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: *2009.006a-dP* (to be completed by ICTV officers)

Short title: create 9 species in the genus Potyvirus and 1 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** ☒	

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

Mike Adams (mike.adams@bbsrc.ac.uk) and Jari Valkonen (jari.Valkonen@helsinki.fi) on behalf of the Potyviridae SG

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

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

Date first submitted to ICTV: May 13, 2009
Date of this revision (if different to above): June 13, 2009

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.006aP***	(assigned by ICTV officers)

To create 9 new species with the name(s):

Arracacha mottle virus
Brugmansia suaveolens mottle virus
Chilli ringspot virus
Hardenbergia mosaic virus
Malva vein clearing virus
Telosma mosaic virus
Twisted-stalk chlorotic streak virus
Vallota mosaic virus
Wild tomato mosaic virus

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.006bP***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***Potyvirus***
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.

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Species demarcation criteria published in the 8th report are:

- Genome sequence relatedness.
  - CP aa sequence identity less than ca. 80%,
  - nt sequence identity of less than 85% over whole genome,
  - different polyprotein cleavage sites.
- Natural host range.
  - host range may be related to species but usually not helpful in identifying species; may delineate strains.
- Pathogenicity and cytopathology.
  - different inclusion body morphology,
  - lack of cross protection,
  - seed transmissibility, or lack thereof,
  - some aspects of host reaction may be useful (e.g., different responses in key host

    species, and particular genetic interactions).

- Antigenic properties.
    - serological differences.

In a more recent and comprehensive analysis, the most appropriate species threshold for the polyprotein or coat protein nucleotide sequence was found to be 76% identity (around 80-82% amino acids) [Adams et al., 2005]. Each of these viruses has been characterized and the sequence of the 3'-end of the genome (or more) determined. Comparisons of the coat protein genes (or the whole polyprotein sequence) justify their status as distinct species but within the genus *Potyvirus* (i.e. with 50-76% nt identity to existing species in their coat protein or entire polyprotein sequence). Details of the accession numbers, comparisons and associated references are listed below.

Arracacha mottle virus
Identified and characterized in Brazil. 3'-part sequence DQ925486 has <70% sequence identity to know potyviruses. Orilio et al., 2009.

Brugmansia suaveolens mottle virus
Identified and characterized in Brazil. 3'-part sequence AB370296 shared 71% nucleotide identity with *Pepper mottle virus*, the best-matched potyvirus sequence. Lucinda et al., 2008.

Chilli ringspot virus
Identified in Vietnam. 3'-part sequences DQ925438/9. The two sequences share about 92% identity, while the most closely related sequences on databases are four isolates of *Tobacco vein banding mosaic virus* (TVBMV), with identities ranging from 72.3–73.5% and 58.4– 60% identity over the CP gene and 3' UTR, respectively. Ha et al., 2008b.

Hardenbergia mosaic virus
Well characterized virus from native legume species in Western Australia. CP sequences DQ898188-214/EF375606-8 show that the closest existing species is *Passionfruit woodiness virus* (71.3-75.9% nt identity). Webster et al., 2007.

Malva vein clearing virus
Well characterized virus from Spain. Various 3'-part sequences FM212972/FJ539084/FJ561293/EU884405-10. CP sequences most closely related to *Pea seed-borne mosaic virus* (56.8% identity). Lunello et al., 2009.

Telosma mosaic virus
Identified in Vietnam. Complete sequence DQ851493; Ha et al., 2008a. Virus is a new member of the bean common mosaic subgroup. The complete polyprotein sequence has 67% nt identity to that of East Asian passiflora virus and >60% to other members of the subgroup.

Twisted-stalk chlorotic streak virus
Identified from native plant in Alaska. 3'-part sequence (AY954248) shows that it is not closely related to any existing species. (Nearest match is 63.6% aa identity in partial polyprotein to Tobacco etch virus.) Robertson (2005).

Vallota mosaic virus
First identified many years ago. 3'-part sequences EF441726/EF507688/FJ618540 now available. Inouye & Hakkaart, 1980; Monger & Mumford 2008. These have 68-69% sequence identity in the partial NIb and complete CP regions to their most closely related potyvirus, Ornithogalum mosaic virus.

Wild tomato mosaic virus
Identified in Vietnam. Complete sequence DQ851495; Ha et al., 2008a. The most closely related of the existing species is Chilli veinal mottle virus (the complete polyprotein sequences have 63% nt identity).

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.006cP***	(assigned by ICTV officers)

To create 1 new species with the name(s):

Wheat Eqlid mosaic virus

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family.

Code	***2009.006dP***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

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.

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Species demarcation criteria published in the 8th report are identical to those for the genus *Potyvirus* (see above) and include:

- Genome sequence relatedness.
    - CP aa sequence identity less than ca. 80%,
    - nt sequence identity of less than 85% over whole genome,
    - different polyprotein cleavage sites.

In a more recent and comprehensive analysis, the most appropriate species threshold for the polyprotein or coat protein nucleotide sequence was found to be 76% identity (around 80-82% amino acids) [Adams et al., 2005].

Wheat Eqlid mosaic virus causes a minor disease of wheat in Iran and is mite-transmitted. The complete nucleotide sequence of the WEqMV genome (EF608612; Rastegar et al., 2008) has now been determined and shown to have the genome organization typical of a member of the family *Potyviridae*. It is most closely related to other mite-transmitted viruses in the genus *Tritimovirus* but is sufficiently different from them in sequence (Annex, Table 1) and polyprotein cleavage sites (Annex, Table 2) to justify classification as a distinct species within the genus. This is also shown in the phylogenetic tree based on the complete polyprotein sequence (Annex, Figure 1).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

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

Ha C, Coombs S, Revill PA, Harding RM, Vu M, Dale JL (2008a). Design and application of two novel degenerate primer pairs for the detection and complete genomic characterization of potyviruses. Arch. Virol. 153:25-36

Ha C, Revill P, Harding RM, Vu M, Dale JL (2008b). Identification and sequence analysis of potyviruses infecting crops in Vietnam. Arch. Virol. 153:45-60.

Inouye N, Hakkaart FA. (1980). Preliminary description of a potyvirus from Vallota speciosa. Neth J. Plant Pathol. 68:265-275.

Lucinda N, Nagata Y, Inoue-Nagata AK, Salaroli RB, Kitajima EW. (2008). Brugmansia suaveolens mottle virus, a novel potyvirus causing leaf mottling of Brugmansia suaveolens in Brazil. Arch. Virol. 153:1971-1976.

Lunello P, Tourino A Nunez Y, Ponz F, Sanchez F. (2009). Genomic heterogeneity and host recovery of isolates of Malva vein clearing virus. Virus Res. 140:91-97.

Monger WA, Mumford RA (2008). Vallota mosaic virus infecting nerine in the UK. Plant Pathol. 57:768.

A. F. Orílio AF, Dusi AN, Madeira NR, Inoue-Nagata AK. (2009). Characterization of a member of a new Potyvirus species infecting arracacha in Brazil. Arch. Virol. 154:181-185.

Rastegar M, Izadpanah K, Masumi M, Siampour M, Zare A, Afsharifar A. (2008). Analyses of the complete genome of wheat Eqlid mosaic virus, a novel species in the genus Tritimovirus. Virus Genes 37:212-217.

Robertson, N.L. (2005), A newly described plant disease complex involving two distinct viruses in a native Alaskan lily, Streptopus amplexifolius. Can. J. Bot. 83:1257-1267

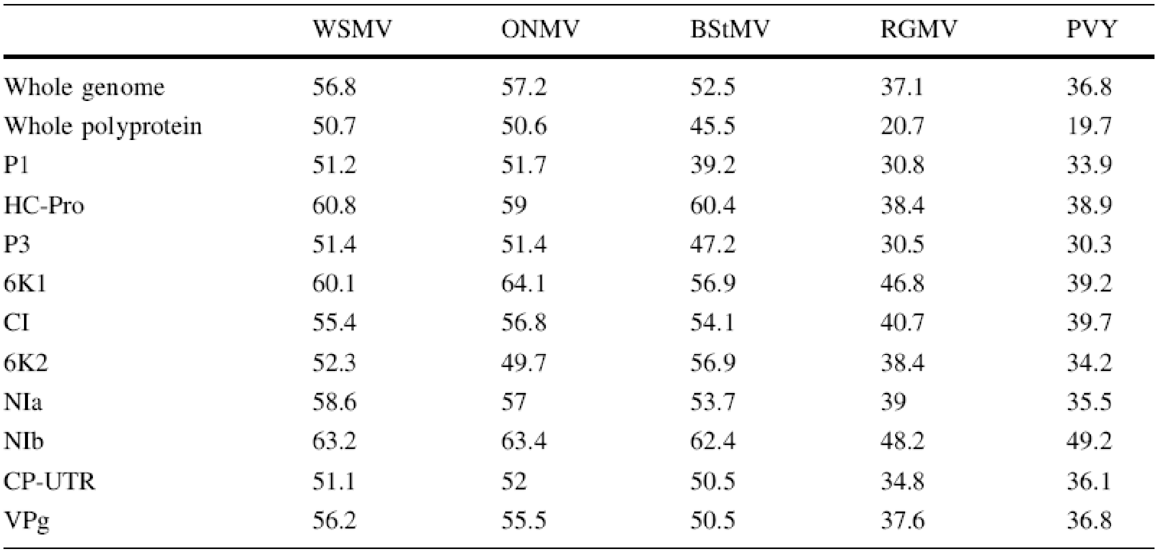
Webster CG, Coutts BA, Jones RAC, Jones MGK, Wylie SJ. (2007). Virus impact at the interface of an ancient ecosystem an a recent agroecosystem: studies on three legume-infecting potyviruses in the southwest Australian floristic region. Plant Pathol. 56:729-742.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.

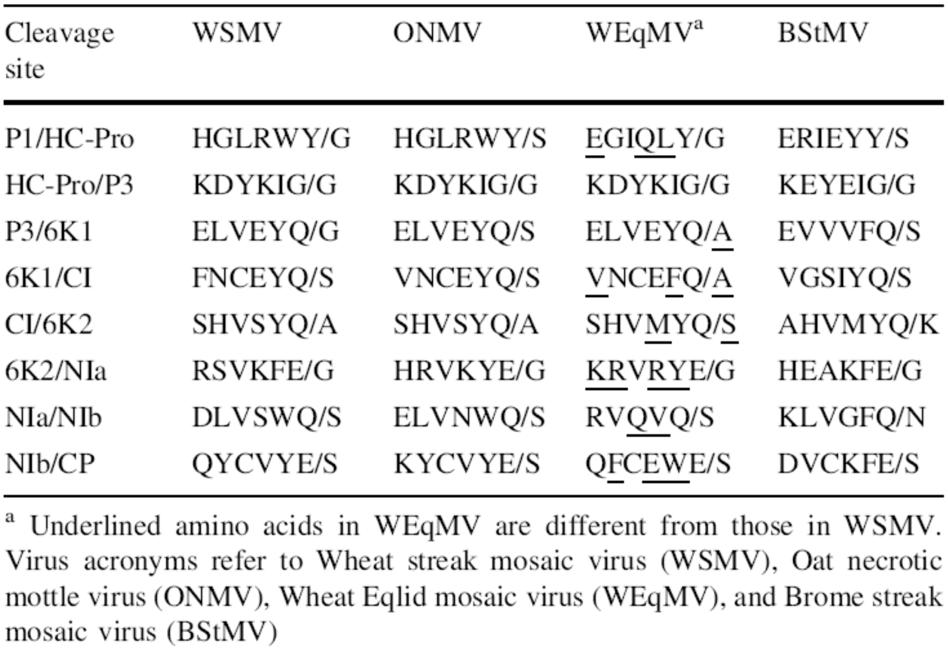
The use of Figures and Tables is strongly recommended.

Table 1. Percent sequence identity between WEqMV and other members of the genus *Tritimovirus*: Wheat streak mosaic virus (WSMV), Oat necrotic mottle virus (ONMV) and Brome streak mosaic virus (BStMV). Comparisons are also shown for Ryegrass mosaic virus (RGMV, genus *Rymovirus* and Potato virus Y (PVY, genus *Potyvirus*) (from Rastegar et al., 2008).



	WSMV	ONMV	BStMV	RGMV	PVY
Whole genome	56.8	57.2	52.5	37.1	36.8
Whole polyprotein	50.7	50.6	45.5	20.7	19.7
P1	51.2	51.7	39.2	30.8	33.9
HC-Pro	60.8	59	60.4	38.4	38.9
P3	51.4	51.4	47.2	30.5	30.3
6K1	60.1	64.1	56.9	46.8	39.2
CI	55.4	56.8	54.1	40.7	39.7
6K2	52.3	49.7	56.9	38.4	34.2
NIa	58.6	57	53.7	39	35.5
NIb	63.2	63.4	62.4	48.2	49.2
CP-UTR	51.1	52	50.5	34.8	36.1
VPg	56.2	55.5	50.5	37.6	36.8

Table 2. Predicted proteinase cleavage sites of polyprotein in WEqMV and other tritimoviruses (from; Rastegar et al., 2008).



Cleavage site	WSMV	ONMV	WEqMV[a]	BStMV
P1/HC-Pro	HGLRWY/G	HGLRWY/S	EGIQLY/G	ERIEYY/S
HC-Pro/P3	KDYKIG/G	KDYKIG/G	KDYKIG/G	KEYEIG/G
P3/6K1	ELVEYQ/G	ELVEYQ/S	ELVEYQ/A	EVVVFQ/S
6K1/CI	FNCEYQ/S	VNCEYQ/S	VNCEFQ/A	VGSIYQ/S
CI/6K2	SHVSYQ/A	SHVSYQ/A	SHVMYQ/S	AHVMYQ/K
6K2/NIa	RSVKFE/G	HRVKYE/G	KRVRYE/G	HEAKFE/G
NIa/NIb	DLVSWQ/S	ELVNWQ/S	RVQVQ/S	KLVGFQ/N
NIb/CP	QYCVYE/S	KYCVYE/S	QFCEWE/S	DVCKFE/S

[a] Underlined amino acids in WEqMV are different from those in WSMV. Virus acronyms refer to Wheat streak mosaic virus (WSMV), Oat necrotic mottle virus (ONMV), Wheat Eqlid mosaic virus (WEqMV), and Brome streak mosaic virus (BStMV)

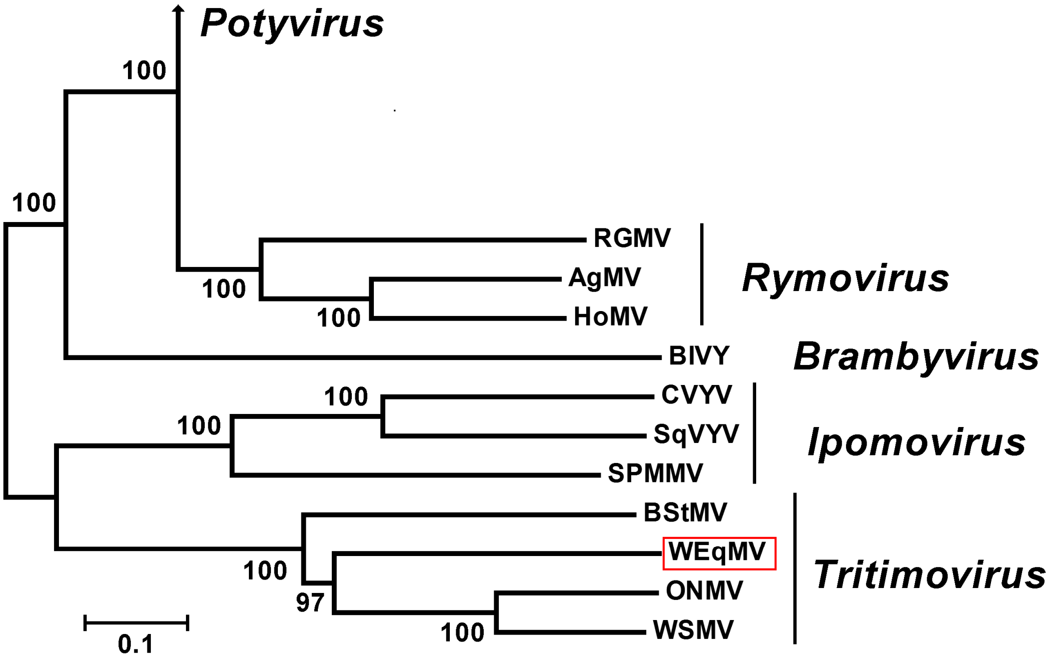


Figure 1. Phylogenetic tree of the codon-aligned polyprotein nucleotide sequences of monopartite members of the family *Potyviridae* to show the position of the proposed new species *Wheat Eqlid mosaic virus* within the genus *Tritimovirus*. The tree was generated in MEGA 4 using maximum composite likelihood distances and 10,000 bootstrap replicates (the large section for the genus *Potyvirus* has been omitted). Bootstrap values are shown at the nodes when >60%. Abbreviations and accession numbers are: AgMV, *Agropyron mosaic virus* (AY623626); BlVY, *Blackberry virus Y* (AY994084); BStMV, *Brome streak mosaic virus* (Z48506); CVYV, *Cucumber vein yellowing virus* (AY578085); HoMV, *Hordeum mosaic virus* (AY623627); ONMV, *Oat necrotic mottle virus* (AY377938); RGMV, *Ryegrass mosaic virus* (Y09854); SPMMV, *Sweet potato mild mottle virus* (Z73124); SqVYV, *Squash vein yellowing virus* (EU259611); WEqMV, *Wheat Eqlid mosaic virus* (EF608612); WSMV, *Wheat streak mosaic virus* (AF057533).