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

Code assigned: *2009.002a,bP* (to be completed by ICTV officers)	

Short title: 1 new species unassigned in the family Betaflexiviridae
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached
(modules 1 and 9 are required)

1 ☒ 2 ☒ 3 ☐ 4 ☐ 5 ☐
6 ☐ 7 ☐ 8 ☐ 9 ☒

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

Francisco Morales   f.morales@CGIAR.ORG
Mike Adams   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	*2009.002aP*	(assigned by ICTV officers)

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

 African oil palm ringspot virus

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	*2009.002bP*	(assigned by ICTV officers)

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

Genus:	**unassigned**
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

The family *Betaflexiviridae* was created for those viruses within the old family *Flexiviridae* that have a carlavirus-like polymerase. This included the genera *Carlavirus, Citrivirus, Capillovirus, Foveavirus, Trichovirus* and *Vitivirus* together with some unassigned species, *Banana mild mosaic virus* (BanMMV), *Cherry green ring mottle virus* (CGRMV), *Cherry necrotic rusty mottle virus* (CNRMV), *Potato virus T* and *Sugarcane striate mosaic-associated virus* (SCSMaV). Classification into genera is based on the genome organization and phylogenetic analyses (particularly of the large replication protein). Throughout the family, species are recognized because of their specific natural host range, serological differences 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).

A filamentous virus causing a serious disease of African oil palm in South America was first identified by Morales et al (2002). Partial sequence data suggested that the virus might be a member of the genus *Foveavirus*.

The complete genome sequence of AOPRV has now been determined (AY072921) and shows that it has a polyadenylated ssRNA of 7781 nt with five ORFs: a large (209 kDa) replication protein, a Triple Gene Block (associated with cell-to-cell movement) and a single 29 kDa coat protein. This organization is typical of the genus *Foveavirus* but also of the unassigned

BanMMV, CGRMV, CNRMV and SCSMaV (which do not group consistently with foveaviruses in phylogenetic analyses).

In sequence comparisons and phylogenetic analyses, AOPRV always groups most closely with CNRMV and CGRMV with 40-50% amino acid identity between their respective ORFs. See Annex Figure 1 for a phylogenetic tree for the replication proteins or AOPRV and selected members of the family. There is therefore no doubt that this virus represents a distinct species within the family but that it cannot be classified within the existing genera. It has not been easy to find consistent criteria to classify most of the unassigned members of the family into genera that can be supported by phylogenetic analyses and therefore, for the present, we propose that *African oil palm ringspot virus* should become a species unassigned within the family.

MODULE 9: **APPENDIX**: supporting material

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

Morales FJ, Lozano I, Velasco AC, Arroyave JA (2002) Detection of a fovea-like virus in African oil palms affected by a lethal 'ringspot' disease in South America. J. Phytopathol. 150:611-615

Fig. 1 Phylogenetic tree of the replication protein of unassigned members of the family *Betaflexiviridae* and representatives of the various genera to show the position of AOPRV. 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%.