

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

Code † **2007.065P.04** To designate the following as species in the genus:

Fabavirus

belonging to the family° :

Comoviridae

Gentian 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

Family *Comoviridae*

Genus *Fabavirus*

Type Species

Broad bean wilt virus 1

Species in the Genus

Broad bean wilt virus 2

Lamium mild mosaic virus

New Taxonomic Order

Order *Picornavirales* (order under consideration by ICTV, see 2006 proposal)

Family *Comoviridae* [but see proposal for family *Secoviridae* (2007.057-9P.02)]

Sub-Family currently none [but see proposal for subfamily *Comovirinae* (2007.053-6P.01) in the proposed family *Secoviridae* (2007.057-9P.02)]

Genus *Fabavirus*

Type Species

Broad bean wilt virus 1

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Gentian mosaic virus

ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

No pseudo-recombination between components possible

Differences in antigenic reactions

Sequence identity lower than 75% in the coat protein and polymerase coding regions

Argumentation to justify the designation of new species in the genus

Gentian mosaic virus (GeMV) was isolated from gentian (*Gentiana scraba*) displaying mosaic symptoms (Kobayashi et al, 2005). It has not been previously classified. GeMV has icosahedral particles approximately 30 nm in diameter and a bipartite positive-strand RNA genome. RNA1 and RNA2 are 5,836 and 3,372 nts in length, respectively. The virus particles consist of two coat proteins of 39.3 and 26.6 kDa. Each RNA encodes a polyprotein from which mature viral proteins are released. The genomic organization of GeMV, the size of the two RNAs and the number of CPs are similar to those of members the genera *Comovirus* and *Fabavirus* within the currently accepted family *Comoviridae*. The family *Comoviridae* is now proposed to become a sub-family within the suggested family *Secoviridae* (see proposal on the creation of the family *Secoviridae*). GeMV has a wide host range which is typical of fabaviruses but not of comoviruses. Phylogenetic studies confirmed that it groups with other members of the genus *Fabavirus* in a branch that is distinct from that shared by members of the genus *Comovirus* (Kobayashi et al, 2005, see also Annex). The vector of GeMV is not known.

GeMV is a distinct species within the genus *Fabavirus* based on the following observation (Kobayashi et al, 2005). Indirect ELISA assays confirmed that GeMV does not cross-react with broad bean wilt virus 2 (BBWV2) or lamium mild mosaic virus, two species of the genus *Fabavirus*. Only a weak cross-reaction was observed with broad bean wilt virus 1 (BBWV1). The level of identity between the deduced amino acid sequence of GeMV and other fabaviruses was between 38 and 66 % depending on the virus and region of the genome considered. The RdRp is generally considered a good indicator for species differentiation. The level of amino acid sequence identity was 64-66% between GeMV and other fabaviruses and was 42% with cowpea mosaic virus (type member of the genus *Comovirus*). These characteristics meet the criteria established for species demarcation in the genus *Fabavirus* (Le Gall et al, 2005)

List of created Species in the genus

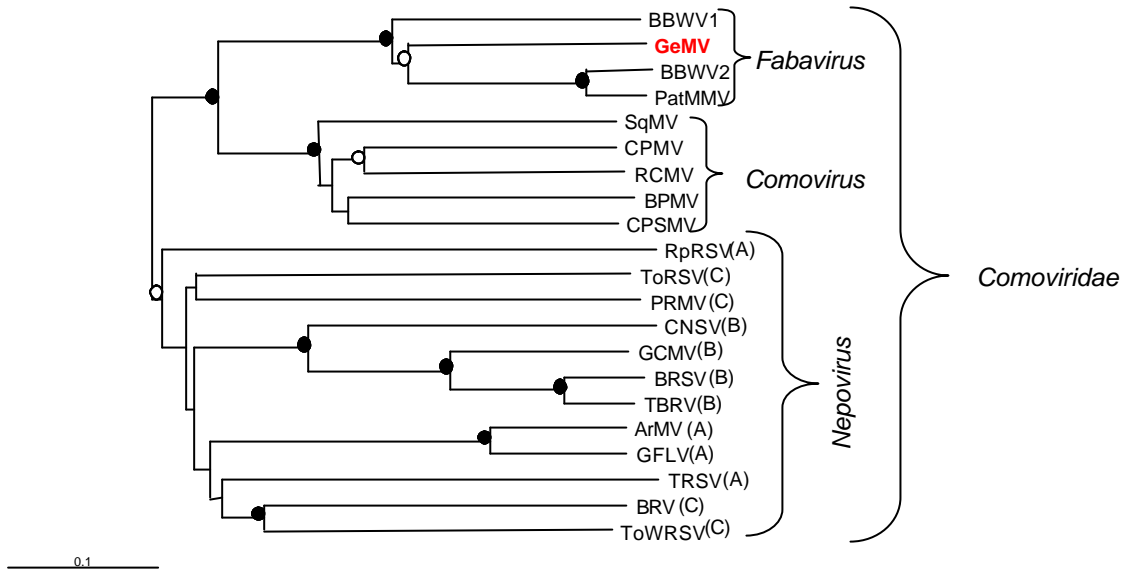
Gentian mosaic virus (GeMV) AB084452/3

References

Kobayashi, Y. O., Kobayashi, A., Hagiwara, D., Uga, H., Mikoshiba, Y., Naito, T., Honda, Y., Omura, T. (2005) Gentian mosaic virus: A new species in the genus Fabavirus. *Phytopathology* 95: 192-197.

Le Gall, O., Iwanami, T., Karasev, A. V., Jones, A. T., Lehto, K., Sanfacon, H., Wellink, J., Wetzel, T., and Yoshikawa, N. (2005) Family Comoviridae. In *Virus Taxonomy: The classification and nomenclature of viruses. The eight report of the International Committee on Taxonomy of Viruses* (Fauquet, C. M., Mayo, M. A., Maniloff, J., Desselberger, U., and Ball, L. A., Eds, Academic Press, San Diego, USA) pp. 807-818

Annex: Phylogenetic tree showing the position of GeMV in the genus *Fabavirus*



Hierarchical clustering of selected plant picorna-like viruses based on the Pro-Pol sequence (region between the CG motif within the proteinase and the GDD motif with the polymerase). The families and genera are delineated on the right. The letter in parenthesis after the nepovirus acronyms refer to the subgroup in which they have been classified (A, B or C). Circles indicate nodes supported by bootstrap values above 80% (closed circles) or 60% (open circles); nodes without circles are not supported to these levels. The bar represents a p-distance of 0.1. The amino-acid sequence clustering is based on the region between the Pro (CG) and the Pol (GDD) sequence motifs. The GenBank accession numbers for each virus were as follows: gentian mosaic virus (GeMV, BAD99001), broad bean wilt virus 1 (BBWV1, AB084450), broad bean wilt virus 2 (BBWV2, AF225953), patchouli mild mosaic virus, an isolate of BBWV2 (PatMMV, AB050782), squash mosaic virus (SqMV, AB054688), bean pod mosaic virus (BPMV, U70866), red clover mosaic virus (RCMV, X64886), cowpea severe mosaic virus (CPSMV, M83830), cowpea mosaic virus (CPMV, X00206), tomato white ringspot virus (ToWRSV which is probably an isolate of artichoke ringspot virus, ABM65096), peach rosette mosaic virus (PRMV, AAB69867), blackcurrant reversion virus (BRV, AF3682772), tomato ringspot virus (ToRSV, L19655), tomato black ring virus (TBRV, AY157993), grapevine chrome mosaic virus (GCMV, X15346), cycas necrosis stunt virus (CNSV, AB073147), beet ringspot virus (BRSV, D00322), tobacco ringspot virus (TRSV, U50869), raspberry ringspot virus (RpRSV, AY303787), arabis mosaic virus (ArMV, AY303786), grapevine fanleaf virus (GFLV, D00915)