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:	***2012.016aP***	(to be completed by ICTV officers)

Short title: One new species in the genus Carlavirus
(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:

Kreuze, J.F. (j.kreuze@cgiar.org); Cuellar, W.; De Souza, J.; Fuentes, S.; Savenkov, E.

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: 22 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	**2012.016aP**	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Carlavirus***
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:**
Sweet potato C6 virus	JX212747

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

Sweet potato C6 virus (SPC6V) has previously been named in the literature as 'C-6 virus' and the availability of its partial genome sequence has been used to confirm its status as a carlavirus related to *Sweet potato chlorotic fleck virus* (SPCFV) [1,3]. It can be distinguished from SPCFV biologically by its host range (restricted to *Convolvulaceae*) and by its distinct symptoms produced in the indicator host *Ipomoea setosa*. Serologically each virus is only detected by their cognate antibodies. The complete genome sequence of SPC6V now determined is 8857nt excluding its poly-A tail, and its genome structure is typical for that of other carlaviruses except that an ORF6 encoding a cystein rich protein is missing (see Appendix Figure 1). Instead there is a putative ORF lacking an ATG start codon predicted to encode a protein without similarity to other known proteins. Since the putative ORF6 overlaps the CP by 7 nts including a potential slippery AAAA motif, it may be possible that it is translated through ribosomal frameshift or alternatively internal initiation as has been shown to occur for Potato virus M [2]. SPC6V is most closely related to SPCFV (see Appendix Figure 2) with which it shares only 48.2% nt identity over the entire genome. The complete replicase protein shows only 38% aa identity between SPC6V and SPCFV and ≤ 64% aa identity in the conserved RdRp domain, whereas their coat proteins share only 34.7% aa identity. Each of these identity values are well below the species demarcation threshold in the family *Betaflexiviridae* (isolates of different species are expected to have less than about 72% nt identity - or 80% aa identity - between their respective CP or polymerase genes). Because the virus has previously been identified as C-6 virus, included in the widely distributed sweetpotato virus detection kit produced by CIP, we propose the name *Sweet potato C6 virus* (SPC6V).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Clark, C.A., Davis, J.A., Abad, J.A., Cuellar, W.J., Fuentes, S., Kreuze, J.F., Gibson, R.W., Mukasa, S.B., Tugume, A.K., Tairo, F.D. and Valkonen, J.P.T. 2012. Sweetpotato viruses: 15 years of progress on understanding and managing complex diseases Plant Disease, 96 (2). pp. 168-185. ISSN 0191-2917
2. Gramstat, A., Prufer, D., Rohde, W. 1994. The nucleic acid-binding zinc finger protein of potato virus M is translated by internal initiation as well as by ribosomal frameshifting involving a shifty stop codon and a novel mechanism of P-site slippage. Nucleic Acids Research 22, 19: 3911 -3917
3. Untiveros, M., Fuentes, S., and Salazar, L. F. 2007. Synergistic interaction of *Sweet potato chlorotic stunt virus* (*Crinivirus*) with carla-, cucumo-, ipomo-, and potyviruses infecting sweet potato. Plant Dis. 91:669-676.

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 Sweet potato C6 virus indicating its position in the Carlavirus genome structure.

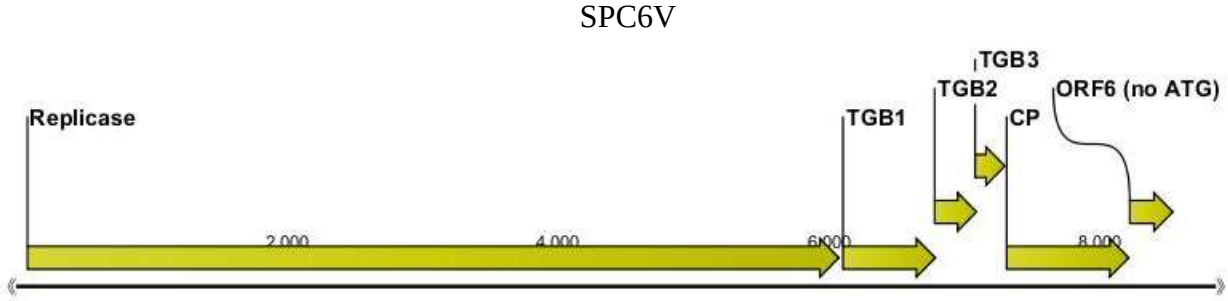
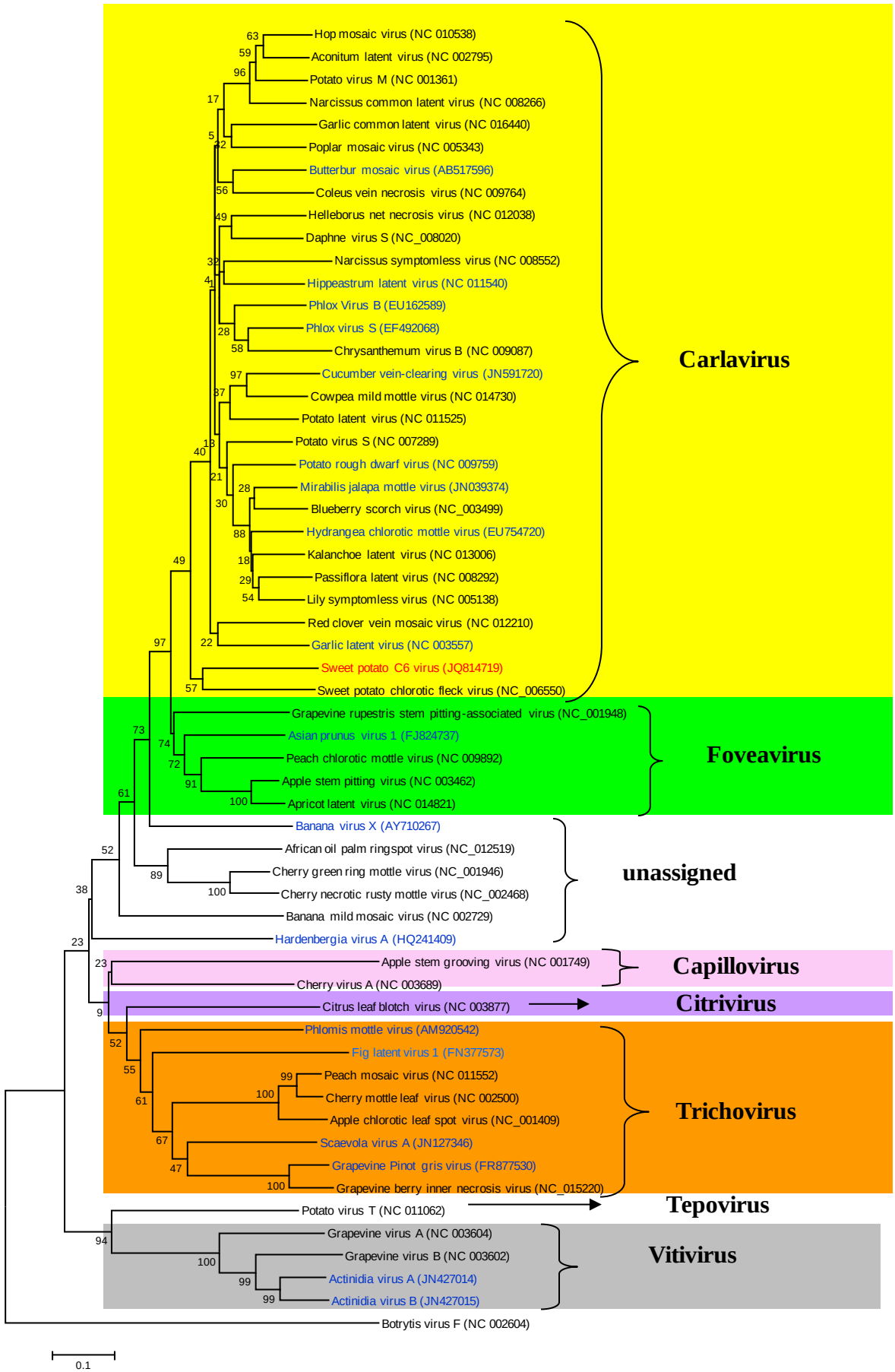


Figure 2 (next page): Phylogenetic tree based on the amino acid sequences of the entire replication protein of species of the family *Betaflexiviridae*. Sequences from classified and unclassified (blue color) species in the family were included and aligned using the ClustalW algorithm and a tree was generated using the Neighbour-Joining and Maximum composite likelihood method. Tree is rooted with Botrytis virus F (genus *Mycoflexivirus*, family *Gammaflexiviridae*). Numbers on branches indicate percentage of bootstrap support out of 1000 bootstrap replications (when > 60%). Tree produced in MEGA4.


Hop mosaic virus (NC 010538)
Aconitum latent virus (NC 002795)
Potato virus M (NC 001361)
Narcissus common latent virus (NC 008266)
Garlic common latent virus (NC 016440)
Poplar mosaic virus (NC 005343)
Butterbur mosaic virus (AB517596)
Coleus vein necrosis virus (NC 009764)
Helleborus net necrosis virus (NC 012038)
Daphne virus S (NC_008020)
Narcissus symptomless virus (NC 008552)
Hippeastrum latent virus (NC 011540)
Phlox Virus B (EU162589)
Phlox virus S (EF492068)
Chrysanthemum virus B (NC 009087)
Cucumber vein-clearing virus (JN591720)
Cowpea mild mottle virus (NC 014730)
Potato latent virus (NC 011525)
Potato virus S (NC 007289)
Potato rough dwarf virus (NC 009759)
Mirabilis jalapa mottle virus (JN039374)
Blueberry scorch virus (NC_003499)
Hydrangea chlorotic mottle virus (EU754720)
Kalanchoe latent virus (NC 013006)
Passiflora latent virus (NC 008292)
Lily symptomless virus (NC 005138)
Red clover vein mosaic virus (NC 012210)
Garlic latent virus (NC 003557)
Sweet potato C6 virus (JQ814719)
Sweet potato chlorotic fleck virus (NC_006550)
Carlavirus
Grapevine rupestris stem pitting-associated virus (NC_001948)
Asian prunus virus 1 (FJ824737)
Peach chlorotic mottle virus (NC 009892)
Apple stem pitting virus (NC 003462)
Apricot latent virus (NC 014821)
Foveavirus
Banana virus X (AY710267)
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)
Hardenbergia virus A (HQ241409)
unassigned
Apple stem grooving virus (NC 001749)
Cherry virus A (NC 003689)
Capillovirus
Citrus leaf blotch virus (NC 003877)
Citrivirus
Phlomis mottle virus (AM920542)
Fig latent virus 1 (FN377573)
Peach mosaic virus (NC 011552)
Cherry mottle leaf virus (NC 002500)
Apple chlorotic leaf spot virus (NC_001409)
Scaevola virus A (JN127346)
Grapevine Pinot gris virus (FR877530)
Grapevine berry inner necrosis virus (NC_015220)
Trichovirus
Potato virus T (NC 011062)
Tepovirus
Grapevine virus A (NC 003604)
Grapevine virus B (NC 003602)
Actinidia virus A (JN427014)
Actinidia virus B (JN427015)
Vitivirus
Botrytis virus F (NC 002604)
0.1