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:	***2011.012aP***	(to be completed by ICTV officers)

Short title: create one new species in the genus *Furovirus* family *Virgaviridae*
(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:

Yukio Shirako, yshirako@anesc.u-tokyo.ac.jp

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)	Furovirus and allies

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

Majority of SG in favour

Date first submitted to ICTV:	18 August 2011
Date of this revision (if different to above):	

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	***2011.012aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Furovirus***
Subfamily:	
Family:	***Virgaviridae***
Order:	

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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Japanese soil-borne wheat mosaic virus	AB033689/90

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

The genus *Furovirus* contains viruses with rod-shaped particles that infect cereal crops and are transmitted by a root-infecting 'fungoid protist' *Polymyxa graminis*. The genomes have two ssRNA components: RNA1 (ca. 7100 nt) encodes a large replication polyprotein and a cell-to-cell movement protein; RNA2 (ca. 3600 nt) encodes the coat protein with a readthrough domain involved in vector transmission and a small protein that is a suppressor of gene silencing.

There are currently 5 species, *Soil-borne wheat mosaic virus* (SBWMV) as the type species, *Soil-borne cereal mosaic virus* (SBCMV), *Chinese wheat mosaic virus* (CWMV), *Oat golden stripe virus* (OGSV) and *Sorghum chlorotic spot virus* (SrCSV). These species are differentiated partly on the basis of host range and serological properties and also on the basis of sequence comparisons. RNA1 sequences from different species have <75% nt identity and RNA2 sequences have <80% identity.

Amongst the viruses described in the literature as SBWMV, those from the US and Japan differ from each other considerably at the nucleotide and the translated amino acid levels. Following determination of the sequences of both genome segments of a Japanese isolate (Shirako et al., 2000) it became clear that:

- In RNA1, SBWMV from US is more closely related to CWMV whereas the Japanese virus resembles OGSV (68% nt identity).
- In RNA2, the Japanese 'SBWMV' isolate is more closely related to SBCMV (80% nt identity) followed by the US SBWMV isolates.

Phylogenetic analyses are presented in Annex, Figure 1.

To be consistent with the species demarcation criteria already applied in the genus, it is now appropriate for the SBWMV Japanese isolate to be separated from the SBWMV US isolates to form an independent species. Since the virus name SBWMV has been used for decades in the Japanese and English language literature and recognized widely not only among plant virologists but also among researchers in plant breeding as well as by farmers, it is best to keep the name Soil-borne wheat mosaic virus associated with the Japanese isolate. It is therefore proposed to name the species first reported from Japan *Japanese soil-borne wheat mosaic virus*.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Shirako Y., Suzuki N., French R.C. (2000). Similarity and divergence among viruses in the genus Furovirus. Virology 270:201-207.

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.

Fig. 1. Phylogenetic trees of the codon-aligned nucleotide sequences of the combined ORFs on RNA1 and RNA2 of fully sequenced members of the genus *Furovirus*. Trees were produced in MEGA4 using the Maximum Composite Likelihood method and 10,000 bootstrap replicates