Taxonomic proposal to the ICTV Executive Committee

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:	*2008.003P*	(to be completed by ICTV officers)

Short title: 1 new species in the genus Foveavirus
(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	*2008.003P*	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	***Foveavirus***
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:

Peach chlorotic mottle 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:

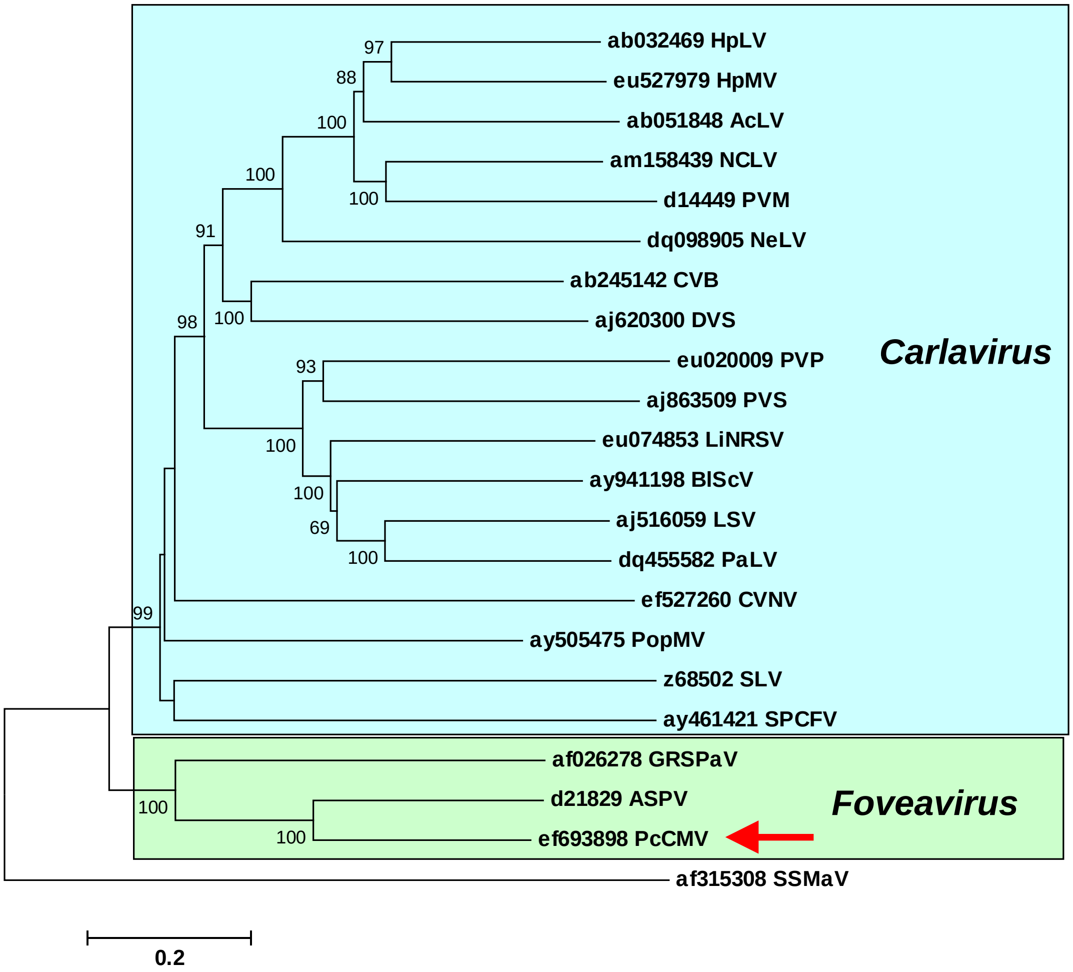
Each distinct species usually has a specific natural host range. Distinct species do not cross-protect in infected common host plant species. Distinct species are readily differentiated by serological procedures; strains of individual species are often distinguishable in reactions with polyclonal antisera, 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.

The virus isolated from peach cross-reacts with antisera to diverse viruses, such as plum pox virus

Argument to justify the creation of the new species:

(PPV), genus *Potyvirus*, family *Potyviridae*; and apple stem pitting virus (ASPV), genus *Foveavirus*, family *Flexiviridae*. The PCMV genome (EF693898) consists of 9005 nucleotides and has an organisation similar to that of ASPV but the two genomes share a nucleotide (nt) sequence identity of only 58%. Despite the serological cross reaction, the amino acid sequences of the CPs of PCMV and ASPV CP share only 37% identity (James et al., 2007). Phylogenetic analyses (Fig. 1) and sequence comparisons justify its status as a distinct species within the genus *Foveavirus* (it has 55% aa identity to ASPV in its polymerase sequence)

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:

James D., Varga A., Croft H. (2007). Analysis of the complete genome of peach chlorotic mottle virus: identification of non-AUG start codons, in vitro coat protein expression, and elucidation of serological cross-reactions. Arch. Virol. 152:2207-2215