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:	***2012.012aP***	(to be completed by ICTV officers)

Short title: create one new species in the genus *Tenuivirus*
(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:

T. Sasaya (tsasaya@affrc.go.jp) on behalf of Tenuivirus study group

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)	Tenuivirus SG

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

Date first submitted to ICTV:
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	***2012.012aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Tenuivirus***
Subfamily:	
Family:	
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:**
Iranian wheat stripe virus	AY312434/35/36

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

This proposal suggests that Iranian wheat stripe virus (IWSV) should be considered a new species of the genus *Tenuivirus*.

Viruses in the genus *Tenuivirus* have plant host ranges limited to the family *Gramineae*, and are transmitted by a particular species of planthopper in a circulative-propagative manner. The multiple-sized filamentous viral particles appear to be branched, spiral or circular. The genome of tenuiviruses consists of four or more single-stranded RNA segments. All RNAs of segments 2, 3 and 4 in tenuiviruses have an ambisense coding strategy. There are currently 6 species, *Rice stripe virus* (RSV) as the type species, *Maize stripe virus* (MSpV), *Rice hoja blanca virus* (RHBV), *Echinochloa hoja blanca virus* (EHBV), *Urochloa hoja blanca virus* (UHBV) and *Rice grassy stunt virus* (RGSV) [1].

IWSV is characterized as a tentative member of the genus *Tenuivirus* and was not approved as species in the 9th report of ICTV.

According to the 9th report of ICTV, species are distinguished by the following criteria:

- Vector specificity, i.e. transmission by different vector species
- Host range, i.e. different abilities to infect key plant species
- Different sizes and/or numbers of RNA components
- <85% amino acid sequence identity between any corresponding gene products
- <60% nucleotide sequence identity between corresponding non-coding intergenic regions

IWSV is transmitted to wheat plants in a persistent manner by the delphacid planthopper, *Unkanodes tanasijevici* [2]. No other tenuiviruses besides IWSV are known to propagate in *U. tanasijevici*. The natural host of IWSV is only wheat but IWSV has a broad host range in *Gramineae*, including rice, barley and sorghum [2].

The IWSV particle has a thin filamentous shape similar to other tenuiviruses. IWSV is serologically related to RHBV but not to MSpV by the agar gel diffusion method with IWSV-antiserum [2].

The genome of IWSV tentatively consists of four RNA segments, which are designated RNAs 1 to 4 in order of decreasing molecular mass. The complete nucleotide sequences of RNAs 2 (3469 nt), 3 (2337 nt) and 4 (1831 nt) of IWSV were reported, and have been deposited in GenBank under AY312434, AY312435 and AY312436, respectively. The 5′- and 3′-terminal sequences of IWSV RNAs 2, 3 and 4 are very similar to those of other tenuivuruses and are complementary to each other for 16 and 15 terminal nucleotides, respectively. Furthermore, all these segments contain two open reading frames each in an ambisense arrangement [3].

The amino acid sequence homologies between the six proteins on RNAs 2, 3 and 4 of IWSV and each of the corresponding proteins of other tenuiviruses (excluding RGSV) range from 42.7 to 83.3% (Annex, Figure 1). In addition, the nucleotide sequence homologies between intergenic regions for RNAs 2, 3 and 4 of IWSV and their counterparts in other tenuiviruses (excluding RGSV) range from 34.4 to 58.8% [3]. These differences in both nucleotide and amino acid sequences fall outside the limits set by the species demarcation criteria in the 9th ICTV report.

Information on IWSV is sufficient to meet the criteria for species classification in the genus *Tenuivirus*. Thus, in essence, it is now appropriate for IWSV to be considered as a definitive species of the genus *Tenuivirus*. This is supported by phylogenetic analysis (Annex, Figure 2).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Shirako Y, Falk BW, Haenni A-L (2012). The *Tenuivirus*. In: Virus Taxonomy-Classification and Nomenclature of Viruses, 9th Report of the International Committee on Taxonomy of Viruses. King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (eds) Elsevier Academic Press, San Diego, CA, pp 771-776.
2. Heydarnejad J, Izadpanah K (1992). Isolation and partial characterization of a Tenuivirus from wheat in iran. J. Phytopathology 136:279-287.
3. Heydarnejad J, Barclay WS, Izadpanah K, Hunter FR, Gooding MJ (2006). Molecular characterization of Iranian wheat stripe virus shows its taxonomic position as a distinct species in the genus Tenuivirus. Arch. Virol. 151:217-227.

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.

Figure 1. Percentage amino acid identity between the proteins encoded by ORFs on IWSV RNAs 2, 3 and 4 and the corresponding ORFs on RNAs 2, 3 and 4 from other tenuiviruses. Similarities between IWSV, EHBV and RHBV are shaded. Viruses included in the analysis and accession numbers used [ ] are: IWSV [AY312434, AY312435, AY312436]; UHBV [U82447, U82446]; EHBV [L75930, L48441]; RHBV [L54073, L07940, AF004657]; MSpV [U53224, M57426, L13438]; RSV [D13176, X53563, D10979]; RGSV [AB010376, AB000403, AB000404].
* RGSV RNAs 5 and 6 correspond to RNAs 3 and 4 of other tenuiviruses.

RNA2

Nonstructural protein (p2)

	IWSV	RHBV	MSpV	RSV	RGSV
IWSV		68.5%	44.7%	42.7%	25.4%
RHBV	69.0%		46.7%	40.2%	23.7%
MSpV	43.9%	42.5%		61.1%	22.4%
RSV	44.3%	44.8%	53.3%		30.2%
RGSV	24.3%	21.5%	21.0%	20.7%	

Nonstructural protein (pC2)

RNA3

Nonstructural protein (p3)

	IWSV	UHBV	EHBV	RHBV	MSpV	RSV	RGSV*
IWSV		79.6%	79.1%	79.1%	51.9%	46.1%	25.2%
UHBV	70.7%		95.4%	94.0%	49.2%	50.0%	21.4%
EHBV	69.6%	89.5%		96.4%	49.2%	48.6%	20.2%
RHBV	71.1%	93.7%	89.9%		48.7%	48.8%	22.9%
MSpV	43.9%	48.5%	46.9%	48.3%		65.9%	20.2%
RSV	47.4%	48.1%	47.1%	48.3%	65.1%		18.0%
RGSV*	22.6%	23.0%	22.5%	23.0%	21.7%	20.0%	

Nucleocapsid protein (pC3)

RNA4

Nonstructural protein (p4)

	IWSV	UHBV	EHBV	RHBV	MSpV	RSV	RGSV*
IWSV		83.3%	81.6%	82.1%	61.1%	62.7%	27.8%
UHBV	80.2%		93.6%	93.6%	62.9%	60.9%	31.0%
EHBV	80.2%	93.2%		93.6%	59.4%	59.7%	29.8%
RHBV	77.0%	90.1%	88.6%		61.7%	60.9%	29.8%
MSpV	57.9%	56.8%	57.8%	56.8%		74.1%	27.8%
RSV	60.2%	57.8%	57.4%	57.0%	76.7%		25.7%
RGSV*	29.2%	27.6%	28.4%	27.2%	27.4%	28.0%	

Nonstructural protein (pC4)

Figure 2. Phylogenetic tree based on the aligned nucleotide sequences of the combined ORFs on RNAs 3 and 4 of members of the genus *Tenuivirus*. The phylogenetic tree was generated using the neighbour-joining method algorithm implemented in the MEGA5.05 program. Numbers on branches indicate percentage of bootstrap support out of 10,000 bootstrap replications (when > 50%). The scale indicates maximum composite likehood distance. The tree based on the combined four ORFs is more robust than other trees based on each ORF and has been used in the past to evaluate the relationship of members of the genus with a reference to the taxonomy report. This tree supports the position of IWSV as a distinct species of *Tenuivirus*. Viruses included in the analysis and accession numbers used [ ] are: IWSV [AY312435, AY312436]; RHBV-co [AF004658, L14952]; RHBV-cr [L07940, AF004657]; EHBV [L75930, L48441]; UHBV [U82447, U82446]; RSV-jp(t) [X53563, D10979]; RSV-jp(m) [D01094, D01039]; RSV-cn [Y11095, Y11096]; MSpV-us [M57426, L13438]; RGSV-cn [AF290947, AF287949]; RGSV-ph(l) [AB000403, AB000404]; RGSV-ph(sc) [AB023779, AB023780].