

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

Code<sup>†</sup>  To designate the following as species in the genus:

belonging to the family<sup>°</sup> :

<sup>†</sup> Assigned by ICTV officers

<sup>°</sup> leave blank if inappropriate or in the case of an unassigned genus

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

## Old Taxonomic Order

Order	
Family	<i>Closteroviridae</i>
Genus	<i>Closterovirus</i>
Type Species	<i>Beet yellows virus</i>
Species in the Genus	6
Tentative Species in the Genus	4
Unassigned Species in the family	5

## New Taxonomic Order

Order	
Family	<i>Closteroviridae</i>
Genus	<i>Closterovirus</i>
Type Species	<i>Beet yellows virus</i>
Species in the Genus	7
Tentative Species in the Genus	4
Unassigned Species in the family	5

## ICTV-EC comments and response of the SG

## Species demarcation criteria in the genus

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 new species in the genus

Mint virus 1 (MV-1), a virus described by Tzanetakis *et al.* (2005), infects variegated mint (*Mentha x gracilis*) and is part of a virus complex that induces leaf crinkling and distortion.

MV-1 properties:

- (i) Virus particles: no data
- (ii) dsRNA: multiple bands. The largest, thought to represent the viral genome, is c. 15 kbp in size
- (iii) CP: 22 kDa (determined by deduced sequence data)
- (iv) Nucleic acid: ssRNA 15,450 nt in size
- (v) Genome: totally sequenced (NC\_006944) comprising 8 ORFs organized (relative position) like those of *Beet yellow virus*, the type species of the genus *Closterovirus*. The 5' untranslated region has no significant similarity with any of the closterovirus species so far sequenced and none of the ORF products has an amino acid sequence identity higher than 55% with the comparable proteins of other closteroviruses.
- (vi) Phylogenetic relationships: MV-1 clusters with members of the genus *Closterovirus* in trees constructed with CP and HSP70 homologue sequences
- (vii) Mechanical transmission : unsuccessful to a range of herbaceous hosts
- (viii) Transmission by vectors: successful from mint to mint, mediated by the aphid *Ovatus crategarius*. Modality of transmission undetermined
- (ix) Cytopathology: no information

Despite the fact that MV-1 particles were not seen, its physico-chemical (size of dsRNA and CP), molecular (genome structure and sequence), and epidemiological (aphid transmission) properties tally with those of recognized closterovirus species. These data and the fact that MV-1 has a clear-cut phylogenetic relationship with members of the genus *Closterovirus* support its assignment to this genus as a definitive species

### List of created Species in the genus

Mint virus 1 (MV-1)

### References

Tzanetakis, I.E., Postman, J.D. and Martin, R.R., 2005. Characterization of a novel member of the family *Closteroviridae* from *Mentha* spp. *Phytopathology*, **95**: 1043-1048.

### Annexes: