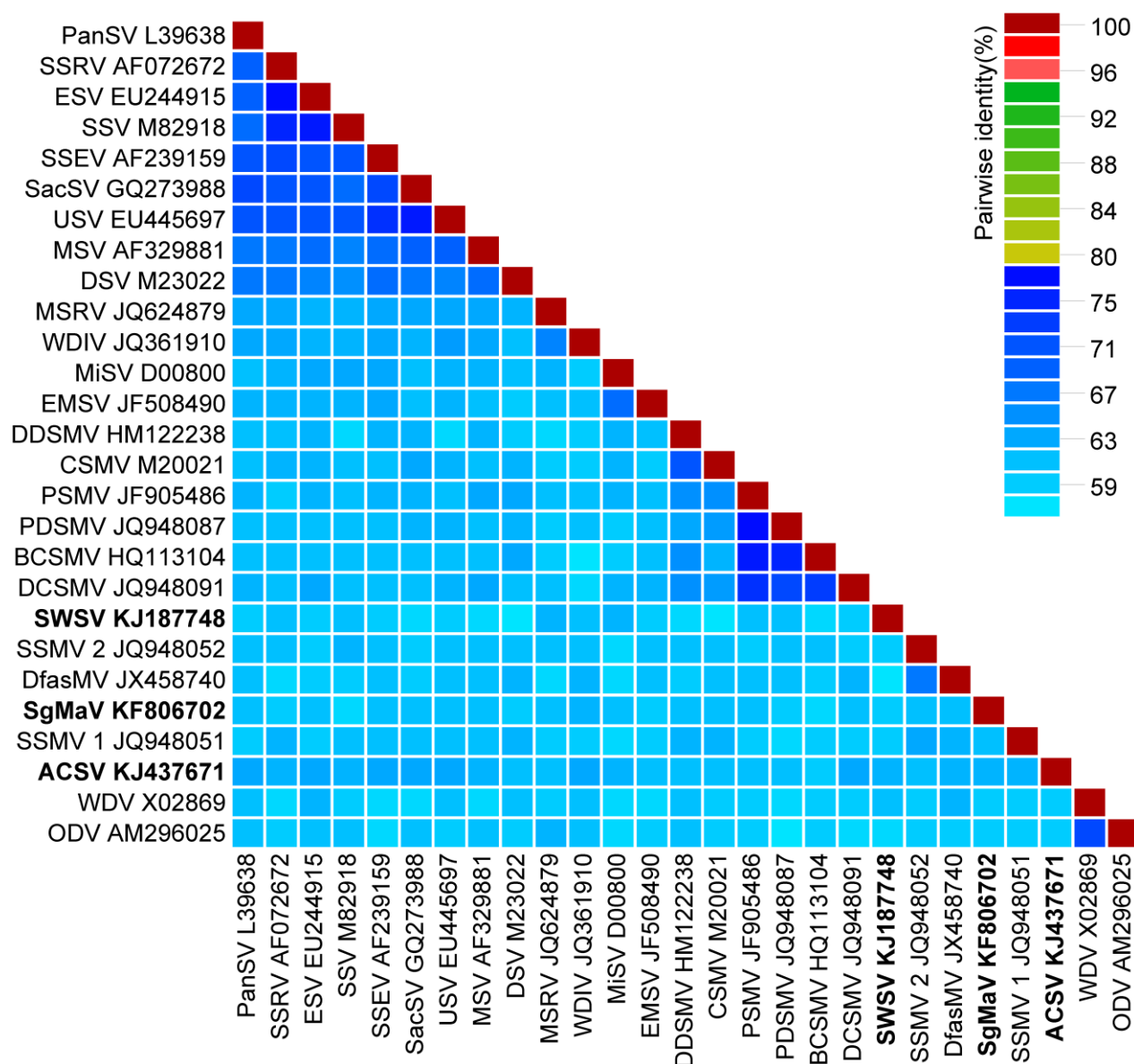


Figure A1. Pairwise genome-wide nucleotide sequence identities between the three proposed species (in bold) and currently accepted species in the genus Mastrevirus. Note that the blue colour of all cells off the horizontal indicates that all of the listed species share less than 78% genome-wide nucleotide sequence identity. The three new proposed species actually all share less than 70% identity with any mastrevirus isolates belonging to any of the currently accepted mastrevirus species. ACSV = axonopus compressus streak virus; BCSMV = bromus catharticus striate mosaic virus; CSMV = chloris striate mosaic virus; DCSMV = digitaria ciliaris striate mosaic virus; DDSMV = digitaria didactyla striate mosaic virus; DfasMV = dragonfly associated mastrevirus; DSV = digitaria streak virus; EMSV = eragrostis minor streak virus; ESV = eragrostis streak virus; MSV = maize streak virus; MiSV = miscanthus streak virus; MSRV= maize streak Reunion virus; ODV = oat dwarf virus; PanSV = panicum streak virus; PDSMV = paspalum dilatatum striate mosaic virus; PSMV = paspalum striate mosaic virus; SacSV = saccharum streak virus; SSMV-1 = Sporobolus striate mosaic virus-1; SSMV-2 = sporobolus striate mosaic virus-2; SgMaV = switchgrass mosaic associated virus; SSEV = sugarcane streak Egypt virus; SSRV = sugarcane streak Reunion virus; SSV = sugarcane streak virus; SWSV = sugarcane white streak virus; USV = urochloa streak virus; WDIV = wheat dwarf India virus; WDV = wheat dwarf virus.

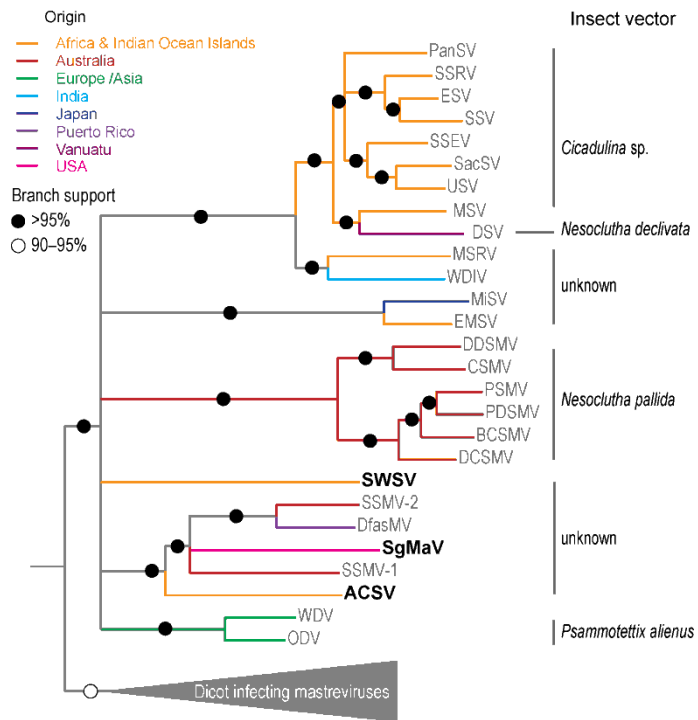


Figure A2. Maximum likelihood phylogenetic tree indicating the distant evolutionary relationships between the three newly proposed species (indicated in bold) and other accepted mastrevirus species. Abbreviations as in Figure A1.