

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

Code † **2007.074P.04** To remove the following as species in the genus:

Potyvirus

belonging to the family° : *Potyviridae*

Zantedeschia mosaic virus

† Assigned by ICTV officers

° leave blank if inappropriate or in the case of an unassigned genus

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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 separate proposal) and 1 current species to be removed

ICTV-EC comments and response of the SG

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Species demarcation criteria in the genus

Criteria published in the 8ⁿ 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].

Argumentation to justify the removal of a species in the genus

Both *Zantedeschia mosaic virus* and *Konjac mosaic virus* were listed as species in the 8th report. There are 11 partial (3'-terminal) sequences of ZaMV but only recently have there been molecular data for KoMV. The complete sequence of KoMV (AB219545) has recently been published (Nishiguchi et al., 2006) and shows that these sequences have >90% amino acid identity in the overlapping region. Additional unpublished data for the complete sequence of a Chinese isolate of ZaMV shows that the complete polyproteins have 92.0% aa identity and that the two complete sequences have 85.6% nt identity. These are well above the species demarcation threshold values and indicate that ZaMV and KoMV are isolates of the same virus species. The SG recommends that the older name, *Konjac mosaic virus*, should be the official species name.

List of Species removed from the genus

Zantedeschia mosaic virus

Revised species

Konjac mosaic virus

Konjac mosaic virus	(KoMV)	AB219545
Zantedeschia mosaic virus	(ZaMV)	AF332872 etc
Japanese hornwort mosaic virus	(JHMV)	AB081518/52/53/54 AB251346

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.

Nishiguchi M., Yamasaki S., Lu X.-Z., Shimoyama A., Hanada K., Sonoda S. Shimono M., Sakai J., Mikoshiba Y., Fujisawa I. (2006). Konjak mosaic virus: the complete nucleotide sequence of the genomic RNA and its comparison with other potyviruses. *Arch. Virol.* 151:1643-1650

Annex: