MODULE 1: TITLE, AUTHORS, etc

Code assigned:	***2012.011a-dP***	(to be completed by ICTV officers)

Short title: create species *Hibiscus green spot virus 2* in a new unassigned genus named *Higrevirus*

Modules attached	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

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

Michael Melzer (melzer@hawaii.edu)

List the ICTV study group(s) that have seen this proposal:

Plant virus sub-committee	*Cilevirus* study group

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

Cilevirus Study Group response to the EC (June 2013):

As suggested by the ICTV-EC, the Cilevirus Study Group has discussed the possibility to create one or two families to accommodate both genera Cilevirus and Higrevirus. Based on the available information, probably both genera should be in a single family. Perhaps even the proposed genus Blunervirus[1] would also be placed in this family. However, some members of the Study Group, as well as some other scientific groups, are sequencing viruses that may belong to these new genera both in Brazil and in the USA and, hence, we decided to wait for the characterization of more short bacilliform viruses in order to build a stronger proposal and submit a more robust document to the ICTV-EC. In the meantime, we suggest that they should be considered as free-floating genera at this point. It should be noted, however, that our Study Group is committed to address this issue of creating one or two family(ies) for the next year.

Regarding the name of the species, our Study Group suggests that Hibiscus green spot virus 2 (HGSV 2) is maintained, but agrees with the elimination of the hyphen. If HGSV A is used, this virus would have at least three different names in the literature: HGSV in the original publication[2], HGSV 2 in a recent publication[3], and HGSV A in future publications. This could lead to confusion. HGSV 2 seems the most adequate, especially considering that HGSV 1 is one of the viruses that will soon be sequenced.

1.Quito-Ávila, D.F., Brannen, P.M., Cline, W.O., Harmond, P.F., Martin, R.R. 2013. Genetic characterization of Blueberry necrotic ring blotch 1 virus, a novel RNA virus with unique genetic features. Journal of General Virology doi:10.1099/vir.0.050393-0

2.Melzer, MJ, Sether, DM, Borth, WB, and Hu, JS. 2012. Characterization of a virus infecting Citrus volkameriana with citrus leprosis-like symptoms. Phytopathology 102:122-127.

3.Melzer, M.J., Simbajon, N., Carillo, J., Borth, W.B., Freitas-Astúa, J., Kitajima, E.W., Neupane, K.R., Hu, J.S. 2013. A cilevirus infects ornamental hibiscus in Hawaii. 2013. Archives of Virology 158: DOI 10.1007/s00705-013-1745-0

ICTV-EC comment to the study group (July 2012):

The EC would like the study group to consider whether one family could be created for both genera Cilevirus and Higrevirus, or whether two families could be created, one for each genus. Hyphens are not acceptable before a number at the end of a virus name. Given the possible confusion with the already existing hibiscus green spot virus 1, which is not currently an accepted species, the EC suggested that the name Hibiscus green spot virus A could be used for the new species rather than Hibiscus green spot virus 2.

Cilevirus Study Group response to Michael Melzer (2012):

The proposal is well written and the results support the creation of a new genus, with the proposed type species. However, there is a conflict involving the name of the type species, Hibiscus green spot virus (HGSV), since this name was used to denominate an apparently different virus infecting that ornamental host in Brazil. The only available information on the Brazilian virus refers to the symptoms it induces (localized green spots), morphology (bacilliform), cytopathic effects caused in the cytoplasm of infected cells, and possible vector (*Brevipalpus phoenicis* mites). Since there are no sequences available of this virus, it has not been proposed as a new species to the ICTV, but there are at least two publications describing it (Kitajima et al., 2003; 2010)*.
All of those above-mentioned characteristics are similar to the ones caused by the species proposed here. However, there are minor differences in symptoms, and the primes designed to the Hawaiian HGSV fail to amplify the Brazilian virus, suggesting that they are different. Hence, since the official description of the disease should have priority over subsequent reports, we suggest that the Brazilian virus, once fully characterized, should be named Hibiscus green spot virus-1, while the Hawaiian virus could be named *Hibiscus green spot virus-2* (HGSV-2). The genus name may remain as Higrevirus.

*Kitajima et al., Experimental & Applied Acarology 30(1-3): 135-160. 2003; Kitajima et al., Scientia Agricola 67(3): 348-371. 2010.

Date first submitted to ICTV:	Feb 9 2012
Date of this revision (if different to above):	June 26, 2012

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

Code	***2012.011aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Higrevirus* (new)**
Subfamily:	***unassigned***
Family:	***unassigned***
Order:	***unassigned***

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Hibiscus green spot virus 2	HQ852052, HQ852053,HQ852054

Reasons to justify the creation and assignment of the new species:

Hibiscus green spot virus 2 (HGSV-2) is proposed to be type species of a new viral genus, Higrevirus. HGSV-2 is a tripartite virus, and based on the polymerase domain, is most closely related to the bipartite *Citrus leprosis virus C* (CiLV-C) of the genus *Cilevirus*. The amino acid identity between homologous products for these two viruses range from 26 to 48%.

MODULE 3: **NEW GENUS**

creating a new genus

Code	***2012.011bP***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***unassigned***
Family:	***unassigned***
Order:	***unassigned***

naming a new genus

Code	***2012.011cP***	(assigned by ICTV officers)

To name the new genus: *Higrevirus*

Assigning the type species and other species to a new genus

Code	***2012.011dP***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Hibiscus green spot virus 2

Please enter here the TOTAL number of species (including the type species) that the genus will contain:

1

Reasons to justify the creation of a new genus:

The proposed genus Higrevirus, and its proposed type member Hibiscus green spot virus 2 (HGSV-2), is most closely related to the genus *Cilevirus*, and its type member *Citrus leprosis virus C* (CiLV-C). HGSV-2 is a tripartite virus (8.4, 3.2, and 3.1kb), while CiLV-C is bipartite (8.7 and 5.0kb). HGSV-2 has a triple gene block movement module, while CiLV-C encodes a 3A type movement protein. HGSV-2 encodes 8 ORFs, while CiLV-C encodes 6 ORFs; only two of these ORFs are orthologs. The phylogenetic distance between the polymerase domain of HGSV-2 and CiLV-C is similar to the distance between members of the genus *Tobravirus* and the genera *Pomovirus*/*Furovirus*. A tree is included in the appendix.

Origin of the new genus name:

Hibiscus green spot virus 2 – Higrevirus

Reasons to justify the choice of type species:

The genome of Hibiscus green spot virus 2 has been completely sequenced and its putative virions have been observed by TEM.

Species demarcation criteria in the new genus:

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Melzer, MJ, Sether, DM, Borth, WB, and Hu, JS. 2012. Characterization of a virus infecting Citrus volkameriana with citrus leprosis-like symptoms. Phytopathology 102:122-127

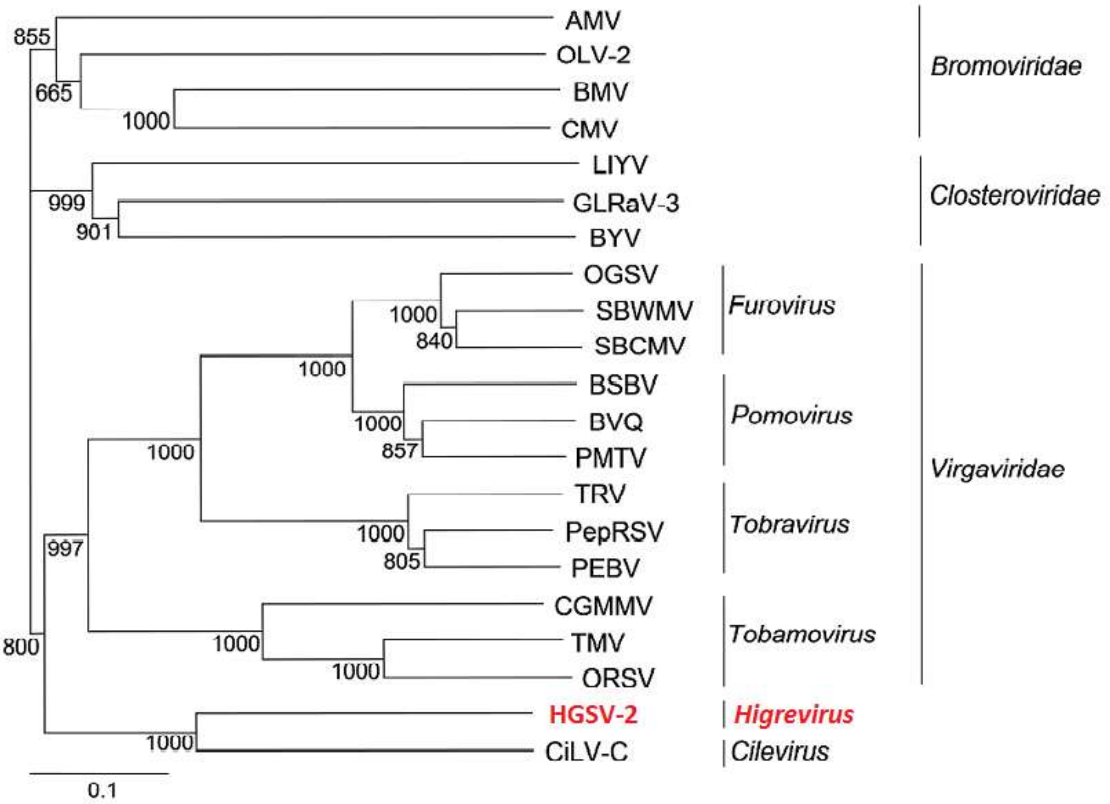
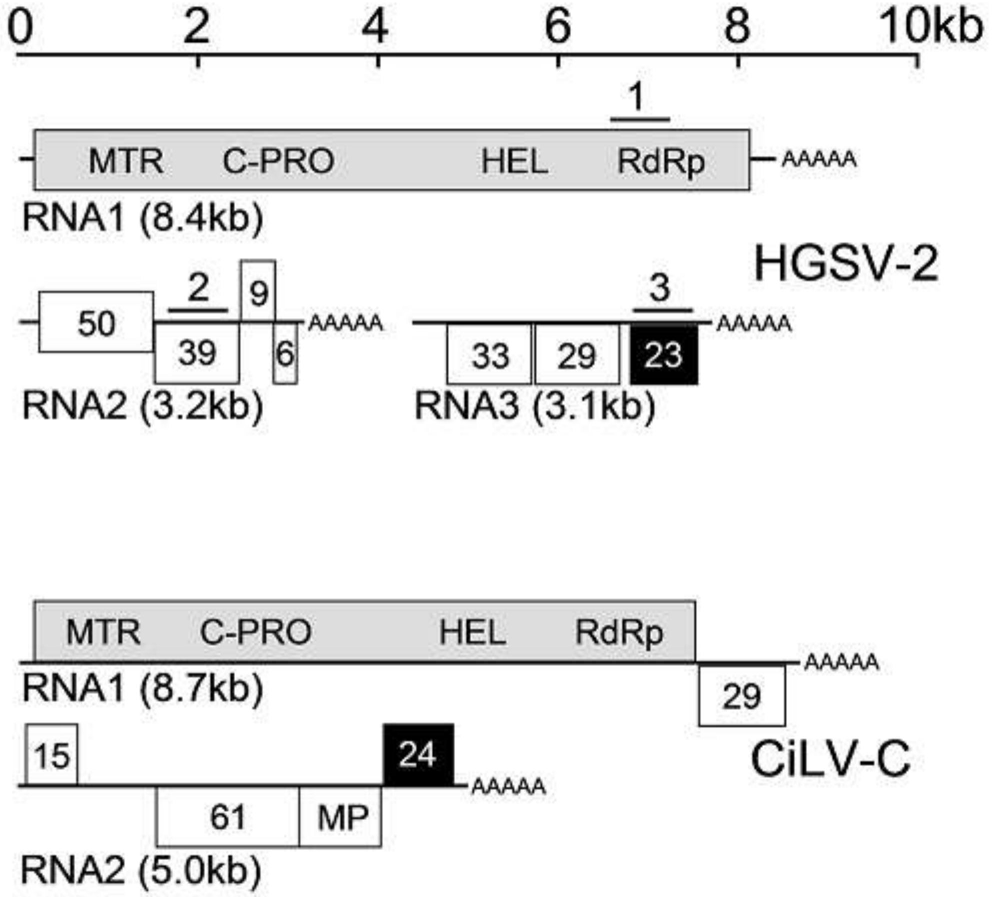


Figure 1. Phylogenetic placement of HGSV-2, of the proposed genus "*Higrevirus*", and other viruses inferred by a neighbor-joining algorithm using the RNA-dependent RNA polymerase domain. Bootstrap values are indicated on branches, and branches with a support of less than 600 of 1000 replications were collapsed. The scale indicates the number of substitutions for the given branch length. Virus abbreviations; AMV, *Alfalfa mosaic virus* (GenBank accession P03593); BMV, *Brome mosaic virus* (P03594); BSBV, *Beet soil-borne virus* (ABU63612); BVQ, *Beet virus Q* (NP_612605); BYV, *Beet yellows virus* (NP_733949); CiLV-C, *Citrus leprosis virus – cytoplasmic* (YP_654538); CGMMV, *Cucumber green mosaic mottle virus* (ACP17898); CMV, *Cucumber mosaic virus* (P16490); GLRaV-3, *Grapevine leafroll associated virus 3* (O71189); HGSV, Hibiscus green spot virus (HQ852052); LIYV, *Lettuce infectious yellows virus* (Q83045); OGSV, *Oat golden stripe virus* (NP_059510); OLV-2, *Olive latent virus 2* (CAA64073); ORSV, *Odontoglossum ringspot virus* (AAB53794); PEBV, *Pea early-browning virus* (CAB37343); PepRSV, *Pepper ringspot virus* (NP_620033); PMTV, *Potato mop-top virus* (NP_620444); SBCMV, *Soil-borne cereal mosaic virus* (CAB56599); SBWMV, *Soil-borne wheat mosaic virus*

(NP_049335); TMV, *Tobacco mosaic virus* (ABN79257); TRV, *Tobacco rattle virus* (NP_620444).



Figrue 2. Genome organization of Hibiscus green spot virus 2 (HGSV-2) and *Citrus leprosis virus-C* (CiLV-C). Similarly shaded open reading frames are orthologs; unshaded open reading frames are unrelated.

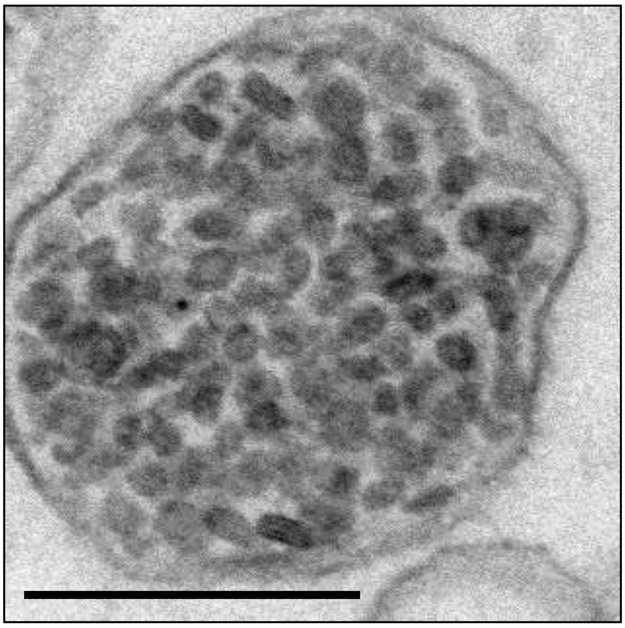


Figure 3. Membrane-bound vesicle containing virus like particles (VLPs) were present in tissues infected with Hibiscus green spot virus 2, but not healthy controls. These VLPs are similar to those associated with *Citrus leprosis virus C* infection. Bar is 250nm.