This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned: ***2008.005P*** (to be completed by ICTV officers)

Short title: 2 new species in the genus Carlavirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached
(please check all that apply):

1 ☐ **2** ☐ **3** ☐ **4** ☐ **5** ☒
6 ☐ **7** ☐

Author(s) with e-mail address(es) of the proposer:

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

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

MODULE 5: **NEW SPECIES**

Code ***2008.005P*** (assigned by ICTV officers)

To create 2 new species assigned as follows:

Genus:	***Carlavirus***
Subfamily:	
Family:	**proposed family *Betaflexiviridae* (formerly *Flexiviridae*)**
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Coleus vein necrosis virus
Ligustrum necrotic ringspot virus

Argument to justify the creation of the new species:
If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Species demarcation criteria published in the 8th report are:

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.

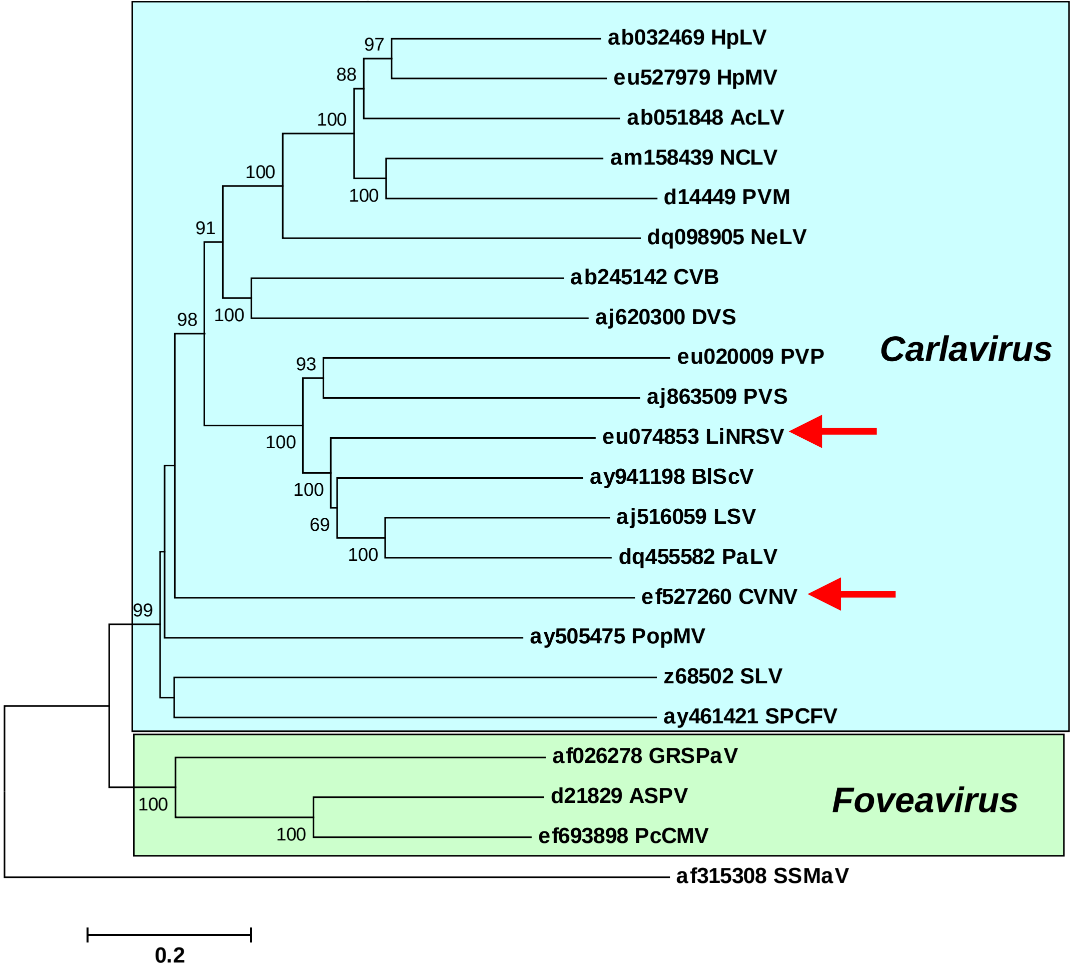
Argument to justify the creation of the new species:

Both viruses have been characterized and the sequence of their entire genomes determined. Phylogenetic analyses (Fig. 1) and sequence comparisons justify their status as distinct species within the genus *Carlavirus* (i.e. with less than 80% amino acid identity to existing species in their polymerase sequence):

Coleus vein necrosis virus
A filamentous virus identified in coleus in Minnesota and New York was found to cause veinal necrosis in coleus and could be transmitted readily by mechanical inoculation to coleus and Nicotiana spp. It was not transmitted by Myzus persicae. A 2-kb fragment of the 3' terminus (DQ915963) showed its relationship to carlaviruses (Mollov et al., 2007). The complete sequence of a Verbena isolate (EF527260; Kraus et al., 2008) has also been reported. The two sequences have 90% aa identity between their coat proteins. The polymerase has <40% aa identity to other species in the genus.

Ligustrum necrotic ringspot virus
Complete sequence (EU074853); Scott & Zimmerman, 2008. Polymerse has 55% aa identity to Blueberry scorch virus (BlScV), its nearest relative in the genus.

Fig. 1. Phylogenetic (NJ) tree of the amino acid sequences of the polymerase (ORF1) of members of the genera *Carlavirus* and *Foveavirus* with an unassigned member of the family, Sugarcane streak mosaic associated virus, as an outgroup. JTT distances and 100 bootstrap replicates. From MEGA4.



References:

Kraus J., Tzanetakis I.E., Putnam M.L., Martin R.R. (2008). Complete nucleotide sequence of an isolate of coleus vein necrosis virus from verbena. Arch. Virol. 153:381-384

Mollov D.S., Hayslett, M.C., Eichstaedt, K.A., Beckman, N.G., Daughtrey, M.L., Lockhart, B.E. (2007). Identification and characterization of a carlavirus causing veinal necrosis of coleus. Plant Dis 91:754-757

Scott S.W., Zimmerman M.T. (2008). The complete sequence of ligustrum necrotic ringspot virus, a novel carlavirus. Arch. Virol. 153:393-396