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:	***2014.005aP***	(to be completed by ICTV officers)

Short title: Create the species *Tall oatgrass mosaic virus* 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** ☒	

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

Members of the ICTV Potyviridae SG:

Rabenstein, Frank (Chair)	frank.rabenstein@jki.bund.de
Adams, Michael J.	mike.adams.ictv@gmail.com
Kreuze, Jan F.	j.kreuze@cgiar.org
Lopez-Moya, Juan Jose	juanjose.lopez@cragenomica.es
Ohshima, Kazusato	ohshimak@cc.saga-u.ac.jp
Stenger, Drake C.	dstenger@fresno.ars.usda.gov
Wang, Aiming	aiming.wang@agr.gc.ca
Wylie, Stephen	s.wylie@murdoch.edu.au
Zerbini, F. Murilo	zerbini@ufv.br

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 2014
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	***2014.005aP***	(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.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Tall oatgrass mosaic virus	Benesov	KF260962

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

Hassan et al. (2013) reported a virus infecting tall oat grass (*Arrhenatherum elatius*) from various sites in the Czech Republic. Flexuous particles about 700-720 nm long and pin-wheel inclusion bodies seen in infected cells by electron microscopy suggested the presence of a virus in the family *Potyviridae* but no positive reactions were obtained in ELISA tests using antisera raised to known members of the family infecting monocotyledonous plants. The virus was transferred by mechanical inoculation to *A. elatius* and a small number of other grasses, in which mosaic symptoms were induced, but appeared to have a narrow host range. The virus was named tall oatgrass mosaic virus (TOgMV).

The complete genome sequence of an isolate from Benesov was obtained by sequencing RT-PCR products generated using degenerate potyvirid primers and 5’-RACE. The sequence consisted of 9359 nucleotides excluding the 3’-proximal polyadenylated tail (accession number KF260962) and had the genome organization typical of monopartite viruses of the family *Potyviridae*, with one large polyprotein ORF. A blastn search of NCBI databases revealed that wheat streak mosaic virus, the type member of the genus *Tritimovirus*, was the virus most closely related to TOgMV with 60.8 % nt and 61 % aa sequence identity. Nine putative cleavage sites were identified and these were similar, although not identical, to those of other tritimoviruses

According to criteria published in the ICTV 9th Report (Adams et al., 2011), different species in the family usually have CP aa sequence identity less than ca. 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. Polyproteins of viruses in the same genus have >40% aa identity (Adams et al., 2005). TOgMV-Benesov is thus clearly a representative of a new species in the genus *Tritimovirus*, and this conclusion is confirmed by phylogenetic analysis (Annex Fig. 1).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adams MJ, Antoniw JF, Fauquet CM (2005). Molecular criteria for genus and species discrimination within the family *Potyviridae*. Arch. Virol. 150:459–479

Adams MJ, Zerbini FM, French R, Rabenstein F, Stenger DC, Valkonen JPT. (2011). Family *Potyviridae*. 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. 1069-1089. Elsevier Academic Press, London.

Hassan M, Lenka Širlová L, Vacke J (2013). Tall oatgrass mosaic virus (TOgMV): a novel member of the genus *Tritimovirus* infecting *Arrhenatherum elatius*. Arch. Virol. DOI 10.1007/s00705-013-1905-2

Annex:

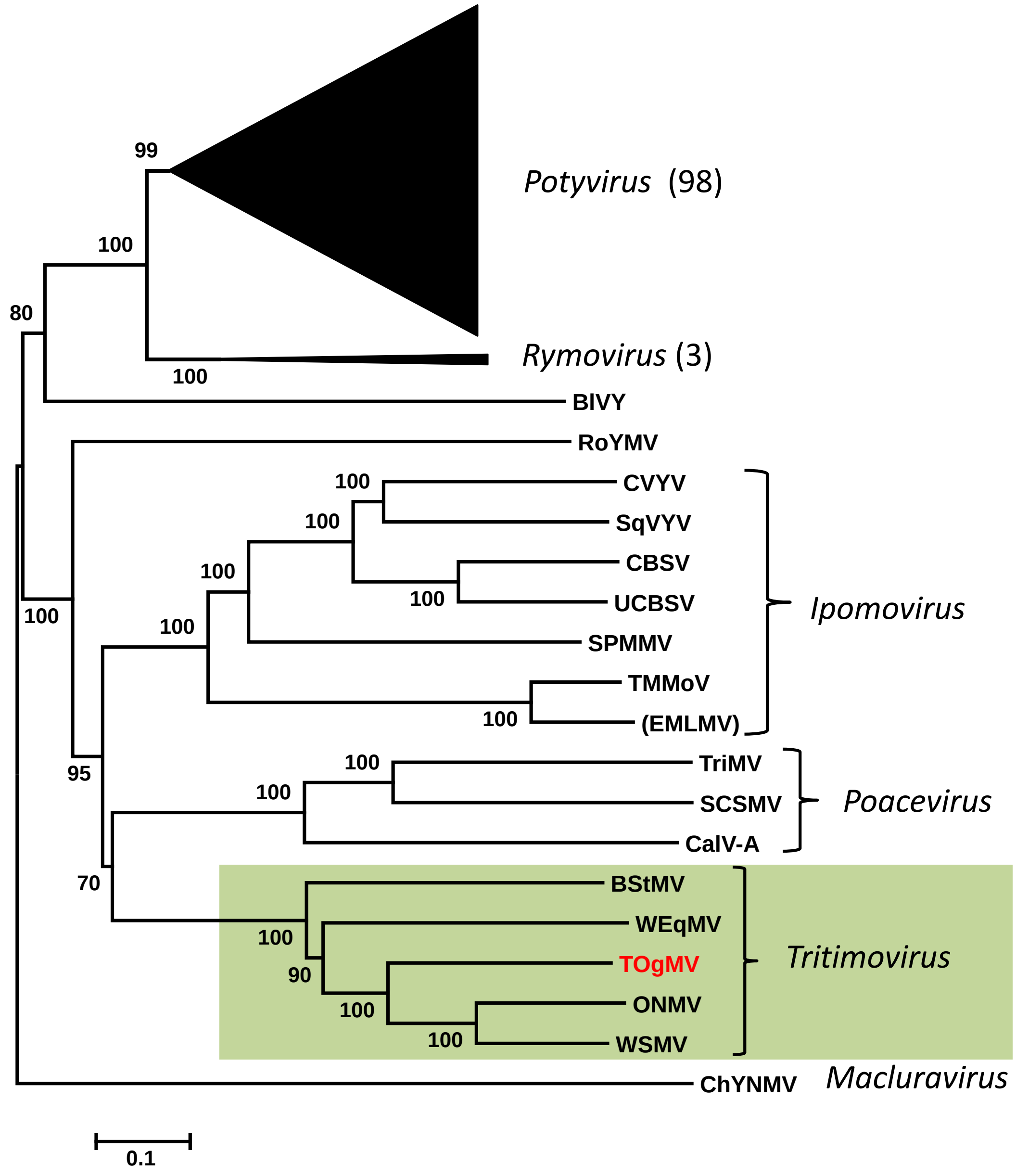

Figure 1: Distance (Maximum composite likelihood) phylogenetic tree using the codon-aligned complete polyprotein coding sequences of fully sequenced members of the family *Potyviridae*. The branches for the genera *Rymovirus* and *Potyvirus* are collapsed; the other branches represent a single isolate of an approved species (except for CalV-A, EMLMV and the new TOgMV). Tree produced in MEGA5.10 with 10,000 bootstrap replicates. Tall oatgrass mosaic virus (TOgMV) is highlighted in red. Other abbreviations are: BlVY, Blackberry virus Y; BStMV, Brome streak mosaic virus; CalV-A, Caladenia virus A; CBSV, Cassava brown streak virus; ChYNMV, Chinese yam necrotic mosaic virus; CVYV, Cucumber vein yellowing virus; EMLMV, Eggplant mild leaf mottle virus (strain of TMMoV); ONMV, Oat necrotic mottle virus; RoYMV, Rose yellow mosaic virus; SCSMV, Sugarcane streak mosaic virus; SPMMV, Sweet potato mild mottle virus; SqVYV, Squash vein yellowing virus; TMMoV, Tomato mild mottle virus; TriMV, Triticum mosaic virus; UCBSV, Ugandan cassava brown streak virus; WEqMV, Wheat eqlid mosaic virus; WSMV, Wheat streak mosaic virus.