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

Code[†] 2007.004P.04</sup> To designate the fo

To designate the following as species in the genus:

Crinivirus

belonging to the family°:

Closteroviridae

Potato yellow vein virus

[†] Assigned by ICTV officers

 $^{\circ}$ 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
Genus	Crinivirus
Type Species	Lettuce infectious yellows virus
Species in the Genus	8
Tentative Species in the Genus	3
Unassigned Species in the family	5
New Taxonomic Order	
Order	
Family	Closteroviridae
Genus	Crinivirus
Type Species	Lettuce infectious yellows virus
Species in the Genus	9
Tentative Species in the Genus	2
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

Potato yellow vein is a disease known for over 50 years to affect potato crops in South America (Alba, 1950, 1952, in Salazar *et al.*, 2000). Its agent was recently recognized as a virus denoted Potato yellow vein virus (PYVV), described by Salazar *et al.* (2000), sequenced and characterized molecularly by Livieratos *et al.* (2004).

PYVV properties:

- (i) Virus particles: Filamentous. Modal length undetermined
- (ii) dsRNA: at least 5 species approximately 8, 5.3, 3.8, 2.0 and 1.8 kbp in size
- (iii) CP: 28.2 kDa (determined by deduced sequence data)
- (iv) CPm: 77.5 kDa (determined by deduced sequence data)
- (v) Nucleic acid: three molecules of ssRNA: 8035 nt (RNA-1), 5339 nt (RNA-2), and 3892 nt in size
- (vi) Genome: tripartite, totally sequenced. RNA-1 has a single ORF encoding the replication associated proteins. RNA-2 consists of 5 ORFs encoding, the HSP70 homologue followed by 7K, 60K, 10 K proteins and the CP, homologous to products encoded by the first half or RNA-2 of criniviruses. RNA-3 has three ORFs coding for: a 4K protein that has no counterpart with any other protein described for members of the family *Closteroviridae*; the CPm (77.5 kDa), and a 26.4 kDa protein that seems to be unique to the genus *Crinivirus*. In the 3' untranslated regions, the viral genome possesses secondary structures conserved in all criniviruses.
- (vii) Phylogenetic relationships: PYVV clusters with members of the genus *Crinivirus* in trees constructed with polymerase, CP, HSP70 homologue and p60 sequences, the closest species being Cucumber yellows virus (CuYV, Hartono *et al.*, 2003). Amino acid identity in the HSP70 homologue is 67.5%
- (viii) Mechanical transmission: Negative
- (ix) Transmission by grafting: Positive only to tomato cv. Rugters out of 15 different hosts tested in the family *Solanaceae*
- (x) Transmission by vectors: Transmitted in a semi-persistent manner by *Trialeurodes vaporariorum*
- (xi) Cytopathology: no data

Biological, epidemiological and molecular data (sequence and phylogene tic relationships) indicate that PYVV is a distinct member of the genus *Crinivirus*. The major difference from other members of the genus resides in the presence of a tripartite rather than a bipartite genome. Whether this calls for the establishment of a new genus is an issue to be addressed if and when other viruses with a similar genome organization are found.

List of created definitive Species in the genus

Potato yellow vein virus (PYVV) AJ557128, AJ557129, AJ508757

References

Hartono, S. Natsuaki, T., Genda, Y and Okuda, S., 2003. Nucleotide sequence and genome organization of Cucumber yellows virus, a member of the genus *Crinivirus*. *Journal of General Virology*, **84**: 1007-1012

Livieratos, I.C., Eliaso, E., Müller, G., Olsthoom, R.C.L., Salazar, L.F., Pleji, C.W.A, Coutts, R.H.A., 2004. Analysis of the RNA of Potato yellow veing virus: evidence for a tripartite genome and conserved 3' terminal structures among members of the genus *Crinivirus. Journal of General Virology*, **85**: 2065-2075.

Salazar, L.F., Müller, G., Quesri, M., Zapata, J.L. and Owens, R.A., 2000. Potato yellow vein virus: its host range, distribution in South America and identification as a crinivirus transmitted by *Trialeurodes vaporariorum*. *Annals of Applied Biology*, **137**: 7-19