

Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

Code To designate the following as species in the genus:

belonging to the family[°] :

Narcissus symptomless virus
Potato virus P
Sweet potato chlorotic fleck virus

[†] Assigned by ICTV officers

[°] leave blank if inappropriate or in the case of an unassigned genus

Author(s) with email address(es) of the Taxonomic Proposal

Mike Adams (mike.adams@bbsrc.ac.uk) on behalf of the Flexiviridae SG

Old Taxonomic Order

Order	
Family	<i>Flexiviridae</i>
Genus	<i>Carlavirus</i>
Type Species	<i>Carnation latent virus</i>
Species in the Genus	(37)

New Taxonomic Order

Order	
Family	<i>Flexiviridae</i>
Genus	<i>Carlavirus</i>
Type Species	<i>Carnation latent virus</i>
Species in the Genus	<i>Narcissus symptomless virus</i> <i>Potato virus P</i> <i>Sweet potato chlorotic fleck virus</i> (plus 37 as before)

ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

Each distinct species usually has a specific natural host range. Distinct species do not cross-protect in infected common host plant species. Distinct species are readily differentiated by serological procedures; strains of individual species are often distinguishable in reactions with polyclonal antisera, but more readily so with monoclonal antibodies. Distinct species have less than *ca.* 72% identical nt or 80% identical aa between their CP or polymerase genes.

Argumentation to justify the designation of new species in the genus

Narcissus symptomless virus

This is a newly described virus from daffodils that, in mechanical inoculation tests, was able to infect only some species of *Narcissus* and always without causing symptoms. The complete genome sequence (AM182569, 8281 nt) had an organization typical of the genus *Carlavirus* and this was consistent with its virion morphology. Phylogenetic analysis (Annex, Fig. 1) confirms that it is a member of the genus and in sequence comparisons, it has < 50% nt identity to other members of the genus in the polymerase gene (<47% nt identity in the coat protein). It therefore clearly satisfies the criteria to be regarded as a distinct species in the genus. See Chen et al., 2006.

Potato virus P

Potato virus P and Potato rough dwarf virus have been listed as tentative members of the genus *Carlavirus* in recent reports. They can be distinguished by the symptoms caused on some plant indicator species but they have many similar properties and cannot be distinguished by polyclonal antibodies. Sequence data from the 3'-ends of both these viruses show typical properties of a carlavirus in genome organization and in conserved genus-specific motifs. Phylogenetic analysis of the coat protein (Annex, Fig. 2) places them clearly within the genus *Carlavirus*. The coat proteins had 90.8% amino acid identity in an ungapped alignment, suggesting that they represent strains of the same species. The name Potato virus P was the first to be used and is preferred for the species (see Nisbet et al., 2006). In coat protein comparisons, these potato isolates had 67% amino acid identity to their nearest neighbour, Blueberry scorch virus, justifying their recognition as a distinct species.

Sweet potato chlorotic fleck virus

This filamentous virus (particles 12 x 750–800 nm) was first detected in a sweet potato accession showing fine chlorotic spots in Peru and, following the production of an antiserum, has been detected in sweet potato crops of several countries including Bolivia, Brazil, Colombia, Cuba, Indonesia, Japan, Kenya, Panama, Peru, Philippines and Uganda. Available evidence indicates that the virus is transmitted by sap but not by aphids and has a limited host range in the families Convolvulaceae and Chenopodiaceae. SPCFV is serologically unrelated to known filamentous viruses infecting sweet potato: the crinivirus sweet potato chlorotic stunt virus (SPCSV), the potyviruses sweet potato feathery mottle virus (SPFMV), sweet potato latent virus, sweet potato mild speckling virus, and the ipomovirus sweet potato mild mottle virus (SPMMV). Many of these viruses occur as mixed infections on crops. The complete genome has now been determined (AY461421, Aritua et al., 2007) and shown to be 9104 nucleotides (nt) long, and with the typical genome organisation of a carlavirus. This taxonomic placement is supported by phylogenetic analysis (Annex, Fig. 1). In sequence comparisons, it has < 40% nt identity to other fully sequenced members of the genus in the polymerase and coat protein genes but the CP has 61.2% nt identity to that of the partially sequenced Melon yellowing-associated virus (AY373028).

List of created Species in the genus

<i>Narcissus symptomless virus</i>			
Narcissus symptomless virus	(NSV)	AM182569	
<i>Potato virus P</i>			
Potato virus P	(PVP)	DQ516055	
Potato rough dwarf virus	(PRDV)	AJ250314	
<i>Sweet potato chlorotic fleck virus</i>			
Sweet potato chlorotic fleck virus	(SPCFV)	AY461421	

References

Aritua V, Barg E, Adipala E, Vetten HJ. (2007). Sequence analysis of the entire RNA genome of a sweet potato chlorotic fleck virus isolate reveals that it belongs to a distinct carlavirus species. *Archives of Virology* **152**, 813-818.

Chen J, Shi Y-H, Lu Y-W, Adams MJ, Chen J-P. (2006). Narcissus symptomless virus: a new carlavirus of daffodils. *Archives of Virology* **151**, 2261-2267.

Nisbet C, Butzonitch I, Colavita M, Daniels J, Martin J, Burns R, George E, Akhond MAY, Mulholland V, Jeffries CJ. (2006). Characterization of Potato rough dwarf virus and Potato virus P: distinct strains of the same viral species in the genus *Carlavirus*. *Plant Pathology* **55**, 803-812.

Annexes:

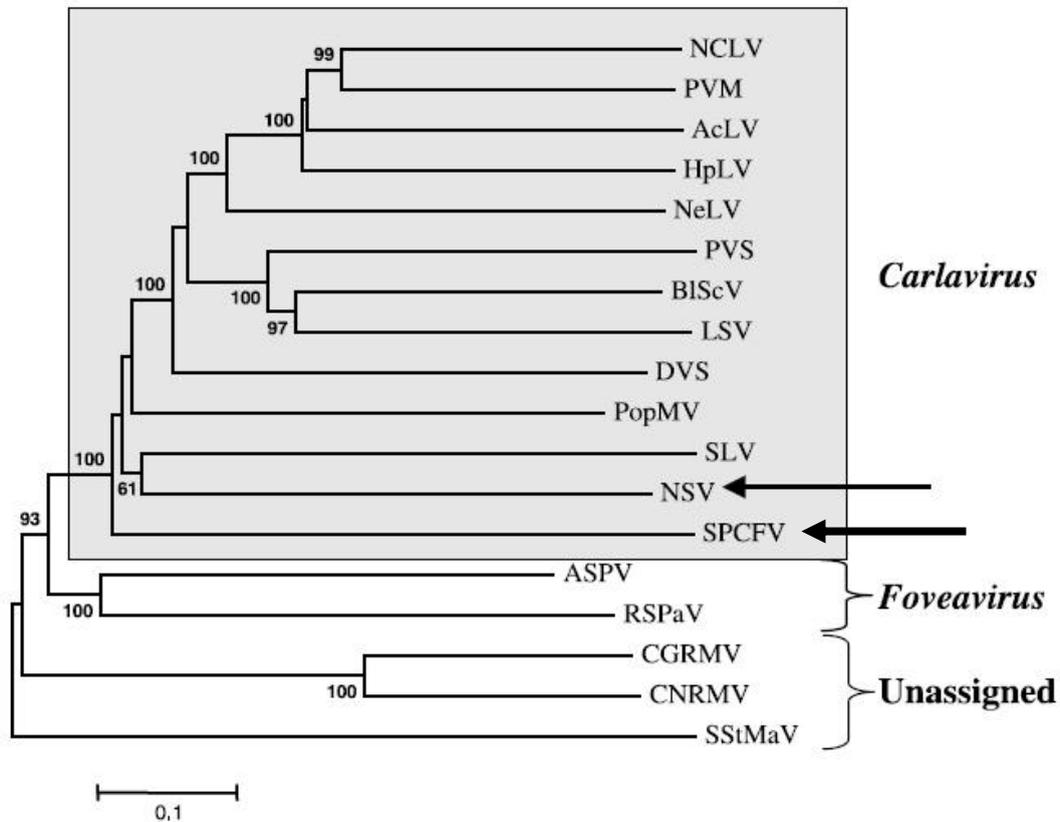


Figure 1. Phylogenetic tree for the coding sequence (ORFs 1–5) of the completely sequenced carlaviruses to show the position of two proposed new species, *Narcissus symptomless virus* and *Sweet potato chlorotic fleck virus*.

The sequences and abbreviations are as follows: Genus *Carlavirus*: Aconitum latent virus (AcLV; AB051848), blueberry scorch virus (BLSv; L25658), daphne virus S (DVS; AJ620300), hop latent virus (HpLV; AB032469), lily symptomless virus (LSV; AJ564638), *Narcissus common latent virus* (NCLV; AM158439), *Narcissus symptomless virus* (NSV; AM182569), Nerine latent virus (NeLV; DQ098905), poplar mosaic virus (PopMV; X65102), potato virus M (PVM; AJ437481), potato virus S (PVS; AJ863510), shallot latent virus (SLV; AJ292226), sweet potato chlorotic fleck virus (SPCFV; AY461421), Genus *Foveavirus*: apple stem pitting virus (ASPV; D21829), Rupestris stem pitting-associated virus (RSPaV; AF026278), Unassigned *Flexiviridae*: cherry green ring mottle virus (CGRMV; AF017780), cherry necrotic rusty mottle virus (CRMV; AF237816), sugarcane striate mosaic-associated virus (SStMaV; AF315308). The values at the forks indicate the percentage of trees in which this grouping occurred after bootstrapping the data with 10,000 replicates (shown only when >60%). The scale bar shows the number of substitutions per base.

(This is figure 2 in Chen et al., 2006)

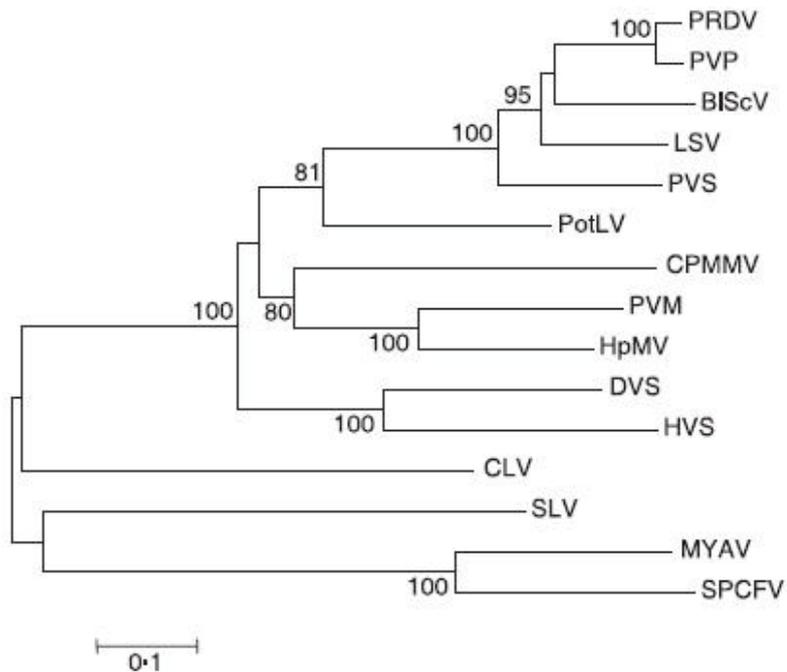


Figure 2. Phylogenetic tree for the coat protein amino acid sequences of carlavirus isolates to show the position of Potato virus P and Potato rough dwarf virus.

The dendrogram was constructed using neighbour-joining (Dayhoff PAM formula) with bootstrap test of phylogeny (250 replicates) and complete deletion of gaps. Bootstrap values of greater than 60% are included in the dendrogram. Virus names, coat-protein accessions and abbreviations are as follows: BLSvV, Blueberry scorch virus [NP_612812]; CLV, Carnation latent virus (CAA36854); CPMMV, Cowpea mild mottle virus (AAB94082); DVS, daphne virus S (CAI96553); HVS, Helenium virus S (Q00556); HpMV, Hop mosaic virus (BAB72006); LSV, Lily symptomless virus (CAB57961); MYAV, melon yellowing-associated virus (AAR19039); PotLV, Potato latent virus (AAG23710); PVM, Potato virus M (AAB81272); PVS, Potato virus S (CAA75701); SLV, Shallot latent virus (BAA25779); SPCFV, sweet potato chlorotic fleck virus (CAH03136).

(This is figure 3 in Nisbet et al., 2006)