

## 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>Crinivirus</i>
Type Species	<i>Lettuce infectious yellows virus</i>
Species in the Genus	8
Tentative Species in the Genus	2
Unassigned Species in the family	5

### New Taxonomic Order

Order	
Family	<i>Closteroviridae</i>
Genus	<i>Crinivirus</i>
Type Species	<i>Lettuce infectious yellows virus</i>
Species in the Genus	8
Tentative Species in the Genus	3
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

Blackberry yellow vein-associated virus (BYVaV) is a virus described by Martin *et al.* (2004) from blackberry plants showing yellow vein, ringspots, leaf distortion and decline.

### BYVaV properties:

- (i) Virus particles: no data
- (ii) dsRNA: multiple bands, the largest c. 9 kbp in size
- (iii) CP: 28 kDa (determined by deduced sequence data)
- (iv) Nucleic acid: two molecules of ssRNA 7801 nt (RNA-1) and 7917 nt (RNA-2) in size
- (v) Genome: bipartite totally sequenced. RNA-1 has a single ORF encoding the replication associated proteins. RNA-2 consists of 9 ORFs similar in size and position to the comparable genes of criniviruses,
- (vi) Phylogenetic relationships: BYVaV clusters with members of the genus *Crinivirus* in trees constructed with polymerase, CP, and HSP70 homologue sequences, the closest species being *Beet pseudoyellows virus* (BPYV)
- (vii) Serology: no data
- (viii) Mechanical transmission: negative
- (ix) Transmission by vectors: *Trialeurodes packardii* and *T. ruborum* both negative
- (x) Cytopathology: proliferation of vesicles and tubules
- (xi) Transmission by grafting: Transmitted to 'Marion' blackberry, 'Meeker' red raspberry and 'Munger' black raspberry, all remained symptomless

Molecular data (genome sequence and organization) indicate that BYVaV is a member of the genus *Crinivirus*. The protease near the 5' end of RNA 1 has 42% aa identity to that of BPYV and the corresponding values for the helicase, polymerase and HSP70 homologue are respectively 65%, 70% and 72% indicating that BYVaV should be classified as a distinct definitive species.

## List of created definitive Species in the genus

Blackberry yellow vein-associated virus	(BYVaV)	AY776334-5
---	---------	------------

## References

Martin, R.R., Tzanetakis, I.E., Gergerich, R., Fernadez, G. and Pesic, Z., 2004. Blackberry yellow vein associated virus: a new crinivirus found in blackberry. *Acta Horticulturae*, **565**: 127-142.

Susaimuthu, J., Gergerich, R.C., Bray, M.M., Clay, K.B., Clark, J.R., Tzanetakis, I.E. and Martin, R.R. 2007. The incidence and ecology of Blackberry yellow vein associated virus. *Plant Dis.* **91**(accepted).

Susaimuthu, J., Tzanetakis, I.E., Gergerich, R.C. and Martin, R.R. 2006. Yellow vein-affected blackberries and the presence of a novel crinivirus. *Plant Pathol.* **55**:607-613.

Tzanetakis, I.E., Susaimuthu, J., Gergerich, R. and Martin, R.R., 2006. Nucleotide sequence of Blackberry yellow vein associated virus, a novel member of the *Closteroviridae*. *Virus Research*, **116**: 196-200.