

# Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

Code 2007.073P.04 To designate the following as species in the genus:

<i>Potyvirus</i>
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belonging to the family<sup>°</sup> : 

<i>Potyviridae</i>
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<p><i>Amazon lily mosaic virus</i>  <i>Basella rugose mosaic virus</i>  <i>Chinese artichoke mosaic virus</i>  <i>Daphne mosaic virus</i>  <i>East Asian Passiflora virus</i>  <i>Euphorbia ringspot virus</i>  <i>Fritillary virus Y</i>  <i>Meadow saffron breaking virus</i>  <i>Passiflora chlorosis virus</i>  <i>Pennisetum mosaic virus</i>  <i>Pfaffia mosaic virus</i>  <i>Ranunculus leaf distortion virus</i>  <i>Ranunculus mild mosaic virus</i>  <i>Ranunculus mosaic virus</i>  <i>Spiranthes mosaic virus 2</i>  <i>Sweet potato virus 2</i>  <i>Thunberg fritillary mosaic virus</i>  <i>Tradescantia mild mosaic virus</i>  <i>Tuberose mild mottle virus</i>  <i>Zantedeschia mild mosaic virus</i></p>
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<sup>†</sup> Assigned by ICTV officers

<sup>°</sup> leave blank if inappropriate or in the case of an unassigned genus

## Author(s) with email address(es) of the Taxonomic Proposal

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## Old Taxonomic Order

Order	
Family	<i>Potyviridae</i>
Genus	<i>Potyvirus</i>
Type Species	<i>Potato virus Y</i>
Species in the Genus	(109 species)

## New Taxonomic Order

Order	
Family	<i>Potyviridae</i>
Genus	<i>Potyvirus</i>
Type Species	<i>Potato virus Y</i>
Species in the Genus	128 species: 20 new species (see list) and 1 current species to be removed

## ICTV-EC comments and response of the SG



### Species demarcation criteria in the genus

Criteria published in the 8<sup>th</sup> 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]. Members of different genera usually had <50% nt identity.

### Argumentation to justify the designation of new species in the genus

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 Annex Table 1.

## List of created Species in the genus

<b><i>Amazon lily mosaic virus</i></b> Amazon lily mosaic virus	(ALiMV)	AB158523
<b><i>Basella rugose mosaic virus</i></b> Basella rugose mosaic virus	(BaRMV)	DQ394891
<b><i>Chinese artichoke mosaic virus</i></b> Chinese artichoke mosaic virus	(ChAMV)	AB099711
<b><i>Daphne mosaic virus</i></b> Daphne mosaic virus Daphne virus Y	(DapMV)	DQ299908
<b><i>East Asian Passiflora virus</i></b> East Asian Passiflora virus	(EAPV)	AB246773 etc
<b><i>Euphorbia ringspot virus</i></b> Euphorbia ringspot virus	(EuRSV)	AY697300
<b><i>Fritillary virus Y</i></b> Fritillary virus Y	(FVY)	AM039800
<b><i>Meadow saffron breaking virus</i></b> Meadow saffron breaking virus	(MSBV)	AY388995
<b><i>Passiflora chlorosis virus</i></b> Passiflora chlorosis virus	(PaChV)	DQ860147
<b><i>Pennisetum mosaic virus</i></b> Pennisetum mosaic virus	(PenMV)	AY642590
<b><i>Pfaffia mosaic virus</i></b> Pfaffia mosaic virus	(PfMV)	AY485276
<b><i>Ranunculus leaf distortion virus</i></b> Ranunculus leaf distortion virus	(RanLDV)	DQ152190
<b><i>Ranunculus mild mosaic virus</i></b> Ranunculus mild mosaic virus	(RanMMV)	DQ152191
<b><i>Ranunculus mosaic virus</i></b> Ranunculus mosaic virus	(RanMV)	DQ152192
<b><i>Spiranthes mosaic virus 2</i></b> Spiranthes mosaic virus 2	(SpMV2)	AY685219
<b><i>Sweet potato virus 2</i></b> Sweet potato virus 2 Sweet potato virus Y Ipomoea vein mosaic virus	(SPV2) (SPVY)	AY232437, AY459603 etc

<b><i>Thunberg fritillary mosaic virus</i></b>	Thunberg fritillary mosaic virus	(TFMV)	AJ851866
<b><i>Tradescantia mild mosaic virus</i></b>	Tradescantia mild mosaic virus	(TraMMV)	AY861351
<b><i>Tuberose mild mottle virus</i></b>	Tuberose mild mottle virus	(TuMMV)	AJ581528; AY833736
<b><i>Zantedeschia mild mosaic virus</i></b>	Zantedeschia mild mosaic virus	(ZaMMV)	AY626825 etc

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## Annex:

**Table 1:** proposed new species: accession numbers, relationships and references

New species	Sequence <sup>2</sup>	Nearest other species by BLAST	% identity			Reference/comment
			All nt <sup>3</sup>	CP nt	CP aa	
Amazon lily mosaic virus <sup>1</sup>	AB158523	Pepper mottle virus AF227728	65.9	70.1	72.8	Fuji et al., 2004
Basella rugose mosaic virus	DQ394891	Beet mosaic virus AY2063944	64	66	67	Huang & Chang 2006
Chinese artichoke mosaic virus	AB099711	Ornithogalum mosaic virus AJ493580	57.9	62.3	61.3	Fuji et al., 2003
Daphne mosaic virus	DQ299908*	Peanut mottle virus L32957*	56	55	52	Fránová et al., 2006. Formerly Daphne virus Y <sup>1</sup>
East Asian Passiflora virus	D85849	Wisteria vein mosaic virus AF484549	72.1	73.0	73.1	Only 65-70% identity to <i>Passiflora woodiness virus</i> to which these isolates were originally assigned; Iwai et al., 2006
	AB185021	Bean common mosaic virus AY575773	69.8	70.8	75.3	
	AF208662	Wisteria vein mosaic virus AF484549	72.0	72.7	72.0	
	AB246773*	Wisteria vein mosaic virus AY656816*	70			
Euphorbia ringspot virus <sup>1</sup>	AY697300	Narcissus late seasons yellows virus AJ493579	52.0	66.0	63.5	Guaragna et al., 2004a
Fritillary virus Y	AM039800*	Soybean mosaic virus AB100443*	68.9	74.8	79.2	Chen et al., 2006
		Bean common mosaic necrosis virus AY282577*	66.7	72.5	81.2	
Meadow saffron breaking virus	AY388995	Zucchini yellow mosaic virus AY188994	60.4	63.5	64.5	Poutaraud et al, 2004.
Passiflora chlorosis virus	DQ860147	Bean common mosaic necrosis virus AY864314	72	73	78	Baker & Jones 2007
Pennisetum mosaic virus	AY642590*	Sorghum mosaic virus AJ310196*	73.3	73.8	79.0	Fan et al., 2003
Pfaffia mosaic virus	AY485276	Potato virus Y AY841267	74.2	74.2	76.1	Mota et al., 2004
Ranunculus leaf distortion virus	DQ152190	Bean yellow mosaic virus AB032023	60.3	63.2	62.4	Turina et al., 2006
Ranunculus mild mosaic virus	DQ152191	Japanese yam mosaic virus AB029504	64.3	66.3	67.9	Turina et al., 2006
Ranunculus mosaic virus	DQ152192	Peanut mottle virus X73422	53.0	60.0	49.8	Turina et al., 2006
Spiranthes mosaic virus 2	AY685219	Verbena canadensis potyvirus AY825284	56.8	58.4	53.8	Guaragna et al., 2004b
Sweet potato virus 2	AY232437	Sweet potato virus G AJ515380	72.3	73.1	80.1	Synonyms: Sweet potato virus Y and Ipomoea vein mosaic virus. Ateka et al., 2004, Tairo et al., 2006 and Ateka et al., 2007
	AY459603		73.4	72.7	80.0	
Thunberg fritillary mosaic virus	AJ851866*	Lycoris mild mottle virus AF399672	69.1	72.8	72.5	Wei et al., 2005
Tradescantia mild mosaic virus	AY861351	Onion yellow dwarf virus AJ409311	55.7	57.3	53.0	Ciuffo et al., 2006
Tuberose mild mottle virus	AJ581528	Tuberose mild mosaic virus AF062926	68.3	71.1	76.6	Lin et al., 2004
	AY833736		67.7	69.8	75.5	
Zantedeschia mild mosaic virus	AY518550	Ornithogalum virus 2 AB079654	53.2	61.3	58.4	Chen C. et al., 2003; Huang & Chang, 2005; Huang et al., 2007
	AY626825*	Zucchini yellow mosaic virus AY278998	60.6	64.5	63.7	
		Wisteria vein mosaic virus AY656816*	61			

<sup>1</sup> listed as tentative species in the 8th report (others not listed)

<sup>2</sup> 3'-end sequence including partial NIB, CP and 3'-UTR except where shown \* (for complete sequence)

<sup>3</sup> comparisons over the entire overlapping regions between the two sequences listed