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:	***2013.002a-cP***	(to be completed by ICTV officers)

Short title: 4 new species in the family *Betaflexiviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

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

Jan Kreuze (j.kreuze@cgiar.org) on behalf of the *Flexiviridae* SG

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 SG

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

Date first submitted to ICTV:	June 2013
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	***2013.002aP***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***unassigned***
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.

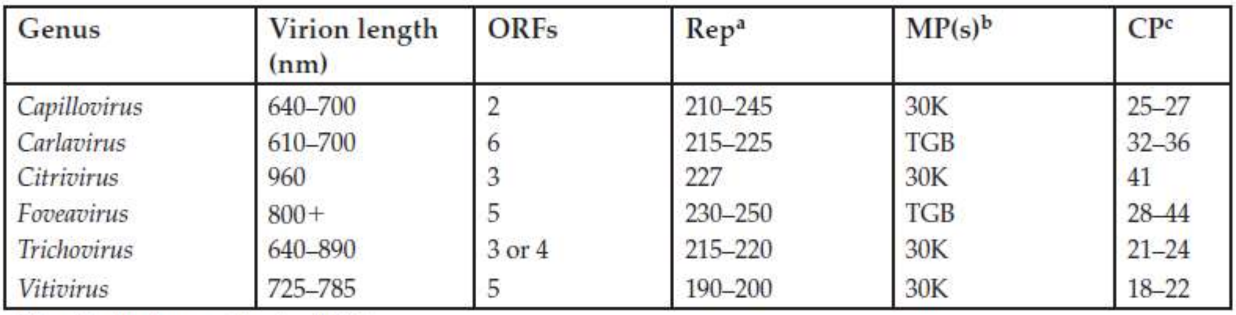
And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Diuris virus A	JX173276
Diuris virus B	JX173277

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 family *Betaflexiviridae* contains viruses with flexuous filamentous virions that infect plants They share a distinct lineage of alphavirus-like replication proteins that is unusual in lacking any recognized protease domain. Throughout the family, isolates of different species should have less than about 72% nt identity (or 80% aa identity) between their respective CP or polymerase genes. Viruses from different genera usually have less than about 45% nt identity in these genes.

Table 1: Distinguishing properties of genera in the family *Betaflexiviridae*



Genus	Virion length (nm)	ORFs	Rep[a]	MP(s)[b]	CP[c]
Capillovirus	640–700	2	210–245	30K	25–27
Carlavirus	610–700	6	215–225	TGB	32–36
Citrivirus	960	3	227	30K	41
Foveavirus	800+	5	230–250	TGB	28–44
Trichovirus	640–890	3 or 4	215–220	30K	21–24
Vitivirus	725–785	5	190–200	30K	18–22

[a] Rep, Replication protein size (kDa).
[b] MP, Movement protein either of the "30K" superfamily or a triple gene block (TGB).
[c] CP, Coat protein size (kDa).

Diuris virus A and Diuris virus B (DiVA, DiVB; Wylie et al., 2013)

These viruses were identified by mRNA sequencing from Diuris orchids. Their genome structure is similar to Capilloviruses and *Hardenbergia virus A* (HarVA) to which they are most similar and which is unclassified within the family *Betaflexiviridae* The two viruses were found co-infecting the same orchid plant. Both were inoculated to a range of experimental host plants, including *N. benthamiana*, *N. glutinosa*, *Chenopodium amaranticolor* and *C. quinoa*. No systemic infection was obtained on non-orchids but local lesions develop on both *Chenopodium* species and fragments of both viruses are readily amplified from these lesions by RT-PCR (Steve Wylie, personal communication). *Apple stem grooving virus* (ASGV), the type capillovirus, is not closely related to *Cherry virus A*, HarVA, DiVA and DiVB. Thus, until more related virus sequences become available so as to confidently be able to decide if these viruses should be classified as capilloviruses or perhaps a new genus, it is recommended to accept these viruses as unclassified species within the family *Betaflexiviridae*

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	***2013.002bP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Foveavirus***
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:**
Rubus canadensis virus 1	JX277553

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

Rubus canadensis virus 1 (RuCV-1, *Abou Ghanem-Sabanadzovic et al.*, 2013).

Clearly this is a distinct Foveavirus (<52% aa identity over replicase protein to related viruses). Sequenced from a plant showing mild virus-like symptoms and containing flexuous filamentous virions. RT-PCR from 230 blackberry samples detected RuCV-1 in only one additional plant and showed 98% sequence similarity.

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	***2013.002cP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Vitivirus***
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 virus F	JX105428

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 virus F (GVF; Al Rwahnih et al., 2012)

Sequenced from dsRNA from black grape accession AUD46129. Bioassay of that accession resulted in death within 1 to 2 years of Cabernet Sauvignon plants propagated on Freedom, 420A, 3309C, and 101-14 rootstocks. ORFs 1 through 5 shared 31 to 49%, 8 to 26%, 28 to 47%, 40 to 70%, and 19 to 51% homologies, respectively, with other previously known grapevine vitiviruses. Field surveys and biological studies appear to show the involvement of this novel virus in graft incompatibility reactions.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Abou Ghanem-Sabanadzovic N, Tzanetakis IE, Sabanadzovic S. (2013). Rubus canadensis virus 1, a novel betaflexivirus identified in blackberry. Arch. Virol. 158(2):445-449

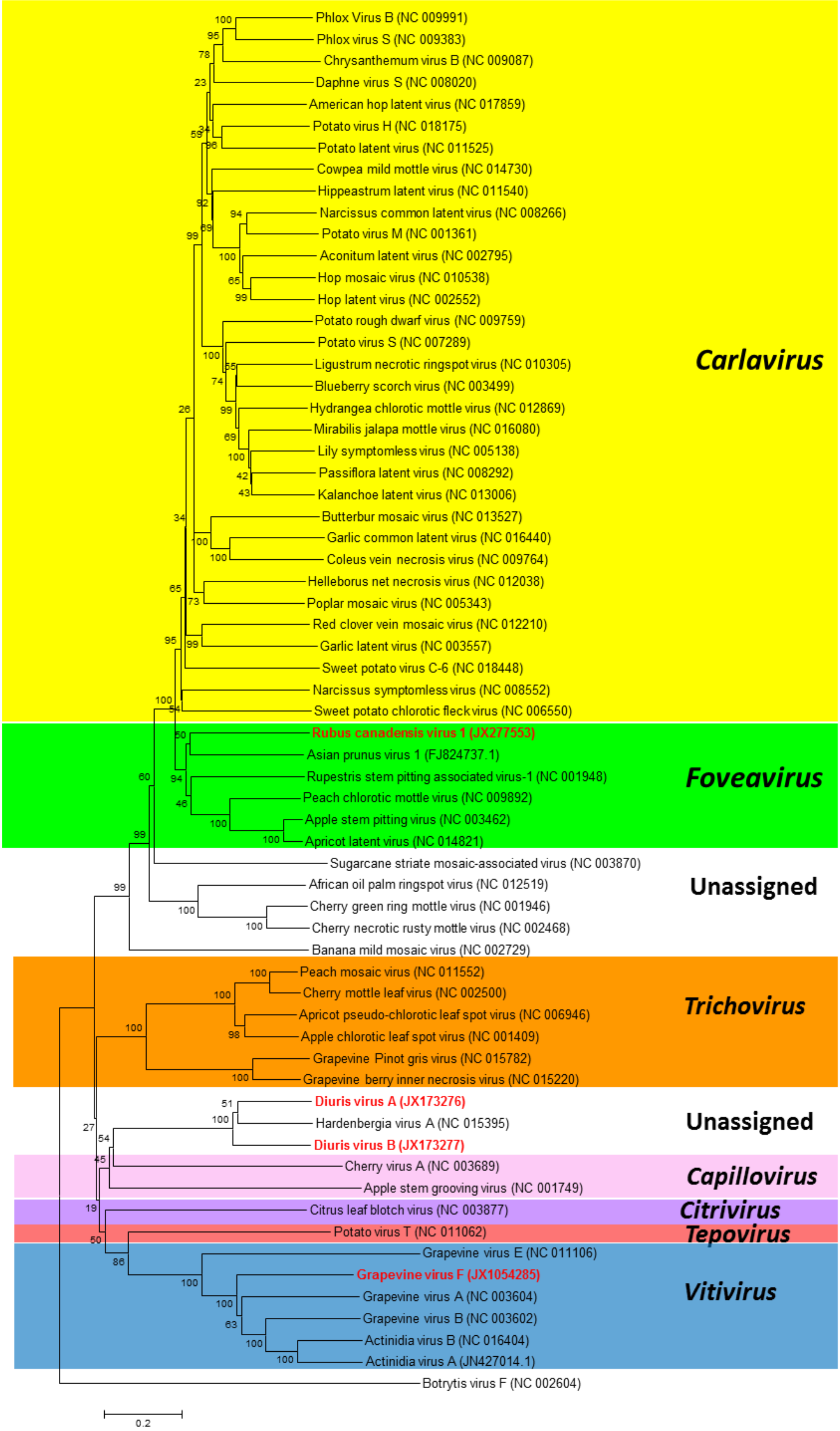
Al Rwahnih M, Sudarshana MR, Uyemoto JK, Rowhani A. (2012). Complete genome sequence of a novel vitivirus isolated from grapevine. J. Virol. 86(17):9545-9545(2012).

Wylie SJ, Li H, Dixon KW, Richards H, Jones MG (2013). Exotic and indigenous viruses infect wild populations and captive collections of temperate terrestrial orchids (Diuris species) in Australia. Virus Res. 171(1):22-32.

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.

Fig 1 (next page). Phylogenetic tree of Betaflexiviridae based on ClustalW alignment of the complete replicase amino acid sequences. Proposed new viruses from this proposal are indicated with red font.


Phlox Virus B (NC 009991)
Phlox virus S (NC 009383)
Chrysanthemum virus B (NC 009087)
Daphne virus S (NC 008020)
American hop latent virus (NC 017859)
Potato virus H (NC 018175)
Potato latent virus (NC 011525)
Cowpea mild mottle virus (NC 014730)
Hippeastrum latent virus (NC 011540)
Narcissus common latent virus (NC 008266)
Potato virus M (NC 001361)
Aconitum latent virus (NC 002795)
Hop mosaic virus (NC 010538)
Hop latent virus (NC 002552)
Potato rough dwarf virus (NC 009759)
Potato virus S (NC 007289)
Ligustrum necrotic ringspot virus (NC 010305)
Blueberry scorch virus (NC 003499)
Hydrangea chlorotic mottle virus (NC 012869)
Mirabilis jalapa mottle virus (NC 016080)
Lily symptomless virus (NC 005138)
Passiflora latent virus (NC 008292)
Kalanchoe latent virus (NC 013006)
Butterbur mosaic virus (NC 013527)
Garlic common latent virus (NC 016440)
Coleus vein necrosis virus (NC 009764)
Helleborus net necrosis virus (NC 012038)
Poplar mosaic virus (NC 005343)
Red clover vein mosaic virus (NC 012210)
Garlic latent virus (NC 003557)
Sweet potato virus C-6 (NC 018448)
Narcissus symptomless virus (NC 008552)
Sweet potato chlorotic fleck virus (NC 006550)
Carlavirus
Rubus canadensis virus 1 (JX277553)
Asian prunus virus 1 (FJ824737.1)
Rupestris stem pitting associated virus-1 (NC 001948)
Peach chlorotic mottle virus (NC 009892)
Apple stem pitting virus (NC 003462)
Apricot latent virus (NC 014821)
Foveavirus
Sugarcane striate mosaic-associated virus (NC 003870)
African oil palm ringspot virus (NC 012519)
Cherry green ring mottle virus (NC 001946)
Cherry necrotic rusty mottle virus (NC 002468)
Banana mild mosaic virus (NC 002729)
Unassigned
Peach mosaic virus (NC 011552)
Cherry mottle leaf virus (NC 002500)
Apricot pseudo-chlorotic leaf spot virus (NC 006946)
Apple chlorotic leaf spot virus (NC 001409)
Grapevine Pinot gris virus (NC 015782)
Grapevine berry inner necrosis virus (NC 015220)
Trichovirus
Diuris virus A (JX173276)
Hardenbergia virus A (NC 015395)
Diuris virus B (JX173277)
Unassigned
Cherry virus A (NC 003689)
Apple stem grooving virus (NC 001749)
Capillovirus
Citrus leaf blotch virus (NC 003877)
Citrivirus
Potato virus T (NC 011062)
Tepovirus
Grapevine virus E (NC 011106)
Grapevine virus F (JX1054285)
Grapevine virus A (NC 003604)
Grapevine virus B (NC 003602)
Actinidia virus B (NC 016404)
Actinidia virus A (JN427014.1)
Vitivirus
Botrytis virus F (NC 002604)
0.2