

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[°] :

Tobacco latent virus
Wasabi mottle virus
Hibiscus latent Singapore virus
Hibiscus latent Fort Pierce virus

[†] Assigned by ICTV officers

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

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TLV proposal initiated by Dr. R. Koenig (R.Koenig@BBA.DE); proposed name change and additional sequence comparisons to the other proposed species made by DJL.

New Taxonomic Order

Order

Family

Genus *Tobamovirus*

Type Species *Tobacco mosaic virus*

List of Species in the genus *Tobacco latent virus*

Wasabi mottle virus

Hibiscus latent Singapore virus

Hibiscus latent Fort Pierce virus

List of Tentative Species in the Genus

List of Unassigned Species in the Family

Species demarcation criteria in the genus

Sequence similarity; less than 10% overall nucleotide sequence difference is considered to characterize strains of the same species, although most of the sequenced species have considerably less than 90% sequence identity,
Host range; however many of these viruses have wider and more overlapping host ranges in experimental rather than natural situations,
Antigenic relationships between the CPs.

Argumentation to justify the designation of new species in the genus

Complete nucleotide sequence for the movement protein (MP) and coat protein (CP) open reading frames (ORF) are now available for Tobacco latent virus (TLV). This virus is referred to in a single reference as Nigerian tobacco latent virus. However, as there are no reports of other latent tobamoviruses isolated from tobacco, the simplified name 'Tobacco latent virus' is proposed. TLV is most similar to *Tobacco mild green mosaic virus* (TMGMV). The region encompassing the MP and CP ORFs has 63% nucleotide sequence identity with the corresponding regions of TMGMV, which is well below the species demarcation criteria. The MP has 64% and the CP has 73% amino acid identity with TMGMV. TLV forms rod-shaped virions typical of the genus. Antisera produced from TLV virions did not react with TMGMV, although one of two TMGMV antiseras reacted with TLV virions, demonstrating an antigenic relationship. This virus produces a non-symptomatic (latent) infection in tobacco, which is different from other tobamoviruses that naturally infect tobacco.

GenBank accession number: AY137775

The complete genome sequences are available for two isolates of Wasabi mottle virus (WMoV). This virus is referred to in the literature and GenBank as a 'wasabi strain of crucifer tobamovirus', which does not conform to the rules of nomenclature. The proposed name incorporates the host (*Eutrema wasabi* – Japanese horseradish or wasabi) from which this virus was isolated and the characteristic symptoms produced. The genome organization is typical of tobamoviruses and the two isolates of WMoV (6297 and 6298 nucleotides of single strand RNA) are 98% identical. WMoV is more similar to tobamoviruses isolated from brassicas than those isolated from other hosts. WMoV genomic RNA has 84% and 82% nucleotide sequence identity with *Youcai mosaic virus* (YoMV) and *Turnip vein clearing virus* (TVCV), respectively. WMoV replicase, MP and CP have 92-93%, 87-89% and 89-90% amino acid identity, respectively, to strains of TVCV, and 89-90%, 82-83% and 91-92% amino acid identity to strains of YoMV.

GenBank accession numbers: NC_003355 (derived from AB017503), AB017504

Nucleotide sequence for the complete MP and CP ORFs are now available for Hibiscus latent Singapore virus (HLSV). HLSV was isolated from hibiscus in Singapore and is most similar to Hibiscus latent Fort Pierce virus (HLFPV), described below. HLSV has 39-44% MP ORF nucleotide sequence identity and 31-38% MP amino acid identity with the currently recognized tobamovirus species. HLSV has 68% MP ORF nucleotide sequence identity and 60% MP amino acid identity with a partial clone encoding the 3'-proximal one-third of the HLFPV MP. HLSV is more similar to HLFPV (68% CP ORF nucleotide sequence and 73% CP amino acid identity), than to all recognized tobamovirus species (46-52% CP ORF nucleotide sequence and 45-57% CP amino acid identity). The percent nucleotide sequence identity within the MP and CP ORFs are below the species demarcation criteria. HLSV produces rod-shaped virions typical of tobamoviruses. HLSV CP cross-reacts with one of three tobamovirus antisera. The proposed name in the single reference (Hibiscus virus S) does not conform to rules of nomenclature. Because this virus produces a latent or symptomless infection in at least some cultivars of hibiscus and the description of another latent or symptomless tobamovirus from hibiscus in Florida, it is proposed that the name contains the country of origin of the virus (Singapore) to distinguish it as a distinct species from HLFPV.
GenBank accession numbers: AF395898, AF395899

The sequence of the Hibiscus latent Fort Pierce virus (HLFPV) CP ORF is now available. HLFPV was isolated from hibiscus in Fort Pierce, Florida, USA and is most similar to Hibiscus latent Singapore virus (HLSV). HLFPV has 68% CP ORF nucleotide sequence and 73% CP amino acid identity with HLSV. Percent nucleotide sequence and amino acid identity with recognized species are 44-53% and 45-51%, respectively. The 3'-proximal one-third of the MP ORF is most similar to HLSV, having 68% nucleotide and 60% amino acid sequence identity. Percent identity for CP and partial MP nucleotide sequences are below the species demarcation criteria. HLFPV forms virions of the shape and size characteristic of the genus. HLFPV CP antisera weakly cross-reacts with PMMoV and TMV CPs. One experimental host (*Chenopodium quinoa*) gives a differential response to HLFPV and HLSV. HLFPV was isolated from hibiscus plants that were co-infected with other virus(es), but appears to cause a latent or symptomless infection in at least some hibiscus cultivars. It is proposed that this virus have a name similar to, yet distinct from HLSV. The city (Fort Pierce) was chosen rather than the state (Florida) due to detection of other, different putative tobamoviruses in other regions of Florida.
GenBank accession number: AY250831

List of created Species in the genus

Tobacco latent virus

Wasabi mottle virus

Hibiscus latent Singapore virus

Hibiscus latent Fort Pierce virus

Ladipo, J. L., Koenig, R., and Lesemann, D.-E. 2003. Nigerian tobacco latent virus: a new tobamovirus from tobacco in Nigeria. *Eur. J. Plant Pathol.* 109, 373-379.

Shimamoto, I., Sonoda, S., Vazquez, P., Minaka, N. and Nishiguchi, M. 1998. Nucleotide sequence analysis of the 3' terminal region of a wasabi strain of crucifer tobamovirus genomic RNA: subgrouping of crucifer tobamoviruses. *Arch. Virol.* 143 (9), 1801-1813.

Kashiwazaki, S., Shimazu, K., and Tsuchizaki, T. 1990. Serological properties of wasabi strain of tobacco mosaic virus. *Ann. Phytopathol. Soc. Jpn.* 56: 257-260.

Srinivasan, K.G., Narendrakumar, R. and Wong, S.M. 2002. Hibiscus virus S is a new subgroup II tobamovirus: evidence from its unique coat protein and movement protein sequences. *Arch. Virol.* 147 (8), 1585-1598.

Adkins, S., Kamenova, I., Achor, D., and Lewandowski, D. J. 2003. Biological and molecular characterization of a novel tobamovirus with a unique host range. *Plant Disease* 87 (in press).

Adkins, S., Achor, D., and Lewandowski, D. J. 2002. Characterization of a tobamovirus from hibiscus. *Phytopathology* 92, 1024.

Adkins, S. 2001. Detection and characterization of a virus from hibiscus. *Phytopathology* 91, S2.