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

Code[†] 005.009P.04

To designate the following as species in the genus: ***Carlavirus***

belonging to the family° : ***Flexiviridae***

Daphne virus S
Daphne virus S (DVS)
AJ620300
Melon yellowing-associated virus
Melon yellowing-associated virus (MYaV)
AY373028

[†] Assigned by ICTV officers
° leave blank if inappropriate or in the case of an unassigned genus

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Old Taxonomic Order

Order	
Family	*Flexiviridae*
Genus	*Carlavirus*
Type Species	
Species in the Genus	
Tentative Species in the Genus	
Unassigned Species in the family	

New Taxonomic Order

Order	
Family	*Flexiviridae*
Genus	*Carlavirus*
Type Species	
Species in the Genus	*Daphne virus S* *Melon yellowing-associated virus*
Tentative Species in the Genus	
Unassigned Species in the family	

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

Daphne virus S:
This species has been classified as a tentative member of the genus but the complete nucleotide sequence is now available (AJ620300) and this confirms earlier suggestions (Lee et al., 2003) that is should be regarded as a distinct species. Phylogenetic analyses (Annex, Figs. 1 and 2) confirm that it is a member of the genus and in sequence comparisons, it has < 55% nt identity to other members of the genus in the replicase gene (<58% nt identity in the coat protein).

Melon yellowing-associated virus:
This is a newly described virus, causing a disease of melon and transmitted by whitefly (Nagata et al., 2003; 2005). A sequence of the 3'-end of the genome, including the entire coat protein, has been reported (AY373028). Genome organization resembles that of the genus and phylogenetic analyses of the coat protein (Annex, Fig. 2) places it within the genus *Carlavirus*. It has ≤50% nt identity in its coat protein to other members of the genus and thus clearly satisfies the criteria for a new species.

List of created Species in the genus

Daphne virus S
Melon yellowing-associated virus

References

Lee BY, Choi SH, Ryu KH (2003) Characterization of the 3 '-terminal nucleotide sequence of two Korean isolates of Daphne virus S support its placement as a distinct species of the genus Carlavirus. Arch Virol 148: 1915-1924.

Nagata T, Kitajima EW, Alves DMT, Cardoso JE, Inoue-Nagata AK, de Oliveira MRV, de Avila AC (2003) Isolation of a novel carlavirus from melon in Brazil. Plant Pathology 52: 797-797.

Nagata T, Alves DM, Inoue-Nagata AK, Tian TY, Kitajima EW, Cardoso JE, de Avila AC (2005) A novel melon flexivirus transmitted by whitefly. Arch. Virol. 150: 379-387.

Annexes: Figs 1 and 2

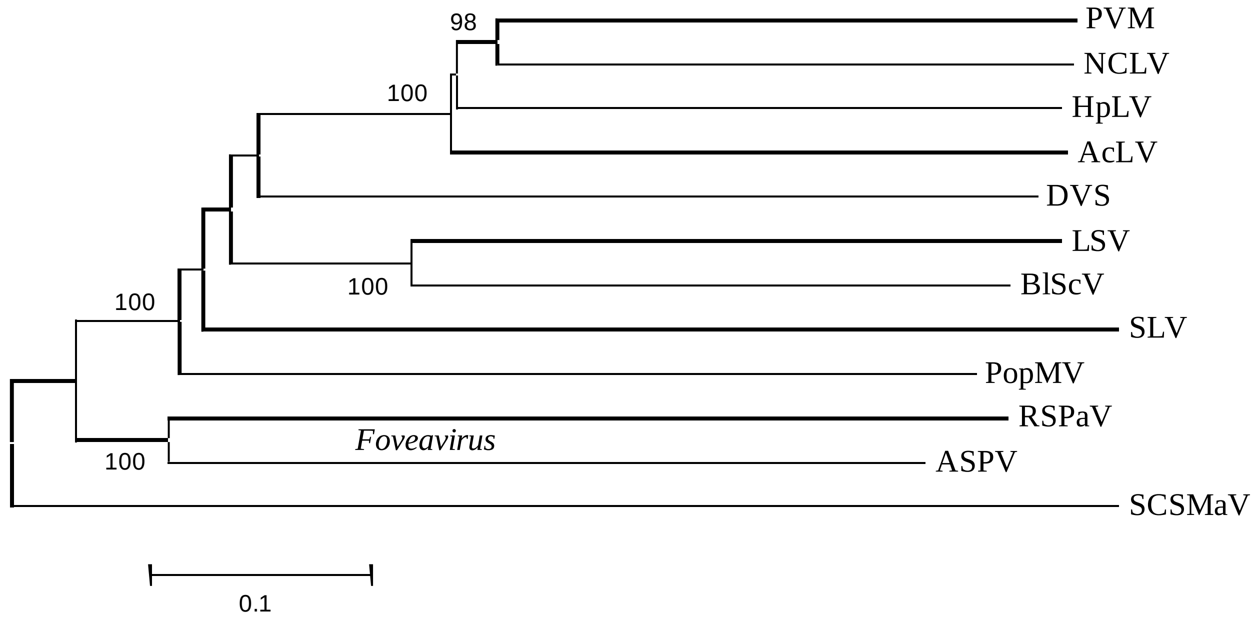

Fig. 1. Phylogenetic (Neighbor-Joining) tree of the complete coding nucleotide sequences of species in the genera *Carlavirus* and *Foveavirus* to show the position of *Daphne virus S* (DVS) in the genus *Carlavirus*. Bootstrap values (%), based on 1000 replicates, are shown where >70.

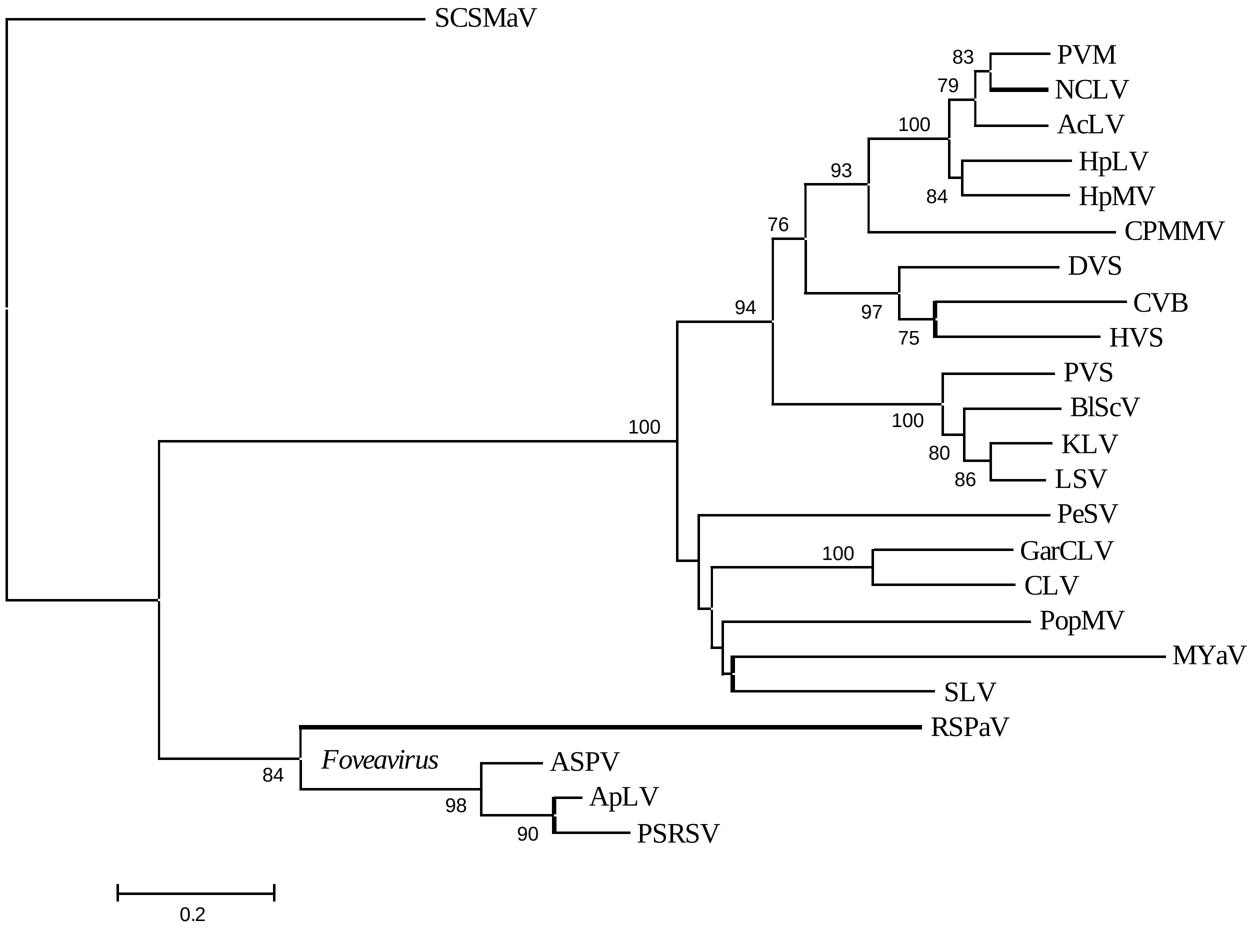

Fig. 2. Phylogenetic (Neighbor-Joining) tree of the coat protein amino acid sequences of species in the genera *Carlavirus* and *Foveavirus* to show the position of *Daphne virus S* (DVS) and *Melon yellowing associated virus* (MYaV) in the genus *Carlavirus*. Bootstrap values (%), based on 1000 replicates, are shown where >70.