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

Code[†] 2006.004P.04 To designate the following as unassigned species in the family:

Closteroviridae

Mint vein banding-associated virus (MVBaV)

[†] Assigned by ICTV officers
° leave blank if inappropriate or in the case of an unassigned genus

Author(s) with email address(es) of the Taxonomic Proposal

GP Martelli on behalf of the ICTV Study Group on *Closteroviridae*

Old Taxonomic Order

Order	
Family	**Closteroviridae**
Unassigned Species in the family	**5**

New Taxonomic Order

Order	
Family	***Closteroviridae***
Unassigned Species in the family	**6**

ICTV-EC comments and response of the SG

Species demarcation criteria in the genera

Particle size
Size of CP, as determined by deduced aa sequence data
Serological specificity using discriminatory monoclonal or polyclonal antibodies
Genome structure and organisation (number and relative location of the ORFs)
Amino acid sequence of relevant gene products (CP, CPm, HSP70) differing by more than 10%
Vector species and specificity
Magnitude and specificity of natural and experimental host range
Cytopathological features (aspects of inclusion bodies and origin of cytoplasmic vesicles)

Argumentation to justify the designation of unassigned species in the family

Mint vein banding associated virus (MVBaV) is a virus described by Tzanetakis *et al.* (2005) from variegated mint (*Mentha x gracilis* cv. Variegata) with outstanding yellow vein banding symptoms that contribute to its uses as an ornamental clone. The vein banding symptoms are caused by a virus complex.

MVBaV properties:

(i) Virus particles: Flexuous filaments about 1500 x 12 nm
(ii) dsRNA: multiple bands, the largest c. 14 kbp in size
(iii) CP: 25 kDa (determined by deduced sequence data)
(iv) Nucleic acid: single molecule of ssRNA
(v) Genome: monopartite, sequenced in part (8008 nt comprising helicase, polymerase, HSP70h and CP genes) (AY548173)
(vi) Phylogenetic relationships: characteristics shared with all there genera of the family. Viral CP shows homology with both types of CP genes of other members of the family, thus could not be identified as the major or minor CP of the virus. In trees constructed with polymerase and HSP70h sequences, MVBaV does not cluster with any of the three genera of the family, standing pretty much on its own.
(vii) Mechanical transmission: unsuccessful to a moderate range of herbaceous hosts
(viii) Transmission by vectors: successful successful from mint to mint, mediated by the aphid *Ovatus crataegarius*. Modality of transmission undetermined
(ix) Cytopathology: No information

Particle morphology, biological, epidemiological, and molecular data clearly show that MVBaV is a member of the family *Closteroviridae*. However, the peculiarity of its genome organization and phylogenetic relationships which, as pointed out by Tznanetakis *et al.* (2005) "*place this virus in the center of the family as known today*" suggest that MVBaV should be placed as a non-assigned species to the family, until more exhaustive molecular information is obtained.

List of created Unassigned Species in the family

Mint vein banding-associated virus (MVBaV)

References

Tzanetakis, I.E., Postman, J.D. and Martin, R.R., 2005. A member of the *Closteroviridae* from mint with similarities to all three genera of the family. *Plant Disease*, **89**:654-658.

Annexes: