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:	***2011.002aP***	(to be completed by ICTV officers)

Short title: One new species in the proposed genus Solendovirus
(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.; Fuentes, S.; De Souza, J.; Barrantes, I.

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)	Caulimoviridae 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: 28 June 2011
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	***2011.002aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Solendovirus***
Subfamily:	
Family:	***Caulimoviridae***
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:**
Sweet potato vein clearing virus	HQ694979 = NC_015228

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 vein clearing virus (SPVCV), is a circular sweetpotato infecting DNA virus which is phylogenetically most closely related to *Tobacco vein clearing virus* (TVCV) (currently genus *Cavemovirus* but the proposed type member of the new genus *Solendovirus* – see proposal 2010.017a-eP.U) [1]. SPVCV shares 45.8% nucleotide identity with TVCV over its entire genome which is well below the 80% species demarcation threshold for the family, and it shares the characteristic genome structure of TVCV in contrast to the continuing members of the genus *Cavemovirus*, *Cassava vein mosaic virus* (CsVMV) and the proposed *Sweet potato collusive virus* (SPCV) (see Appendix Figure 1).

1. Cuellar, W. J., De Souza, J., Barrantes, I., Fuentes, S., and Kreuze, J. F. 2011. Distinct cavemoviruses interact synergistically with sweet potato chlorotic stunt virus (genus Crinivirus) in cultivated sweet potato. Journal of General Virology. 92:1233-1243

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Cuellar, W. J., De Souza, J., Barrantes, I., Fuentes, S., and Kreuze, J. F. 2011. Distinct cavemoviruses interact synergistically with sweet potato chlorotic stunt virus (genus Crinivirus) in cultivated sweet potato. Journal of General Virology. 92:1233-1243

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 (reproduced from Cuellar et al., 2011): Genome structure of the two currently accepted species in the genus *Cavemovirus*, CsVMV and TVCV, and the proposed species SPVCV and SPCV, shows similar structure between SPVCV and TVCV in the newly proposed genus *Solendovirus*, as compared to SPCV and CsVMV. Line arrows indicate the position of the first nucleotide of the genome (tRNAmet sequence). Black block arrows indicate ORFs found in all caulimoviruses while white block arrows (a–e) indicate ORFs for which no function could be assigned on the basis of sequence similarity. The black solid line indicates the relative position of the 59 leader sequence (hairpin) in each genome. CP, Coat protein; IBP, inclusion body protein; MP,movement protein.

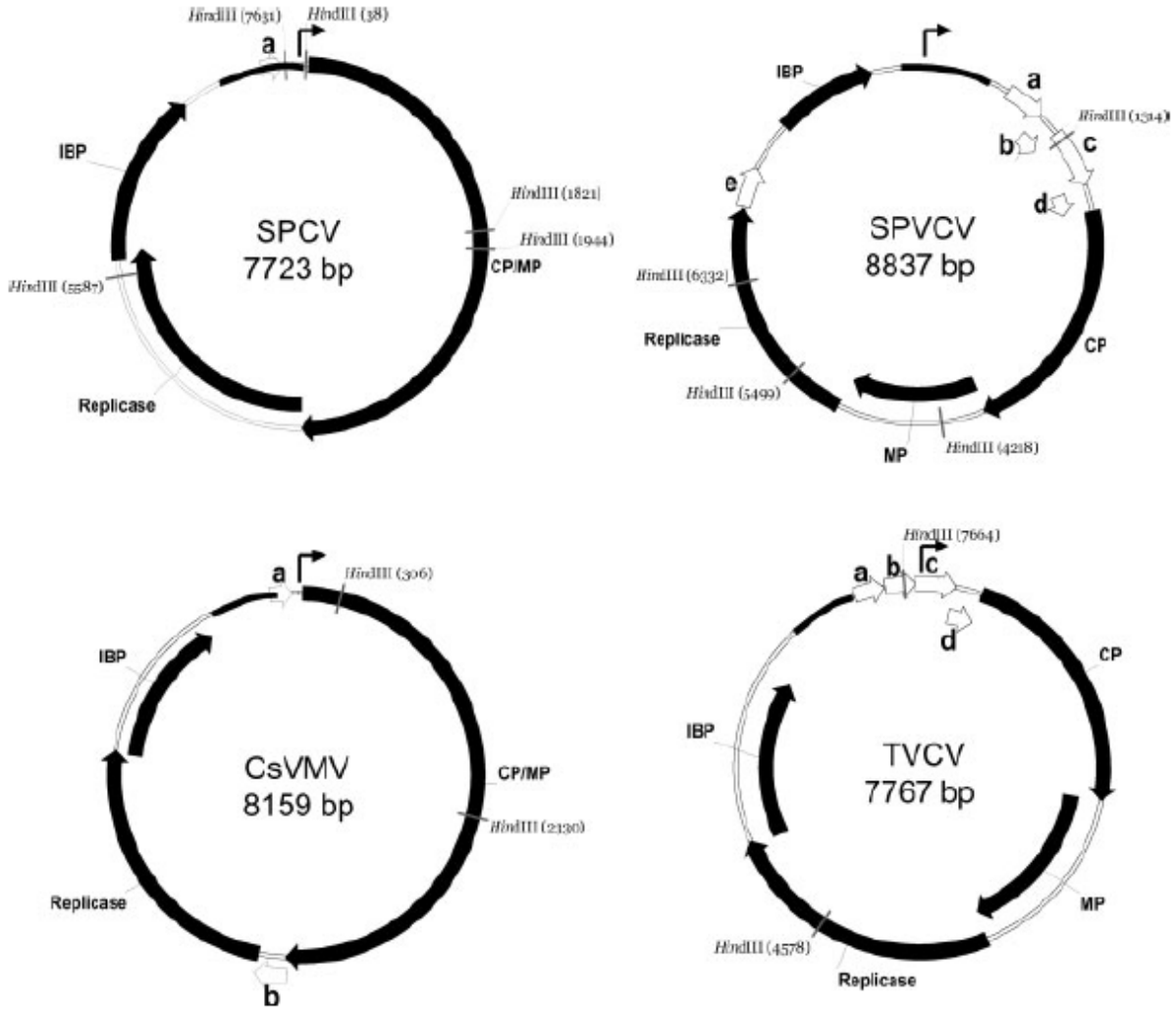

Figure 2 (adapted from Cuellar et al., 2011): Phylogenetic tree of complete genome sequences of viruses from the family *Caulimoviridae* showing the grouping of SPVCV with TVCV within the proposed genus Solendovirus and separate from the viruses in the genus *Cavemovirus*. Sequences were aligned using the ClustalW algorithm and a tree was generated using the Neighbour-Joining and Maximum composite likelihood method and 1000 bootstrap replicates, as implemented in MEGA5.05.