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:	***2012.021aP***	(to be completed by ICTV officers)

Short title: create a new species in the genus *Trichovirus*, family *Betaflexiviridae*
(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:

Saldarelli, P.S. (p.saldarelli @ba.ivv.cnr.it); Giampetruzzi, A., Roumi, V.; Malossini, U.

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)	Flexiviridae Study Group

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

This proposal is endorsed by the Study Group in its original form.

Date first submitted to ICTV: 25 June 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	***2012.021aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Trichovirus***
Subfamily:	
Family:	***Betaflexiviridae***
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 Pinot gris virus	FR877530

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

Grapevine Pinot gris virus (GPGV) was identified in grapevine (*Vitis vinifera*) cv Pinot gris. Attempts to mechanically transmit the virus to *Nicotiana benthamiana*, *Nicotiana occidentalis*, and *Chenopodium quinoa* were unsuccessful.

GPGV RNA genome has been sequenced (FR877530) and consists of 7275 nucleotides excluding the poly A tail. GPGV genome organization is typical of the genus *Trichovirus* showing three overlapping open reading frames (ORFs) which encode putative replicase-associated (ORF1), movement (ORF2) and coat proteins (ORF3) (see Appendix 9). Pairwise comparisons of the three ORFs reveals strong similarities with homologous genes of *Grapevine berry inner necrosis virus* (GINV), the most related species in the *genus*, with amino acid identities of 66.1% (ORF1), 64.9 % (ORF2) and 71.4% (ORF3). These values are lower than the 80% identity considered as boundary for the species demarcation.

Neighbour-joining phylogenetic trees with RNA dependent RNA polymerase domains and coat proteins of species in the *Betaflexiviridae* family, consistently grouped GPGV with GINV in the genus *Trichovirus* (see Appendix 9).

No serological reactivity was detected with an antiserum to GINV.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

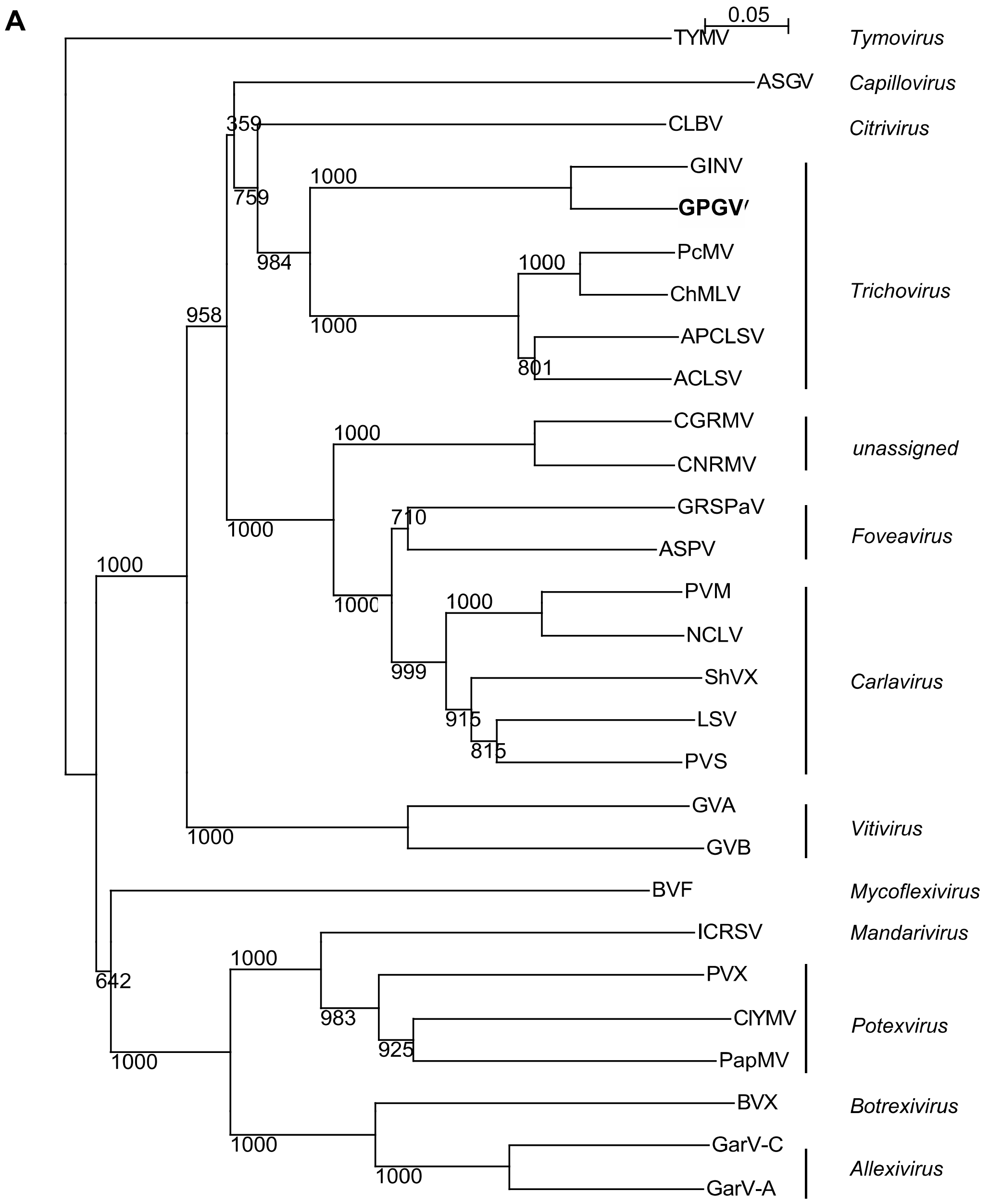
Giampetruzzi, A., Roumi, V., Roberto, R., Malossini, U., Yoshikawa, N., La Notte, P., Terlizzi, F., Credi, R., Saldarelli, P. 2012. A new grapevine virus discovered by deep sequencing of virus and viroid-derived small RNAs in cv Pinot gris. Virus Research 163: 262-268.

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 1: Genome structure of Grapevine Pinot gris virus (grey open boxes represent position of open reading frames; RdRpol: Replicase; MP: movement protein; CP: coat protein)

Fig. 3. Phylogenetic trees constructed with RdRp (A) and CP (B) protein sequences of GPGV and members of the family Flexiviridae. In both trees GPGV clusters with GINV in a separate clade. Numbers at branches indicate occurrence of bootstrap replicates out of the 1000 replicatesperformed in the test. Bars denote evolutionary distances corresponding to number of amino acids substitution per site. GenBank ID of the amino acid sequences are: TYMV (*Turnip yellow mosaic virus)* AAB92649; ASGV (*Apple stem grooving virus*) AAP80757; GarV-A (*Garlic virus A)NC* 003375; GarV-C (*Garlic virus C*) NC 003376; BVX (*Botrytis virus X*) NC 005132; PVX (*Potato virus X*) AAA47167; PapMV (*Papaya mosaic virus*) NC 001748; NCLV (*Narcissus common latent virus*) NC 008266; PVM (*Potato virus M*) AAP76207; PVS (*Potato virus S*) NC 007289; CNRMV (*Cherry necrotic rusty mottle virus*) NC 002468; ASPV (*Apple stem pitting virus*)NC 003462; BVF (*Botrytis virus F*) NC 002604; ACLSV (*Apple chlorotic leaf spot virus*) CAA68080; APsCLSV (*Apricot pseudo-chlorotic leaf spot virus*) NC 006946; ChMLV (*Cherry mottle leaf virus*) NC 002500; PcMV (*Peach mosaic virus*) NC 011552; GVB (*Grapevine virus B*) NC 003602; GVA (*Grapevine virus A*) NC 003604; LSV (*Lily symptomless virus*) NC 005138; GRSPaV (*Grapevine rupestris stem pitting-associated virus*) AF026278; CGRMV (*Cherry green ring mottle virus*) NC 001946; ICRSV (*Indian citrus ringspot virus*) NC 003093; ShVX (*Shallot virus X*) NC 003557; ClYMV (*Clerodendron yellow mosaic virus*) NC 001753; CLBV (*Citrus leaf blotch virus*) NC 003877; GINV (*Grapevine berry inner necrosis virus*) NC 015220.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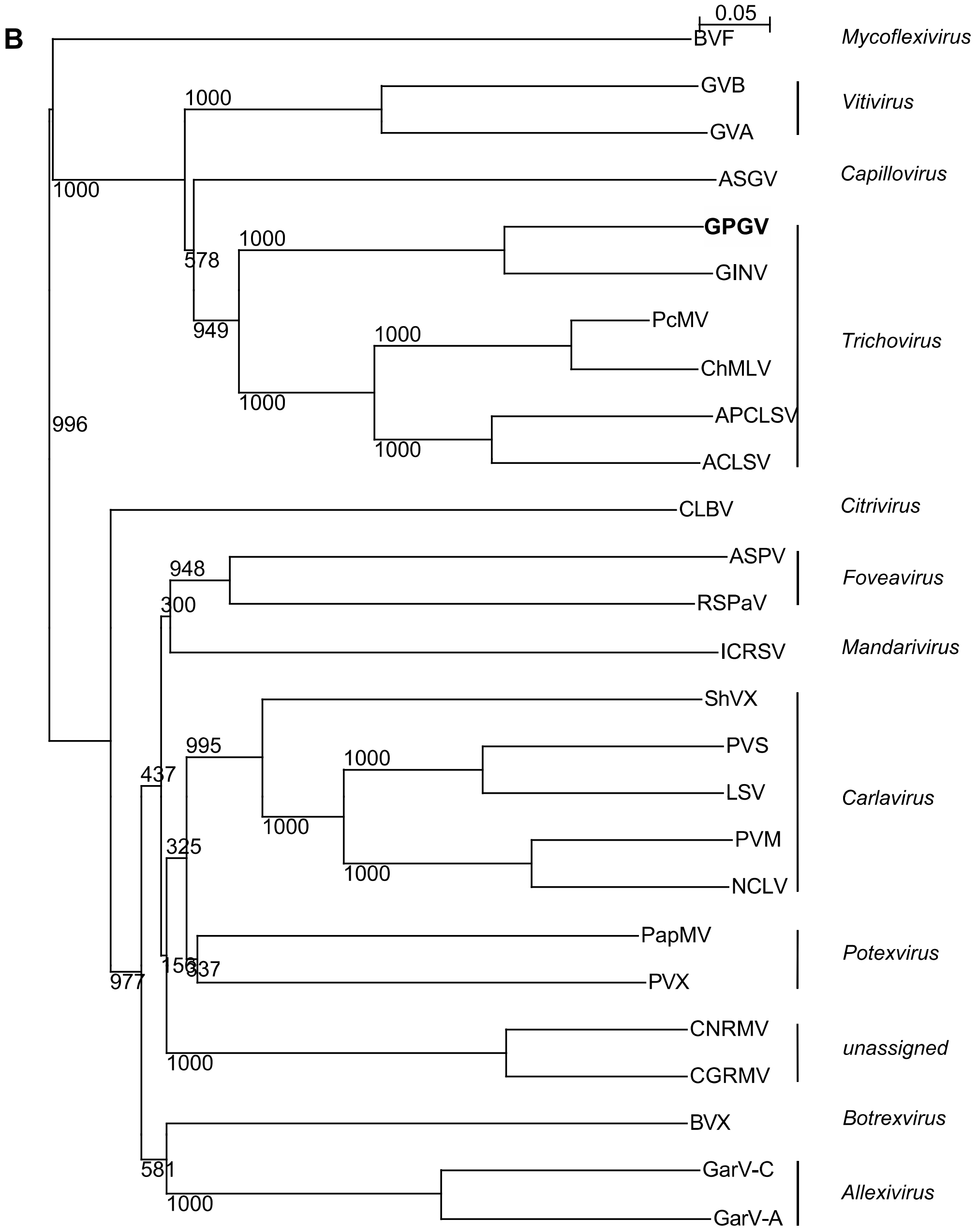
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