

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

Code[†] **2007.072P.04** To designate the following as species in the genus:

Ipomovirus

belonging to the family[°] : *Potyviridae*

Squash vein yellowing 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>Ipomo virus</i>
Type Species	<i>Sweet potato mild mottle virus</i>
Species in the Genus	(3)

New Taxonomic Order

Order	
Family	<i>Potyviridae</i>
Genus	<i>Ipomo virus</i>
Type Species	<i>Sweet potato mild mottle virus</i>
Species in the Genus	<i>Squash vein yellowing 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., 2005].

Argumentation to justify the designation of new species in the genus

There has been a thorough study of the symptomatology of this virus and the sequence of the 3'-end of the genome determined (DQ812125; Adkins et al., 2007). Its whitefly transmission and phylogenetic analysis (see Annex Fig. 1) clearly places it within the genus *Ipomovirus* and its coat protein has 64% nt (66% aa) identity with that of the existing species, Cucumber vein yellowing virus (AY578085).

List of created Species in the genus

<i>Squash vein yellowing virus</i>		
Squash vein yellowing virus	(SqVYV)	DQ812125

References

- Adams M.J., Antoniwi J.F., Fauquet C.M. (2005). Molecular criteria for genus and species discrimination within the family *Potyviridae*. *Arch. Virol.* 150:459-479.
- Adkins S., Webb S. E., Achor D., Roberts P. D., Baker C. A. (2007). Identification and characterization of a novel whitefly-transmitted member of the family *Potyviridae* isolated from cucurbits in Florida. *Phytopathol.* 97:145-154.

Annex:

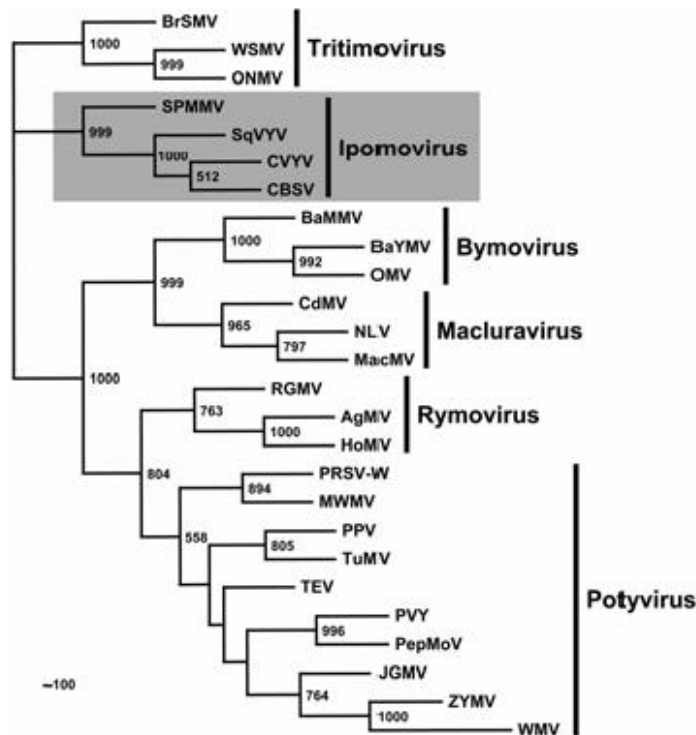


Figure 1. Phylogenetic analysis of the amino acid sequences of the conserved core of the coat protein of Squash vein yellowing virus (SqVYV) and other members of the family *Potyviridae*. Sequences were aligned using CLUSTALX (47) with gap opening and extension penalties of 10 and 0.2, respectively, and Gonnet series protein weight matrix. Phylogenetic trees were inferred using the JTT model and neighbor-joining method using Phylip version 3.65 (17) with Brome streak mosaic virus (BrSMV) as an outgroup. The significance of the branching order was assessed by bootstrap resampling of 1,000 replicates, and values =50% are indicated. Viruses included (listed with abbreviation and GenBank accession number for nucleotide sequence) are Agropyron mosaic virus (AgMV, NC_005903), Barley mild mosaic virus (BaMMV, NC_003483), Barley yellow mosaic virus (BaYMV, AJ132268), Brome streak mosaic virus (BrSMV, NC_003501), Cardamom mosaic virus (CdMV, AF189125), Cassava brown streak virus (CBSV, AY007597), Cucumber vein yellowing virus (CVYV, NC_006941), Hordeum mosaic virus (HoMV, NC_005904), Johnsongrass mosaic virus (JGMV, Z26920), Maclura mosaic virus (MacMV, U58771), Moroccan watermelon mosaic virus (MWMV, AF305545), Narcissus latent virus (NLV, U58770), Oat mosaic virus (OMV, AJ306718), Oat necrotic mottle virus (ONMV, AY377938), Papaya ringspot virus type W (PRSV-W, AY027812), Pepper mottle virus (PepMoV, M96425), Plum pox virus (PPV, NC_001445), Potato virus Y (PVY, X12456), Ryegrass mosaic virus (RGMV, Y09854), Squash vein yellowing virus (SqVYV, DQ812125), Sweet potato mild mottle virus (SPMMV, Z73124), Tobacco etch virus (TEV, M15239), Turnip mosaic virus (TuMV, NC_002509), Watermelon mosaic virus (WMV, NC_006262), Wheat streak mosaic virus (WSMV, AF057533), and Zucchini yellow mosaic virus (ZYMV, L31350). The six recognized genera are indicated, with the ipomoviruses shaded. This is an unrooted tree. This is Fig. 6 from Adkins et al., 2007.