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:	***2012.013aP***	(to be completed by ICTV officers)

Short title: create new species in the genus *Tritimovirus*, family *Potyviridae*
(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** ☒	

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and in consultation with Hélène Sanfaçon (Helene.Sanfacon@agr.gc.ca)

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)	*Potyviridae*

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

Date first submitted to ICTV: June 2012
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	***2012.013aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Tritimovirus***
Subfamily:	
Family:	***Potyviridae***
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:**
Yellow oat-grass mosaic virus	GQ259764

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 new virus, tentatively named Yellow oat-grass mosaic virus (YOgMV), has been isolated from Yellow oat-grass plants (*Trisetum flavescens* L.) with mild mosaic and pronounced dwarfing symptoms at different locations in the Czech Republic (Širlova *et al.*, 2004). Electron microscopic investigations revealed the presence of filamentous particles and cytoplasmic inclusion bodies characteristic of members of the family *Potyviridae*.
The 3’end of the viral genome was cloned, sequenced and compared to sequences of species in the family *Potyviridae*. The virus appeared more closely related to viruses in the genus *Tritimovirus* than to other genera within the *Potyviridae*. Based on phylogenetic analyses of the coat protein cistron and flanking genomic regions, it was proposed that YOgMV is a distinct species of the genus *Tritimovirus* (Hassan et al. 2009).

Current species demarcation criteria within the family *Potyviridae* (as defined in the Ninth Report) are:
Genome sequence relatedness: different species have CP aa sequence identity less than about 80%; and nt sequence identity less than 76% either in the CP or over the whole genome. There are also differences in polyprotein cleavage sites.

The phylogenetic analysis of CP confirmed the grouping of YOgMV with other members of the genus *Tritimovirus* (Fig. 1). Amino acid identities to other members of the genus are in the range 41-61%.

Other useful criteria include antigenic reactions, host range and vector specificity.
Host range studies showed that the virus was readily mechanically transmitted to its original

host plus a narrow range of monocot species including all tested *Avena* species, *Bromus mollis* and *Lagurus ovatus*. It could not be transmitted to barley, wheat or maize. The mode of vector transmission is not yet determined. An antiserum to the virus has not been produced so far but serological tests of infected plant extracts using antisera specific to the closest viruses in the family *Potyviridae* (wheat streak mosaic virus and oat necrotic mottle virus) were negative (Hassan et al., 2009).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Širlova, L., Vacke, J., Jokeš, M. (2004): Characteristics of a potyvirus associated with a mosaic-like disease of yellow oat-grass. Plant Protect. Sci. 40 (2): 37-41.

Hassan, M., Širlova, L., Jokeš, M., Vacke, J. (2009). Identification and characterization of a novel Tritimovirus species isolated from wild *Trisetum flavescens* L., family *Poaceae*. Virus Genes 39:146-152.

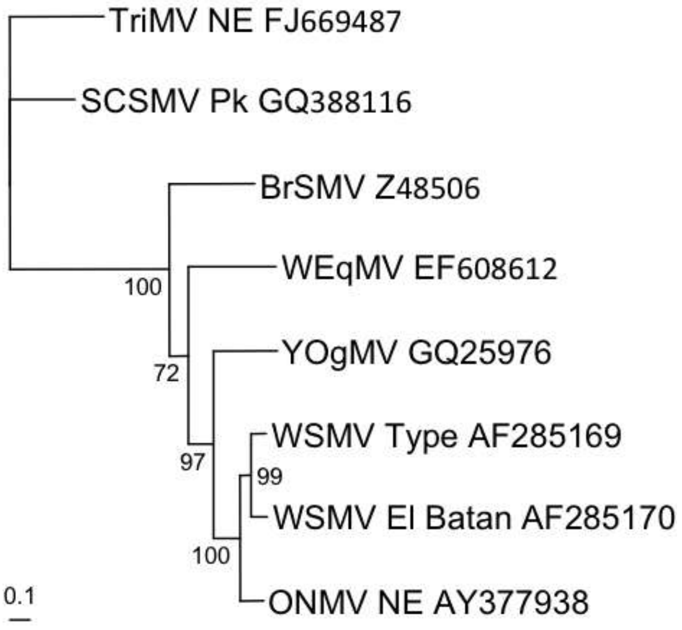

Figure 1: Neighbor-joining tree of the Coat protein amino acid sequences of members of the genus *Tritimovirus*.

Abbreviations: BrSMV = *Brome streak mosaic virus*, WEqMV = *Wheat eqlid mosaic virus*, WSMV = *Wheat streak mosaic virus* (type member of the genus, and strain El Batan3), ONMV (Oat necrotic mottle virus). The two members (*Triticum mosaic virus*, TriMV and *Sugarcane streak mosaic virus*, SCSMV) of the recently established sister genus *Poacevirus* are also presented.