



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**

<b>Code assigned:</b>	<b>2015.013aP</b>	(to be completed by ICTV officers)			
<b>Short title:</b> 1 new species in the genus <i>Potexvirus</i> , family <i>Alphaflexiviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

**Author(s):**

Mike Adams & Jan Kreuze on behalf of the *Flexiviridae* SG

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**List the ICTV study group(s) that have seen this proposal:**

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

*Flexiviridae* SG

**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):

July 28, 2015

**ICTV-EC comments and response of the proposer:**

EC comments: Define abbreviations in Fig. 1. A typo was also corrected in the reference list.

Response: Done

## MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	<b>2015.013aP</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<b><i>Potexvirus</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<b><i>Alphaflexiviridae</i></b>	
Order:	<b><i>Tymovirales</i></b>	
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Yam virus X</i>	T551	KJ711908

### Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria.**
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Yam virus X was first described in yam plants from a collection in Guadeloupe showing mild mosaic symptoms. It was detected in plants using potexvirus consensus primers and the entire genome was subsequently determined by sequencing of PCR products and 5'-RACE (KJ711908; Mambole et al., 2014). Genome organization (5ORFs: a replicase, a Triple Gene Block and a coat protein) together with phylogenetic analyses of the replicase and coat protein amino acid sequences (Annex Fig. 1), place YVX within the genus *Potexvirus* and most closely related to Nerine virus X but amino acid sequence identities between their polymerase or coat protein sequences were only ~50%. The virus could not be transmitted to a range of commonly-used plant virus indicator hosts. Using PCR primers designed from the sequence, YVX was also detected in several other accessions in the germplasm collection. Small genome fragments of two other phylogenetically distinct potexviruses were also identified from yam accessions.

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: isolates of different species have less than about 72% nt identity (or 80% aa identity) between their CP or polymerase genes.

YVX clearly meets the criteria to be a new species in the genus *Potexvirus*.

**Note:** Five complete sequences from China labelled Yam virus X have also been deposited in the sequence databases (KJ789131-34; KM009120). There are no publications associated with them. They have 88-99% nucleotide identity between themselves and have the genome characteristics of a potexvirus, but comparisons show that they do not belong to the same species as isolate T551 (only 49% aa identity between their replicase proteins) and they are not closely related to the sequences of any other member of the genus. In the absence of a publication, these are not being used to propose a further species at this stage but one of the sequences is included in the phylogenetic trees for comparative purposes (labelled YCVX).

MODULE 10: **APPENDIX:** supporting material

additional material in support of this proposal

**References:**

Mambole I.A., Bonheur L., Dumas L.S., Filloux D., Gomez R.M., Faure C., Lange D., Anzala F., Pavis C., Marais A., Roumagnac P., Candresse T., Teycheney P.Y. (2014). Molecular characterization of yam virus X, a new potexvirus infecting yams (*Dioscorea* spp) and evidence for the existence of at least three distinct potexviruses infecting yams. Arch. Virol. 159:3421-3426.

**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.

Fig 1. Phylogenetic tree of the concatenated replicase and coat protein amino acid sequences of members of the family *Alphaflexiviridae*. Neighbor-Joining Tree (JTT substitution model) with 1000 bootstrap replicates produced in MEGA6 with Donkey orchid symptomless virus (DOSV) as outgroup. Percentage bootstrap support is shown at all branches if >60%. Yam virus X (YVX) is shown in red. Other abbreviations: AAV-1, Ambrosia asymptomatic virus 1; ActVX, Actinidia virus X; AlsVX, Alstroemeria virus X; AltMV, Alternanthera mosaic virus; AlVX, Allium virus X; AV-3, Asparagus virus 3; BaMV, Bamboo mosaic virus; BotV-F, Botrytis virus F; BotV-X, Botrytis virus X; BVE, Blackberry virus E; CIYMV, Clover yellow mosaic virus; CsCMV, Cassava common mosaic virus; CVX, Cactus virus X; CymMV, Cymbidium mosaic virus; CYVCV, Citrus yellow vein clearing virus; FoMV, Foxtail mosaic virus; GarV-A, Garlic virus A; GarV-B, Garlic virus B; GarV-C, Garlic virus C; GarV-D, Garlic virus D; GarV-E, Garlic virus E; GarV-X, Garlic virus X; HdRSV, Hydrangea ringspot virus; HVX, Hosta virus X; ICRSV, Indian citrus ringspot virus; LeVX, Lettuce virus X; LoLV, Lolium latent virus; LVX, Lily virus X; MalMV, Malva mosaic virus; MVX, Mint virus X; NMV, Narcissus mosaic virus; NVX, Nerine virus X; OpVX, Opuntia virus X; PAMV, Potato aucuba mosaic virus; PapMV, Papaya mosaic virus; PepMV, Pepino mosaic virus; PhVX, Phaius virus X; PitVX, Pitaya virus X; PIAMV, Plantago asiatica mosaic virus; PVX, Potato virus X; SchVX, Schlumbergera virus X; ShVX, Shallot virus X; SMYEV, Strawberry mild yellow edge virus; SSDaV, Sclerotinia sclerotiorum debilitation-associated RNA virus; SSDaV-2, Sclerotinia sclerotiorum debilitation-associated RNA virus 2; TRMV, Tamus red mosaic virus; TVX, Tulip virus X; WCIMV, White clover mosaic virus; ZyVX, Zygocactus virus X.

