

# Template for Taxonomic Proposal to the ICTV Executive Committee

## Creating Species in an existing genus

Code†  To designate the following as species in the genus:

*Potexvirus*

belonging to the family° : *Flexiviridae*

*Opuntia virus X*  
Opuntia virus X, (OpVX) AY366209  
*Schlumbergera virus X*  
Schlumbergera virus X, (SchVX) AY366207  
*Zygocactus virus X*  
Zygocactus virus X, (ZyVX) AY366208

† Assigned by ICTV officers

° leave blank if inappropriate or in the case of an unassigned genus

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Order

Family

*Flexiviridae*

Genus

*Potexvirus*

Type Species

Species in the Genus

Tentative Species in the Genus

Unassigned Species in the family

### New Taxonomic Order

Order

Family

*Flexiviridae*

Genus

*Potexvirus*

Type Species

Species in the Genus

*Opuntia virus X*  
*Schlumbergera virus X*  
*Zygocactus virus X*

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 list of species demarcation criteria in the genus is:

- Host range : the natural host range is usually specific to different species.
- Distinct species fail to cross-protect in infected plants.
- Serology; species and strains of some species are also readily distinguishable in differential reactions with monoclonal antibodies.
- Sequence: Distinct species have less than *ca.* 72% identical nt or 80% identical aa between their CP or polymerase genes.

## Argumentation to justify the designation of new species in the genus

Two complete sequences (Opuntia virus X, AY366209; and Zygocactus virus X, AY366208) together with 3030 nts representing the 3'-half of the genome of Schlumbergera virus X (AY366207) were reported by Koenig et al (2004). The sequences were all derived from virus isolates previously regarded as serologically distinct strains of *Cactus virus X* (CVX) but the sequences proved to be sufficiently distinct from one another (<c. 67% nt identity; see Annex, Table 1) to justify regarding them as from different species according to the currently accepted criteria. The authors recommended discontinuation of the name CVX in favour of the three new species. However, independently and simultaneously, the complete sequence of a further isolate was published by Liou et al (2004) under the name Cactus virus X (AF308158). This is clearly related to the other sequences and is most closely related to the Zygocactus virus X sequence of Koenig et al. Comparisons between the two sequences fall very close to the species demarcation criteria previously established (see Annex, Table 1). It seems simplest to retain the species names attached to the sequences and to regard these as four related species within the genus. A phylogenetic tree of the capsid protein sequences, showing their relationships to other members of the genus *Potexvirus* is provided in Annex, Fig. 1.

## List of created Species in the genus

*Opuntia virus X*  
*Schlumbergera virus X*  
*Zygocactus virus X*

## References

Koenig R, Pleij CWA, Loss S, Burgermeister W, Aust H, Schiemann J (2004) Molecular characterisation of potexviruses isolated from three different genera in the family *Cactaceae*. Arch. Virol. 149: 903-914.

Liou MR, Chen YR, Liou RF (2004) Complete nucleotide sequence and genome organization of a *Cactus virus X* strain from *Hylocereus undatus* (Cactaceae). Arch Virol 149: 1037-1043

**Annexes: Table 1 and Fig. 1.**

Table 1. Percentage nucleotide (nt) or amino acid (aa) identity in pairwise comparisons between the replication protein (Rep) or capsid protein (CP) of potexvirus isolates from species in the family Cactaceae (CVX, Cactus virus X, AF308158; OpVX, Opuntia virus X, AY366209; SchVX, Schlumbergera virus X, AY366207 and ZyVX, Zygocactus virus X, AY366208)

	<b>Rep</b>				<b>CP</b>			
	CVX	OpVX	ZyVX		CVX	OpVX	SchVX	ZyVX
				<b>%nt ide</b>				
CVX	*	65.1	72.3		*	57.9	68.9	72.4
OpVX		*	65.6			*	62.8	60.0
SchVX			-				*	66.8
								*
				<b>%aa ide</b>				
CVX	*	66.5	80.5		*	59.4	76.4	78.2
OpVX		*	67.9			*	62.2	61.5
SchVX			-				*	75.7

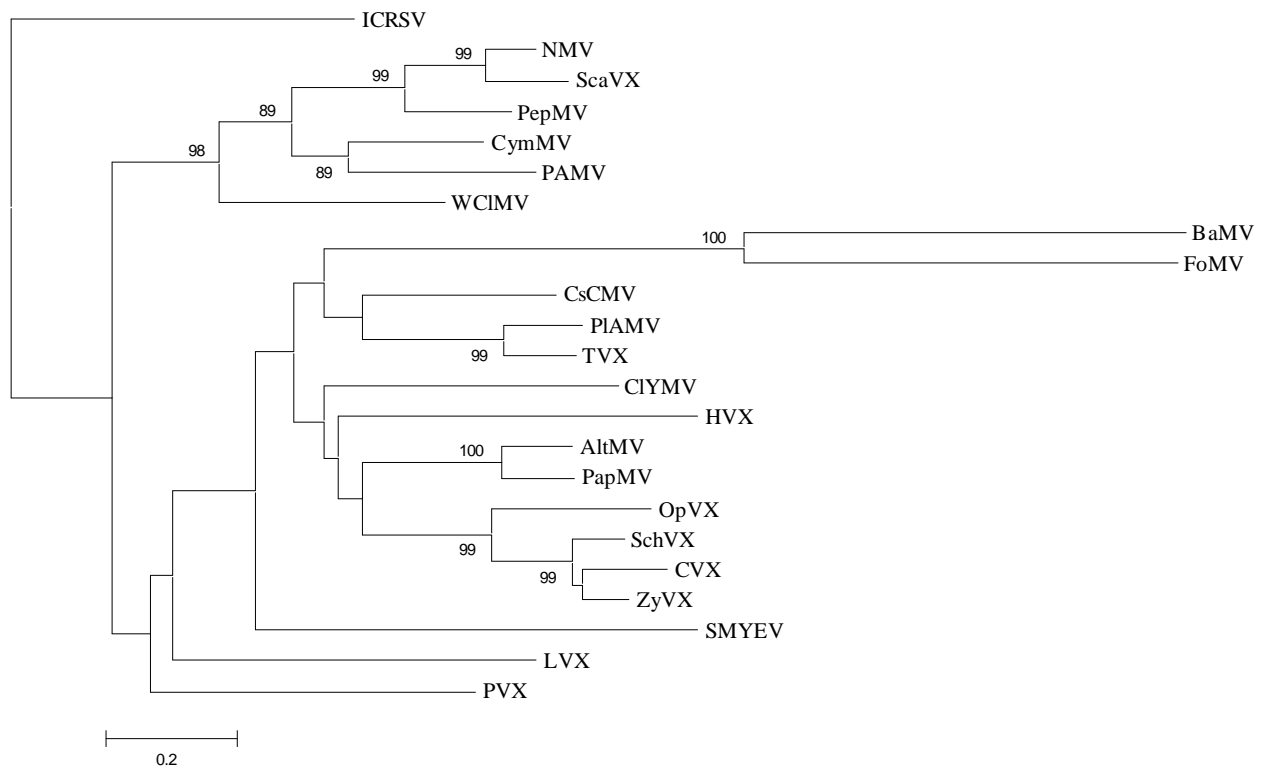


Fig. 1. Phylogenetic (Neighbor-Joining) tree of the capsid protein amino acid sequences of species in the genus *Potexvirus* to show the position of the species infecting members of the Cactaceae, *Cactus virus X* (CVX), *Opuntia virus X* (OpVX), *Schlumbergera virus X* (SchVX) and *Zygocactus virus X* (ZyVX). Bootstrap values (%), based on 1000 replicates, are shown where >70.