MODULE 1: **TITLE, AUTHORS, etc**

Code assigned: *2009.005a,bP* (to be completed by ICTV officers)	

Short title: 1 new species in the genus Potexvirus
(e.g. 6 new species in the genus *Zetavirus*)

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

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

Mike Adams on behalf of the Flexiviridae Study Group mike.adams@bbsrc.ac.uk

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

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

Date first submitted to ICTV: May 2009
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	*2009.005aP*	(assigned by ICTV officers)

To create 1 new species with the name(s):

Lettuce virus X

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	*2009.005bP*	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	*Potexvirus*
Subfamily:	
Family:	*Alphaflexiviridae* **(awaiting ratification)**
Order:	*Tymovirales* **(awaiting ratification)**

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.

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Throughout the family, species are recognized because of their specific natural host range, serological and molecular differences; distinct species have less than *ca.* 72% identical nt or 80% identical aa between their CP or polymerase genes (Adams et al., 2004; Martelli et al., 2007).

The following details (from Dizadji et al., 2008) show that lettuce virus X (LeVX) clearly satisfies the criteria to be recognized as an independent species in the genus *Potexvirus*.

LeVX was isolated from lettuce plants in Iran and shown to be infectious. Lettuce plants may contain high concentrations of the virus but remain apparently free from symptoms. The virus causes systemic vein yellowing in the assay host *Chenopodium quinoa* and can also infect *Nicotiana benthamiana*. The full genome sequence has been determined (AM745758) and an infectious clone prepared. Particle morphology and genome organization are typical of member of the genus *Potexvirus*. No member of this genus has previously been reported from lettuce and the virus did not react with a range of potexvirus antisera. In sequence comparisons, LeVX was most closely related to Alstroemeria virus X (68% aa identity in the replication protein; 62% aa identity in the coat protein). It also groups with this virus and with Narcissus mosaic virus and Asparagus virus 3 in phylogenetic analyses of these genes (see Annex, Figure 1).

additional material in support of this proposal

References:

Adams MJ, Antoniw JF, Bar-Joseph M, Brunt AA, Candresse T, Foster GD, Martelli GP, Milne RG, Zavriev SK, Fauquet CM (2004) The new plant virus family Flexiviridae and assessment of molecular criteria for species demarcation. Arch. Virol. 149:1045-1060.

Dizadji A, Koohi-Habibi M, Izadpanah K, Dietrich C, Mossahebi GH, Winter S. (2008). Characterisation of lettuce virus X, a new potexvirus infecting lettuce in Iran. Arch Virol 153:1867-1875.

Martelli G, Adams MJ, Kreuze JF, Dolja VV (2007) Family Flexiviridae: a case study in virion and genome plasticity. Ann. Rev. Phytopathol. 45:73-100

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.

Fig. 1 Phylogenetic tree of the replication protein of all sequenced members of the genus
Potexvirus and Shallot virus X (genus *Allexivirus*). The tree was generated from a codon-aligned
nucleotide sequence using MEGA4 (Neighbor-Joining, Maximum Composite Likelihood method
with 10,000 bootstrap replicates. Bootstrap values shown when >60%. The position of lettuce
virus X (LeVX) is highlighted.