



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:	2010.002aP	(to be completed by ICTV officers)			
Short title: Reclassification of Sweet potato feathery mottle virus strain C as a separate species Sweet potato virus C in the genus Potyvirus (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input 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:

Jari Valkonen (jari.Valkonen@helsinki.fi) on behalf of Potyviridae SG

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)

Potyviridae

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

EC requested name change of Sweetpotato virus C in v1 to Sweet potato virus C as here

Date first submitted to ICTV:

27/05/2010

Date of this revision (if different to above):

03/07/2010

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	2010.002aP	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Potyvirus</i>	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.
Subfamily:		
Family:	<i>Potyviridae</i>	
Order:		
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Sweet potato virus C</i>		GU207957

Reasons to justify the creation and assignment of the new species:
<p>This proposal suggests the creation of a separate potyvirus species for viruses belonging to the current C-strain of <i>Sweet potato feathery mottle virus</i>. Complete genomic sequence analysis of a representative C-strain isolate has shown that nucleotide and amino-acid sequence identities of ~71% (complete genome) and ~77.6% (polyprotein) are clearly below the recommended potyvirus species demarcation limit: 76% and 83%, respectively [1]. Only the 5’ (46.9%) and 3’ (81.2-83.5%) UTR region are more conserved than what is usually found between different potyvirus species ($\leq 39.7\%$ and $\leq 76\%$ respectively) [1]. Because the three other currently recognized SPFMV strains (EA, RC and O) have been studied much more thoroughly and are in the majority as compared to C-strain it would be preferable to maintain the name Sweet potato feathery mottle virus for those viruses, and rename only the C-strain as a new species, for which the name sweetpotato virus C was previously proposed [2]. Additional support for this proposal is included in the appendix and in [3].</p>

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Adams MJ, Antoniw JF, Fauquet CM (2005) Molecular criteria for genus and species discrimination within the family Potyviridae. *Arch Virol* 150:459–479
2. Tairo F, Mukasa SB, Jones RAC, Kullaya A, Rubaihayo PR, and Valkonen JPT (2005) Unravelling the genetic diversity of the three main viruses involved in sweet potato virus disease (SPVD) and its implications. *Mol Plant Pathol* 6:199-211
3. Untiveros M, Quispe D, Kreuze J (2010) Analysis of complete genomic sequences of isolates of the Sweet potato feathery mottle virus strains C and EA: molecular evidence for two distinct potyvirus species and two P1 protein domains. *Arch Virol*, in press

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.

Table 1 Percentage of nucleotide and amino acid sequence identity between SPFMV-C1, and isolates Piu, S and 10-O

Virus region	% nt and (aa) sequence identity with SPFMV-C1			Recommended % nt and (aa) sequence identities threshold for different potyvirus species (Adams et al., 2005)
	Piu (EA ^a)	S(RC)	O-10(O)	
Polyprotein	71,8 ^b (77,8 ^c)	71,7 (77,4)	71,8 (77,5)	76 (82.9)
5'UTR	46.9	46.9	46.9	39.7
P1	56.4 (55.0)	55.5 (54.5)	56.0 (54.5)	58 (27.8)
Hc-Pro	74.4 (83.8)	74.8 (82.5)	74.3 (83.2)	76 (85.2)
P3	68.4 (67.3)	66.9 (67.3)	68.5 (68.2)	74 (76.6)
6K1	69.9 (78.8)	69.9 (78.8)	71.2 (74.9)	- ^d
CI	74.7 (85.5)	74.7 (85.1)	74.9 (85.7)	78 (88)
6K2	66.7 (71.7)	67.9 (71.7)	67.3 (71.7)	-
Nla-Vg	72.6 (82.2)	73.6 (81.2)	73.3 (83.3)	76 (81.4)
Nla-Pro	76.8 (91.8)	77.6 (91.4)	76.7 (88.9)	76 (88.5)
Nib	76.3 (86.2)	76.3 (87.1)	75.4 (86.0)	76.5 (89)
CP	77.1 (81.7)	76.3 (82.1)	76.9 (81.4)	76 (79.6)
3'UTR	82.6	83.5	81.2	76

^a Strain group to which each isolate corresponds.

^b % nucleotide identity

^c % amino acid identity is given between brackets

^d Not applicable

Figure 1 Plot of nucleotide identities over the entire genome between SPFMV isolate C1 (C strain) and Piu3 (EA strain), S (RC strain), and 10-O (O strain) using a 200nt sliding window. Recommended species demarcation thresholds (nt) for each protein region are indicated by black dotted lines.

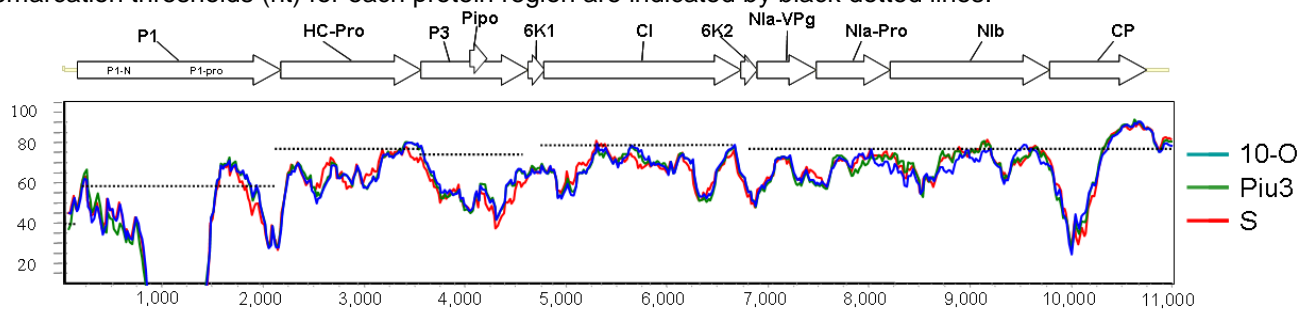


Figure 2 Phylogenetic tree (using Kimura 2 parameter distance and neighbor joining) of Coat protein nucleotide sequences showing the distinct and consistent phylogenetic position of SPFMV strain C as compared to the remaining SPFMV strain groups.

