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

Code[†] 2006.007P.04

To designate the following as species in the genus: ***Potexvirus***

belonging to the family° : ***Flexiviridae***

Alstroemeria virus X
Mint virus X

[†] 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

Mike Adams (on behalf of Flexiviridae SG)
mike.adams@bbsrc.ac.uk

Old Taxonomic Order

Order	
Family	*Flexiviridae*
Genus	*Potexvirus*
Type Species	*Potato virus X*
Species in the Genus	**(28)**
Tentative Species in the Genus	
Unassigned Species in the family	

New Taxonomic Order

Order	
Family	*Flexiviridae*
Genus	*Potexvirus*
Type Species	*Potato virus X*
Species in the Genus	(30)
Tentative Species in the Genus	
Unassigned Species in the family	

ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

The criteria demarcating species in the genus (Adams et al., 2004) are:

- Members of distinct species have less than *ca.* 72% identical nt or 80% identical aa between their CP or polymerase genes
- Different reactions with antisera.

Argumentation to justify the designation of new species in the genus

Alstroemeria virus X: A flexuous virus was isolated in Japan from an Alstroemeria plant showing mosaic symptoms. The virus had a broad host range but had systemically latent infectivity in alstroemeria. The virion morphology and complete sequence (AB206396) confirmed that it was a member of the genus *Potexvirus* (Fuji et al., 2005).

Mint virus X is one of three distinct RNA viruses cloned and sequenced from variegated mint plants in the USA. Detection tests based on the sequence determined showed that the virus was widespread in variegated mint clones and was also present (apparently without symptoms) in other mint species in the clonal collection. The complete sequence of Mint virus X (AY789138) and some other partial sequences, confirmed that the genomic organization was that of a potexvirus (Tzanetakis et al., 2006).

Phylogenetic analyses of the replication protein gene (Figure 1) and the coat protein gene (Figure 2) consistently grouped AlsVX with *Narcissus mosaic virus* and Scallion mosaic virus and MVX with *Lily virus X* (Figure 1). Key sequence comparisons (Table 1) indicate that both viruses meet the criteria needed to be recognized as new species in the genus.

Table 1: Percentage identity in nt and aa sequences between selected potexviruses

Gene		AlsVX v. NMV	AlsVx v. ScaMV	MVX v. LVX
Pol	nt	60.8	62.2	62.5
	aa	61.6	62.7	63.6
CP	nt	66.5	65.9	56.2
	aa	63.5	70.0	57.5

List of created Species in the genus

Alstroemeria virus X		
Alstroemeria virus X	(AlsVX)	AB206396
Mint virus X		
Mint virus X	(MVX)	AY789138

References

Adams, M.J., Antoniw, J.F., Bar-Joseph, M., Brunt, A.A., Candresse, T., Foster, G.D., Martelli, G.P., Milne, R.G., Zavriev, S.K. and Fauquet, C.M. (2004). The new plant virus family *Flexiviridae* and assessment of molecular criteria for species demarcation. *Arch. Virol.*, **149,** 1045-1060.

Fuji, S., Shinoda, K., Ikeda, M, Furuya, H., Naito, H., Fukutomo, F. (2005). Complete nucleotide. sequence of the new potexvirus “Alstroemeria virus X”. *Arch. Virol.*, **150,** 2377-2385.

Tzanetakis I.E., Postman J.D., Martin R.R. (2006). Mint virus X: a novel potexvirus associated with symptoms in 'Variegata' mint. *Arch. Virol.*, **151,** 143-153.

Annexes:

Figure 1. Neighbor-Joining Distance trees of the polymerase nucleotide sequences of members of the genus *Potexvirus* showing the positions of Alstroemeria virus X (AlsVX) and Mint virus X (MVX). Values on the branches show the percentage of trees in which this grouping occurred after bootstrapping the data (10,000 replicates; shown only where >50%). The scale bar shows the number of substitutions per base.

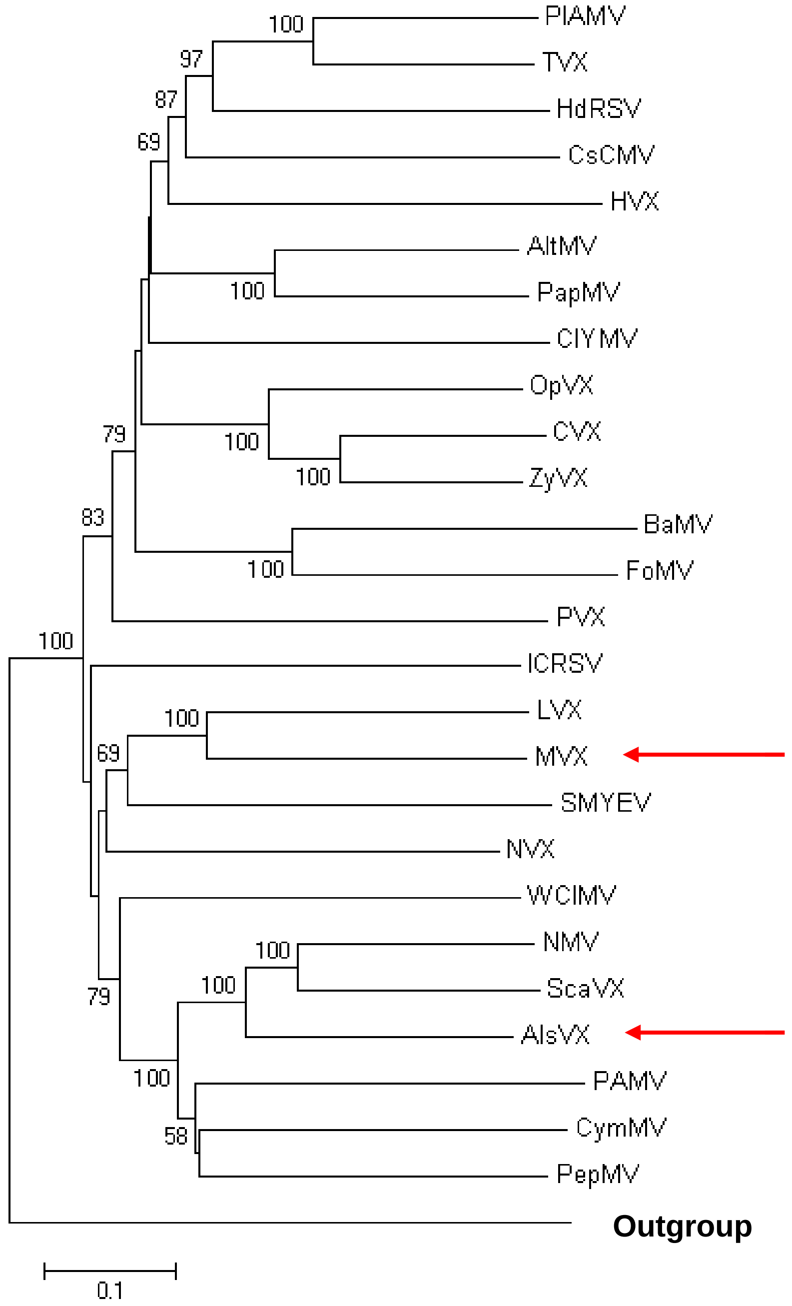

Figure 2. Neighbor-Joining Distance trees of the coat protein nucleotide sequences of selected members of the genus *Potexvirus* showing the positions of Alstroemeria virus X (AlsVX) and Mint virus X (MVX). Values on the branches show the percentage of trees in which this grouping occurred after bootstrapping the data (10,000 replicates; shown only where >60%). The scale bar shows the number of substitutions per base.