Taxonomic proposal to the ICTV Executive Committee

This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.006P***	(to be completed by ICTV officers)

Short title: 2 new species in the genus Potexvirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached
(please check all that apply)**:**

1 ☐	2 ☐	3 ☐	4 ☐	5 ☒
6 ☐	7 ☐			

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

Mike Adams (mike.adams@bbsrc.ac.uk) on behalf of the Flexiviridae SG

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

MODULE 5: **NEW SPECIES**

Code	***2008.006P***	(assigned by ICTV officers)

To create 2 new species assigned as follows:

Genus:	*Potexvirus*
Subfamily:	
Family:	**proposed family *Alphaflexiviridae* (formerly *Flexiviridae*)**
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Malva mosaic virus
Phaius virus X

Argument to justify the creation of the new species:
If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Species demarcation criteria published in the 8th report are:

Each distinct species usually has a specific natural host range. Distinct species do not cross-protect in infected common host plant species. Distinct species are readily differentiated by serological procedures; strains of individual species are often distinguishable in reactions with polyclonal antisera, but more readily so with monoclonal antibodies. Distinct species have less than *ca.* 72% identical nt or 80% identical aa between their CP or polymerase genes.

Argument to justify the creation of the new species:

Both viruses have been characterized and the sequence of their entire genomes determined. Phylogenetic analyses (Fig. 1) and sequence comparisons justify their status as distinct species within the genus *Potexvirus* (i.e. with less than 80% amino acid identity to existing species in their polymerase sequence):
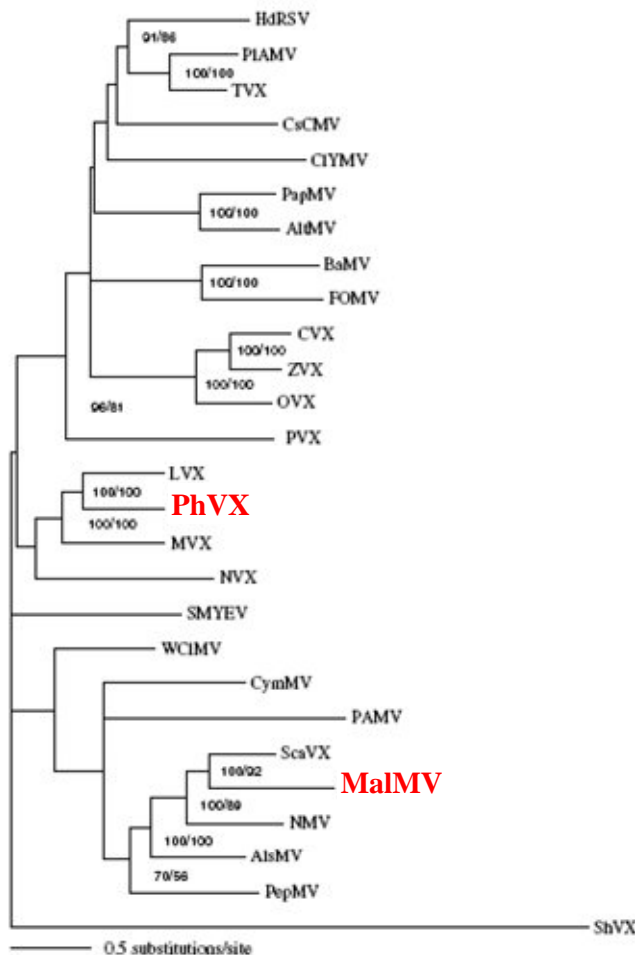
Malva mosaic virus
The virus was isolated from *Malva neglecta* (common mallow) and propagated in *Chenopodium quinoa*. The complete sequence (DQ660333; originally labeled Chenopodium virus X) was determined (Cote et al., 2008). The polymerase has 63-67% amino acid identity its nearest relatives in the genus (ScaVX and other isolates of Asparagus virus 3).

Phaius virusX
Complete sequence (AB353071); Kawakami et al., 2008. Polymerse has 69% aa identity to Lily virus X (LVX), its nearest relative in the genus. Following mechanical inoculation, the virus caused systemic, but symptomless, infection in *Phaius flavus* but did not infect a range of other common indicator plants.

Fig. 1. Phylogenetic tree of the nucleotide sequences of the polymerase (ORF1) of members of the genus *Potexvirus* with Shallot virus X (ShVX, genus Allexivirus), as an outgroup. Tree constructed in PAUP 4.0; the bootstrap values from 1000 replicates using two methods (NJ/maximum parsimony) are shown at the right of the branches. From Kawakami et al., 2008.

References:

Cote F., Pare C., Majeau N., Bolduc M., Leblanc E., Bergeron M.G., Bernardy M.G., Leclerc D. (2008). Nucleotide sequence and phylogenetic analysis of a new potexvirus: Malva Mosaic Virus. Infect. Genet. Evol. 8:83-93

Kawakami, K., Fuji, S., Miyoshi, K. (2008). Complete nucleotide sequence of a new potexvirus, "Phaius virus X", isolated from *Phaius flavus* Lindl. Arch. Virol. 153:527-531