

Template for Taxonomic Proposal to the ICTV Executive Committee

Creating Species in an existing genus

Code[†] To designate the following viruses as species in the genus:

belonging to the family[°] :

Cherry Mottle leaf virus (CMLV)
Peach mosaic virus (PcMV)

[†] Assigned by ICTV officers

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

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New Taxonomic Order

Order

Family

Genus

Trichovirus

Type Species

List of Species in the genus

Cherry Mottle leaf virus (CMLV)

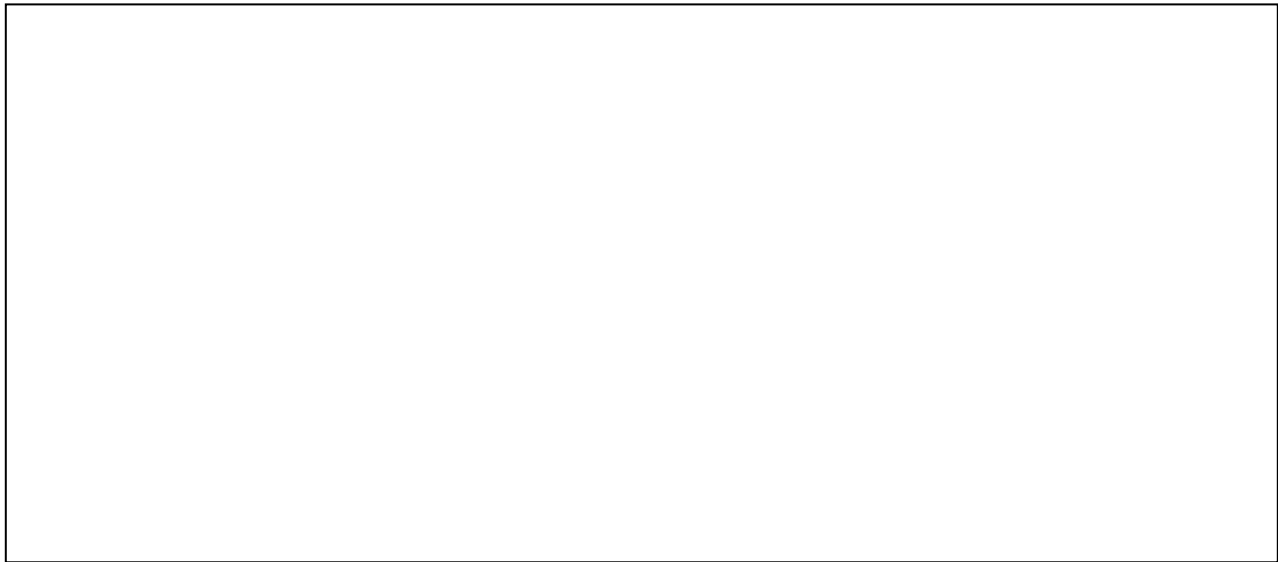
Peach mosaic virus (PcMV)

List of Tentative Species in the Genus

List of Unassigned Species in the Family

Argumentation to justify the designation of new species in the genus

Species demarcation criteria in the genus



Argumentation to justify the designation of new species in the genus

Cherry mottle leaf virus (CMLV) and *Peach mosaic virus* (PcMV) are important pathogens effecting *Prunus* species. These two viruses are transmitted by eriophyid mites and have flexuous elongated particles. Although they induce distinctly different diseases in their natural woody hosts, these two viruses appear to be closely related in that they show similar dsRNA patterns, have coat protein subunits of similar molecular mass and show serological cross-reaction using both polyclonal and monoclonal antibodies.

CMLV was initially considered as a member of the subgroup II of the *Closterovirus* group based on its particle structure. This initial link has been rejected and the two viruses are currently unclassified in virus genus, despite the fact that their proximity to *Apple chlorotic leaf spot virus* (ACLSV), the type member of the *Trichovirus* genus has been pointed out.

The genome of CMLV has been completely sequenced (James *et al.*, 2000, Genbank AF170028) and shown to consist of a single ssRNA of 8003 nucleotides. Its genomic organisation is similar to that of other Trichoviruses, with the exception of the existence of an additional ORF (ORF4) at the 3' end of the genome. Comparisons on the shared ORFs (polymerase, movement protein, capsid protein) clearly indicate that CMLV is phylogenetically closely related to ACLSV with amino-acids sequence identity values of ~63% (polymerase), ~47% (movement protein) and ~53% (capsid protein).

Partial sequence information obtained in the polymerase of PcMV (James & Upton, 1999) confirms that PCMV and CMLV are closely related viruses with a nucleotide sequence identity level of 79.5%.

Summarizing, with the exception of the presence of an additional ORF at the 3' end of its genome, CMLV has all the allmarks of a *Trichovirus* and sequence data analysis supports the its classification as a definitive species in this genus. The close relationships between CMLV and PcMV also support inclusion of PcMV as a definitive species in the *Trichovirus* genus.

List of created Species in the genus

Cherry Mottle leaf virus (CMLV)
Peach mosaic virus (PcMV)

References

James, D. & Upton, C., 1999. Single primer pair designs that facilitate simultaneous detection and differentiation of peach mosaic virus and cherry mottle leaf virus. *J. Virol. Meth.*, **83**, 103-111.

James, D., Jelkmann, W. & Upton, C., 2000. Nucleotide sequence and genome organisation of cherry mottle leaf virus and its relationship to members of the *Trichovirus* genus. *Arch. Virol.*, **145**, 995-1007.

James, D. & Howell, W.E., 1998. Isolation and partial characterization of a filamentous virus associated with peach mosaic disease. *Plant Dis.*, **82**, 909-913.

James, D. & Mukerji, S., 1993. Mechanical transmission, identification and characterization of a virus associated with mottle leaf in cherry. *Plant Dis*, **77**, 271-275.

Oldfield, G.N., 1970. Mite transmission of plan viruses. *Ann. Rev. Entomol.*, **15**, 343-380.

Annexes: