Recogize Diodia vein chlorosis virus as a definitive species in the genus Crinivirus

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:	***2012.009aV***	(to be completed by ICTV officers)

Short title: *Diodia vein chlorosis* virus is a definitive species in the genus *Crinivirus*
(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:

I.E. Tzanetakis (itzaneta@uark.edu) on behalf of the SG on *Closteroviridae*

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)	Closteroviridae

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

Date first submitted to ICTV: 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	***2012.009aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Crinivirus***
Subfamily:	
Family:	***Closteroviridae***
Order:	

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:**
Diodia vein chlorosis virus	GQ225585 and GQ376201

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

Diodia vein chlorosis virus (DVCV) was first identified by Larsen et al. (1991) in Virginia buttonweed (*Diodia virginiana*) showing vein clearing and chlorosis. The authors determined that the virus was transmitted efficiently by the banded-winded whitefly (*Trialurodes abutilonea*). Purifications yielded flexuous fragmented elongated particles with a diameter of ~ 12 nm whereas thin section EM revealed closterovirus-like inclusion bodies in the phloem tissue. The virus did not react to antisera against *Lettuce infectious yellows virus* or *Beet yellows virus.*

Tzanetakis *et al.* (2011) used a clone of a plant used in the Larsen *et al*. study. The complete genome of the virus was determined and phylogenetic analysis performed. Transmissions onto *Nicotiana benthamiana* and Virginia buttonweed seedlings with the banded-winged and greenhouse (*T. vaporiorum*) whiteflies were performed.

DVCV properties

Virus particles: flexuous elongated particles with a diameter of ~ 12nm (Larsen *et al*.,1991)
(i) dsRNAs: observed but not appropriate marker used (Larsen *et al*.,1991)
(ii) CP: 28 kDa (determined from deduced sequence data; Tzanetakis *et al*., 2011)
(iii) Nucleic acid: two molecules of ssRNA. RNA-1 8,010 nt in size and RNA-2 8,220 nt in size, respectively (Tzanetakis *et al*., 2011)
(iv) Genome: bipartite made up of a total of 10 ORFs, two of which comprised in RNA-

1 (accession No. GQ225585) and eight in RNA-2 (accession No. GQ376201) (Tzanetakis *et al*., 2011). Genome structure resembling that of members of the genus *Crinivirus* subgroup 1 but with differences in the relative position of some ORFs.
(v) Phylogenetic relationships: DVCV groups with members of the genus *Crinivirus* in trees constructed with RdRp, HSP70h and CP sequences (Tzanetakis *et al*., 2011). The closest crinivirus species is *Strawberry pallidosis associated virus* (SPaV) with which DVCV clusters in a distinct clade (Annex, Tzanetakis *et al.*, 2011). At the amino acid level, DVCV and SPaV show 77%, 81% and 47% amino acid identities with the RdRp, HSP70h and CP respectively.
(vi) Serological relationships: no similarities to anti-LIYV or BYV antisera (Larsen *et al.*,1991)
(vii) Mechanical transmission: Negative (Larsen *et al.*,1991)
(viii) Transmission by vectors: transmitted by *Trialurodes abutilonea* and *T. vaporariorum* (Larsen *et al.*,1991; Tzanetakis *et al.*, 2011). The closest relative, SPaV is only transmitted by *T. vaporariorum.*
(ix) Cytopathology: Inclusion bodies of the *Beet yellows virus* type in phloem tissue plus unusual double membrane-bound bodies never reported previously in closterovirus-infected cells (Larsen *et al*.,1991)
(x) Natural host range: *Diodia virginiana*

Species demarcation criteria in the genus *Crinivirus* (taken from the Ninth Taxonomy report) include: particle size, size of CP, serological specificity, genome structure and organization (number and relative location of the ORFs), amino acid sequence of relevant gene products (polymerase, CP, HSP70h) differing by more than 25%, vector specificity, magnitude and specificity of natural and experimental host range and cytopathological features. The above data support the notion that DVCV is a crinivirus species of good standing.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Larsen, R.C, Kim, K.S. and Scott, H.A. 1991 Properties and cytopathology of Diodia vein chlorosis virus – a new whitefly-transmitted virus. *Phytopathology* 81: 227-232.
2. Tzanetakis, I.E., Wintermantel, W.M., Poudel, B. and Zhou, J. 2011. Diodia vein chlorosis virus is a group-1 crinivirus. *Archives of Virology* 156: 2033-2037.

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.

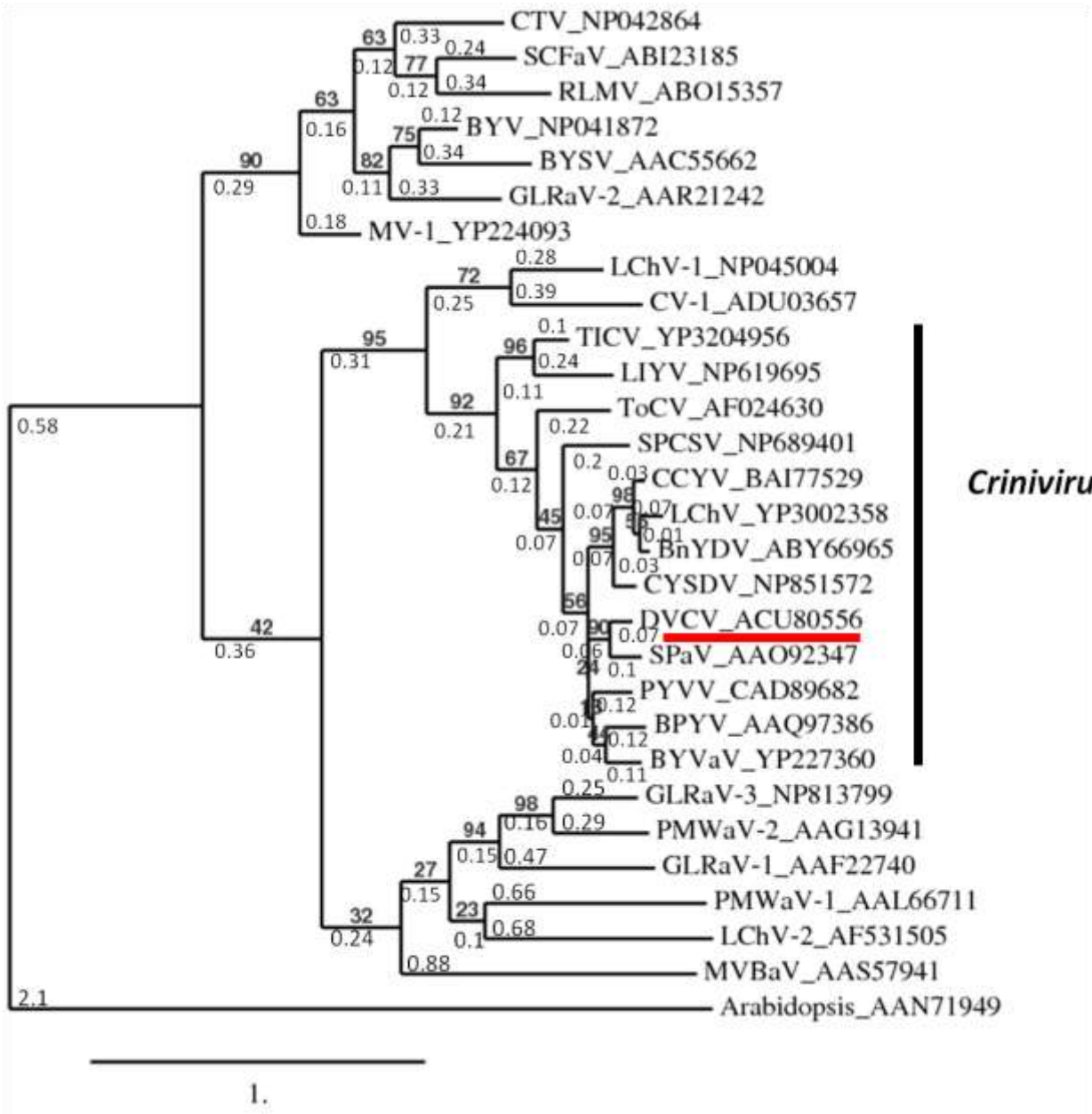

Figure 1. Phylogram of the heat shock protein 70 homolog of viruses in the family *Closteroviridae*. Abbreviations: BPYV, beet pseudoyellows virus; BnYDV, bean yellow disorder virus, BYV, beet yellows virus; BYSV, beet yellow stunt virus; BYVaV, blackberry yellow vein-associated virus; CTV, citrus tristeza virus; CV-1, cordyline virus-1; CCYV, cucurbit chlorotic yellows virus; CYSDV, cucurbit yellow stunting disorder virus; GLRaV-1, grapevine leafroll-associated virus 1; GLRaV-2, grapevine leafroll-associated virus 2,; GLRaV-3, grapevine leafroll-associated virus 3; LIYV, lettuce infectious yellows virus; LChV, lettuce chlorosis virus; LChV-1, little cherry virus-1, LChV-2, little cherry virus 2; MVBaV, mint vein banding-associated virus; MV-1, mint virus-1, PMWaV-1, pineapple mealybug wilt associated virus-1; PMWaV-2, pineapple mealybug wilt-associated virus-2; PYVV, potato yellow vein virus; RLMV, raspberry leaf mottle virus; SCFaV, strawberry chlorotic fleck-associated virus; SPaV, strawberry pallidosis-associated virus; SPCSV, sweet potato chlorotic stunt virus; TICV, tomato infectious chlorosis virus; ToCV, tomato chlorosis virus. Arabidopsis, *Arabidopsis thaliana* putative heat shock protein 70. The Arabidopsis protein is used as the outgroup. Bootstrap values are shown as percentages and Genbank accession numbers and branch length is shown on the figure.

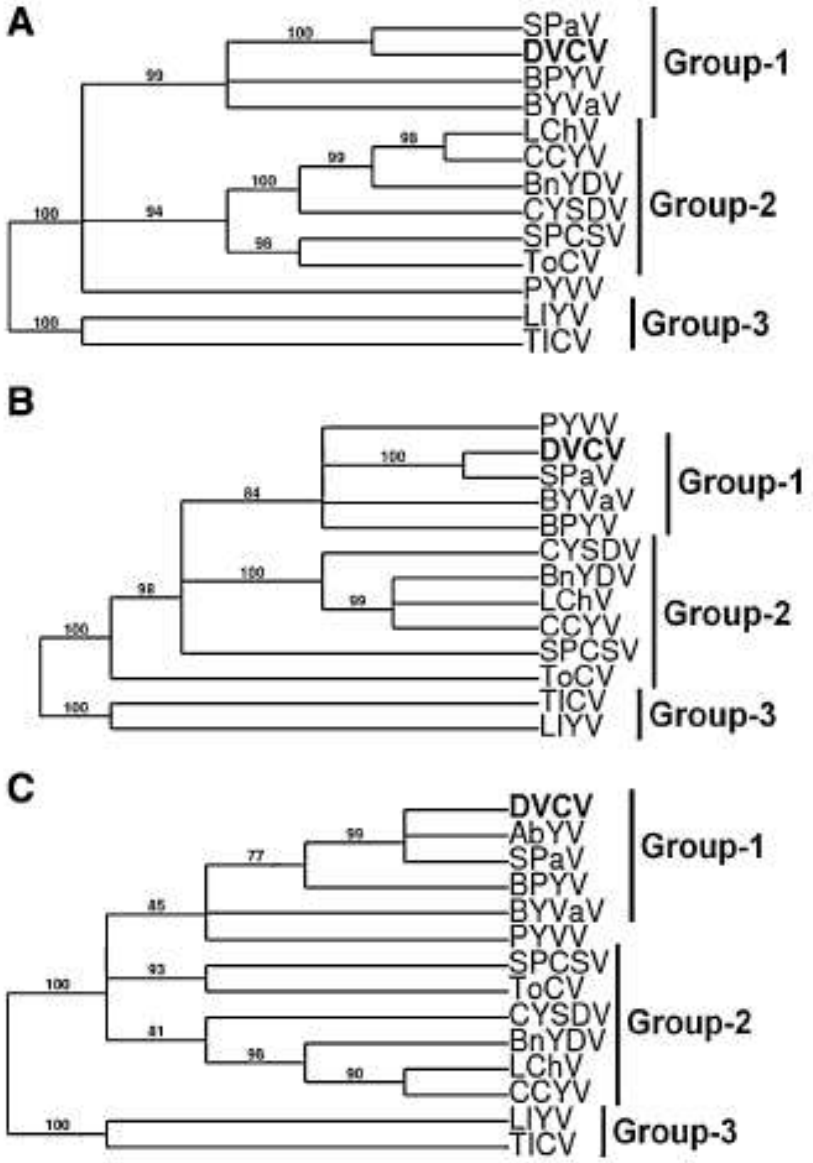

Fig. 3 Cladograms of the polymerase domain (A), heat shock protein 70 homolog (B) and coat protein (C) of members of the genus *Crinivirus*. All protein sequences have been obtained from the genome sequence of the respective virus, other than abutilon mosaic virus, where accession numbers are provided. Abbreviations: abutilon mosaic virus (AbYV, AAR00224), bean yellow disorder virus (BnYDV), blackberry yellow vein-associated virus (BYVaV), beet pseudo-yellows virus (BPYV), cucurbit chlorotic yellows virus (CCYV), cucurbit yellow stunting disorder virus (CYSDV), lettuce infectious chlorosis virus (LChV), lettuce infectious yellows virus (LIYV), potato yellow vein virus (PYVV), strawberry pallidosis-associated virus (SPaV), sweet potato chlorosis stunt virus (SPCSV), tomato chlorosis virus (ToCV), tomato infectious chlorosis virus (TICV). Nodes with bootstrap values <70% have been collapsed, as they are considered insignificant