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

Code[†] 2005.122P.04 To designate the following as species in the genus:

belonging to the family° :

Marafivirus

Tymoviridae

Citrus sudden death-associated virus

Citrus sudden death-associated virus –P15 (CSDaV-P15) DQ185573

Citrus sudden death-associated virus –BZ (CSDaV-BZ) AY884005

[†] Assigned by ICTV officers

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

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Old Taxonomic Order

Order: None

Family: *Tymoviridae*

GenusMarafivirus

Type Species: *Maize rayado fino virus*

Species in the Genus: 3

Tentative Species in the Genus: 2

Unassigned Species in the family: None

New Taxonomic Order

Order: None

Family: *Tymoviridae*

Genus: *Marafivirus*

Type Species: *Maize raydo fino virus*

Species in the Genus: 4

Tentative Species in the Genus: 2

Unassigned Species in the family: none

ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

The criteria demarcating species in the genus are:

Overall sequence identity of less than 80%
CP sequences less than 90% identical,
Differences in the 3'-terminal structure and in the number of ORFs
Differential host range
Vector specificity
Serological specificity
Different effects on cell ultrastructure
Marafibox that is distinct in sequence from the tymobox

Argumentation to justify the designation of new species in the genus

To give a taxonomic allocation to a recently described citrus virus with isometric particles, based on biological, morphological (aspect and size of virus particles), physico-chemical (type, size, and high C content of nucleic acid), and molecular (structural organization of genomic RNA, presence of marafibox) properties, as detailed in the annex.

List of created Species in the genus

Citrus sudden death-associated virus

References

Bassanezi R.B., Bergamin Filho A., Amorim L., Gimenes-Fernades N., Gottwald T.R., Bové J.M., 2003. Spatial and temporal analyses of citrus sudden death as a tool to generate hypotheses concerning its aetiology. *Phytopathology* **93**: 502-512.

Maccheroni W. *et al*., 2005. Identification and genomic organization of a new virus (*Tymoviridae* family) associated with citrus sudden death disease. *Journal of Virology* **79**:3028-3037.

Roman M.P. *et al*., 2004. Sudden death of citrus in Brazil: a graft transmissible bud union disease. *Plant Disease* **88**: 453-467.

ANNEX

Biological properties. Citrus sudden death-associated virus (CSDaV) is a non-mechanically transmissible virus associated with a devastating disease of citrus, first reported in Brazil in 1999. It has no known host other than citrus.

Epidemiology. Sudden death spreads naturally in the field. CSDaV can be transmitted by grafting and is disseminated by infected propagating material over long distances. Although not experimentally proven, spread at a site may be mediated by the brown citrus aphis *Toxoptera citricida* in association with the closterovirus Citrus tristeza virus (CTV), which is consistently found together with CSDaV both in infected citrus plants and in *T. citricida*

Physico-chemical properties. CSDaV has isometric particles about 30 nm in diameter with a rounded contour and prominent surface structure. Some particles are apparently intact whilst others are penetrated by the negative stain, thus resembling the non infectious empty shells of *Tymoviridae*. The nucleic acid is a polyadenylated single-stranded RNA about 2.4 Kb in size, with a cytosine content of 37.4%.

Molecular properties. The genomic RNA (6,805 nt in size) has been totally sequenced. It contains a putative marafibox (nt 5956-5971) and comprises two ORFs, the largest of which encodes a protein with Mr 240 kDa, containing in succession the conserved signature domains of methytransferase, papain-like protease, helicase, RdRp, and the major (22.5 kDa) and minor (21 kDa) coat protein. The 3' most ORF2 encodes a 16 kDa polypeptide with an overall identity of 43% to the putative movement protein of *Maize rayado fino virus.*

Phylogenetic tree generated from the alignment of the overall coat protein amino acid sequences of members of the *Nepovirus* genus

Figure 4.
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