



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**

<b>Code assigned:</b>	<b><i>2011.001aP</i></b>	(to be completed by ICTV officers)			
<b>Short title:</b> One new species in the genus Cavemovirus (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

**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	<b>2011.001aP</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<i>Cavemovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<i>Caulimoviridae</i>	
Order:		
<b>And name the new species:</b>		<b>GenBank sequence accession number(s) of reference isolate:</b>
<i>Sweet potato collusive virus</i>		HQ694978 = <a href="#">NC_015328</a>

**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 collusive virus (SPCV), is a circular sweetpotato infecting DNA virus which is phylogenetically most closely related to *Cassava vein mosaic virus* (CsVMV) within the genus *Cavemovirus* [1, 2]. SPCV shares 63.1% nucleotide identity with CsVMV over its entire genome which is well below the 80% threshold determined for species demarcation in the family *Caulimoviridae*, but also shares a characteristic genome structure with CsVMV in contrast to *Tobacco vein clearing virus* (TVCV) and the proposed *Sweet potato vein clearing virus* (SPVCV) which belong to the proposed new genus *Solendovirus* (see proposal 2010.017a-eP.U).

SPCV has been named in the literature as ‘Sweet potato caulimo-like virus’, but this is inappropriate and potentially confusing because it could suggest that it belongs to the genus *Caulimovirus*.

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
2. De Souza J, Cuellar W. 2011. Sequence analysis of the replicase gene of 'sweetpotato caulimo-like virus' suggests that this virus is a distinct member of the genus *Cavemovirus*. *Archives of Virology* 156:535-537.

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
2. De Souza J, Cuellar W. 2011. Sequence analysis of the replicase gene of 'sweetpotato caulimo-like virus' suggests that this virus is a distinct member of the genus Cavemovirus. *Archives of Virology* 156:535-537.

**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 SPCV and SPVCV, shows the similar genome structures between SPCV and CsVMV, in contrast to SPVCV and TVCV in the newly proposed genus *Solendovirus*. Line arrows indicate the position of the first nucleotide of the genome (tRNA<sup>met</sup> 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.

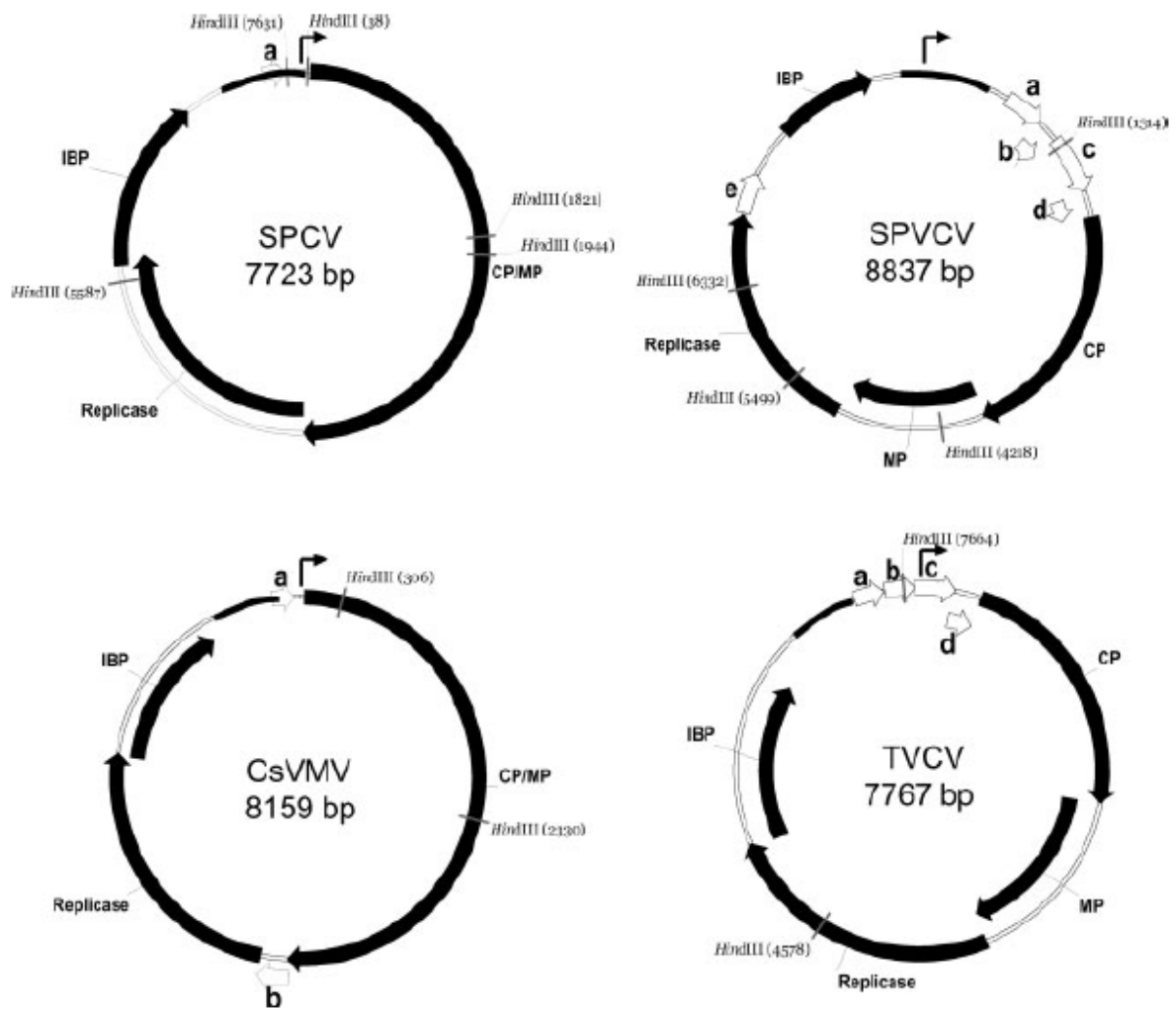


Figure 2 (adapted from Cuellar et al., 2011): Phylogenetic tree of complete genome nucleotide sequences of viruses from the family *Caulimoviridae* showing the grouping of SPCV with CsVMV within the genus *Cavemovirus* in a separate clade from TVCV and the proposed SPVVCV in the genus *Solendovirus*.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

