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:	***2012.017a,bP***	(to be completed by ICTV officers)

Short title: create three species in the family *Alphaflexiviridae*, one to be unassigned in the family and two assigned to the genus *Potexvirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒ **6** ☐	**2** ☒ **7** ☐	**3** ☐ **8** ☐	**4** ☐ **9** ☒	**5** ☐

Author(s) with e-mail address(es) of the proposer:

Jan Kreuze (j.kreuze@cgiar.org) on behalf of the *Flexiviridae* SG

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-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:
Date of this revision (if different to above):

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	***2012.017aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***unassigned***
Subfamily:	
Family:	***Alphaflexiviridae***
Order:	***Tymovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

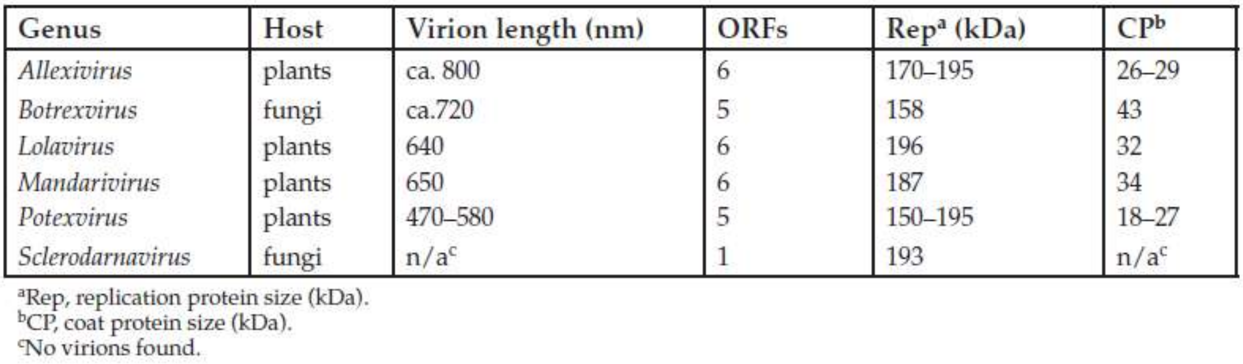
And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Blackberry virus E	JN053266

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

The family *Alphaflexiviridae* contains viruses with flexuous filamentous virions that infect plants and a few viruses discovered in plant-infecting fungi. They share a distinct lineage of alphavirus-like replication proteins that is unusual in lacking any recognized protease domain. Throughout the family, isolates of different species should have less than about 72% nt identity (or 80% aa identity) between their respective CP or polymerase genes. Viruses from different genera usually have less than about 45% nt identity in these genes.

Table 1: Distinguishing properties of genera in the family *Alphaflexiviridae*



Genus	Host	Virion length (nm)	ORFs	Rep[a] (kDa)	CP[b]
Allexivirus	plants	ca. 800	6	170–195	26–29
Botrexvirus	fungi	ca.720	5	158	43
Lolavirus	plants	640	6	196	32
Mandarivirus	plants	650	6	187	34
Potexvirus	plants	470–580	5	150–195	18–27
Sclerodarnavirus	fungi	n/a[c]	1	193	n/a[c]

[a] Rep, replication protein size (kDa).
[b] CP, coat protein size (kDa).
[c] No virions found.

Blackberry virus E (BVE; Sabanadzovic et al., 2011)

BVE was found in blackberry plants co-infected with Blackberry virus Y (*Brambyvirus*, *Potyviridae*), Phylogenetic analysis of BVE clearly puts it in same clade with other allexiviruses (Sabanadzovic et al., 2011; Fig 1); it contains the 'halmark' 40 k protein, and overall nt identity (~60%) consistent with same genus. However phylogenetically it is on its own branch as an outgroup from other allexivirueses (Sabanadzovic et al., 2011; Fig 1) and lacks the last ORF I, typical of allexiviruses. Therefore it is proposed that BVE be included as an unassigned species within the family *Alphaflexiviridae* until more information is available that may aid in its final classification.

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	***2012.017bP***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Potexvirus***
Subfamily:	
Family:	***Alphaflexiviridae***
Order:	***Tymovirales***

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Allium virus X *Lagenaria mild mosaic virus*	FJ670570 AB546335

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

Two new species in the genus *Potexvirus*

Allium virus X (AlVX; Miglino et al., 2010) and *Lagenaria mild mosaic virus* (LaMMoV; Kim et al., 2011), are two proposed new species in the genus potexvirus. AlVX was identified in plants of *Allium christophii, Allium giganteum, Allium unifolium* and *Allium globemaster* showing diffuse yellow stripes or leaf mottling in the Netherlands.
LaMMoV and was isolated from bottle gourd (*Lagenaria siceraria*) showing mosaic and mottle symptoms in Myanmar in 2007. In artificial inoculation tests, infectivity of LaMMoV was

limited to two families: *Chenopodiaceae* and *Cucurbitaceae*. The host range of LaMMoV differs from those of the two cucurbit-infecting potexviruses, *Alternanthera mosaic virus* (AltMV) and *Papaya mosaic virus* (PapMV) to which it is related.

The complete genomes of AlVX and partial genome sequence of LaMMoV (3'-terminal 3,859 nts) nucleotides, show that sequence similarity with other viruses within the genus are well below the species demarcation limit for the genus Potexvirus. In the case of AlVX it was 52 and 26% identical to its closest relative in the RDRP and CP, respectively (Miglino et al., 2010), and in the case of LaMMoV the CP gene showed less than 69% identity with those of AltMV and PapMV isolates at the nucleotide level, and 75% identity with that of AltMV and 73 to 76% identities with those of PapMV isolates at the amino acid level.

The list of species demarcation criteria in the genus Potexvirus 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.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Kim O.-K., Mizutani T., Khin Soe, Lee K.-W., Natsuaki K.T. (2010). Characterization of Lagenaria mild mosaic virus, a New Potexvirus from Bottle Gourd in Myanmar. Plant Dis. 94:1225-1230.

Miglino R., Druffel K.L., van Schadewijk A.R., Pappu H.R. (2011). Molecular characterization of allium virus X, a new potexvirus in the family Alphaflexiviridae, infecting ornamental allium. Arch. Virol. 156(11):2113-2115.

Sabanadzovic S., Abou Ghanem-Sabanadzovic N., Tzanetakis I.E. (2011). Blackberry virus E: an unusual flexivirus. Arch. Virol. 156(9):1665-1669.

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.

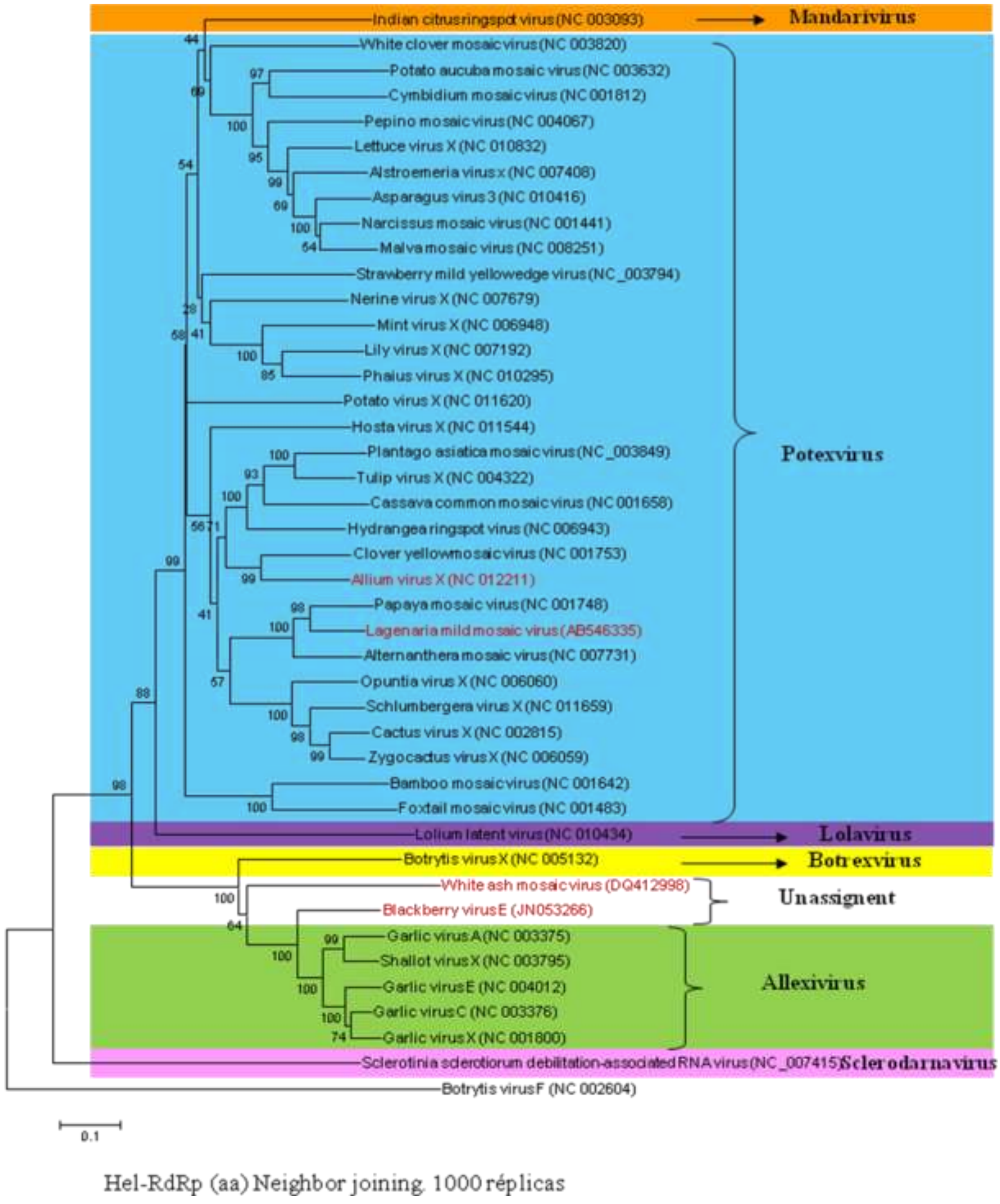


Fig 1. Phylogenetic tree of Alphaflexiviridae based on ClustalW alignment of Helicase and RdRp domain amino acid sequences. Putative new viruses are indicated with red font.