

This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: TITLE, AUTHORS, etc

Code assigned:				(to be cor	to be completed by ICTV officers)		
Short title: Abolish 3 species from the genus (e.g. 6 new species in the genus Zetavirus) Modules attached (modules 1 and 10 are required)		Potexvirus 1 6	s, family 2 2 □ 7 ⊠	Alphaflexi 3	iviridae 4 □ 9 □	5 □ 10 ⊠	
Author(s):							
Mike Adams & Jan Kreuze on behalf of the Flexiviridae SG							
Corresponding author with e-mail address:							
Jan Kreuze, j.kreuze@cgiar.org							
List the ICTV study group(s) that have seen this proposal:							
A list of study groups and contacts http://www.ictvonline.org/subcommin doubt, contact the appropriate schair (fungal, invertebrate, plant, poetebrate viruses)	mittees.asp . If subcommittee	Flexiviri	idae				
ICTV Study Group comments (if any) and response of the proposer:							
Date first submitted to ICTV: June 2015 Date of this revision (if different to above):							
ICTV-EC comments and response of the proposer:							

MODULE 7: REMOVE and MOVE

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)
- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	201	5.014aP	(assigned by ICTV officers)			
To remove the following taxon (or taxa) from their present position:						
Commelina virus X						
Daphne virus X						
Plantago severe mottle virus						
The present taxonomic position of these taxon/taxa:						
G	enus:	Potexvirus				
Subfa	mily:		Fill in all that apply			
Fa	mily:	Alphaflexiviridae	Fill in all that apply.			
C	rder:	Tymovirales				
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" YES						
in the box on the right						

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

These species have been included in the Master Species List for many years but there are no sequences (even genome fragments) and most were created on the basis of a single research report 30-40 years ago. Genus assignment was done on the basis of particle morphology and sometimes serological affinities but cannot be assured without sequence data. There has been no published work on any of these viruses for over 30 years and the viruses are not represented in any culture collection. In the absence of authentic material associated with the viruses it seems inappropriate to retain the species on the ICTV list. Names will of course remain in the historical records and the Study Group will include them in lists of viruses that are possible members of the genus.

In particular:

Commelina virus X: Known from one brief report in the UK (Stone, 1980).

Daphne virus X: Studied in New Zealand 1975-1978 (Forster & Milne, 1978).

Plantago severe mottle virus: Known from one study in Canada (Rowhani & Peterson, 1980).

MODULE 10: APPENDIX: supporting material

additional material in support of this proposal

References:

Forster RL, Milne KS. (1978) Daphne virus X AAB Descriptions of Plant Viruses no. 195 Rowhani A, & Peterson JF. (1980). Characterization of a Flexuous Rod-Shaped Virus from Plantago. Can J Plant Pathol 2:12-18

Stone, O.M. (1980). Two new potexviruses from monocotyledons. Acta Hort. 110: 59.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.