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:	***2012.022aP***	(to be completed by ICTV officers)

Short title: create three new species in the genus *Carlavirus*, family *Betaflexiviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

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

John Hammond; john.hammond@ars.usda.gov

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)	(Flexivirus study group)

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	***2012.022aP***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Carlavirus***
Subfamily:	
Family:	***Betaflexiviridae***
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:**
Phlox virus S	EF492068 (NC_009383)
Phlox virus B	EU162589 (NC_009991)
Phlox virus M	EF507476

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

Phlox virus S

Phlox virus S (PhlVS) was initially isolated from *Phlox stolonifera* (*Polemoniaceae*), and is readily mechanically transmissible, having an experimental host range including systemic infection of *Phlox drummondii* (*Polemoniaceae*), *Nicotiana benthamiana, N. clevelandii, N. edwardsonii, N. megalosiphon*, and *N. debneyi* (*Solanaceae*), and (local infection only) three species in the *Scrophulariaceae* (*Verbascum phoeniceum, Antirrhinum majus*, and *Digitalis purpurea*), *Nicotiana glutinosa*, and *Polemonium caeruleum* (*Polemoniaceae*).

The full genome of PhlVS has been sequenced (EF492068; NC_009383), and consists of 8590 nt not including the poly(A) tail. The genome organization (Polymerase, Triple gene block, Coat protein, and Nucleic acid binding protein) is typical of the genus Carlavirus. Full genome analysis using the PASC tool at NCBI (http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview) reveals a 51.5-53.56% match to four isolates of *Chrysanthemum virus B* (CVB) by BLAST-based alignment, and 61.03-62.79% to *Chrysanthemum virus B* by global alignment, with lower degrees of identity to other species of the genus *Carlavirus*. These include Phlox virus B (51.2% by BLAST-based alignment; 60.6% by global alignment).

Pairwise comparisons of the polymerase and coat protein amino acid sequences reveal identities of 54% or less for the polymerase, and 62% or less for the coat protein. These values are lower than the species demarcation value of <80% identity. Nucleotide sequence comparisons revealed maximum identities of 69% (CVB) or 73% (PhlVB) over only portions (less than 2.5 Kb of the c.6 Kb polymerase gene) of the equivalent polymerase sequences of other carlaviruses; and 68% (*Helenium virus S*, HelVS), 67% (CVB), 71% (*Cowpea mild mottle virus*, CpMMV), and 71% (*Daphne virus S*, DVS) over the core region of the coat protein nucleotide sequence. The overall nucleotide identities of the complete polymerase and coat protein genes are clearly lower than the 72% identity established for demarcation between carlavirus species.

A Neighbor-joining phylogenetic tree of all available carlavirus CP sequences groups PhlVS with HelVS, PhlVB, CVB, and DVS, at equivalent distance to other distinct carlavirus sequences; a similarly constructed tree of polymerase sequences groups PhlVS, PhlVB, CVB, and DVS, consistent with each being distinct species (see Appendix).

Serological cross-reactivity was detected with antisera prepared against *Potato virus S* (PVS) and *Kalanchoe latent virus* (KLV); no serological reactivity to PhlVS was detected with antisera against *Blueberry scorch virus* (BlScV), *Carnation latent virus* (CLV), CVB, *Garlic common latent virus* (GCLV), *Lily symptomless virus* (LSV), *Potato virus M* (PVM), or *Shallot latent virus* (ShLV). Comparison of aligned sequences revealed that PhlVS, PVS, and KLV share a conserved five residue sequence (PKPDP) close to the coat protein N-terminus, which differs from CVB (PKPAP) by a single residue, and which is not present in other carlavirus coat protein sequences examined. A polyclonal antiserum raised against purified PhlVS has been used to specifically detect PhlVS in infected plants by ELISA.

Electron microscopy reveals particles of typical carlavirus morphology, of mean length c. 640nm.

Phlox virus B

Phlox virus B (PhlVB) was initially detected in *Phlox divaricata*, and is mechanically transmitted with some difficulty to a very limited host range, including *Phlox drummondii* (*Polemoniaceae*) and *Digitalis purpurea* (*Scrophulariaceae*).

The full genome of PhlVB has been sequenced (EU162589; NC_009991), and consists of 9058 nt not including the poly(A) tail. The genome organization (Polymerase, Triple gene block, Coat protein, and Nucleic acid binding protein) is typical of the genus Carlavirus. Full genome analysis using the PASC tool at NCBI (http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview) reveals a 51.2% match to PhlVS, 48.9% to DVS, 48.33-48.69% match to five isolates of CVB, and lower matches to other carlaviruses by BLAST-based alignments; and 60.58% to PhlVS, 58.96-60.29% to five isolates of CVB, 59.11% to DVS, and lower matches to other carlaviruses by global alignment.

Pairwise comparisons of the polymerase and coat protein amino acid sequences reveal identities of 55% or less for the polymerase, and 67% or less for the coat protein. These values are lower than the species demarcation value of <80% identity. Nucleotide sequence comparisons revealed maximum identities of 67-77% (CVB) or 73% (PhlVS) over only portions (less than 2.5 Kb of the c.6 Kb polymerase gene) of the equivalent polymerase sequences of other carlaviruses; and 69-72% (DVS), 67-70% (CVB), 71% (PhlVM), and 70%

(PhlVS) over the core region of the coat protein nucleotide sequence. The overall nucleotide identities of the complete polymerase and coat protein genes are clearly lower than the 72% identity established for demarcation between carlavirus species.

A Neighbor-joining phylogenetic tree of all available carlavirus CP sequences groups PhlVB with CVB, PhlVS, HelVS, and DVS, at equivalent distance to other distinct carlavirus sequences; a similarly constructed tree of polymerase sequences groups PhlVB, PhlVS, CVB, and DVS, consistent with each being distinct species (see Appendix).

No serological reactivity to PhlVB was detected with antisera against PhlVS, PVS, KLV, BlScV, CLV, CVB, GCLV, LSV, PVM, or ShLV.

Electron microscopy reveals particles of typical carlavirus morphology.

Phlox virus M

Phlox virus M (PhlVM) was initially detected in an annual phlox hybrid, and has been mechanically transmitted only to *Phlox drummondii*.

To date the partial Triple gene block 2 (TGB2), TGB3, Coat protein, Nucleic acid binding protein, and 3' non-coding region of one isolate (EF507476), and the TGB3, Coat protein, Nucleic acid binding protein, and 3' non-coding region of a second isolate (FJ159381) have been sequenced.

Analysis using the PASC tool at NCBI (http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview) reveals highest identity of the partial genome to *Potato virus M* (PVM), *Narcissus common latent virus* (NCLV), and *Aconitum latent virus* (AcLV) by BLAST-based alignments; and to PVM, NCLV, and *Hop latent virus* (HpLV) by global alignment.

Pairwise (BLAST) comparisons of the coat protein amino acid sequence reveals identities of 80-83% (PVM), 72-77% (NCLV), 73% (AcLV), 64-70% (HpLV) or less; and nucleotide identities of 72-75% (PVM), 70-71% (NCLV), 71% (AcLV) and 70% (HpLV) over aligned (incomplete) regions. Whereas these values fall close to the 80% (amino acid) and 72% (nucleotide) demarcation values for carlavirus species, the most closely related species (PVM) has a much wider host range, being readily transmissible to tomato. Pairwise alignment of PhlVM and PVM using ALIGN (Myers and Miller, CABIOS, 1999, 4:11-17) reveals 71.7% amino acid identity and 67.2% nucleotide identity over the full CP sequence, consistent with PhlVM being a distinct species; there is minimal amino acid identity within the CP N-terminal domain (see Appendix).

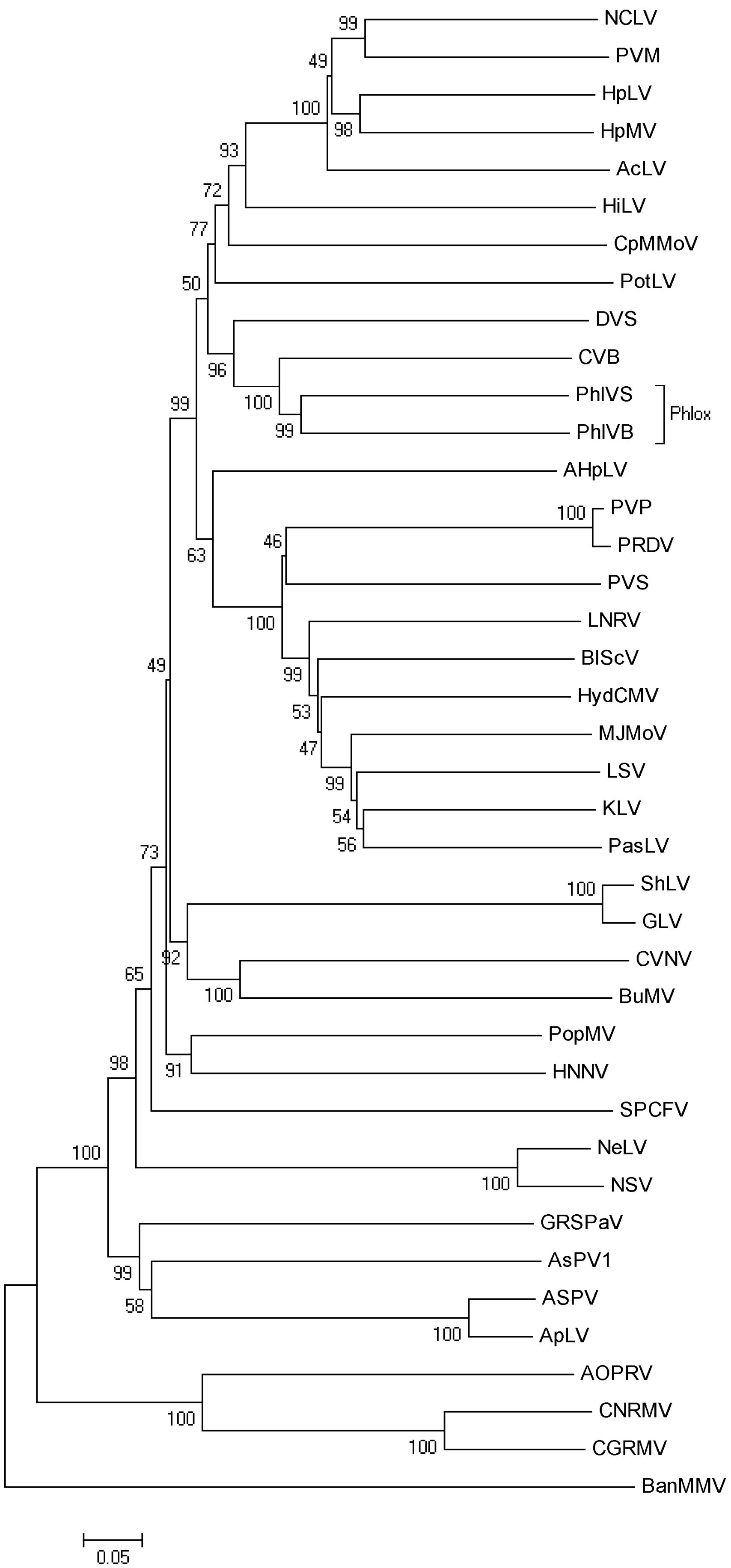
A Neighbor-joining phylogenetic tree of all available carlavirus CP sequences groups PhlVM most closely with AcLV, PVM, and NCLV, at equivalent distance as other distinct species (see Appendix).

Electron microscopy reveals particles of typical carlavirus morphology.

MODULE 9: **APPENDIX**: supporting material

A) Neighbor-joining tree of Carlavirus polymerase amino acid sequences; the position of PhlVS and PhlVB RdRp in the tree are indicated by a bracket.

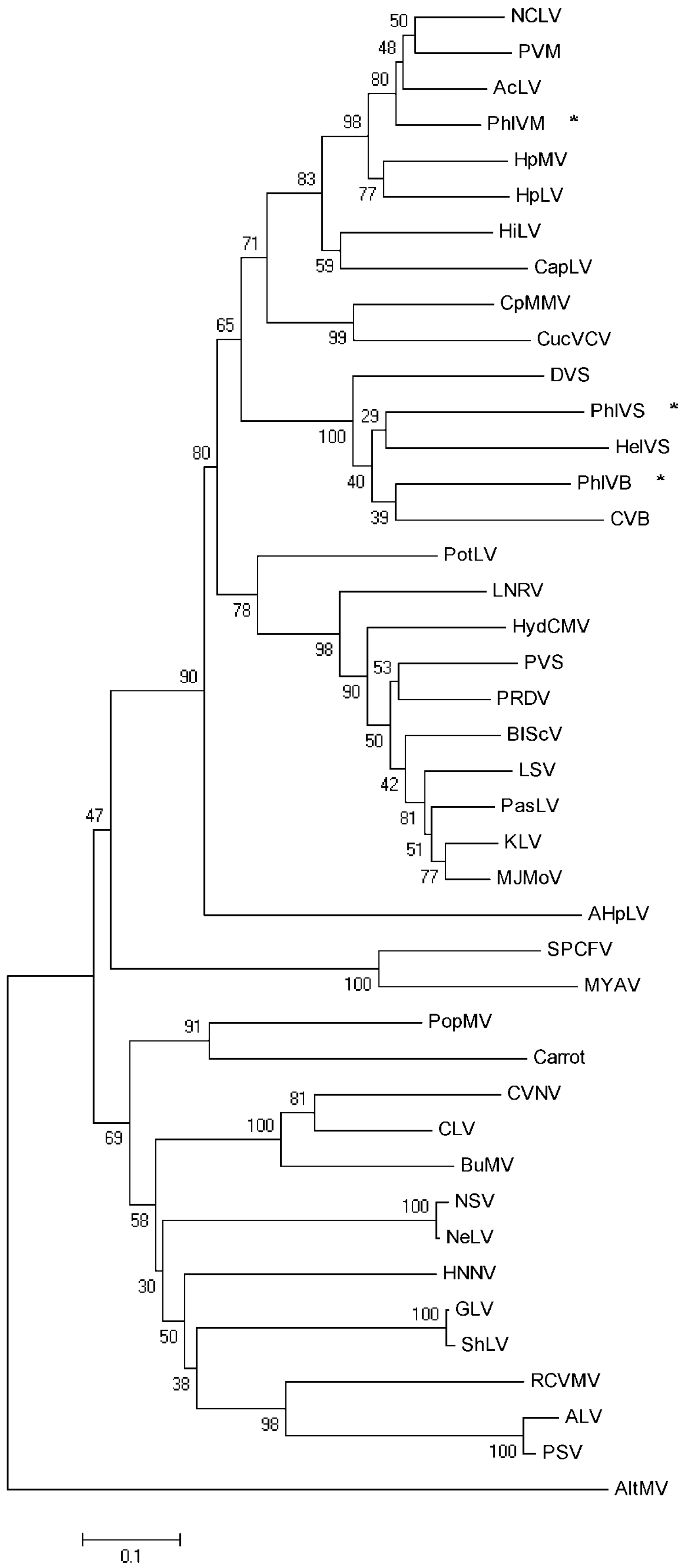
Virus abbreviations and accession numbers from which sequences were utilized: AcLV = *Aconitum latent virus*, NC002795; AHpLV = *American hop latent virus*, NC017859; AOPRV = *African oil palm ringspot virus* (unassigned), NC017859; ApLV = *Apricot latent virus* (*Foveavirus*), NC014821; ASPV = *Apple stem pitting virus* (*Foveavirus*), NC003462; AsPV1 = Asian prunus virus 1 (proposed Foveavirus), FJ824737; BanMMV = *Banana mild mosaic virus* (unassigned); BlScV = *Blueberry scorch virus*, NC003499; BuMV = Butterbur mosaic virus, NC013527; CGRMV = *Cherry green ring mottle virus* (unassigned), NC001946; CNRMV = *Cherry necrotic rusty mottle virus* (unassigned), NC002468; CpMMV = *Cowpea mild mottle virus*, NC014730; CVB = *Chrysanthemum virus B*, NC009087; CVNV = *Coleus vein necrosis virus*, NC009764; DVS = *Daphne virus S*, NC008020; GLV = Garlic latent virus, NC003557; GRSPaV = *Grapevine rupestris stem pitting-associated virus* (*Foveavirus*), NC_001948; HiLV = Hippeastrum latent virus, NC011540; HNNV = *Helleborus net necrosis virus*, NC012038; HpLV = *Hop latent virus*, NC002552; HpMV = *Hop mosaic virus*, NC010538; HydCMV = Hydrangea chlorotic mottle virus, NC012869; KLV = *Kalanchoe latent virus*, NC013006; LNRV = *Ligustrum necrotic ringspot virus*, NC010305; LSV = *Lily symptomless virus*, NC005138; MJMoV = Mirabilis jalapa mottle virus, NC016080; NCLV = *Narcissus common latent virus*, NC008266; NeLV = *Nerine latent virus*, JQ395043; NSV = *Narcissus symptomless virus*, NC008552; PasLV = *Passiflora latent virus*, NC008292; PhlVB = Phlox virus B, NC009991; PhlVS = Phlox virus S, NC009383; PopMV = *Poplar mosaic virus*, NC005343; PotLV = *Potato latent virus*, NC011525; PRDV = Potato rough dwarf virus, NC009759; PVM = *Potato virus M*, NC001361; PVP = *Potato virus P*, EU338239; PVS = *Potato virus S*, NC007289; ShLV = *Shallot latent virus*, JF320811; SPCFV = *Sweet potato chlorotic fleck virus*, NC006550.


NCLV
PVM
HpLV
HpMV
AcLV
HiLV
CpMMoV
PotLV
DVS
CVB
PhlVS
PhlVB
Phlox
AHpLV
PVP
PRDV
PVS
LNRV
BlScV
HydCMV
MJMoV
LSV
KLV
PasLV
ShLV
GLV
CVNV
BuMV
PopMV
HNNV
SPCFV
NeLV
NSV
GRSPaV
AsPV1
ASPV
ApLV
AOPRV
CNRMV
CGRMV
BanMMV
0.05

A.

B) Neighbor-joining tree of Carlavirus coat protein amino acid sequences; the positions of PhlVS, PhlVB, and PhlVM CP in the tree are indicated by aaterisks (*).

Virus abbreviations and accession numbers from which sequences were utilized: AcLV = *Aconitum latent virus*, NC002795; AHpLV = *American hop latent virus*, NC017859; ALV = Alfalfa latent virus, AY037925; AltMV = *Alternanthera mosaic virus* (*Potexvirus*, outgroup), NC007731; BlScV = *Blueberry scorch virus*, NC003499; BuMV = Butterbur mosaic virus, NC013527; CapLV = *Caper latent virus*, HQ588148; Carrot = carrot carlavirus, EU881919; CLV = *Carnation latent virus*, X52627; CpMMV = *Cowpea mild mottle virus*, NC014730; CucVCV = Cucumber vein-clearing virus, JN591720; CVB = *Chrysanthemum virus B*, NC009087; CVNV = *Coleus vein necrosis virus*, NC009764; DVS = *Daphne virus S*, NC008020; GLV = Garlic latent virus, NC003557; HelVS = *Helenium virus S*, D10454; HiLV = Hippeastrum latent virus, NC011540; HNNV = *Helleborus net necrosis virus*, NC012038; HpLV = *Hop latent virus*, NC002552; HpMV = *Hop mosaic virus*, NC010538; HydCMV = Hydrangea chlorotic mottle virus, NC012869; KLV = *Kalanchoe latent virus*, NC013006; LNRV = *Ligustrum necrotic ringspot virus*, NC010305; LSV = *Lily symptomless virus*, NC005138; MJMoV = Mirabilis jalapa mottle virus, NC016080; MYAV = Melon yellowing associated virus, AB510477; NCLV = *Narcissus common latent virus*, NC008266; NeLV = *Nerine latent virus*, JQ395043; NSV = *Narcissus symptomless virus*, NC008552; PasLV = *Passiflora latent virus*, NC008292; PhlVB = Phlox virus B, NC009991; PhlVM = Phlox virus M, EF507476; PhlVS = Phlox virus S, NC009383; PopMV = *Poplar mosaic virus*, NC005343; PotLV = *Potato latent virus*, NC011525; PRDV = Potato rough dwarf virus, NC009759; PSV = *Pea streak virus*, AF354652; PVM = *Potato virus M*, NC001361; PVS = *Potato virus S*, NC007289; RCVMV = *Red clover vein mosaic virus*, NC012210; ShLV = *Shallot latent virus*, JF320811; SPCFV = *Sweet potato chlorotic fleck virus*, NC006550.



NCLV
PVM
AcLV
PlVM *
HpMV
HpLV
HiLV
CapLV
CpMMV
CucVCV
DVS
PlVS *
HelVS
PlVB *
CVB
PotLV
LNRV
HydCMV
PVS
PRDV
BlScV
LSV
PasLV
KLV
MJMoV
AHpLV
SPCFV
MYAV
PopMV
Carrot
CVNV
CLV
BuMV
NSV
NeLV
HNNV
GLV
ShLV
RCVMV
ALV
PSV
AltMV
0.1

B.

C) Phlox virus S host range:

Species	**Local/Systemic**	**Symptoms**
Phlox stolonifera	+ / +	Mosaic*
Nicotiana benthamiana	+ / +	CLL/Chl or bronze mos.
N. clevelandii	+ / +	CLL/Chl or bronze mos
N. edwardsonii	+ / +	CLL/Chl or bronze mos
N. megalosiphon	+ / +	CLL/Chl or bronze mos
N. debneyi	+ / +	CLL/Chl or bronze mos
N. glutinosa	+ / -	CLL
N. tabacum	- / -	
N. sylvestris	- / -	
Verbascum phoeniceum	+ / -	Symptomless
Antirrhinum majus	+ / -	CLL
Polemonium caeruleum	+ / -	Symptomless
Digitalis purpurea	+ / -	Symptomless
Aquilegia hybrid	- / -	
Consolida ambigua	- / -	
Phlox drummondii	+ / +	No clear symptoms

*Note that initial infection was mixed with *Alternanthera mosaic virus* and *Tobacco ringspot virus.*

D) Phlox virus B host range

Species	**Local/Systemic**	**Symptoms**
Phlox divaricata	+ / +	Mosaic
Digitalis purpurea	+ / +	Mild mottle

E) Phlox virus M host range

Species	**Local/Systemic**	**Symptoms**
Annual *Phlox* hybrid	+ / +	Mosaic
Phlox drummondii	+ / +	Mosaic

F) Pairwise comparison of Phlox virus M (PhlVM) and Potato virus M (PVM) CP amino acid sequences

```
ALIGN calculates a global alignment of two sequences
 version 2.0

Please cite: Myers and Miller, CABIOS (1989) 4:11-17

PhlVM_CP                                    302 aa vs.
PVM_CP                                      304 aa
scoring matrix: BLOSUM50, gap penalties: -12/-2
71.7% identity;        Global alignment score: 1455


                      10        20             30        40        50
PhlVM_CP      MENEKKVAEDAQKKEQLKLKIQER-----AEASRTNNAKLQKFIEPEENMTEEEATLEQR
              : .  : :: :..    .    .:     ::    .:.   .  . : :   :::.::.:
PVM_CP        MGDSTKKAEVAKEAGTSQAAKGNRPLPTAAEFEGDDNSGDASVRDAEAN---EEASLERR
                      10        20        30        40           50

                 60        70        80        90       100       110
PhlVM_CP      LDSLRNWLRERRSATRVTNPGLETGRPQLKLASDMRPDPTNPYNRPSIDELSKIMPRAIS
              :.:::..:::::.: ::::::::::::.::::.::::::::::::::.. ::.: : :.:
PVM_CP        LNSLREFLRERRGAIRVTNPGLETGRPRLKLADDMRPDPTNPYNRPSLEALSRIKPIAVS
               60        70        80        90       100       110

                120       130       140       150       160       170
PhlVM_CP      NNMATSEDMMRIYVNLEGLGVPTEQVQKIVIQAVIYCKDASSSAYLDPRGSFEWPGGAIT
              :::::::::::::::::::::::: ::..:::::..:::::::.::::::::::: ::::
PVM_CP        NNMATSEDMMRIYVNLEGLGVPTEYVQQVVIQAVLFCKDASSSVYLDPRGSFEWPRGAIT
              120       130       140       150       160       170

                180       190       200       210       220       230
PhlVM_CP      ADAVLAVLKRDAETLRRVCRLYAPVTWNYMLTHNAPPSDWAAMGFQYEDRFAAFDCFDYV
              :::::::.:.::::::::::::::::::.::.::.::.::::::::::::::::::::::
PVM_CP        ADAVLAVMKKDAETLRRVCRLYAPVTWNHMLAHNSPPADWAAMGFQYEDRFAAFDCFDYV
              180       190       200       210       220       230

                240       250       260       270       280       290
PhlVM_CP      VNAAAVQPLEGLIRRPTPREQIAHNTHKDLALRAANRNQAFGNTSTEITGGKNGPELTRD
               :.:::::::::::::::::..:::::::.:::.:::::.:.. ..:.::: ::::::::
PVM_CP        ENTAAVQPLEGLIRRPTPREKVAHNTHKDIALRGANRNQVFSSLNAEVTGGMNGPELTRD
              240       250       260       270       280       290

                300
PhlVM_CP      YRKSNNQ
              . ::::.
PVM_CP        FSKSNNK
              300
```

G) Pairwise comparison of Phlox virus M (PhlVM) and Potato virus M (PVM) CP nucleotide sequences

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989) 4:11-17
PhlVM-IC_CP                                         909 nt vs.
PVM-Ru_CP                                           915 nt
scoring matrix: DNA, gap penalties: -16/-4
67.2% identity;        Global alignment score: 1796


                      10        20        30         40        50
PhlVM-IC_CP   ATGGAGAACGAGAAGAAGGCAGCGGAAGACGCTCAAAA-GAAGGAACAGCTGAAGTTGAA
              ::::   :    : ::::  ::: :::   ::  :: : :: :: ::  :  :::   :
PVM-Ru_CP     ATGGGAGATTCAACGAAGAAAGCTGAAACTGCCAAAGATGAGGGCACTTCGCAAGAA-AG
                      10        20        30        40        50

             60        70        80        90                100       110
PhlVM-IC_CP   GATACAGGAGCGCGCTGAGGCCTCACGTACTAAC---------AATGCCAAACTACAGAA
              :: : : : :::  :   : :  :   : :: ::         :: : :: :    ::::
PVM-Ru_CP     GAGAGAAGCGCGACCACTGCCGACTGCTGCTGACTTTGAGGGGAAGGACACATCGGAGAA
             60        70        80        90       100       110

                     120       130       140       150       160       170
PhlVM-IC_CP   ATTTATCGAGCCTGAAGAGAACATGACCGAAGAAGAAGCCACACTCGAGCAGCGCCTCGA
                 :   : :: ::  :   : ::: : :: : ::::    :: : :::: : : :: ::
PVM-Ru_CP     CACTGATGGGCGTGCTGC--AGATG-CTGATGGAGAAATGTCATTGGAGCGGAGGCTTGA
            120       130         140        150       160       170

                     180       190       200       210       220       230
PhlVM-IC_CP   TAGTCTGCGTAATTGGCTTCGTGAGCGTCGTAGCGCCACGCGCGTTACTAATCCTGGCCT
               :: :: ::  : :  :: :: :::::  :  :::: :  :: :: :: :: :: ::  :
PVM-Ru_CP     CAGCCTCCGAGAATTCCTGCGAGAGCGGAGGGGCGCAATTCGAGTGACAAACCCAGGGTT
               180       190       200       210       220       230

                     240       250       260       270       280       290
PhlVM-IC_CP   TGAGACTGGCCGTCCGCAGTTGAAGCTTGCAAGTGACATGCGTCCCGATCCAACTAACCC
               ::::::::: : ::   :::: :::: ::     : ::::: :: ::::: :: :: ::
PVM-Ru_CP     AGAGACTGGCAGGCCAAGGTTGCAGCTAGCTGAAAATATGCGCCCTGATCCCACGAATCC
               240       250       260       270       280       290

                     300       310       320       330       340       350
PhlVM-IC_CP   CTACAATCGCCCTTCTATTGACGAGTTGAGCAAAATTGTGCCGCGAGCCATTTCAAACAA
               :::::  : :: :: :: :: :   : :::   ::   :::    :: :: ::::::::
PVM-Ru_CP     GTACAACAGGCCGTCCATAGAAGCTCTCAGCCGGATCAAGCCAATCGCGATCTCAAACAA
               300       310       320       330       340       350

                     360       370       380       390       400       410
PhlVM-IC_CP   CATGGCTACCTCAGAAGACATGATGCGCATCTACGTGAATCTCGAGGGACTTGGCGTGCC
               ::::: :: :: :: :: :::::::::::: :: ::::: :: ::::: :: :: :::::
PVM-Ru_CP     TATGGCCACATCTGAGGATATGATGCGCATATATGTGAACCTGGAGGGGCTAGGGGTGCC
               360       370       380       390       400       410

                     420       430       440       450       460       470
PhlVM-IC_CP   CACGGAACAGGTCCAGAAAATTGTCATACAAGCGGTGATATATTGCAAGGATGCGAGTAG
               :: :: :: :: ::: :  : :: :: :: :: ::: ::: ::::::::: :: :: ::
PVM-Ru_CP     GACTGAGCACGTGCAGCAGGTAGTGATTCAGGCTGTGCTATTTTGCAAGGACGCAAGCAG
               420       430       440       450       460       470
```

```
                     480       490       500       510       520       530
PhlVM-IC_CP   TTCAGCTTATCTTGACCCGAGGGGCTCTTTTGAGTGGCCCGGTGGGGCCATCACTGCTGA
               :: :  :  :: :: ::: : ::::: :: ::::::::  : :: :: :: ::::: ::
PVM-Ru_CP     CTCCGTATTCCTGGATCCGCGAGGCTCGTTCGAGTGGCCAAGAGGTGCTATAACTGCAGA
               480       490       500       510       520       530

                     540       550       560       570       580       590
PhlVM-IC_CP   TGCGGTCTTGGCTGTACTTAAACGTGATGCTGAGACGCTTCGTAGGGTGTGTAGACTGTA
              ::: ::::::::::: :: ::    ::::: :: :: :: :: ::::::::::: :::::
PVM-Ru_CP     TGCCGTCTTGGCTGTGCTGAAGAAGGATGCAGAAACACTGCGAAGGGTGTGTAGGCTGTA
               540       550       560       570       580       590

                     600       610       620       630       640       650
PhlVM-IC_CP   TGCACCCGTCACATGGAATTACATGTTGACTCACAATGCCCCGCCGTCTGATTGGGCCGC
              ::: :: :: ::::::::: : ::: :::: ::::: :: :: ::: : :::::::: ::
PVM-Ru_CP     TGCCCCGGTGACATGGAATCATATGCTGACGCACAACGCGCCTCCGGCCGATTGGGCTGC
               600       610       620       630       640       650

                     660       670       680       690       700       710
PhlVM-IC_CP   TATGGGTTTCCAATATGAGGATAGATTTGCCGCTTTCGACTGCTTCGACTATGTGGTAAA
               ::::: :: :: ::::::::: : :: :: :::::::::::::: :: :: :: :  ::
PVM-Ru_CP     CATGGGGTTTCAGTATGAGGATCGCTTCGCTGCTTTCGACTGCTTTGATTACGTTGAGAA
               660       670       680       690       700       710

                     720       730       740       750       760       770
PhlVM-IC_CP   TGCAGCAGCAGTGCAACCTCTTGAAGGTCTCATCCGTAGGCCAACCCCACGGGAGCAGAT
              : : :: ::::: ::::: :: :: ::  : ::: :  : :: :::::: ::::  :: :
PVM-Ru_CP     TACTGCTGCAGTCCAACCCCTAGAGGGATTGATCAGGCGACCTACCCCAAGGGAAAAGGT
               720       730       740       750       760       770

                     780       790       800       810       820       830
PhlVM-IC_CP   TGCGCACAATACGCATAAGGATCTAGCGCTGCGTGCAGCCAACCGCAATCAGGCTTTTGG
               :: ::::::::::: :: ::  : ::  :::::: ::: :: ::::::::::  ::
PVM-Ru_CP     AGCTCACAATACGCACAAAGACATCGCAGTGCGTGGAGCAAATCGCAATCAGGTGTT---
               780       790       800       810       820       830

                      840         850       860       870       880
PhlVM-IC_CP   CAACACT-TCAA--CTGAGATTACGGGGGGAAAGAATGGTCCTGAGCTCACTAGAGATTA
              :: : :: ::::  : ::: : :: :: :: : ::::::::: :::::::::::::::::
PVM-Ru_CP     CAGCTCTCTCAATGCCGAGGTCACTGGTGGTATGAATGGTCCGGAGCTCACTAGAGATTA
                  840       850       860       870       880       890

              890       900
PhlVM-IC_CP   TAGAAAGTCGAACAATCAATGA
              :  :::::: :: :   :::::
PVM-Ru_CP     TGTAAAGTCTAATAGAAAATGA
                  900       910
```

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.