Taxonomic proposal to the ICTV Executive Committee

This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.001P***	(to be completed by ICTV officers)

Short title: 2 new species in the genus Nucleorhabdovirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☐	**5** ☒
	6 ☐	**7** ☐			

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

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

MODULE 5: **NEW SPECIES**

Code	***2008.001P***	(assigned by ICTV officers)

To create 2 new species assigned as follows:

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

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Maize fine streak virus
Taro vein chlorosis virus

Argument to justify the creation of the new species:
If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

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. 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 defined.

Biological data and the complete genome sequences of MFSV and TaVCV support their assignment

Argument to justify the creation of the new species:

as species within the genus *Nucleorhabdovirus*:

MFSV

- Bacilliform (~231 x 71 nm) particles
- Thin section electron microscopy of infected maize leaves showed particles accumulating in the nucleus and budding into the perinuclear space
- Serologically unrelated to other maize-infecting nucleorhabdovirus species
- Serologically distantly related to the unassigned rhabdovirus sorghum stunt mosaic virus (SSMV)
- Vectored by the leafhopper *Graminella nigrifrons*, unlike SSMV
- Comparison of virion and vector properties and known distribution of maize-infecting nucleorhabdoviruses suggests that MFSV is a distinct species (Annex, Table 1)
- Genome sequence distinct from that of other plant and animal rhabdoviruses: the complete sequence of 13,782 nt negative-sense RNA genome is available (AY618417) and shows seven ORFs in anti-genomic strand in the order of putative proteins N, P, 3, 4, M, G, L. The N, ORF 4 and M proteins localize to nuclei of infected cells. Phylogenetic analysis of rhabdovirus L gene sequences places MFSV in a clade with all other sequenced nucleorhabdoviruses, separate from the cytorhabdovirus clade (Annex, Figure 1)

TaVCV

- Thin section electron microscopy of infected leaves showed bacilliform virions (200 x 70 nm) accumulating in the nucleus and budding into the perinuclear space
- Serologically distinct from another putative rhabdovirus that infects taro, *Colocasia* bobone disease virus (CBDV) (syn. Taro large bacilliform virus)
- The vector for TaVCV is unknown, but CBDV is transmitted by the taro planthopper *Tarophagus proserpina*. MMV vector is the leafhopper *Peregrinus maidis*;
- Genome sequence distinct from that of other sequenced plant and animal rhabdoviruses: the complete sequence of 12,020 nt negative-sense RNA genome is available (AY674964) and shows six ORFs in anti-genomic strand equivalent to putative N, P, 3, M, G, L genes. Based on deduced amino acid sequence identity, TaVCV is most closely related to the respective proteins of the nucleorhabdovirus species *Maize mosaic virus* (N: 63%, P:46%, gene 3: 43%, M: 46%, G: 50%, L: 68%). Phylogenetic analysis of the L gene deduced amino acid grouped TaVCV in a clade with all other sequenced nucleorhabdoviruses, separate from the cytorhabdovirus clade (Annex, Figure 1)

References:

MFSV

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 steak virus, a new leafhopper-transmitted rhabdovirus. *Phytopathology* **92**, 1167-1174.

Tsai C-W, Redinbaugh MG, Willie KJ, Reed S, Goodin M, Hogenhout SA (2005) Complete genome sequence and in planta subcellular localization of maize fine streak virus proteins. *Journal of Virology* **79**, 5304-5314.

TaVCV

Revill P, Trinh X, Dale J, Harding R (2005) Taro vein chlorosis virus: characterization and variability of a new nucleorhabdovirus. *Journal of General Virology* **86**, 491-499.

Pearson MN, Jackson GVH, Saelea J, Morar SG (1999) Evidence for two rhabdoviruses in taro (*Colocasia esculenta*) in the Pacific region. *Australasian Plant Pathology* **28**, 248-253.

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

Table 1. Properties of some maize infecting rhabdoviruses (taken 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
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*.
[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.

Figure 1. Phylogenetic (Neighbor-joining) tree of the codon-aligned nucleotide sequences of the L-gene of fully sequenced members of the family *Rhabdoviridae* showing the position of MFSV and TaVCV within the genus *Nucleorhabdovirus*. Tree produced in MEGA4 using Composite Maximum Likelihood option and 10,000 boostrap replicates.