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:	***2012.019a,bP***	(to be completed by ICTV officers)

Short title: create 17 species and remove 2 species in the genus *Mastrevirus*, family *Geminiviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

J.K. Brown jbrown@ag.arizona.edu (on behalf of the Geminiviridae Study Group)

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)	Geminiviridae

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV: June 26, 2012
Date of this revision (if different to above):

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	***2012.019aP***	(assigned by ICTV officers)

To create 17 new species within:

Genus:	***Mastrevirus***
Subfamily:	
Family:	***Geminiviridae***
Order:	

Fill in all that apply.
- 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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Bromus catharticus striate mosaic virus	HQ113104
Digitaria ciliaris striate mosaic virus	JQ948088, JQ948089, JQ948090, JQ948091
Paspalum dilatatum striate mosaic virus	JQ948085, JQ948086, JQ948087, JQ948061, JQ948077, JQ948062
Oat dwarf virus	AM296025
Chickpea chlorosis virus	JN989413,JN989414,JN989415, GU256530,GU256531,JN989416, JN989417, JN989432, JN989424, JN989425, JN989426, JN989427, JN989428, JN989429, JN989430, JN989431, JN989433, JN989434, JN989435, JN989436, JN989437, JN989438
Chickpea chlorosis Australia virus	JN989418, JN989419, JN989420, JN989421, JN989422, JN989423

Chickpea redleaf virus	GU256532
Chickpea yellows virus	JN989439
Eragrostis minor streak virus	JF508490
Digitaria didactyla striate mosaic virus	HM122238
Chickpea chlorotic dwarf virus	AM849097, AM850136, AM900416, FR687960, AM933134, AM933135, FR687959, AM849096, DQ458791. Y11023
Maize streak Reunion virus	JQ624879, JQ624880
Saccharum streak virus	GQ273988
Paspalum striate mosaic virus	JF905486
Wheat dwarf India virus	JQ361911, JQ361910
Sporolobus striate mosaic virus 1	JQ948052
Sporolobus striate mosaic virus 2	JQ948051

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

All meet the >78% proposed genome-wide sequence similarity species demarcation criteria, based on re-evaluated % pairwise identity comparisons (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps, Figure 1; Figure 2). Prior to the re-evaluation of pairwise distances the working species cutoff was considered 75% based on

Clustal V analysis, which considers gaps as additional characters. The revised analysis does not consider a gap as a character state and therefore is expected to result in more reliable species demarcations. Phylogenetically, they all group within the *Mastrevirus* genus (based on maximum likelihood analysis with best fit model – GTR+I+G4 selected by jModeltest; Posada, 2008; Guindon *et al.*, 2010; Figure 3). All have a distinctly mastrevirus-like genome organization.

Pairwise comparisons

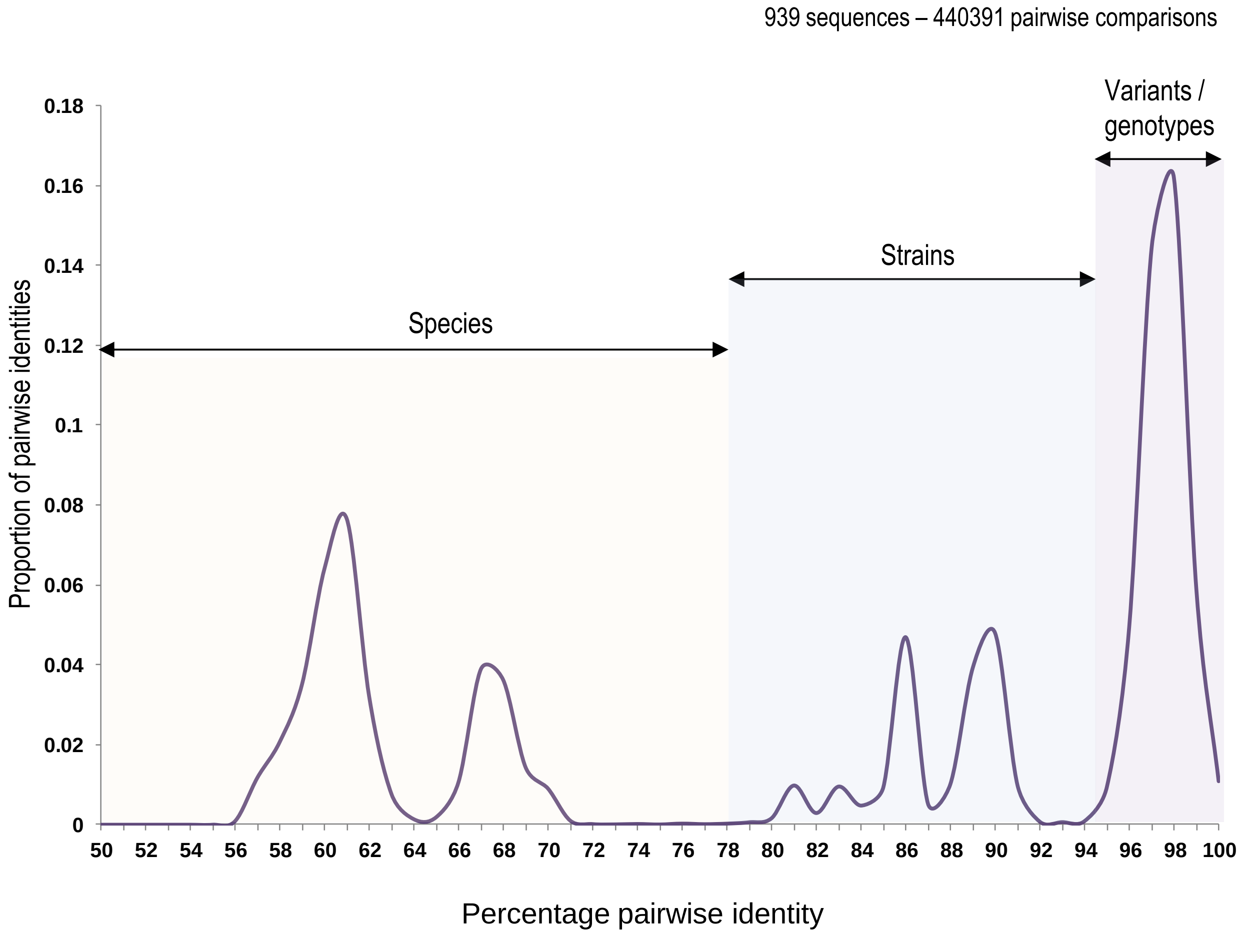

Figure 1. Distribution of mastreviral full genome pairwise sequence similarity scores. All sequence pairs were individually aligned to one-another using Muscle (Edgar, 2004) and pairwise Hamming distances (equivalent to p-distances calculated in Mega5.0) were calculated with pairwise deletion of gaps. Similarity scores were calculated as one minus the Hamming distances. Between 71 and 77% minimum representation of pairwise identities <0.000288 proportion of pairwise identities (0.028% of all pairwise comparisons) is present, hence we propose >78% as the most credible species cut off and employ it here to support the proposed new and revised mastrevirus species (Geminiviridae).

References

Edgar RC. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research. 32: 1792-97.

Guindon S., Dufayard J.F., Lefort V., Anisimova M., Hordijk W. & Gascuel O. (2010) New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. Systematic Biology, 59:307-21, 2010.

Posada D. (2008) jModelTest: Phylogenetic Model Averaging. Molecular Biology and Evolution. 25: 1253-1256

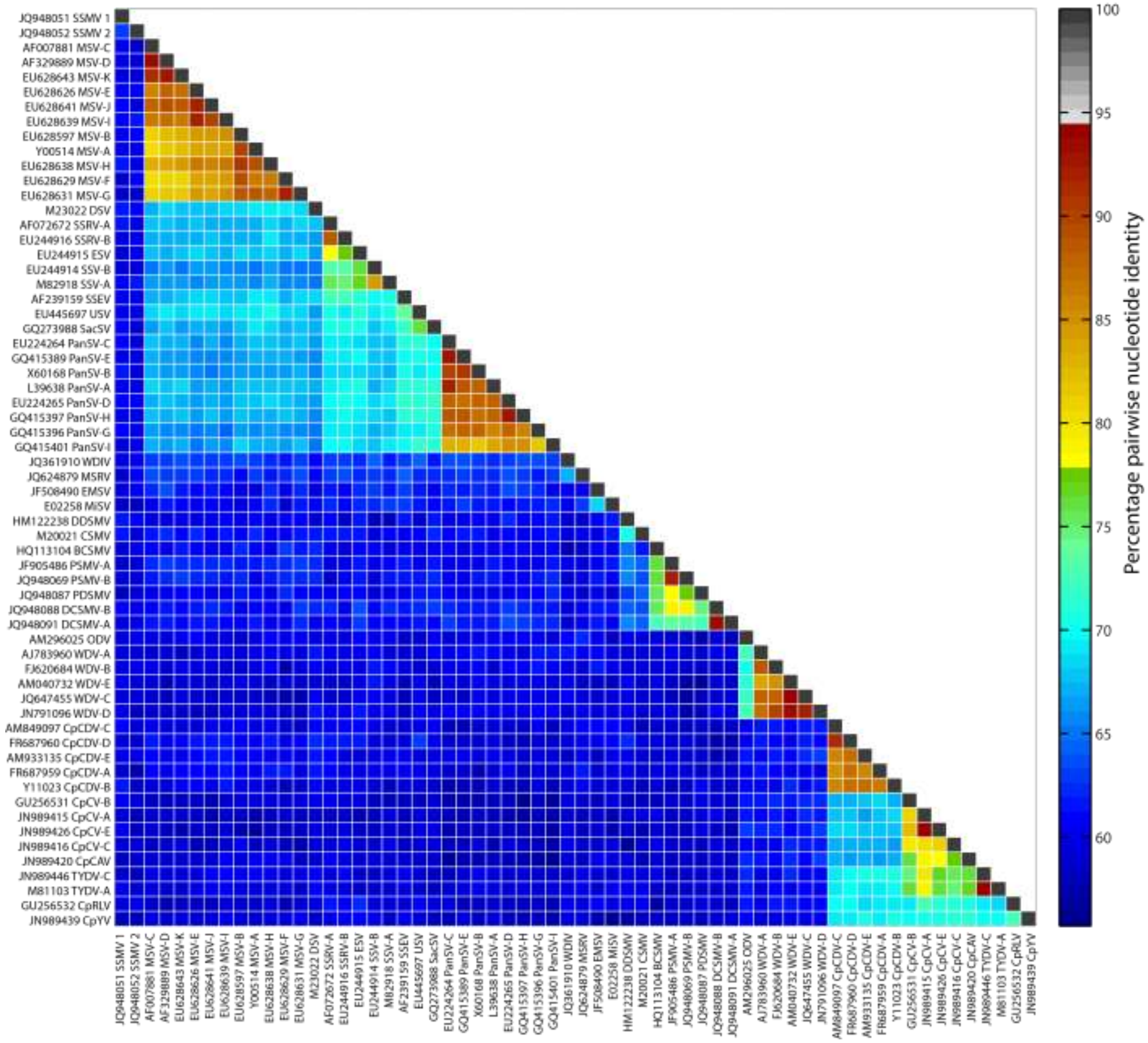

Figure 2. Distance matrix of representative full genome sequences from each accepted and proposed Mastrevirus species. Note representatives of the major strain variants for different species are also included. The colour key indicates percentage pairwise similarity scores. Yellow/orange shades represent pairwise similarities that are above the proposed species demarcation threshold (78%). BCSMV = Bromus catharticus striate mosaic virus; CpCAV = Chickpea chlorosis Australia virus; CpCV = Chickpea chlorosis virus; CpCDV = Chickpea chlorotic dwarf virus; CpRLV = Chickpea redleaf virus; CpYV = Chickpea yellows virus; CSMV = Chloris striate mosaic virus; DCSMV = Digitaria ciliaris striate mosaic virus; DDSMV = Digitaria didactyla striate mosaic virus; DSV = Digitaria streak virus; ESV = Eragrostis streak virus; MiSV = Miscanthus streak virus; MSRV= Maize streak Reunion virus; MSV = Maize streak 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; SSEV = Sugarcane streak Egypt virus; SSRV = Sugarcane streak Reunion virus; SSV = Sugarcane streak virus; TYDV= Tobacco yellow dwarf virus; USV = Urochloa streak virus; WDIV = Wheat dwarf India virus; WDV = Wheat dwarf virus.

Maximum likelihood phylogenetic tree (GTR+I+G4)

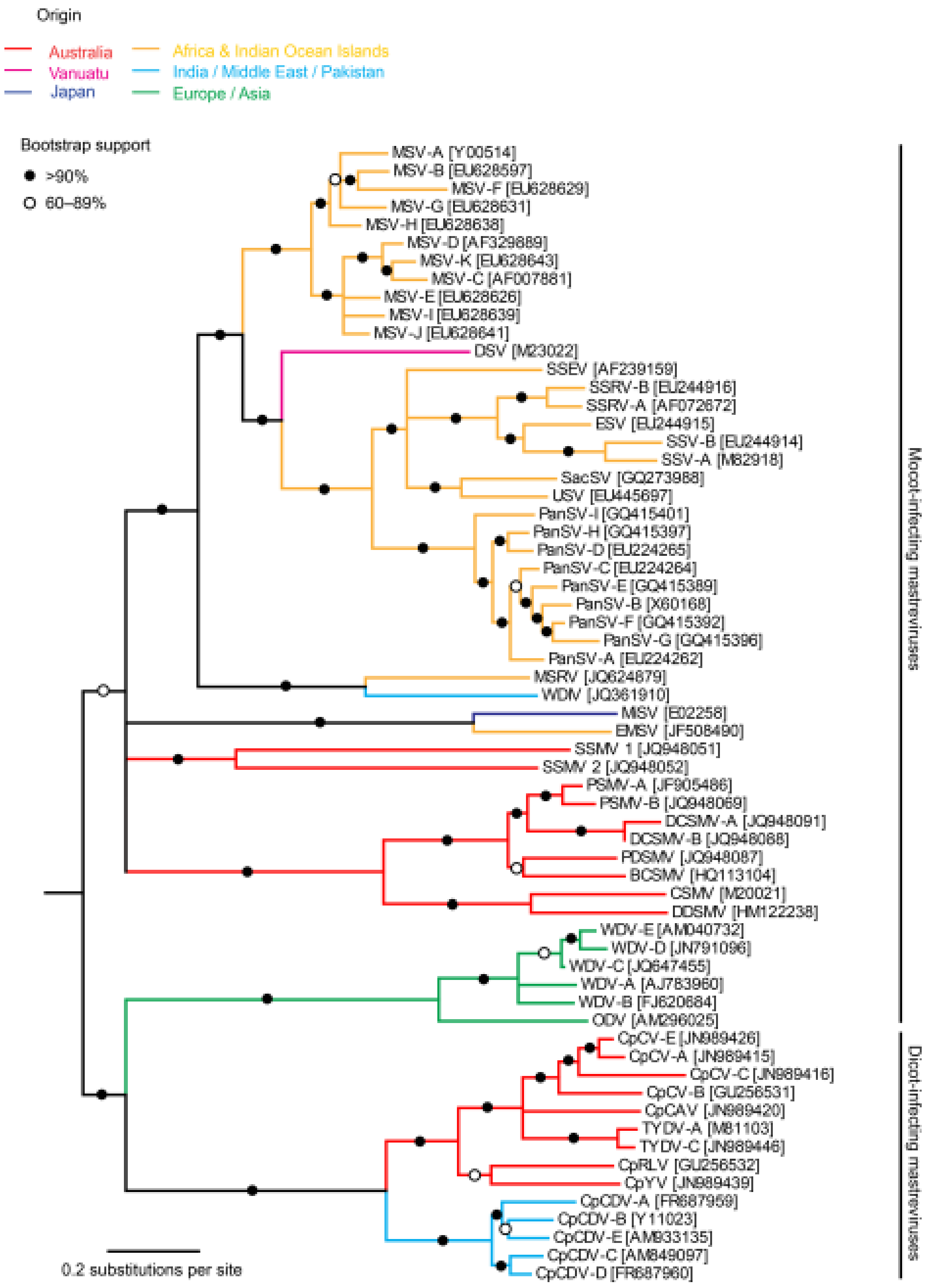

Figure 3. Maximum likelihood phylogenetic tree (constructed using full genome sequences and with nucleotide substitution model GTR+I+G4; Posada, 2008; Guindon et al., 2010) depicting the likely evolutionary relationships of *Mastrevirus* species and proposed strain groupings. African, European, Asian and Australasian origins of the various isolates are indicated. Note however, that in the case of CpCDV-B isolates (formerly, *Bean yellow dwarf virus*) have been sampled in both Africa and Asia. Isolates classified as (proposed) mastrevirus species are indicated in bold. Letters after species names denote strains. BCSMV = Bromus catharticus striate mosaic virus; CpCAV = Chickpea chlorosis Australia virus; CpCV = Chickpea chlorosis virus; CpCDV = Chickpea chlorotic dwarf virus; CpRLV = Chickpea redleaf virus; CpYV = Chickpea yellows virus; CSMV = Chloris striate mosaic virus; DCSMV = Digitaria ciliaris striate mosaic virus; DDSMV = Digitaria didactyla striate mosaic virus; DSV = Digitaria streak virus; ESV = Eragrostis streak virus; MiSV = Miscanthus streak virus; MSRV= Maize streak Reunion virus; MSV = Maize streak 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; SSEV = Sugarcane streak Egypt virus; SSRV = Sugarcane streak Reunion virus; SSV = Sugarcane streak virus; TYDV= Tobacco yellow dwarf virus; USV = Urochloa streak virus; WDIV = Wheat dwarf India virus; WDV = Wheat dwarf virus.

Table1: Details of mastrevirus species, representative strains, hosts, country of isolation and relevant references. All full genomes are isolated from natural infected symptomatic hosts (showing streak-like, striate-mosaic or dwarfing symptoms in the case of monocot-infecting mastreviruses and chlorosis coupled with dwarfing in the case of dicot-infecting viruses). All full genomes of the isolates were determined by sanger sequencing (with primer walking) of cloned viral genomes (either PCR amplified and cloned or restriction enzyme digested from purified virus stocks or restriction enzyme digests of rolling circle amplified viral genomes).

Species	**Strain[†] [GenBank no.]**	**Host[#]**	**Country***	
BCSMV	BCSMV [HQ113104]	*Bromus catharticus*	Australia	(Greber, 1989; Hadfield *et al.*, 2011)
CpCAV	CpCAV [JN989420]	*Cicer arietinum* *Phaseolus sp.*	Australia	(Hadfield *et al.*, 2012)
CpCDV	CpCDV-A [FR687959]	*Cicer arietinum*	Syria	(Halley-Stott *et al.*, 2007; Mumtaz *et al.*, 2011; Nahid *et al.*, 2008) (Ali *et al.*, 2004)
	CpCDV-B [Y11023]	*Phaseolus vulgaris*	Pakistan, South Africa	
	CpCDV-C [AM849097]	*Cicer arietinum*	Pakistan	
	CpCDV-D [FR687960]	*Cicer arietinum*	Pakistan	
	CpCDV-E [AM933135]	*Cicer arietinum*	Sudan	
	CpCV-A [JN989415]	*Cicer arietinum*	Australia	(Hadfield *et al.*, 2012; Thomas *et al.*, 2010)
	CpCV-B [GU256531]	*Cicer arietinum*	Australia	
	CpCV-C [JN989416]	*Cicer arietinum*	Australia	
	CpCV-E [JN989426]	*Cicer arietinum* *Phaseolus sp.*	Australia	
CpRLV	CpRLV [GU256532]	*Cicer arietinum*	Australia	(Thomas *et al.*, 2010)
CpYV	CpYV [JN989439]	*Cicer arietinum*	Australia	(Hadfield *et al.*, 2012)
CSMV	CSMV [M20021]	*Chloris gayana* *Eriochloa polystachya* *Paspalum dilatatum* *Triticum aestivum* *Panicum sp.* *Sporobolus sp.* *Digitaria ciliaris*	Australia	(Andersen *et al.*, 1988; Greber, 1989)
DCSMV	DCSMV-A [JQ948091]	*Digitaria ciliaris*	Australia	(Kraberger *et al.*, 2012)
	DCSMV-B [JQ948088]	*Digitaria ciliaris*	Australia	
DDSMV	DDSMV [HM122238]	*Digitaria didactyla*	Australia	(Briddon *et al.*, 2010; Greber, 1989)
DSV	DSV [M23022]	*Digitaria sanguinalis*	Vanuatu	(Donson *et al.*, 1987)
EMSV	EMSV [JF508490]	*Eragrostis minor*	Namibia	(Martin *et al.*, 2011)
ESV	ESV [EU244915]	*Eragrostis curvula*	Zimbabwe	(Shepherd *et al.*, 2008b)
MiSV	MiSV [E02258]	*Miscanthus sacchariflorus*	Japan	(Chatani *et al.*, 1991)
MSRV	MSRV [JQ624879]	*Zea mays*	La Reunion	(Pande *et al.*, 2012)
MSV	MSV-A [Y00514]	*Zea mays* *Axonopus compressus* *Cenchrus myosuroides* *Digitaria sp.* *Eragrostis curvula* *Erharta calcycina* *Eustachys petraea* *Pennisetum sp.* *Rattraya petiolata* *Rottboellia cochinchinensis,* *Saccharum sp.* *Setaria sp.* *Sugarcane* *Urochloa maxima*	Burkina Faso, Cameroon, Central African Republic, Chad, Kenya, La Reunion, Lesotho, Mozambique, Nigeria, South Africa, Uganda, Zambia, Zimbabwe	(Harkins *et al.*, 2009; Martin *et al.*, 2001; Monjane *et al.*, 2011; Owor *et al.*, 2007; Shepherd *et al.*, 2008a; Varsani *et al.*, 2008)
	MSV-B [EU628597]	*Avena sativa* *Cenchrus myosuroides* *Digiteria sp.* *Ehrharta calcycina* *Hordeum vulgare* *Lolium rigidum* *Rattraya petiolata* *Setaria grisebachii* *Urochloa maxima* *Urochloa plantaginea*	La Reunion, Uganda, Rwanda, Kenya, South Africa, Mozambique	
	MSV-C [AF007881]	*Setaria sp.*	South Africa, Uganda	
	MSV-D [AF329889]	*Urochloa sp.*	South Africa	
	MSV-E [EU628626]	*Digitaria ciliaris*	Mozambique, South Africa,	

		Seteria barbata	Uganda	
	MSV-F [EU628629]	*Urochloa maxima* *Digitaria ciliaris*	Burundi, Uganda, Nigeria	
	MSV-G [EU628631]	*Brachriaria deflexa* *Brachriaria lata* *Digitaria sp.* *Panicum maximum* *Paspalum notatum*	Nigeria, Mali	
	MSV-H [EU628638]	*Setaria barbata*	Nigeria	
	MSV-I [EU628639]	*Digitaria ciliaris*	South Africa	
	MSV-J [EU628641]	*Pennisetum sp*	Zimbabwe	
	MSV-K [EU628643]	*Eustachys petraea* *Setaria verticillata*	Uganda, Zimbabwe	
ODV	ODV [AM296025]	*Avena sativa*	Germany	(Schubert *et al.*, 2007)
PanSV	PanSV-A [L39638]	*Ehrharta calycina* *Panicum maximum*	Zimbabwe, South Africa, Mozambique	(Rybicki, 1994; Shepherd *et al.*, 2008a; Varsani *et al.*, 2009)
	PanSV-B [X60168]	*Panicum maximum*	Kenya	
	PanSV-C [EU224264]	*Urochloa plantaginea*	Zimbabwe	
	PanSV-D [EU224265]	*Urochloa maxima*	Nigeria	
	PanSV-E [GQ415389]	*Panicum maximum*	Kenya	
	PanSV-F [GQ415392]	*Panicum maximum*	Kenya	
	PanSV-G [GQ415396]	*Panicum maximum*	Mayotte	
	PanSV-H [GQ415397]	*Panicum maximum* *Brachiaria Deflexa*	Nigeria, Central African Republic	
	PanSV-I [GQ415401]	*Panicum tricholadum* *Brachiaria Deflexa*	Kenya	
PDSMV	PDSMV [JQ948087]	*Paspalum dilatatum* *Digitaria ciliaris*	Australia	(Kraberger *et al.*, 2012)
PSMV	PSMV-A [JF905486]	*Paspalum dilatatum* *Digitaria ciliaris* *Ehrharta erecta*	Australia	(Geering *et al.*, 2012; Greber, 1989; Kraberger *et al.*, 2012)
	PSMV-B [JQ948069]	*Paspalum dilatatum*	Australia	
SacSV	SacSV [GQ273988]	*Saccharum*	South Africa	(Lawry *et al.*, 2009)
SSEV	SSEV [AF239159]	*Saccharum*	Egypt	(Bigarre *et al.*, 1999)
SSMV 1	SSMV 1 [JQ948051]	*Sporobolus australasicus*	Australia	(Kraberger *et al.*, 2012)
SSMV 2	SSMV 2 [JQ948052]	*Sporobolus australasicus*	Australia	(Kraberger *et al.*, 2012)
SSRV	SSRV-A [AF072672]	*Saccharum* *Setaria barbata*	La Reunion	(Bigarre *et al.*, 1999; Shepherd *et al.*, 2008b)
	SSRV-B [EU244916]	*Paspalum conjugatum*	Zimbabwe	
SSV	SSV-A [M82918]	*Saccharum*	South Africa	(Hughes *et al.*, 1993; Shepherd *et al.*, 2008b)
	SSV-B [EU244914]	*Cenchrus myosuroides*	La Reunion	
TYDV	TYDV-A [M81103]	*Nicotinana sp.* *Phaseolus sp.* *Cicer arietinum*	Australia	(Hadfield *et al.*, 2012; Morris *et al.*, 1992)
	TYDV-C [JN989446]	*Cicer arietinum*	Australia	
USV	USV [EU445697]	*Urochloa deflexa*	Nigeria	(Oluwafemi *et al.*, 2008)
WDIV	WDIV [JQ361910]	*Triticum aestivum*	India	(Kumar *et al.*, 2012)
WDV	WDV-A [AJ783960]	*Hordeum vulgare* *Avena sativa*	Bulgaria, Czech Republic, Germany, Hungary, Turkey, Ukraine	(Koklu *et al.*, 2007; Kundu *et al.*, 2009; Kvarnheden *et al.*, 2002; MacDowell *et al.*, 1985; Tobias *et al.*, 2011)
	WDV-B [FJ620684]	*Hordeum vulgare*	Iran	
	WDV-C [JQ647455]	*Triticum aestivum*	China, Hungary, Tibet	
	WDV-D [JN791096]	*Hordeum vulgare*	Iran	
	WDV-E [AM040732]	*Triticum aestivum* *Lolium sp.* *Secale sp.*	China, Czech Republic, Hungary, France, Germany, Iran, Sweden, Ukraine	

[†] Type strains

Hosts from which full genomes have been isolated and deposited in GenBank

* Full genome shave been isolated from these countries and deposited in GenBank

References

Ali, M. A., Kumari, S. G., Makkouk, K. M. & Hassan, M. M. (2004). Chickpea chlorotic dwarf virus (CpCDV) naturally infects Phaseolus bean and other wild species in the Gezira region of Sudan. *Arab Journal of Plant Protection* **22**, 96.

Andersen, M. T., Richardson, K. A., Harbison, S. A. & Morris, B. A. (1988). Nucleotide sequence of the geminivirus chloris striate mosaic virus. *Virology* **164**, 443-449.

Bigarre, L., Salah, M., Granier, M., Frutos, R., Thouvenel, J. & Peterschmitt, M. (1999). Nucleotide sequence evidence for three distinct sugarcane streak mastreviruses. *Arch Virol* **144**, 2331-2344.

Briddon, R. W., Martin, D. P., Owor, B. E., Donaldson, L., Markham, P. G., Greber, R. S. & Varsani, A. (2010). A novel species of mastrevirus (family Geminiviridae) isolated from Digitaria didactyla grass from Australia. *Arch Virol* **155**, 1529-1534.

Chatani, M., Matsumoto, Y., Mizuta, H., Ikegami, M., Boulton, M. I. & Davies, J. W. (1991). The nucleotide sequence and genome structure of the geminivirus miscanthus streak virus. *J Gen Virol* **72 (Pt 10)**, 2325-2331.

Donson, J., Accotto, G. P., Boulton, M. I., Mullineaux, P. M. & Davies, J. W. (1987). The nucleotide sequence of a geminivirus from Digitaria sanguinalis. *Virology* **161**, 160-169.

Geering, A. D., Thomas, J. E., Holton, T., Hadfield, J. & Varsani, A. (2012). Paspalum striate mosaic virus: an Australian mastrevirus from Paspalum dilatatum. *Arch Virol* **157**, 193-197.

Greber, R. (1989). Biological characteristics of grass geminiviruses from eastern Australia. *Annals of Applied Biology* **114**, 471-480.

Hadfield, J., Martin, D. P., Stainton, D., Kraberger, S., Owor, B. E., Shepherd, D. N., Lakay, F., Markham, P. G., Greber, R. S., Briddon, R. W. & Varsani, A. (2011). Bromus catharticus striate mosaic virus: a new mastrevirus infecting Bromus catharticus from Australia. *Arch Virol* **156**, 335-341.

Hadfield, J., Thomas, J. E., Schwinghamer, M. W., Kraberger, S., Stainton, D., Dayaram, A., Parry, J. N., Pande, D., Martin, D. P. & Varsani, A. (2012). Molecular characterisation of dicot-infecting mastreviruses from Australia. *Virus Res* **166**, 13-22.

Halley-Stott, R. P., Tanzer, F., Martin, D. P. & Rybicki, E. P. (2007). The complete nucleotide sequence of a mild strain of Bean yellow dwarf virus. *Arch Virol* **152**, 1237-1240.

Harkins, G. W., Martin, D. P., Duffy, S., Monjane, A. L., Shepherd, D. N., Windram, O. P., Owor, B. E., Donaldson, L., van Antwerpen, T., Sayed, R. A., Flett, B., Ramusi, M., Rybicki, E. P., Peterschmitt, M. & Varsani, A. (2009). Dating the origins of the maize-adapted strain of maize streak virus, MSV-A. *J Gen Virol* **90**, 3066-3074.

Hughes, F. L., Rybicki, E. P. & Kirby, R. (1993). Complete nucleotide sequence of sugarcane streak Monogeminivirus. *Arch Virol* **132**, 171-182.

Koklu, G., Ramsell, J. N. & Kvarnheden, A. (2007). The complete genome sequence for a Turkish isolate of Wheat dwarf virus (WDV) from barley confirms the presence of two distinct WDV strains. *Virus Genes* **34**, 359-366.

Kraberger, S., Thomas, J. E., Geering, A. D., Dayaram, A., Stainton, D., Hadfield, J., Walters, M., Parmenter, K. S., van Brunschot, S., Collings, D. A., Martin, D. P. & Varsani, A. (2012). Australian monocot-infecting mastrevirus diversity rivals that in Africa. *Virus Res*. DOI: 10.1016/j.virusres.2012.07.018

Kumar, J., Singh, S. P. & Tuli, R. (2012). A novel mastrevirus infecting wheat in India. *Arch Virol*.

Kundu, J. K., Gadiou, S. & Cervena, G. (2009). Discrimination and genetic diversity of Wheat dwarf virus in the Czech Republic. *Virus Genes* **38**, 468-474.

Kvarnheden, A., Lindblad, M., Lindsten, K. & Valkonen, J. P. (2002). Genetic diversity of Wheat dwarf virus. *Arch Virol* **147**, 205-216.

Lawry, R., Martin, D. P., Shepherd, D. N., van Antwerpen, T. & Varsani, A. (2009). A novel sugarcane-infecting mastrevirus from South Africa. *Arch Virol* **154**, 1699-1703.

MacDowell, S. W., Macdonald, H., Hamilton, W. D., Coutts, R. H. & Buck, K. W. (1985). The nucleotide sequence of cloned wheat dwarf virus DNA. *Embo J* **4**, 2173-2180.

Martin, D. P., Linderme, D., Lefeuvre, P., Shepherd, D. N. & Varsani, A. (2011). Eragrostis minor streak virus: an Asian streak virus in Africa. *Arch Virol* **156**, 1299-1303.

Martin, D. P., Willment, J. A., Billharz, R., Velders, R., Odhiambo, B., Njuguna, J., James, D. & Rybicki, E. P. (2001). Sequence diversity and virulence in Zea mays of Maize streak virus isolates. *Virology* **288**, 247-255.

Monjane, A. L., Harkins, G. W., Martin, D. P., Lemey, P., Lefeuvre, P., Shepherd, D. N., Oluwafemi, S., Simuyandi, M., Zinga, I., Komba, E. K., Lakoutene, D. P., Mandakombo, N., Mboukoulida, J., Semballa, S., Tagne, A., Tiendrebeogo, F., Erdmann, J. B., van Antwerpen, T., Owor, B. E., Flett, B., Ramusi, M., Windram, O. P., Syed, R., Lett, J. M., Briddon, R. W., Markham, P. G., Rybicki, E. P. & Varsani, A. (2011). Reconstructing the history of maize streak virus strain a dispersal to reveal diversification hot spots and its origin in southern Africa. *J Virol* **85**, 9623-9636.

Morris, B. A., Richardson, K. A., Haley, A., Zhan, X. & Thomas, J. E. (1992). The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants. *Virology* **187**, 633-642.

Mumtaz, H., Kumari, S. G., Mansoor, S., Martin, D. P. & Briddon, R. W. (2011). Analysis of the sequence of a dicot-infecting mastrevirus (family Geminiviridae) originating from Syria. *Virus Genes* **42**, 422-428.

Nahid, N., Amin, I., Mansoor, S., Rybicki, E. P., van der Walt, E. & Briddon, R. W. (2008). Two dicot-infecting mastreviruses (family Geminiviridae) occur in Pakistan. *Arch Virol* **153**, 1441-1451.

Oluwafemi, S., Varsani, A., Monjane, A. L., Shepherd, D. N., Owor, B. E., Rybicki, E. P. & Martin, D. P. (2008). A new African streak virus species from Nigeria. *Arch Virol* **153**, 1407-1410.

Owor, B. E., Martin, D. P., Shepherd, D. N., Edema, R., Monjane, A. L., Rybicki, E. P., Thomson, J. A. & Varsani, A. (2007). Genetic analysis of maize streak virus isolates from Uganda reveals widespread distribution of a recombinant variant. *J Gen Virol* **88**, 3154-3165.

Pande, D., Kraberger, S., Lefeuvre, P., Lett, J. M., Shepherd, D. N., Varsani, A. & Martin, D. P. (2012). A novel maize-infecting mastrevirus from La Reunion Island. *Arch Virol* **157**, 1617-1621.

Rybicki, E. P. (1994). A phylogenetic and evolutionary justification for three genera of Geminiviridae. *Arch Virol* **139**, 49-77.

Schubert, J., Habekuss, A., Kazmaier, K. & Jeske, H. (2007). Surveying cereal-infecting geminiviruses in Germany--diagnostics and direct sequencing using rolling circle amplification. *Virus Res* **127**, 61-70.

Shepherd, D. N., Martin, D. P., Lefeuvre, P., Monjane, A. L., Owor, B. E., Rybicki, E. P. & Varsani, A. (2008a). A protocol for the rapid isolation of full geminivirus genomes from dried plant tissue. *J Virol Methods* **149**, 97-102.

Shepherd, D. N., Varsani, A., Windram, O. P., Lefeuvre, P., Monjane, A. L., Owor, B. E. & Martin, D. P. (2008b). Novel sugarcane streak and Sugarcane streak Reunion mastreviruses from southern Africa and La Reunion. *Arch Virol* **153**, 605-609.

Thomas, J. E., Parry, J. N., Schwinghamer, M. W. & Dann, E. K. (2010). Two novel mastreviruses from chickpea (Cicer arietinum) in Australia. *Arch Virol* **155**, 1777-1788.

Tobias, I., Shevchenko, O., Kiss, B., Bysov, A., Snihur, H., Polischuk, V., Salanki, K. & Palkovics, L. (2011). Comparison of the nucleotide sequences of wheat dwarf virus (WDV) isolates from Hungary and Ukraine. *Pol J Microbiol* **60**, 125-131.

Varsani, A., Monjane, A. L., Donaldson, L., Oluwafemi, S., Zinga, I., Komba, E. K., Plakoutene, D., Mandakombo, N., Mboukoulida, J., Semballa, S., Briddon, R. W., Markham, P. G., Lett, J. M., Lefeuvre, P., Rybicki, E. P. & Martin, D. P. (2009). Comparative analysis of Panicum streak virus and Maize streak virus diversity, recombination patterns and phylogeography. *Virol J* **6**, 194.

Varsani, A., Shepherd, D. N., Monjane, A. L., Owor, B. E., Erdmann, J. B., Rybicki, E. P., Peterschmitt, M., Briddon, R. W., Markham, P. G., Oluwafemi, S., Windram, O. P., Lefeuvre, P., Lett, J. M. & Martin, D. P. (2008). Recombination, decreased host specificity and increased mobility may have driven the emergence of maize streak virus as an agricultural pathogen. *Journal of General Virology* **89**, 2063-2074.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2012.019bP***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Bean yellow dwarf virus
Setaria streak virus

The present taxonomic position of these taxon/taxa:

Genus:	***Mastrevirus***	Fill in all that apply.
Subfamily:		
Family:		
Order:		

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Viruses isolated from bean plants in South Africa and Pakistan and called *Bean yellow dwarf virus* are >80% similar to a diverse group of chickpea-infecting viruses that we proposed to reclassify them as strains or isolates of *Chickpea chlorotic dwarf virus*.

We have therefore assigned isolates previously referred to as *Bean yellow dwarf virus* (AM849096, DQ458791; Y11023) to the species *Chickpea chlorotic dwarf virus.*

Setaria streak virus isolates from Setaria share >80% pairwise identity to all *Maize streak virus* (MSV) isolates. This should be demoted to a strain of MSV (see figure 2 and 3 for pairwise identity and phylogenetic support). The following genbank accession #s need to be demoted: AF007881, AF329889, AF329888, EU628623, EU628625, EU628626, EU628624, EU628639, EU628640, EU628643, EU628641, EU628642, EU628644, EU628622.

MODULE 9: Supporting material

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.

Appendix 1. List of *Mastrevirus* GenBank Accession numbers; yellow highlighting delineates new or revised species, per this proposal