

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

Code † **2007.071P.04** To designate the following as species in the genus:

Macluravirus

belonging to the family° : *Potyviridae*

Alpinia mosaic virus
Chinese yam necrotic mosaic virus
Ranunculus latent 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>Macluravirus</i>
Type Species	<i>Maclura mosaic virus</i>
Species in the Genus	(3)

New Taxonomic Order

Order	
Family	<i>Potyviridae</i>
Genus	<i>Macluravirus</i>
Type Species	<i>Maclura mosaic virus</i>
Species in the Genus	<i>Alpinia mosaic virus</i> <i>Chinese yam necrotic mosaic virus</i> <i>Ranunculus latent virus</i> (plus 3 as before)

ICTV-EC comments and response of the SG

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., 2005a].

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 determined. Phylogenetic analysis (see Annex Fig. 1) clearly places them within the genus *Macluravirus* and they have a Q/M cleavage site between the NIB polymerase (RdRp) and coat protein cistrons of the polyprotein. This site is characteristic of the genus (Adams et al., 2005b). Comparisons of the coat protein genes justify their status as distinct species as described below.

Alpinia mosaic virus

This virus is listed as a tentative member of the genus *Potyvirus* in the 8th report but sequence data from the 3'-end of the genome (AF499025; Liou et al., 2003) now clearly places this within the genus *Macluravirus*. Its coat protein has 61% nt (60% aa) identity with Cardamom mosaic virus (AF189125).

Chinese yam necrotic mosaic virus

This virus is listed as a tentative member of the genus *Macluravirus* in the 8th report. Sequence data from the 3'-end of the genome of 18 isolates support its status as a member of this genus (see Annex) and show that its coat protein has c.62% nt (c.59% aa) identity with Cardamom mosaic virus (AF189125; Kondo, 2001; Kondo *et al.*, 2003).

Ranunculus latent virus

This is one of four different viruses isolated from *Ranunculus asiaticus* (Turina et al., 2006). Sequence data from the 3'-end of the genome (DQ152193) clearly places this within the genus *Macluravirus*. Its coat protein has 65% nt (56% aa) identity with Maclura mosaic virus (U58771).

List of created Species in the genus

<i>Alpinia mosaic virus</i> Alpinia mosaic virus	(AlpMV)	AF499025
<i>Chinese yam necrotic mosaic virus</i> Chinese yam necrotic mosaic virus	(ChYNMV)	AB044386 etc.
<i>Ranunculus latent virus</i> Ranunculus latent virus	(RanLV)	DQ152193

References

- Adams M.J., Antoniw J.F., Fauquet C.M. (2005a). Molecular criteria for genus and species discrimination within the family *Potyviridae*. *Arch. Virol.* 150:459-479.
- Adams M.J., Antoniw J.F., Beaudoin F. (2005b). Overview and analysis of the polyprotein cleavage sites in the family *Potyviridae*. *Mol. Plant Pathol.* 6:471-487.
- Kondo T. (2001). The 3'-terminal sequence of Chinese yam necrotic mosaic virus genomic RNA: a close relationship with macluravirus. *Arch. Virol.* 146:1527-1535.
- Kondo T., Kang D.K., Fuji S., Chang M.U. (2003). Sequence diversity in the coat protein and 3'-untranslated region of Chinese yam necrotic mosaic virus RNA. *J. Gen. Plant Pathol.* 69:397-399.
- Liou R.F., Yan H.Z., Hong J.L. (2003). Molecular evidence that aphid-transmitted Alpinia mosaic virus is a tentative member of the genus Macluravirus. *Arch. Virol.* 148:1211-1218.
- Turina M., Ciuffo M., Lenzi R., Rostagno L., Mela L., Derin E., Palmano S. (2006). Characterization of Four Viral Species Belonging to the Family *Potyviridae* Isolated from *Ranunculus asiaticus*. *Phytopathology* 96:560-566.

Annex:

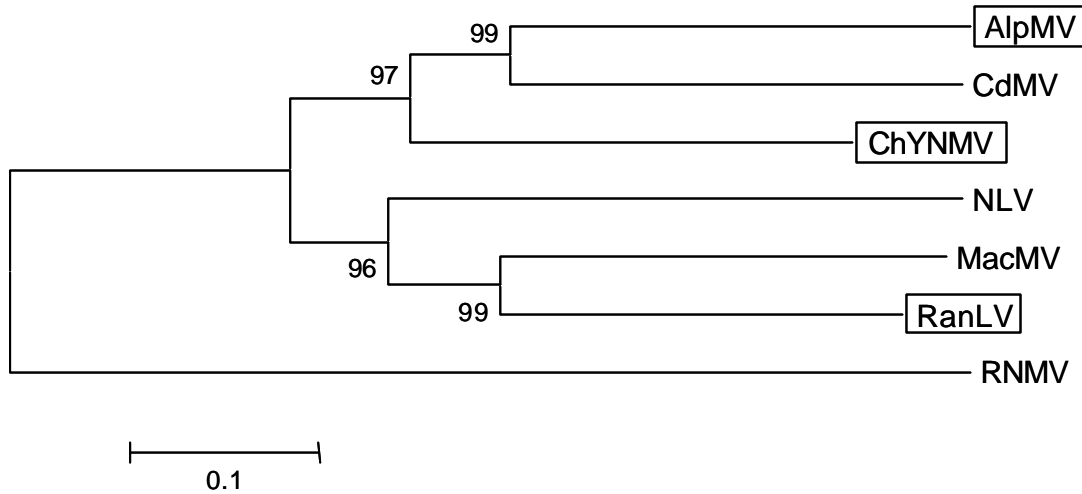


Figure 1. Phylogenetic tree for the 3'-end coding nucleotide sequence of the members of the genus *Macluravirus* to show the position of three proposed new species, Alpinia mosaic virus, Chinese yam necrotic mosaic virus and Ranunculus latent virus.

The sequences and abbreviations are as follows: AlpMV, Alpinia mosaic virus (af499025); CdMV, Cardamom mosaic virus (af189125); ChYNMV, Chinese yam necrotic mosaic virus (ab044386); MacMV, Maclura mosaic virus (u58771); NLV, Narcissus latent virus (u58770); RanLV, Ranunculus latent virus (dq152193); RNMV, Rice necrosis mosaic virus (u95205) genus *Bymovirus* as outgroup. The values at the forks indicate the percentage of trees in which this grouping occurred after bootstrapping the data with 10,000 replicates. The scale bar shows the number of substitutions per base.