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:		(to be completed by ICTV officers)

Short title: 1 new species in the genus Nucleorhabdovirus
(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:

Ralf Dietzgen ralf.dietzgen@deedi.qld.gov.au

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)	Rhabdoviridae SG

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

Date first submitted to ICTV:
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		(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Nucleorhabdovirus***
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

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:**
Maize Iranian mosaic virus	NC_011542

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

The two genera of plant-infecting rhabdoviruses are primarily distinguished on the basis of the sites of virus maturation. Those within the genus *Nucleorhabdovirus* mature in the nucleus and accumulate in perinuclear spaces. Within genera, species are primarily differentiated by host range and vector specificity. Until recently, there have been very limited sequence data and molecular criteria for species discrimination have not been well defined.

Biological data and the near-complete genome sequence of MIMV support its assignment as a species within the genus *Nucleorhabdovirus*:

MIMV

- Bullet-shaped particles (180 x 80 nm)
- Virions budding through inner nuclear and endoplasmic reticulum membranes
- Serologically unrelated to other rhabdoviruses infecting gramineous plants: MMV, BYSMV, CCMoV, CCSV, MSSV, FLSV, NCMV, WCSV, WRSV
- Vectored by planthoppers *Ribautodelphax notabilis, Pregrinus maidis* (low efficiency)
- Comparison of virion and vector properties, host range and geographic distribution of cereal-infecting nucleorhabdoviruses suggests MIMV is distinct (Annex, Tables 1, 2)
- Genome sequence distinct from that of other plant and animal rhabdoviruses: the near-complete sequence of 12,381 nucleotides negative-sense RNA genome is available (NC_011542) and shows six ORFs in anti-genomic strand in the order of putative proteins N, P, 3, M, G, L. Based on deduced amino acid sequence identity, MIMV is most closely related to the respective proteins of the nucleorhabdoviruses MMV and

TaVCV (Annex, Table 3).

- Phylogenetic analysis of the L protein amino acid sequenced grouped MIMV in a clade with all other sequenced nucleorhabdoviruses, separate from the cytorhabdovirus clade and closest to MMV (Annex, Figure 1).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Massah A, Izadpanah K, Afsharifar AR, Winter S (2008) Analysis of nucleotide sequence of Iranian maize mosaic virus confirms its identity as a distinct nucleorhabdovirus. Arch Virol 153:1041-1047

Izadpanah K (1989) Purification and serology of the Iranian maize mosaic virus. J Phytopathol 126:43-50.

Izadpanah K, Ahmadi AA, Parvin S, Jafari SA (1983) Transmission, particle size and additional hosts of the rhabdovirus causing maize mosaic in Shiraz, Iran. Phytopath Z 107:283-288.

Ammar E-D, Gomez-Luengo RG, Gordon DT, Hogenhout SA (2005) Characterization of Maize Iranian mosaic virus and comparison with Hawaiian and other isolates of maize mosaic virus (Rhabdoviridae). J. Phtopathol 153:129-136.

Redinbaugh MG, Seifers DL, Meulia T, Abt JJ, Anderson RJ, Styer WE, Ackerman J, Salomon R, Houghton W, Creamer R, Gordon DT, Hogenhout SA (2002) Maize fine streak virus, a leafhopper-transmitted rhabdovirus. Phytopathology 92, 1167-1174.

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.

Table 1. Comparison of properties between maize Iranian mosaic virus (MIMV) and maize mosaic virus (MMV).

PROPERTIES	MIMV	MMV
Natural insect transmission	*Ribautodelphax notabilis* (dephacid planthopper)	*Peregrinus maidis* (delpahcid planthopper)
Experimental insect transmission	*P. maidis* [0.4-1.6% efficiency after feeding] [64% after hemolymph injection]	*P. maidis* [35% efficiency after feeding]
Host range	wheat (*Triticum aestivum*) barley (*Hordeum vulgare*) maize (*Zea mays*) rice	not reported to infect wheat or barley maize, sorghum
Geographic distribution	Iran	Australia, Brazil, Colombia, Costa Rica, Fiji, Florida, Hawaii, India, Mauritius, Mexico, Peru, Spain, Tanzania, Venezuela
Particle size in negative stained preparations	81 x 179 nm	90 x 225 nm
Cytopathology	virions budding through inner nuclear and ER membranes	virions budding through inner nuclear and ER membranes
Virion proteins in SDS-PAGE	6 proteins N, P and M proteins smaller than those of MMV	6 proteins N, P and M proteins larger than those of MIMV
Serology		
polyclonal antibodies to MIMV	positive	negative with MMV-HI
polyclonal antibodies to MMV-Venezuela	negative	strong positive with all MMV isolates
polyclonal antibodies to MMV-Hawaii	negative in ELISA and western blot	strong positive with all MMV isolates
polyclonal antibodies to MMV-Mauritius	weak reaction in ELISA	strong reaction with MMV-HI and -Florida
	No serological relationship with other rhabdoviruses infecting gramineous plants, ie. MMV, BYSMV, CCMoV, CCSV, MSSV, FLSV, NCMV, WCSV, WRSV	
Nucleotide sequence	12,381+ (incomplete 3' and 5' ends) 3' leader - N - P - 3 - M - G - L - 5' trailer	12,133+ (incomplete 3' and 5' ends) 3' leader - N - P - 3 - M - G - L - 5' trailer

Table 2. Properties of some maize infecting rhabdoviruses (modified from Table 3 in Redinbaugh *et al*., 2002)

Virus[w]	Vectors[x]	Nonvectors[y]	Virion size (nm)	Virion proteins (kDa)	Distribution[z]
MFSV	*Graminella nigrifrons*	*Peregrinus maidis* *Endria inimica* *Dalbulus maidis*	231 × 71	82 50 32	Georgia
MMV	*P. maidis*	*G. nigrifrons* *D. maidis*	225 × 68	75 54 30	Florida, Hawaii, the Carribean, South America, Africa, and Mautritius
MIMV	*Ribautodelphax notabilis; (P. maidis)*		180 × 80	182 73 53 34 27 27	Iran
CCMoV	*Nesoclutha pallida*; *Cicadulina bipunctata*; *C. bimaculata*	*Rhopalosiphum padi, R. maidis, P. maidis, Sogatella kolophon*	214 x 75	77.5 52.5 46.5 32 29	Australia, Morocco
SSMV	*G. sonora*	*G. nigrifrons* *P. maidis*	218 × 70	91 59 36 30	California
WASMV	*E. inimica* *G. nigrifrons*		260 × 80	145 92 59 25	Northern plains of the United States and Canada

[w] MFSV = Maize fine streak virus, MMV = *Maize mosaic virus*, MIMV = *Maize Iranian mosaic virus*, SSMV = *Sorghum stunt mosaic virus*, and WASMV = *Wheat American striate mosaic virus,* CCMoV = Cereal chlorotic mottle virus.
[x] Insects demonstrated to be vectors under persistent transmission conditions.
[y] Insects demonstrated not to be vectors under persistent transmission conditions.
[z] Areas where the virus has been reported.

Table 3. Percent identity of deduced amino acid sequences of MIMV proteins compared with those of other rhabdoviruses (taken from Table 3 in Massah *et al*., 2008)

	N	P	3	M	G	L
MMV	**55**	**42.1**	**41.2**	**41**	**55.6**	**63.9**
TaVCV	**53.9**	**44.3**	**40.4**	**50.6**	**49.6**	**63.4**
RYSV	24.6	16.6	16.5	16	28.5	30.2
MFSV	23.2	15.6	16.2	15.2	21.2	25.7
SYNV	21.3	16.7	14.1	15.1	19.2	24.6
NCMV	19.9	16.6	16.2	13.2	22.4	23.8
LNYV	16.4	18	14.7	14.9	15.9	19.2

MFSV = Maize fine streak virus, MMV = Maize mosaic virus, MIMV = Maize Iranian mosaic virus, TaVCV = Taro vein chlorosis virus, RYSV = Rice yellow stunt virus, SYNV = Sonchus yellow net virus, NCMV = Northern cereal mosaic virus, and LNYV = Lettuce necrotic yellows virus

Figure 1 (taken from Figure 4 in Massah *et al*., 2008)

Phylogenetic analysis of the L protein amino acid sequences of MIMV and other rhabdoviruses. The tree was derived from a parsimony analysis using Phylip. Bootstrap analysis with 1,000 replicates supported each node of the branch to 100%. See Table 3 for acronyms of nucleo- and cytorhabdoviruses.