This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: TITLE, AUTHORS, etc

Code assigned:	***2015.018aM***	(to be completed by ICTV officers)

Short title: One new species in the genus *Fijivirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

Author(s):

Zhou GH, Xu DL, Zhang HM, Chen JP

Corresponding author with e-mail address:

Zhou, Guohui (ghzhou@scau.edu.cn), Chen, Jianping (jpchen2001@126.com)

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Reoviridae SG

ICTV Study Group comments (if any) and response of the proposer:

C1: Please describe clearly the symptoms of SRBSDV-infected rice or maize plants.

Date first submitted to ICTV:	04/22/2015
Date of this revision (if different to above):	06/13/2015

ICTV-EC comments and response of the proposer:

C1: Please describe clearly the symptoms of SRBSDV-infected rice or maize plants.
R1: We described the symptoms in the revised version with highlight color.

C2: As the first Sogatella furcifera-borne reovirus, it would be useful to add some information of the interaction of SRBSDV and its insect vector.
R2: The transmission characters of this virus by its insect vector were added.

C3: Please indicate what is known about SRBSDV, with respect to infection of other crops such as wheat, sorghum, oat and barley, and monocot weeds that most probably are important reservoirs of the virus.
R3: This information was given in the revised version.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2015.018aM***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Fijivirus***
Subfamily:	***Spinareovirinae***
Family:	***Reoviridae***
Order:	***Unassigned***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Southern rice black-streaked dwarf virus	SRBSDV/HN	Seg1 FN563989 Seg2 FN563990 Seg3 FN563991 Seg4 FN563992 Seg5 FN563993 Seg6 FN563994 Seg7 FN563995 Seg8 FN563996 Seg9 EU523359 Seg10 EU523360

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

A fijivirus causing a serious disease on rice and maize in Southern China (and later in Vietnam) was initially identified as rice black-streaked dwarf virus (RBSDV) but studies of several isolates support its classification as a distinct species.

Fijiviruses have 10 dsRNA segments, most of which encode a single protein, although some are bicistronic. Five groups of species have long been recognized and group 2 contains four closely related species: *Rice black streaked dwarf virus, Maize rough dwarf virus* (MRDV), *Mal de Rio Cuarto virus* (MRCV) and *Pangola stunt virus.* According to the ICTV 9th report, MRDV and RBSDV might be considered as one single species. By now, the complete genomic sequences for RBSDV and MRCV, and sequences of segments S8-S10 only for MRDV, are available.

Zhou et al. (2008) first described the genomic segments S9 and S10, the symptoms on rice and maize, the insect vector and the host range of the Hainan (HN) isolate of this virus, and proposed it as a tentative new fijivirus species with the name Southern rice black-streaked dwarf virus (SRBSDV) [1]. Zhang et al. (2008) independently reported the nucleotide sequences of S7~S10 of a Guangdong (GD) isolate [2] and Wang et al. (2010) then completed genomic sequencing and phylogenetic analysis of both isolates [3]. Subsequently, the complete genomic sequences of six other isolates from China and Vietnam have been deposited in the public databases and there are sequences of some genomic segments available for many more isolates. These isolates are very closely related one to another, with over 97% nucleotide and 96% amino acid identities between their corresponding segments or ORFs [3, 6].

Sequence comparisons and phylogenetic analyses clearly identify SRBSDV as a group 2 fijivirus. Comparison between genomic segments of SRBSDV isolates and their counterparts in RBSDV indicates that the two viruses share 78.5-79.2% nt (83.4-89.0% aa) identities in the three most conserved segments, S1, S2 and S10 and 70.6-71.6% nt (63.1-69.9% aa) identities in the two least conserved segments, S5 and S6 (see Annex Table 1). These genetic distances are greater than those between RBSDV and MRDV and similar to those between RBSDV and MRCV [3, 6]. There also are certain genetic differences in the untranslated regions between SRBSDV and the other three members of group 2 fijivirus (see Annex Table 2). For those ORFs that are available, SRBSDV shares amino acid sequence identities of 61-83% with MRDV. Nucleotide diversities among SRBSDV isolates are much lower than those among the corresponding ORFs of the available RBSDV isolates and there is a lower purifying selection pressure on SRBSDV than on RBSDV, providing the molecular evidence for the view that SRBSDV is a recent origin [6].

The ICTV 9th Report [4] has the following entry for species demarcation criteria in the genus:

"Of the seven fijivirus species, the four members of group 2 are relatively closely related to one another. Further information about these viruses may eventually necessitate a revision of their species status. In particular, MRDV and RBSDV may be considered sufficiently closely related to constitute a single species…. In addition to the other general criteria used throughout the family, members of a species in the genus *Fijivirus* may be identified by:

- Sequence analysis: members of different species usually have <40% amino acid identity in comparisons of proteins corresponding to those encoded by RBSDV segments 7, 8, 9 and 10). In comparisons among the genome segments coding for the major capsid protein, viruses from different groups have <55% nucleotide identity (but identities are much higher within group 2).
- Cross-hybridization of less conserved genome segments (Segs-10 of MRDV and RBSDV, encoding a highly conserved major outer shell protein, share 94% nucleotide sequence and so are not suitable). Hybridization using RBSDV Seg5 and Seg6 cDNA probes to detect the homologous sequences is more than 20 times more sensitive than hybridization using their counterparts from MRDV.
- Serological cross-reactions: viruses in different groups do not cross-react; those in group 2 do so to a limited extent that is dependent on the proteins being compared.
- The identity or family of the plant host species (if any) together with the insect vector and its host."

It seems clear that if MRCV, MRDV and RBSDV continue to be considered as separate species, then SRBSDV should be an additional species in the genus. This is supported by phylogenetic analyses (see Annex Figure 1). Furthermore, SRBSDV is transmitted efficiently by a long-distance migratory pest, white-backed planthopper (*Sogatella furcifera* Horváth, Homoptera: Delphacidae) [1], which does not appear to be a vector of the other group 2 fijiviruses, and cannot be transmitted by small planthopper (*Laodelphax striatellus* Fallén) [7], the main vector of RBSDV and MRDV. The white-backed planthopper transmits SRBSDV in a persistent circulative propagative manner, and the insect may acquire the virus by feeding on infected rice plants for 5 min and transmit it to a healthy plant by a 30-min inoculation period [5]. On average, a viruliferous individual of planthopper nymph may transmit the virus to 48 rice seedlings, while a viruliferous adult individual can infect 8–25 rice plants with the virus within 5 days [5].

The host range of SRBSDV includes rice, maize, *Coix lacryma-jobi*, wild oat (*Avena fatua*), barnyard grass (*Echinochloa crusgalli*), goosegrass (*Eleusine indica*), and *Pennisetum flaccidum* [1, 5]. Rice plants infected with the virus show a variety of symptoms including severe stunting, ruffled dark green leaves, failure to elongate, excessive tillering, barren grains, deficient grain weight, poorly-developed brown roots, and small streaked waxy galls on the stems [5]. The maize, barnyard grass and *Juncellus serotinus* grown in and/or adjacent to the diseased rice fields may get infected and show symptoms of stunting, leaf roll and/or dark green [1]. Of the other members of group 2, MRDV and MRCV have not been reported to infect rice. Based on the distinct geographic distribution, vector type and epidemic characteristics of SRBSDV, it is justified to consider the virus to be a novel species in genus *Fijivirus* even when MRDV and RBSDV are regarded as a single species.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Zhou GH, Wen JJ, Cai DJ, et al. (2008). Southern rice black-streaked dwarf virus: a new proposed Fijivirus species in the family Reoviridae. Chin. Sci. Bull. 53, 3677-3685. doi: 10.1007/s11434-008-0467-2.

2. Zhang HM, Yang J, Chen JP, et al. (2008). A black-streaked dwarf disease on rice in China is caused by a novel Fijivirus. Arch. Virol. 153, 1893-1189.doi:10.1007/s00705-008-0209-4

3. Wang Q, Yang J, Zhou GH, et al. (2010). The complete genome sequence of two isolates of Southern rice black-streaked dwarf virus, a new Fijivirus. J. Phytopathol. 158, 733-737.doi:10.1111/j.1439-0434.2010.01679.x

4. Attoui H, Mertens PPC, Becnel J et al. (2011). Family *Reoviridae.* In: *Virus Taxonomy*, Ninth Report of the International Committee on Taxonomy of Viruses (A.M.Q. King, M.J. Adams, E.B. Carstens & E.J. Lefkowitz, eds), pp. 541-637. Elsevier Academic Press, London.

5. Zhou GH, Xu DL, Xu DG et al. (2013). Southern rice black-streaked dwarf virus: a white-backed planthopper transmitted fijivirus threatening rice production in Asia. Front. Microbiol. 4: 270. doi:10.3389/fmicb.2013.00270

6. Xue J, Li J, Zhang HM, et al. (2014). Molecular characterization of Southern rice black-streaked dwarf virus (SRBSDV) from Vietnam. J. Phytopathol. 162: 349-358. doi: 10.1111/jph.12196

7. Jia D, Chen H, Mao Q, et al. (2012). Restriction of viral dissemination from the midgut determines incompetence of small brown planthopper as a vector of Southern rice black-streaked dwarf virus. Virus Res. 167, 404-408. doi: 10.1016/j.virusres

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 but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1. Comparisons between the segments of SRBSDV-HN isolate and the corresponding segments of other fijiviruses. Percentage nucleotide identities are shown for the complete segment comparisons and the percentage amino acid identities for the predicted ORFs are in brackets.

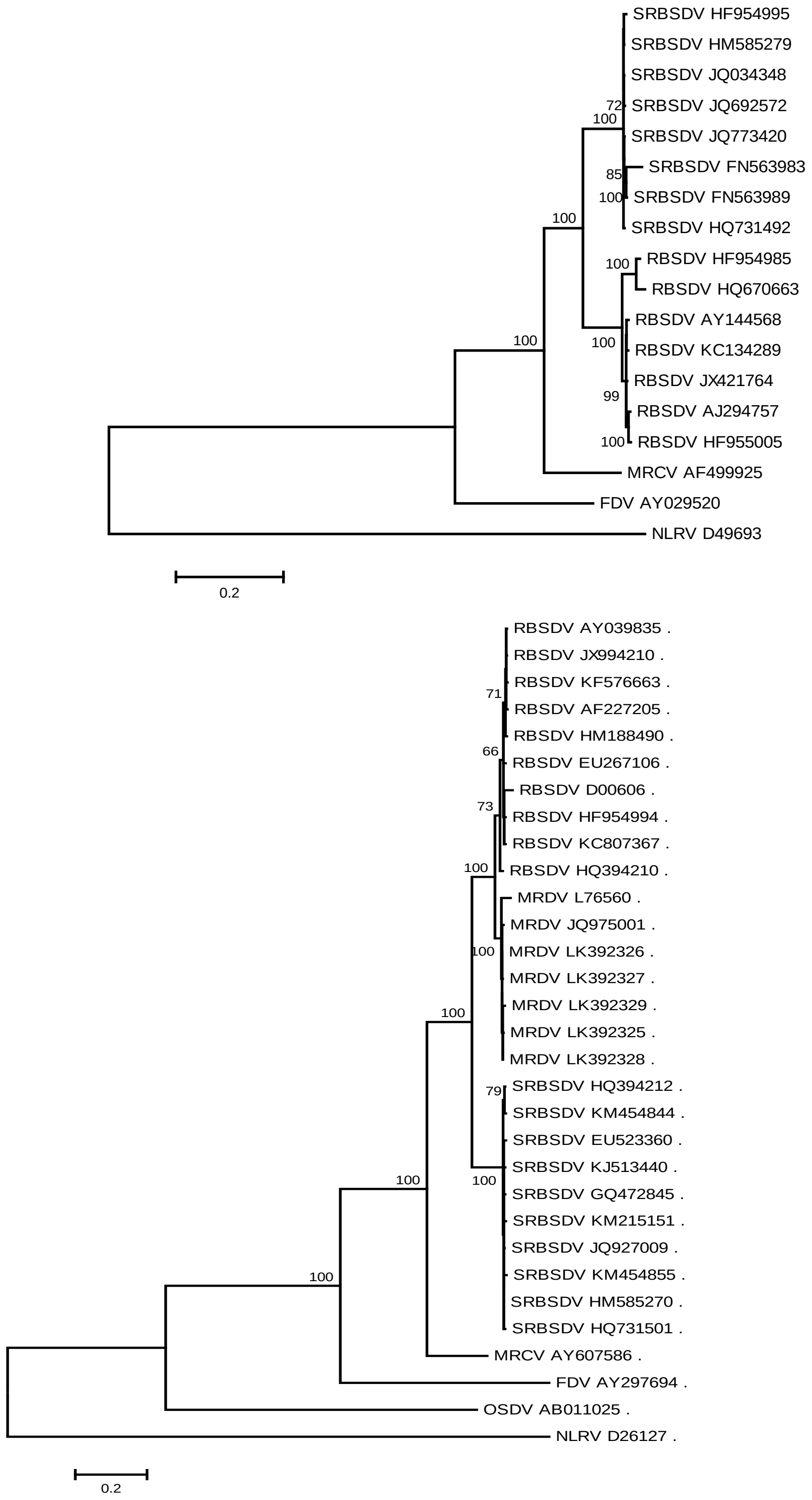
Segment	RBSDV[1]	MRCV	MRDV	FDV	OSDV
S1	79.0 (85.8)	74.1 (78.6)	n/a[2]	67.3 (63.7)	n/a
S2	78.9 (89.0)	75.7 (83.1)	n/a	62.2 (59.4)	n/a
S3	73.0 (73.4)	65.5 (56.8)	n/a	53.8 (37.5)	n/a
S4	77.3 (84.5)	71.1 (72.9)	n/a	63.2 (53.6)	n/a
S5	70.6 (69.9,61.8)	66.3 (59.1,50.5)	n/a	51.1 (30.9, -)	n/a
S6	70.6 (63.1)	62.4 (42.5)	n/a	11.2 (23.2)	n/a
S7	73.3 (80.7, 60.6)	65.5 (61.7,42.3)	74.2 (82.7,61.5)	59.7 (52.5,25.2)	22.8 (34.1,10.2)
S8	72.6 (71.3)	64.2 (55.4)	72.6 (70.3)	40.3 (35.8)	15.1 (22.6)
S9	74.2 (77.4,72.0)	68.8 (67.1,61.6)	74.9 (77.4,73.5)	51.3 (37.1,37.8)	40.5 (26.3,18.0)
S10	78.5 (83.4)	72.5 (71.9)	79.1 (83.5)	56.4 (47.6)	45.4 (33.1)

[1] Zhejiang isolate (Zhang et al., 2001. Arch. Virol. 146:2331-2339; Zhang et al., 2001. Eur. J. Plant Pathol. 107: 563-567). [2] n/a, no sequence available

Table 2. Nucleotide identities of untranslated region between SRBSDV and the other three fijiviruses in group 2

Sequence	RBSDV	MRCV	MRDV
S1-5'UTR	94.3	55.6	n/a
S1-3'UTR	79.7	66.7	n/a
S2-5'UTR	91.1	57.6	n/a
S2-3'UTR	76.7	36.8	n/a
S3-5'UTR	71.4	60.0	n/a
S3-3'UTR	37.3	32.0	n/a
S4-5'UTR	78.6	78.6	n/a
S4-3'UTR	35.1	60.2	n/a
S5-5'UTR	100.0	100.0	n/a
S5-3'UTR	89.0	74.7	n/a
S6-5'UTR	93.8	77.2	n/a
S6-3'UTR	82.2	73.9	n/a
S7-5'UTR	86.7	96.7	n/a
S7-3'UTR	90.1	77.8	n/a
S8-5'UTR	100.0	91.7	100.0
S8-3'UTR	83.6	64.8	83.6
S9-5'UTR	94.1	88.2	92.0
S9-3'UTR	78.4	83.8	82.9
S10-5'UTR	95.2	81.0	85.7
S10-3'UTR	88.3	84.3	89.3

Fig. 1 Phylogenetic trees based on amino acid sequences of the two most conserved proteins: (A) P1 (RNA-dependent RNA polymerase) and (B) P10 (major outer capsid protein), supporting SRBSDV as a new species in the genus *Fijivirus*. All available fijivirus P1 sequences were used, while for P10, 10 geographically diverse sequences were selected to represent each of SRBSDV and RSBDV. The maximum likelihood phylogenetic trees were reconstructed using MEGA version 6.06 (JTT distances and 100 bootstrap replicates; bootstrap percentages shown where >60%). Abbreviations: FDV, *Fiji disease virus*; MRCV, *Mal de Rio Cuarto virus*; MRDV, *Maize rough dwarf virus*; OSDV, *Oat sterile dwarf virus*; NLRV, *Nilaparvata lugens reovirus*;



RBSDV, *Rice black-streaked dwarf virus*.

A