



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**

<b>Code assigned:</b>	<b>2009.008a-fP</b>	(to be completed by ICTV officers)			
<b>Short title:</b> Create genus Tepovirus in the family Betaflexiviridae (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/>	2 <input type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input checked="" type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>	

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

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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 3: **NEW GENUS**

creating and naming a new genus

Code	<b>2009.008aP</b>	(assigned by ICTV officers)
<b>To create a new genus to contain the species listed below</b>		

Code	<b>2009.008bP</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Tepovirus</i></b>		

assigning a new genus to higher taxa

Code	<b>2009.008cP</b>	(assigned by ICTV officers)
<b>To assign the new genus as follows:</b> Ideally, a genus should be placed within a higher taxon, but if not, write " <b>unassigned</b> " in the box below.		
Subfamily:		If any of these taxa has yet to be created (in module 4, 5 or 6) please write " <b>(new)</b> " after its proposed name.
Family:	<b><i>Betaflexiviridae</i></b>	
Order:	<b><i>Tymovirales</i></b>	

assigning type species and other species to a new genus

Code	<b>2009.008dP</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<b><i>Potato virus T</i></b>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
Code		(assigned by ICTV officers)
<b>To assign the following as additional species of the new genus:</b>		

**Reasons to justify the creation of a new genus:**

Additional material in support of this proposal may be presented in the Appendix, Module 9

Potato virus T (PVT), a positive-sense, single-stranded RNA virus with filamentous particles 640 nm in size was first described from Peru and Bolivia by Salazar and Harrison (1978). PVT is pollen- and seed-borne and is readily transmitted by inoculation of sap to a relatively limited range of hosts, but has no known vector (Salazar and Harrison, 1978). This virus had a rather complex taxonomic history. It was first classified as a tentative species in the genus *Closterovirus* (Matthews, 1982) but, because of the distant serological relationship with *Apple stem grooving virus* (ASGV) (Salazar and Harrison, 1978), the type species of the newly established genus *Capillovirus*, it was assigned to it as definitive species (Bar-Joseph and Martelli, 1991). When the sequence of the 3' end of the viral genome became available (Ochi *et al.*, 1992), the structural similarity with the genome of members of the genus *Trichovirus* suggested re-classification of PVT as a definitive trichovirus species (Candresse *et al.*, 1995; Martelli *et al.*, 2000). When the family *Flexiviridae* was established, the incomplete molecular information of the viral genome prompted a further transfer of the virus to become an unassigned species in this family (Adams *et al.*, 2005) and it was then carried over into the family

*Betaflexiviridae* when the family was split and included within a new order *Tymovirales* (ICTV EC decision 2008, due for imminent ratification). Recently, the PVT genome has been totally sequenced (accession EU835937; Russo *et al.*, 2009). It is 6539 nt in size exclusive of the poly(A) tail at the 3' end and contains three slightly overlapping ORFs (Fig. 1) and untranslated regions (UTR) of 74 and 184 nt at the 5' and 3' termini, respectively. ORF 1 codes for replication-associated proteins (185 kDa), ORF 2 for the movement protein (40 kDa) and ORF 3 for the coat protein (24 kDa). Phylogenetic analysis of the proteins encoded by the three PVT ORFs and the corresponding products of all sequenced trichoviruses and of the type member of the other genera of the family *Betaflexiviridae* with 30K-like movement proteins, showed that PVT is clearly separated from all trichoviruses and from ASGV (genus *Capillovirus*) and CLB (genus *Citrivirus*), but groups consistently with *Grapevine virus A* (GVA, genus *Vitivirus*) regardless of the viral gene investigated (replicase, MP, and CP) (Fig. 2).

Pairwise amino acid sequence comparisons of each protein encoded by the PTV genome with the comparable gene products of the type species of the *Trichovirus*, *Vitivirus*, *Capillovirus* and *Citrivirus* genera showed that relationships with all these viruses are distant, with identities at the amino acid level not exceeding 35% for any of the proteins analyzed (Table 1).

PVT has a number of biological, physical, and molecular properties that differentiate it from the type species of all flexiviruses with a 30K-type MP (Table 2). It is phylogenetically very distant from all these viruses, but least so from GVA, with which it groups in all trees. The structural organisation of the viral genome differs from that of ASGV, GVA and CLB, but is comparable with that of definitive trichoviruses (Adams *et al.* 2005). The PVT genome, however, is smaller and does not contain the 3' terminal 4th ORF found in some members of this genus (Saldarelli *et al.*, 2008).

Based on the above, it seems plausible to conclude that PTV is sufficiently distinct to represent a new genus of plant viruses. Russo *et al.* (2009) suggested the name *Andesvirus* for the new genus because of the geographical origin of the virus. To avoid confusion with *Andes virus*, a species in the genus *Hantavirus*, we are now proposing the name *Tepovirus*, derived from the type species.

**Origin of the new genus name:**

Sigla from the (re-arranged) name of the type species **T potato virus**

**Reasons to justify the choice of type species:**

The only species at present

**Species demarcation criteria in the new genus:**

- If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

n/a

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)
- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

**Part (a)** taxon/taxa to be removed or moved

Code	<b>2009.008eP</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
<i>Potato virus T</i>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:	Unassigned	Fill in all that apply.
Subfamily:		
Family:	<i>Betaflexiviridae</i>	
Order:	<i>Tymovirales</i>	
<p>If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right</p>		

<b>Reasons to justify the removal:</b> Explain why the taxon (or taxa) should be removed
To become the type species of a new genus now that complete sequence data are available.

**Part (b)** re-assign to a higher taxon

Code	<b>2009.008fP</b>	(assigned by ICTV officers)
<b>To re-assign the taxon (or taxa) listed in Part (a) as follows:</b>		
Genus:	<i>Tepovirus (new)</i>	Fill in all that apply. • If the higher taxon has yet to be created write " <b>(new)</b> " after its proposed name and complete relevant module to create it. If no genus is specified, enter " <b>unassigned</b> " in the genus box.
Subfamily:		
Family:	<i>Betaflexiviridae</i>	
Order:	<i>Tymovirales</i>	

**Reasons to justify the re-assignment:**

- If it is proposed to re-assign species to an existing genus, please 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

See Module 3 and appendix for justification of the new genus.
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MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Adams MJ, Accotto GP, Agranovsky AA, Bar-Joseph M, Boscia D, Brunt AA, Candresse T, Coutts RHA, Dolja VV, Falk BW, Foster GD, Gonsalves D, Jelkmann W, Karasov A, Martelli GP, Mawassi M, Milne RG, Minafra A, Murrant AF, Namba S, Rowhani A, Vetten HJ, Vishinichenko VK, Wisler GC, Yoshikawa N, Zverev SK (2005). Family Flexiviridae. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA (eds) Virus Taxonomy. Eighth Report of the International Committee on Taxonomy of Viruses. Elsevier/Academic Press, San Diego, USA: 956-960.

Bar-Joseph M, Martelli GP (1991) Capillovirus. In: Francki RIB, Fauquet CM, Knudson DL, Brown F (Eds) Classification and Nomenclature of Viruses. Fifth Report of the International Committee on Taxonomy of Viruses. Arch Virol Suppl 2: 339-340.

Candresse T, Namba S, Martelli GP (1995). Genus Trichovirus. In: Murphy FA, Fauquet CM, Bishop DHL, Ghabrial SA, Jarvis AW, Martelli GP, Mayo MA, Summers MD (eds) Virus Taxonomy. Sixth Report of the International Committee on Taxonomy of Viruses. Springer-Verlag Vienna, Austria: 486-470.

Martelli GP, Agranovsky AA, Bar-Joseph M, Boscia D, Candresse T, Coutts RHA, Dolja VV, Duffus JE, Falk BW, Gonsalves D, Jelkmann W, Karasev A, Minafra A, Murrant AF, Namba S, Niblett CL, Vetten HJ, Yoshikawa N. (2000) Genus Trichovirus. In: Van Regenmortel MHV, Fauquet CM, Bishop DHL, Carstens EB, Estes MK, Lemon SM, Maniloff J, Mayo MA, McGeoch DJ, Pringle CR, Wickner RB (eds). Virus Taxonomy. Seventh Report of the International Committee on Taxonomy of Viruses. Academic Press, San Diego, USA: 956-960.

Matthews REF (1982) Classification and Nomenclature of Viruses. Fourth Report of the International Committee on Taxonomy of Viruses. Intervirology 17, No. 1-3.

Ochi M, Kashiwazaki S, Hiratsuka K, Namba S, Tsuchizaki T (1992) Nucleotide sequence of the 3'-terminal region of Potato virus T RNA. Ann Phytopath Soc Japan 58:416-425.

Russo M, Rubino L, De Stradis A, Martelli GP (2009) The complete nucleotide sequence of potato virus T- Arch Virol 154: 321-325.

Salazar LF, Harrison BD (1978) Host range, purification and properties of potato virus T. Ann Appl Biol 89: 223-235.

Saldarelli P, Boscia D, De Stradis A, Vovlas C (2008). A new member of the family Flexiviridae from *Phlomis fruticosa*. J Plant Pathol 90: 281-286.

**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.

Table 1. Pairwise amino acid sequence comparisons of proteins encoded by the PVT genome with corresponding complete gene products of the type members of the genera *Trichovirus*, *Vitivirus*, *Citrivirus* and *Capillovirus*.

Virus	Genus	Amino acid identity (%)		
		Replicase	Movement protein	Coat protein
ACLSV	<i>Trichovirus</i>	29	22	28
GVA	<i>Vitivirus</i>	30	23	35
CLBV	<i>Citrivirus</i>	28	19	22
ASGV	<i>Capillovirus</i>	28	24	31

Table 2. Properties of PVT compared with those of type members of the other genera of the family *Betaflexiviridae* with a 30K-like movement protein

Virus ...	PVT	ACLSV	GVA	CLBV	ASGV
Genus ...	Proposed <i>Tepovirus</i>	<i>Trichovirus</i>	<i>Vitivirus</i>	<i>Citrivirus</i>	<i>Capillovirus</i>
Natural host	Herbaceous	Woody	Woody <sup>(a)</sup>	Woody	Woody
Vector	None	None	Mealybugs	Not determined	None
Length of virions (nm)	640	680	800	960	620
Aspect of virions in uranyl acetate mounts	Semi rigid, criss-cross pattern	Very flexuous, distinct cross banding	Very flexuous, distinct cross banding	Slightly flexuous, faint cross banding	Very flexuous, distinct cross banding
Serological relationship to PVT		No	No	No	Yes
Genome organization	Three partially overlapping ORFs. No intergenic regions	Three partially overlapping ORFs. No intergenic regions	Five partially overlapping ORFs	Three ORFs. Intergenic region between ORF2 and ORF3	Two nested ORFs
Genome size (nt)	6539	7555	7349	8747	6496
Coat protein size (kDa)	24	22	22	44	27
AlkB domain	No	Yes	Yes	Yes	No
OTu-like domain	No	No	No	Yes	No
Papain-like protease	Yes	Yes	No	Yes	Yes

<sup>(a)</sup> Some vitiviruses infect herbaceous plants

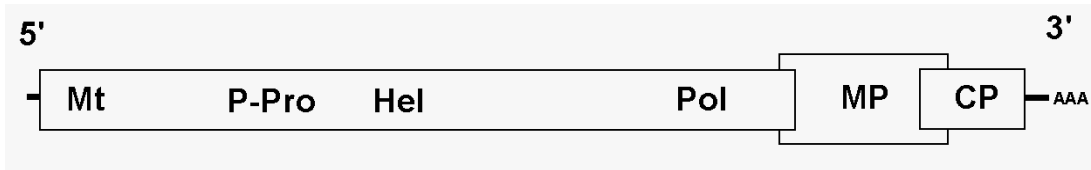


Fig. 1. Schematic representation of PVT genome (EU835937). Motifs in the replicase protein ORF 1 are: Methyltransferase (Mt), Helicase (Hel), Papain-like protease (P-Pro) and RNA-dependent RNA polymerase (Pol).

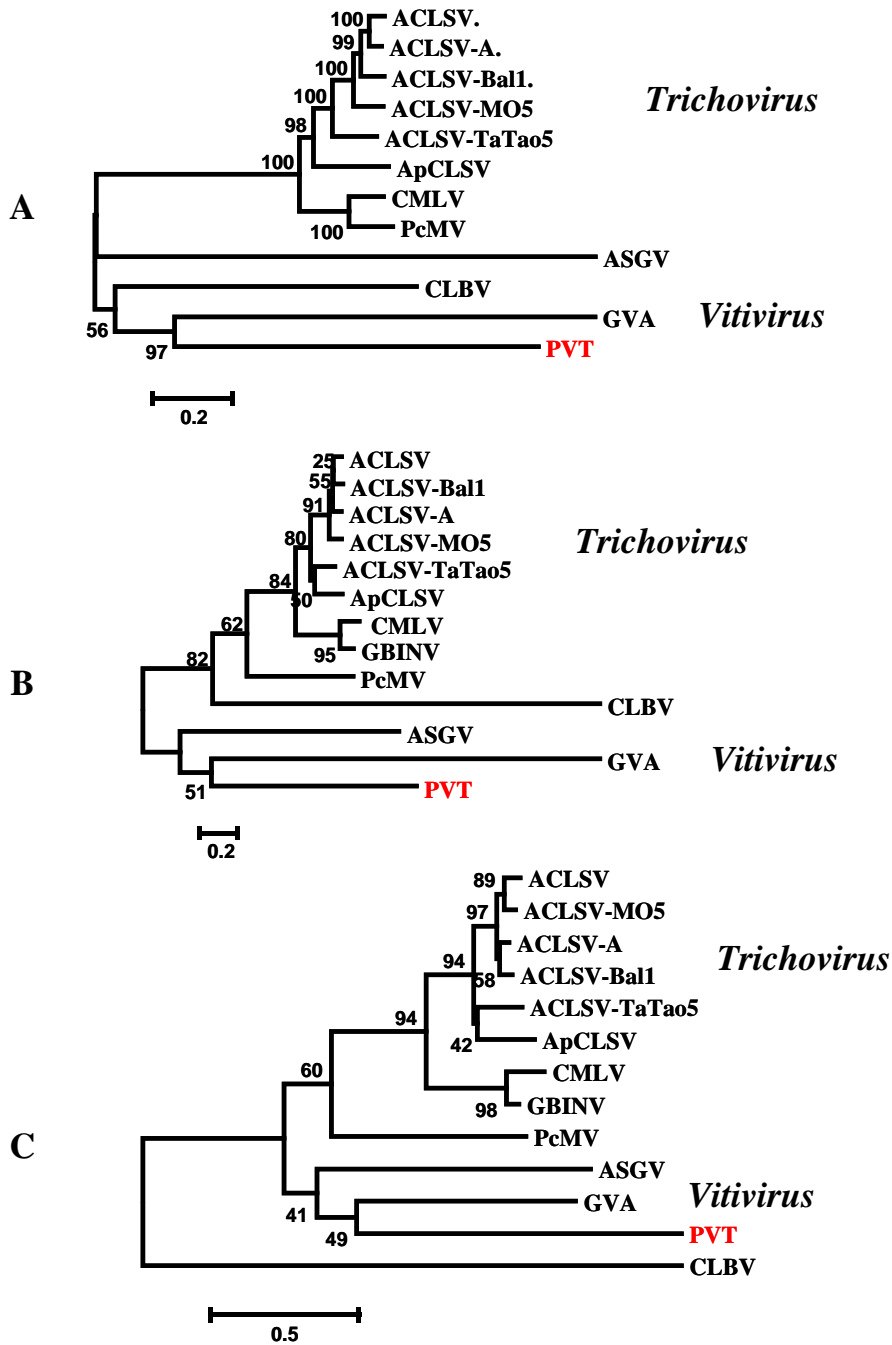


Fig. 2. Unrooted phylogenetic (NJ) trees for amino acid sequences of the replicase (A), MP (B) and CP (C) of PVT, members of the genus *Trichovirus* and one representative member of other genera in the family *Betaflexiviridae*. Accession numbers are: *Apple chlorotic leaf spot virus* (ACLSV), NC\_001409=M58152; ACLSV-A, D14996; ACLSV-Ball1, X99752; ACLSV-MO-5, AB326225; ACLSV-Ta Tao 5, EU223295; *Apricot pseudo-chlorotic leaf spot virus* (ApCLSV), NC\_006946=AY713379; *Apple stem grooving virus* (ASGV), NC\_001749=D14995; *Citrus leaf blotch virus* (CLBV), NC\_003877=AJ318061; *Cherry mottle leaf virus* (CMLV), NC\_002500=AF170028; *Grapevine berry inner necrosis virus* (GBINV), D88448; *Grapevine virus A* (GVA), NC\_003604=X75433; *Peach mosaic virus* (PcMV), DQ117579.



## A

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CVAcP      LGPSQLELKDSEKMSLEDVLQQARRHRVGVYLWKTHIDPAKELLTVPPPEGFKEGESFEG 60
ASGVcP     -----MSLEDVLQQARRHRVGVYLWKTHIDPAKELLTVPPPEGFKEGESFEG 47
PVTcp      -----MDPPTTFVQIRDEVLNLTVAAYSSQWDGQATQALKDG----- 36
           :: :   :: :   : :   : . . . . . : : : : : : * * *

CVAcP      KELYLLLCNHYCKYLFGNIAVFGSSDKTQFPAVGFDTPPVHYNLTTTPKEGETEEQKKAR 120
ASGVcP     KELYLLLCNHYCKYLFGNIAVFGSSDKTQFPAVGFDTPPVHYNLTTTPKEGETDEGRKAR 107
PVTcp      -----AKEQMLRFLFGRIAISSASRNTIWPDEIASEDLQIGMSAASAG-----PP 82
           :: : * * * * * * * : * * * * * : : : : : : : : : : .

CVAcP      EGSSGEKTKIWRIDLNVVPELKTFAATSQRQNSLNECTFRKLCPEFADLAREFLHERWSK 180
ASGVcP     AGSSGEKTKIWRIDLNVVPELKTFAATSQRQNSLNECTFRKLCPEFADLAREFLHERWSK 167
PVTcp      PVAAAPISLIFRVNFNSYVKMLIALSNTSTNSFVKNKTLRQMCMPFAKYAYGYLSE---M 139
           : : . : * * * : : . . * * : : : * * : . : : * * * : * * * * * * *

CVAcP      GLATNIYKKWPKAFEKSPWVAFDFATGLKMN---RLTPDEKQVIDRMTKRLFRTEGQKGV 237
ASGVcP     GLATNIYKKWPKAFEKSPWVAFDFATGLKMN---RLTPDEKQVIDRMTKRLFRTEGQKGV 224
PVTcp      GYATWAYEKMPKLCRKAKWVAFDFASGLLIDTTMQLNDEKTVIQGLGARLFKTKQSQSIQI 199
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

CVAcP      FEAGSESNLELEG- 250
ASGVcP     FEAGSESNLELEG- 237
PVTcp      ADSTMDGEAINREI 213
           : : : : .

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## B

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GVAcP      -----MYLNTLFGYIALVGTSSKAI 20
GVDcP     -----MYLRTLFGYIALVGTSRKAQ 20
GVBcP     MENISRMAKIRSNISELLCAGVTFVTDARETGFDRLP---MYFRTLFGYIALTGTSAKAQ 56
HLVcP     MDGISRSARIRNAVKTLVLAGETLVENASEGGVDAS---MYLRTLFGYIALAGTSAKTE 56
PVTcp     -MDPPTTFVQIRDEVLNLTVAAYSSQWDGQATQALKDGAKEQMLRFLFGRIAISSASRNTI 59
           : . * * * * * * * : : * * *

GVAcP      HYG-----EVDIVGPKASKKTGIDPRGKMVSELVGRMRTLSVAVSEGPKVGA 68
GVDcP     HYG-----VVDVIGPK-SNRSNVDSRGKINISEKVASMMALSRAVSEGPLVGA 67
GVBcP     HYE-----NVDIIGDKVGAEG-IDSRGTINISEQVKKMMGYSRAPVSGVCKGL 103
HLVcP     QYD-----EVDIIGSKYSADS-LDPRGKIKIAEKVRAMMSFARVVPVSGECKKA 103
PVTcp     WPDTEIASEDLQIGMSAASAGPPVAAAPISLIFRVNFNSYVKMLIALSNTSTNSFVKNK 119
           . * * * * * * * : : : : . . * * : : : . . . .

GVAcP      TLRQMCEPFAQNAYDFLVVMAEMGTYSQLATKMTRSGFKEPQVMFDFASGLDLKA---LT 125
GVDcP     TLRQMCEPFAQEAYEMLAKMAEMGLYSQLARKMARLGNKEPQVMFDFASGLDISR---LT 124
GVBcP     TLRQMCEPFAEARECLTILATLRVYSRLALAKMAKLGQKEPQVMFDFNSGLNLLT---LS 160
HLVcP     TLRQMCEPFAEARECLIILSGWGVYSRLACKISKLGQKEPQVMFDFNSGLDLA---LS 160
PVTcp     TLRQMCMPFAKYAYG---YLSMGYATWAYEKMPKLCRKAKWVAFDFASGLLIDTTMQLN 176
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

GVAcP      LQEATVIQAMHSRLFRTEGAKGVFNAQSSIGEQAVEI 162
GVDcP     LQEATVIQAMHSRLFRTEGAKGVFNAQSSVGEQAVEI 161
GVBcP     ATEASAIQSLNSRLFRTEGAKNVFTAQADVGEQSVEI 197
HLVcP     STEAATIQUALNSRLFRTEGAKSVFTAQSSVGEQAVEI 197
PVTcp     DDEKTVIQGLGARLFKTKQSQSIQIADSTMDGEAINREI 213
           * : * * * : : * * * * * : : : : . * *

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Fig. 3. Partial alignments of PVT coat protein with those of capilloviruses (A) and vitiviruses (B). Identical and similar amino acids are indicated by asterisks and dots, respectively. Amino acids between positions 149 and 170 of the PVT CP (alignment A, shadowed) may represent an antigenic determinant in common with ASGV. Accession numbers are: *Grapevine virus B* (GVB) NC\_003602; *Grapevine virus D* (GVD), Y07764; *Heracleum latent virus* (HLV), X79270; *Cherry virus A* (CVA), NC\_003689.