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:	***2010.008aP***	(to be completed by ICTV officers)

Short title: To create a new species in the genus Marafivirus, fam. Tymoviridae
(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:

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on behalf of the Tymoviridae 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)	

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	***2010.008aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Marafivirus***
Subfamily:	
Family:	***Tymoviridae***
Order:	***Tymovirales***

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:**
Grapevine Syrah virus 1	FJ436028

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

According to the 8th ICTV Report (Dreher et al., 2005), the current species demarcation criteria in the genus *Marafivirus* are:

- Overall sequence identity less than 80%
- Coat protein sequences less than 90% identical
- Differences in the 3' terminal structure and number of ORFs
- Differential host range
- Vector specificity
- Serological specificity
- Presence of a marafibox
- Cytopathological features

Grapevine Syrah virus 1 (GSyV-1; Al Rwahnih et al., 2009; FJ436028) and Grapevine virus Q (GVQ; Sabanadzovic et al., 2009; FJ977041) have been recently identified and characterized in two independent studies of grapevine viruses in California and Southeastern United States. Direct comparison shows that the two entities share 98% nucleotide identity and belong to the same viral species. In view of its earlier description, Grapevine Syrah virus 1 (GSyV-1) is proposed as the name for this new species.

GSyV-1 properties:

- **Virus particles**: no information (expected to be isometric of ~ 28-30 nm)
- **Genome:** 6,481 nt-long (without 3' polyA tail) polyadenylated, positive-sense, single stranded RNA (two full genomic sequences are available under accession numbers FJ436028 and FJ977041). Partial sequences are available for three additional strains (FJ977042-FJ977044). The genome contains a large open reading frame (ORF1) putatively encoding a polyprotein with an estimated molecular mass of 229.5 kDa. Conserved domains of viral methyltransferase (MTR), endopeptidase/proteinase (PRO), helicase (HEL), RNA-dependent RNA polymerase (RdRp or POL) and capsid protein (CP) have been identified in the 5' to 3' direction within this ORF. An additional putative ORF, completely overlapping ORF1, with unknown function was identified between nt 752 and 1,555 (Fig. 1). This genome arrangement is consistent with those of known marafiviruses. The genome also

contains conserved signature "marafibox" sequence (Fig. 2).

- **Relationships with closely related species:** Overall nucleotide sequence identities between GSyV-1/GVQ and approved species in the genus *Marafivirus* are in the range of 56-58%. In the replicase-associated polyprotein (REP), the most closely related species in the genus, OBDV and CSDaV, share 50% identical amino acids with GSyV-1. Coat protein(s) of GSyV-1 share limited levels of common residues with orthologs of OBDV and CSDaV (40% and 38%, respectively). Similar levels of identity are shared with Blackberry virus S (BlVS), currently being proposed as a new species in the genus (see separate Taxoprop for BlVS). Grapevine rupestris vein feathering virus, shares 63% identical nucleotides (whole genome) and 51% conserved amino acids (whole polyprotein) with GSyV-1. The coat proteins of GSyV-1 and GRVFV share 61% common residues (Table 1). These data support the distinction of GSyV-1 from other marafiviruses.
- **Phylogeny:** GSyV-1 groups with members of the genus *Marafivirus* independent of the protein used for analyses (Al Rwahnih et al., 2009; Sabanadzovic et al., 2009)(Fig. 3).
- **Serology**: no information.
- **Mechanical transmission:** negative.
- **Vector transmission**: no vector has been experimentally proven. However, GSyV-1 has been detected in leafhopper *Erythroneura variabilis* collected from GSyV-1-infected plants (Al Rwahnih et al., 2009) indicating its likely leafhopper transmission.
- **Cytopathology**: no information.
- **Natural host range**: cultivated and wild *Vitis* spp. Found also in a wild *Rubus* specimen.
- **Distinguishing feature**: The unique feature of this virus is internal permutation of the viral RdRp motifs. Unlike other plant viruses with RNA genomes (including marafiviruses), which all have a "canonical organization" of conserved motifs (A→ B→ C), in this virus 21 aminoacid residues (including a hallmark - GDD), were permuted and positioned upstream of conserved motifs A and B to form a unique arrangement C→A→B (Fig. 4). This phenomenon was not previously reported in plant viruses or alpha-like viruses in general (Sabanadzovic et al., 2009).

In summary, currently available data indicate that GSyV-1 is a distinct species in the genus *Marafivirus.*

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Al Rwahnih M., Daubert S., Golino D., Rowhani A. (2009). Deep sequencing analysis of RNAs from a grapevine showing Syrah decline symptoms reveals a multiple virus infection that includes a novel virus. Virology 387, 395-401

Dreher T.W., Edwards M.C., Gibbs A.J., Haenni A-L., Hammond R.W., Jupin I., Koenig R., Sabanadzovic S., Abou Ghanem-Sabanadzovic N., Martelli G.P. (2005). Family Tymoviridae. In Fauquet C.M., Mayo M., Maniloff J., Desselberger U., Ball L.A. (Eds.): Virus Taxonomy (Eight Report of the ICTV). Elsevier/Academic Press, London pp 1061-1074

Sabanadzovic S., Abou Ghanem-Sabanadzovic N., Gorbalenya A.E. (2009). Permutation of the active site of putative RNA-dependent RNA polymerase in a newly identified species of plant Alpha-like viruses. Virology 294, 1-7

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. Percentage identity between GSyV-1 and other marafiviruses, comparing *a*) nucleotide sequence of the full genomes; *b* and *c*) amino acid sequences of the replication-associated polyprotein, and of the coat protein, respectively (*-in the case of GAMaV only partial sequence are available).

	GSyV-1		
	a. Full genome	*b*. REP polyprotein	*c*. Coat protein
GRVFV	63	51	61
GAMaV	60*	56*	36
OBDV	58	50	40
MRFV	57	48	35
CSDaV	56	50	38
BlVS	56	51	38

Figure 1. Diagrammatic representation of the GSyV-1 genome with nucleotide coordinates.

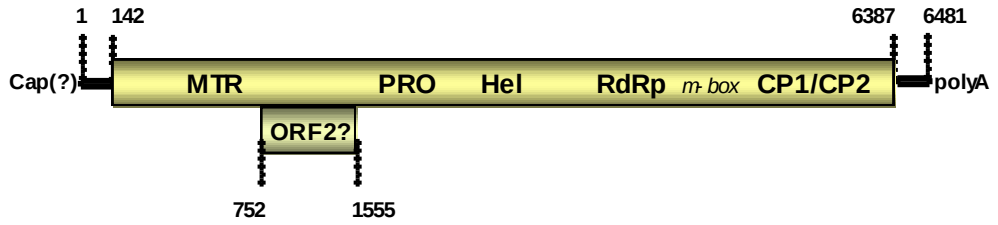

Figure 2. Comparison of the "marafibox" sequences with corresponding genomic regions of some marafi- and tymoviruses. Conserved nucleotides are shown as white characters on black.

Figure 3. Unrooted phenograms depicting the relationships of the whole replication-associated polyprotein (REP, **A**) and coat protein (**B**) sequences of Grapevine Syrah virus 1 with approved species in the genus *Marafivirus* (and related viruses - reported in parentheses), as well as some other members of the family *Tymoviridae*. Trees were generated by the neighbour-joining method and visualized by TreeView. Tymoviruses are reported in red, maculaviruses in black and marafiviruses in blue. Poinsettia mosaic virus (a proposed unassigned species in the family) is reported in green.

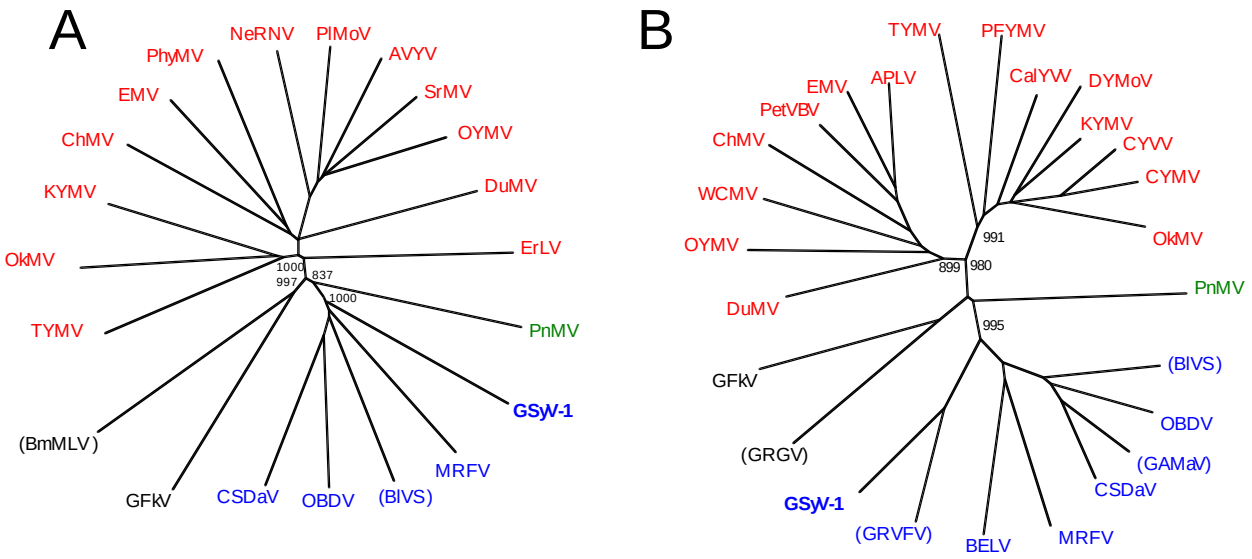

Figure 4. Alignment of the deduced amino acid sequences of RNA-dependent RNA polymerases of GSyV-1 and representatives of the three genera in the family *Tymoviridae*: *Tymovirus* (*Turnip yellow mosaic virus*; TYMV), *Maculavirus* (*Grapevine fleck virus*; GFkV) and *Marafivirus* (*Maize rayado fino virus* - MRFV; *Oat blue dwarf virus* - OBDV; *Citrus sudden death-associated virus* – CSDaV; Grapevine asteroid mosaic associated virus – GAMaV; Grapevine rupestris vein feathering virus – GRVFV). Conserved motifs A, B and C are boxed. A 21 aa-long insertion located upstream of motif A containing GDD tripeptide, uniquely present in GSyV-1/GVQ genome is reported in red.