



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

<b>Code(s) assigned:</b>	<b>2008.002P</b>	<small>(to be completed by ICTV officers)</small>
<b>Short title:</b> 7 new species in the genus Potyvirus <small>(e.g. 6 new species in the genus <i>Zetavirus</i>; re-classification of the family <i>Zetaviridae</i> etc.)</small>		
<b>Modules attached</b> <small>(please check all that apply):</small>	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input type="checkbox"/>
	5 <input checked="" type="checkbox"/>	6 <input type="checkbox"/>
	7 <input type="checkbox"/>	

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

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

MODULE 5: **NEW SPECIES**

<b>Code</b>	<b>2008.002P</b>	<small>(assigned by ICTV officers)</small>
<b>To create 6 new species assigned as follows:</b>		
Genus:	<i>Potyvirus</i>	<small>Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)</small>
Subfamily:		
Family:	<i>Potyviridae</i>	
Order:		

**Name(s) of proposed new species:**

*Algerian watermelon mosaic virus*  
*Alternanthera mild mosaic virus*  
*Angelica virus Y*  
*Butterfly flower mosaic virus*  
*Canna yellow streak virus*  
*Hardenbergia mosaic virus*  
*Spiranthes mosaic virus 3*

**Argument to justify the creation of the new species:**

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Species demarcation criteria published in the 8<sup>th</sup> report are:

- Genome sequence relatedness.

**Argument to justify the creation of the new species:**

- 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 provided in Table 1.

Table 1. Details of sequence comparisons and references for proposed new species

<b>virus</b>	<b>comment</b>
Algerian watermelon mosaic virus	Complete sequence EU410442; Yakoubi et al., 2008. PRV group (71% nt identity to Moroccan watermelon mosaic virus in the coat protein)
Alternanthera mild mosaic virus	3'-part sequence EF442668; first named Alternanthera latent virus. Almedia et al., 2007. PVY subgroup. (74.8% aa identity to Pepper severe mosaic virus and 76.7% aa identity to Pfaffia mosaic virus over C-terminal 486aa).
Angelica virus Y	3'-part sequence EF488740/1; Robertson, 2007. Umbeliferous virus subgroup (70.9% aa identity to Apium virus Y over C-terminal 490aa).
Butterfly flower mosaic virus	3'-part sequence AM774001; Chen et al., 2008. TEV subgroup (73.7% aa identity to Sunflower mosaic virus over C-terminal 470aa).
Canna yellow streak virus	3'-part sequence EF466138/9; Monger et al., 2007. Related to Johnsongrass mosaic virus (71.9% aa identity over C-terminal 490aa)
Hardenbergia mosaic virus	Coat protein sequences DQ898188-214/EF375606-8; Webster et al., 2007. BCMV subgroup. Variable species with CP generally about 76-77% nt or aa identity to Passionfruit woodiness virus isolates.
Spiranthes mosaic virus 3	3'-part sequence AY685218; Guaragna et al., 2004; Related to Colombian datura virus (62.8% aa identity over C-terminal 477aa)

**References:**

- Adams M.J., Antoniw J.F., Fauquet C.M. (2005). Molecular criteria for genus and species discrimination within the family *Potyviridae*. *Arch. Virol.* 150:459-479.
- Almeida A.M., Fukushigue C.Y., Sartori F., Binneck E., Marin S.R., Inoue-Nagata A.K., Chagas C.M., Souto E.R., Mituti T. (2007). Natural infection of *Alternanthera tenella* (*Amaranthaceae*) by a new potyvirus. *Arch. Virol.* 152:2095-2099
- Chen J., Shi Y.H., Li M.Y., Adams M.J., Chen J.P. (2008). A new potyvirus from butterfly flower (*Iris japonica* Thunb.) in Zhejiang, China. *Arch. Virol.* 153:567-569
- Guaragna M.A., Ndum O., Jordan R. (2004). Detection and characterization of two previously undescribed potyviruses in the terrestrial orchid *Spiranthes cernua*. *Acta Hortic.* 0:0-0.
- Monger W.A., Harju V., Skelton A., Seal S.E., Mumford R.A. (2007). Canna yellow streak virus: a new potyvirus associated with severe streaking symptoms in canna. *Arch. Virol.* 152:1527-1530
- Robertson N.L. (2007). Identification and characterization of a new virus in the genus *Potyvirus* from wild populations of *Angelica lucida* L. and *A. genuflexa* Nutt., family *Apiaceae*. *Arch. Virol.* 152:1603-1611
- Yakoubi S., Lecoq, H., Desbiez, C. (2008). Algerian watermelon mosaic virus (AWMV): a new potyvirus in the PRSV cluster. *Virus Genes* DOI 10.1007/s11262-008-0237-x
- Webster C.G., Coutts B.A., Jones R.A.C., Jones M.G.K., Wylie S.J. (2007). Virus impact at the interface of an ancient ecosystem and a recent agroecosystem: studies on three legume-infecting potyviruses in the southwest Australian floristic region. *Plant Pathol.* 56:729-742