MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2009.011a,bP***	(to be completed by ICTV officers)

Short title: create new species in the genus Vitivirus, family Betaflexiviridae
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached	1 ☒	2 ☒	3 ☐	4 ☐	5 ☐
(modules 1 and 9 are required)	6 ☐	7 ☐	8 ☐	9 ☒	

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

Mike Adams on behalf of the Flexiviridae Study Group mike.adams@bbsrc.ac.uk

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

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

Date first submitted to ICTV: May 2009
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	*2009.011aP*	(assigned by ICTV officers)

To create 1 new species with the name(s):

Grapevine virus E

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	*2009.011bP*	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	*Vitivirus*
Subfamily:	
Family:	*Betaflexiviridae* (**awaiting ratification**)
Order:	*Tymovirales* (**awaiting ratification**)

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.

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Throughout the family, species are recognized because of their specific natural host range, serological and molecular differences; distinct species have less than *ca.* 72% identical nt or 80% identical aa between their CP or polymerase genes (Adams et al., 2004; Martelli et al., 2007). Assignment to genera depends on genome organization, particle ultrastructure and biological characteristics including the mode of transmission.

The following details (from Nakaune et al., 2008) show that Grapevine virus E (GVE) clearly satisfies the criteria to be recognized as an independent species in the genus *Vitivirus*.

New virus-like sequences were found in a Japanese grapevine accession. The complete genome sequence (except for the extreme 5'-terminus) was determined (AB432910) and shown to have the characteristic 5 ORFs of a member of the genus *Vitivirus*. The 199-amino-acid sequence deduced from ORF4 has 38.5-54.0% identity with the coat protein (CP) of known grapevine vitiviruses. Phylogenetic analysis of the CP and the replication protein (see Annex, Figure 1) showed that the new virus was clearly related to the vitiviruses. The virus was transmitted from infected grapevine to healthy seedlings by the mealybug *Pseudococcus comstocki* Kuwanae, which is also a characteristic feature of vitiviruses.

additional material in support of this proposal

References:

Adams MJ, Antoniw JF, Bar-Joseph M, Brunt AA, Candresse T, Foster GD, Martelli GP, Milne RG, Zavriev SK, Fauquet CM (2004) The new plant virus family Flexiviridae and assessment of molecular criteria for species demarcation. Arch. Virol. 149:1045-1060.

Martelli G, Adams MJ, Kreuze JF, Dolja VV (2007) Family Flexiviridae: a case study in virion and genome plasticity. Ann. Rev. Phytopathol. 45:73-100

Nakaune R, Toda S, Mochizuki M, Nakano M. (2008). Identification and characterization of a new vitivirus from grapevine. Arch. Virol. 153:1827-1832.

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.

Fig. 1 Phylogenetic tree of the replication protein of representative members of the family *Betaflexiviridae*. The tree was generated from a codon-aligned nucleotide sequence using MEGA4 (Neighbor-Joining, Maximum Composite Likelihood method with 10,000 bootstrap replicates. Bootstrap values shown when >60%. The position of Grapevine virus E (GVE) within the genus *Vitivirus* is highlighted.