Template for Taxonomic Proposal to the ICTV Executive Committee
To create a new Genus in an existing Family

Code[†] 2005.017P.04 To create a new genus in the family* ***Flexiviridae***

Code[†] 2005.018P.04 To name the new genus* ***Citrivirus***

Code[†] 2005.019P.04 To designate the species ***Citrus leaf blotch virus***
As the type species of the new genus*

Code[†] To designate the following as species of the new genus*:

Citrus leaf blotch virus
Citrus leaf blotch virus-SRA-153 (CLBV-SRA153)
AJ318061

Code[†] To designate the following as tentative species in the new genus*:

[†] Assigned by ICTV officers
* repeat these lines and the corresponding arguments for each genus created in the family

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Old Taxonomic Order

Order
Family
Genus
Type Species
Species in the Genus
Tentative Species in the Genus
Unassigned Species in the family

New Taxonomic Order

Order
Family
Genus
Type Species
Species in the Genus
Tentative Species in the Genus
Unassigned Species in the family

ICTV-EC comments and response of the SG

Argumentation to choose the type species in the genus

Presently it is the only species described

Species demarcation criteria in the genus

List of Species in the created genus

List of Tentative Species in the created genus

Argumentation to create a new genus:

1) Although genome organization of CLBV resembles that of trichoviruses, it differs from these in the following aspects aspects: (i) in ACLSV and other trichoviruses ORF2 overlaps ORFs 1 (in 80-92 nt) and 3 (in 88-483 nt), whereas in CLBV, ORFs 2 and 3 are separated by an intergenic region and ORFs 1 and 2 overlap in just one nucleotide; (ii) the CP of CLBV is much larger than the CP of ACLSV and other trichoviruses; and (iii) the 3' untranslated region (3'UTR) of trichoviruses has between 141 and 190 nucleotides, excluding the poly(A) tail, whereas the 3'UTR of CLBV spans 541 nt. (see: http://www.danforthcenter.org/upload/ictvupload/2003.147-9P.05.Flexiviridae.doc)
2) Phylogenetic comparisons with members of the proposed genera within the family *Flexiviridae* (*Potexvirus*, *Mandarivirus, Allexivirus, Carlavirus, Foveavirus, Capillovirus, Vitivirus* and *Trichovirus*) in the RdRp and in the CP regions, show that CLBV is clearly separated from members of all these genera (see description of family *Flexiviridae*).
3) CLBV is seed borne in several citrus species or hybrids. With the exception of some carlaviruses seed transmission has not been reported from other members of the family *Flexiviridae*.

Origin of the proposed genus name

In nature *Citrus leaf blotch virus* has been found infecting only citrus species

References

GALIPIENSO, L., NAVARRO, L., BALLESTER-OLMOS, J.F., PINA, J.A., MORENO, **P.**, GUERRI, J. 2000. Host range and symptomatology of a graft-transmissible pathogen inducing bud union crease of citrus on trifoliate rootstocks. Plant Pathology 49: 308-314.

GALIPIENSO, L., VIVES, M.C., MORENO, P., MILNE, R.G., NAVARRO, L., GUERRI, J. 2001. Partial characterization of citrus leaf blotch virus, a new virus from Nagami kumquat. Archives of Virology 146: 357-368.

VIVES, M.C., GALIPIENSO, L., NAVARRO, L., MORENO, P., GUERRI, J. 2001. The nucleotide sequence and genome organization of *Citrus leaf blotch virus*: Candidate type species for a new virus genus. Virology 287, 226-233.

VIVES, M.C., GALIPIENSO, L., NAVARRO, L., MORENO, P., GUERRI, J. 2002. Characterization of two kinds of subgenomic RNAs produced by *Citrus leaf blotch virus*. Virology 295: 328-336.

VIVES M.C., RUBIO, L., GALIPIENSO, L., NAVARRO, L:, MORENO, P., GUERRI, J. 2002. Low genetic variation between isolates of *Citrus leaf blotch virus* from different host species and of different geographic origins. Journal of General Virology 83: 2587-2591.

GUERRI, J., PINA, J.A., VIVES, M.C., NAVARRO L., MORENO, P. 2004. Seed transmission of Citrus leaf botch virus: Implications in quarantine and certification programs. Plant Disease 88: 906

Annexes:

Genomic organization of CLBV

p227: replicase (includes methyltransferase helicase and RdRp motifs

p40: potential movement protein

p41: coat protein

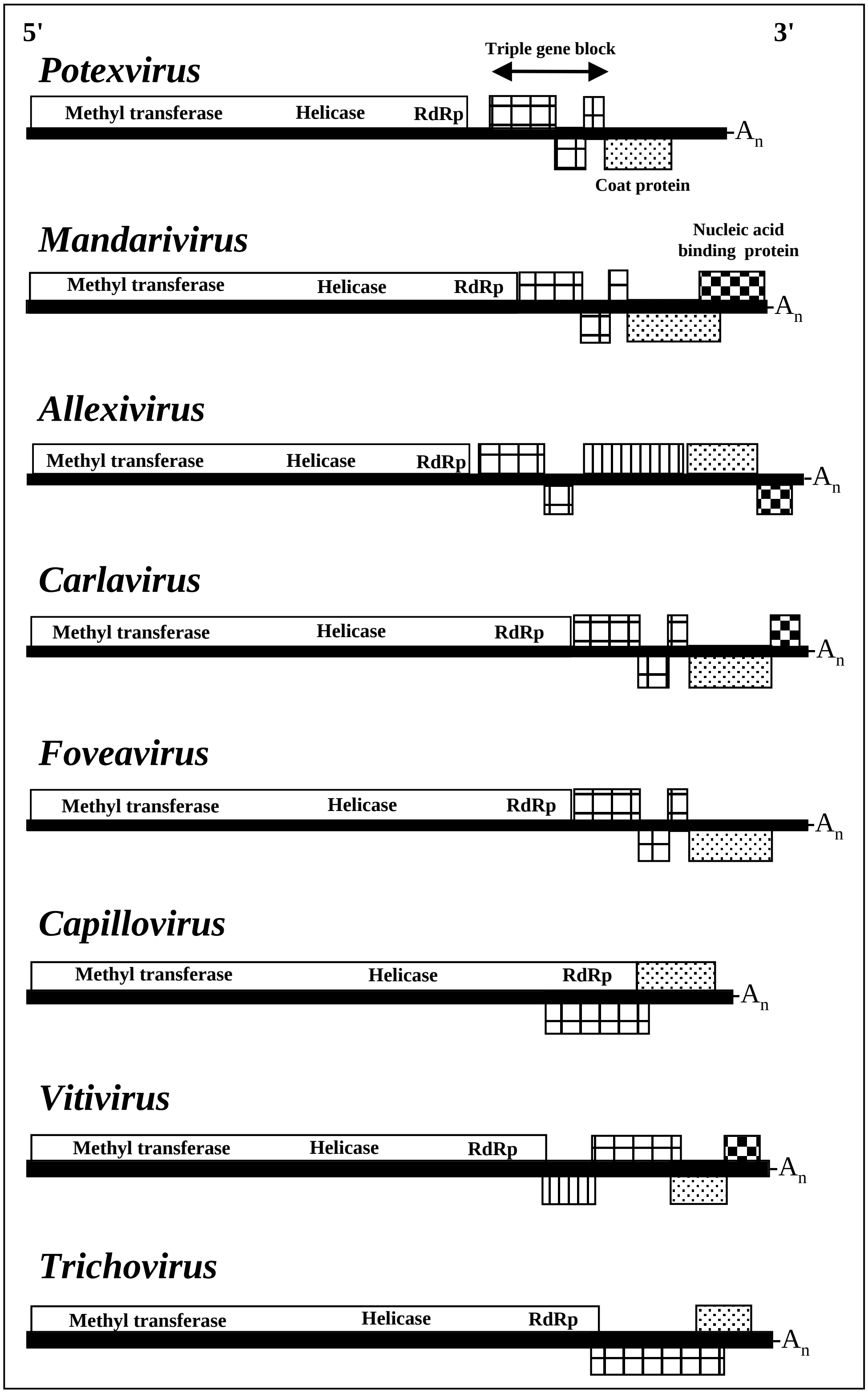

Fig. 1. Phylogenetic (NEIGHBOR) analysis of the members of the proposed family Potexviridae using aa sequences of the RdRp region of the polymerase. Sequences were aligned using GCG PILEUP and genetic distances estimated by PROTDIST (Dayhoff PAM method). Trees were displayed in TreeView. Bootstrap values based on 100 replicates are shown where >60%.

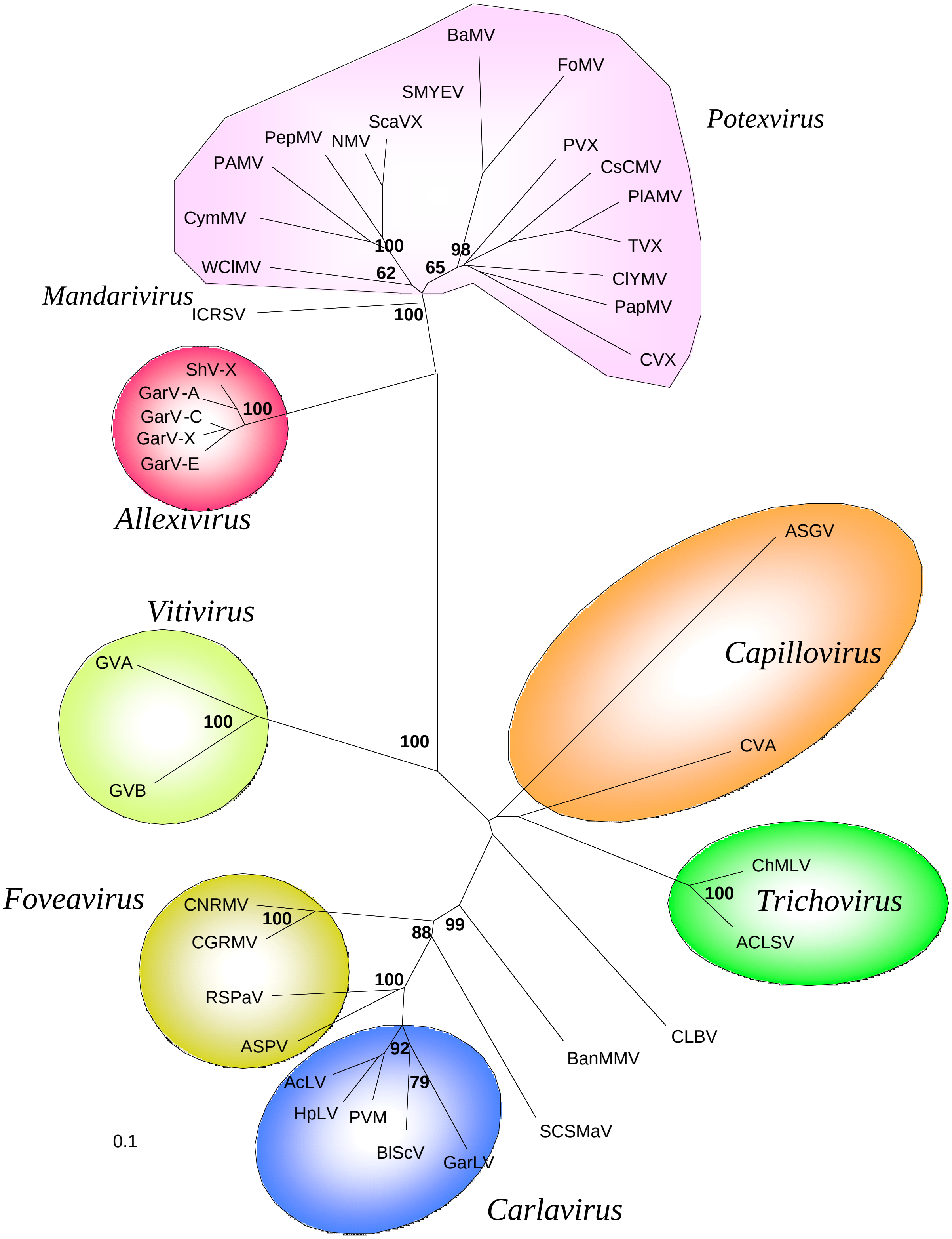

Fig. 2. Phylogenetic (NEIGHBOR) analysis of the members of the proposed family Potexviridae using aa sequences of the core region of the coat protein. Sequences were aligned using GCG PILEUP and genetic distances estimated by PROTDIST (Dayhoff PAM method). Trees were displayed in TreeView. Bootstrap values based on 100 replicates are shown where >60%.